VARIATION AND INTERRELATIONSHIPS AMONG YIELD AND YIELD COMPONENTS IN LOWLAND RICE GENOTYPES (*Oryza sativa* L.) IN MWANZA REGION

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ABSTRACT

Three experiments were conducted at Ukiriguru, Misungwi District, Nansole and Bukindo in Ukerewe district with the aim of investigating genotypic and phenotypic variation, interrelationship and magnitude of Genotype x Environment interactions and stability parameters for rice grain yield and yield components and other agronomic characters in lowland rice genotypes. The experiments, using Randomized Complete Block Design were conducted during 2012 main rain season. Fifteen genotypes obtained from Sokoine University of Agriculture and a local check was used for the experiments. Analysis of variance revealed that there were significant differences among genotypes for all variables studied at all sites. There were no significant differences among locations studied while significant G x E interaction was observed for all the traits except for panicle weight and 1000 grain weight. Furthermore, there was predominance of positive and significant correlation between grain yield and various yield components. In addition, broader genotypic and phenotypic coefficient of variation coupled with higher heritability was observed which emphasizes presence of genetic variability for studied characters. Importantly, grain yield per plant and number of panicles per plant had strong relationship with grain yield reflecting the great contribution of these traits toward grain yield. Thus using these traits as selection criteria would remarkably result into increase in rice grain yield. The presence of significant Genotype x Environment interaction for all characters except for panicle weight and 1000 grain, suggested the need for testing the genotypes in multilocations in order to develop or select genotypes with wide adaptability or recommend varieties for specific environment.

DECLARATION

I, Zakayo Alphaxad Machunde, do hereby declare to the Senate of Sokoine University of Agriculture that this dissertation is my own original work done within the period of registration and that it has neither been submitted nor being concurrently submitted in any other institution.

_____ _____

Zakayo Alphaxad Machunde Date

(MSc. Candidate)

The above declaration is confirmed

_____ _____

Dr. A. Luzi-Kihupi Date

(Supervisor)

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This work is dedicated to my family: my wife, Mary, my son, Solomon, my mom, Jockebeth, my young brothers, Musa, Timothy and Alpha and my sister, Veronica, whose love, encouragement and good wishes vitalized me to this academic accomplishment.

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LIST OF ABBREVIATIONS AND SYMBOLS

%	percentage
AMMI	Additive main multiplicative interaction
ANOVA	Analysis of variance
^0C	degree Celsius
C/N	Carbon nitrogen ratio
Ca	Calcium
CV	Coefficient of variation
DF	Degree of freedom
EAAPP	East Africa Agricultural Productivity Program
EMS	Expected mean squares
FAO	Food Agriculture Organization
FAOSTAT	Food Agriculture Organization Statistics
f	Number of filled grains
FL	50% days to flowering
GCV	Genotypic coefficient of variation
G X E	Genotype by environment
GDP	Gross Domestic Product
GNPP	Grain number per panicle
GWT	1000 grain weight
GY	Grain yield
GYPP	Grain yield per plant
ha	Hectare
H_20	Water

h^2	Heritability
IRRI	International Rice Research Institute
KATRIN	Kilombero Agriculture Training and Research Institute
KCl	Potassium chloride
kg	Kilo gram
L.S.D	Least significant difference
LZARDI	Lake Zone Agricultural Research and Development Institute
m.a.s.l	Meter above sea level
m	Metre
m^2	Square metre
MC	Moisture content
Mg	Magnesium
NERICA	New Rice for Africa
OC	Organic carbon
P	Phosphorus
P	Probability level
PCV	Phenotypic coefficient of variation
PFGPP	Percent filled grain per panicle
pH	Hydrogen ion concentration
PHT	Plant height
PL	Panicle length
PN	Panicle number
PPM	Panicles per square metre
PW	Panicle weight

QTL	Quantitative trait loci
RCBD	Randomized complete block design
s.e	Standard error
S^2d	Deviation from regression
SES	Standard Evaluation System
SUA	Sokoine University of Agriculture
SV	Source of Variation
t	Tonne
TN	Total nitrogen
TPE	Target population environment
u	Unfilled grains from panicles
U	Unfilled grains from bulked sample
URT	United Republic of Tanzania
VA	Additive variance
VD	Dominance variance
VG	Genotypic variance
w	Weight of unfilled grains
W	Weight of filled grains

CHAPTER ONE

1.0 INTRODUCTION

1.1 Background Information

Tanzania's economy is heavily dependent on a combination of subsistence and commercial agricultural activity. Agriculture contributes about 45 percent to GDP, brings approximately 66 percent of foreign exchange and provides the bulk of raw materials for local industries (URT, 2008). Rice is the world's primary source of food for more than half of the world's population, ranking second to wheat (Abodolerendeza and Racionzer, 2009), covering 9% of arable land (Khan *et al*., 2009), with total production of 680 million tones (FAO, 2009). In Tanzania, rice is the second widely cultivated cereal food crop after maize, food in diet of 60% of the population with production of 1 334 000 tones of rice from 904 508 ha (URT, 2008).

Tanzania ranks second after Madagascar as a major rice producer in the eastern and southern Africa. About 94 percent of the crop is cultivated on smallholdings of about 0.5 to 2.0 ha whereas 6 % is produced on large-scale commercial farms (Kanyeka *et al*., 1994). The crop is grown in three agro-ecosystems which comprise of 74% rain-fed lowland, 20% upland and 6% irrigated rice ecosystem (Kanyeka *et al.*, 1995). The leading regions in rice production are Shinyanga, Mwanza, Tabora, Mbeya, Rukwa and Morogoro. The increasing importance of Mwanza region in rice production is due to presence of numerous smallholder rice farmers and some traditional small-scale irrigation schemes. Mwanza Region has rice productivity averages of 2.2 t/ha (RRCoE, 2011). Rice research in Tanzania started earlier even before independence (Dalrymple, 1986). Several traditional rice varieties were improved through selection, hybridization and some were introduced. Until recently, numerous promising rice varieties had been recommended for

growing in the country (URT, 2009a). Despite of all these efforts to increase rice production, the demand for rice in the country remains steadily growing since rice is a highly preferred food in urban areas. A drastic shift of consumer preference both in urban and rural areas from conventional food to rice coupled with rapid urbanization has resulted into simultaneous increase in annual per capital consumption of rice in Tanzania to about 25-30kg/year (Kibanda, 2008). These changes in consumption habit have led to a growing gap between the demand and the supply of rice which has to be filled by imports (Mghase *et al*., 2010). An average of 10 to 25% of the total consumption is imported annually to cover the deficit (URT, 2008). One of reasons for low yield in rice production in Tanzania is that farmers grow a number of traditional varieties which are tall and prone to lodging. They have long maturation period and not suitable for areas with marginal rainfall patterns (Luzi-Kihupi *et al*., 2009). Thus rice yield remains progressively low with average productivity of 1.47 tones per hectare (FAOSTAT, 2009).

Moreover, to sustainably achieve self-suffiency among the majority of rice farmer and consumers, selection of elite genotypes by the breeding programme is an important step in rice improvement program. Interestingly, rice genotypes have a wide range of variability for yield and yield components namely productive tillers per plant, number of spikelets per panicle, 1000 grain weight and grain yield per plant, whose exploitation is potential for increasing productivity. Grain yield is mainly dependent on grain weight, number of grain per panicle and number of panicles per plant (Xing and Zhang, 2010). However, these characters have complex interrelationship; for instance, the number of panicles per plant depends on the development of primary and secondary branches while the grain weight is a function grain width and length (Xing and Zhang, 2010).

1.2 Justification

It is obvious that plant breeders commonly select some of these yield components which directly and positively correlate with increase in yield. Thus prior knowledge regarding the relative contribution of individual traits to yield may be accomplished by correlation studies, however simple correlation does not alone provide adequate information about the contribution of each factor towards yield. Therefore correlation along with path coefficient analysis is utilized to have an idea of direct and indirect contribution of various traits on grain yield (Rangare *et al*., 2012). On the other hand, selection will only be effective if heritability of these components is high. Selection based on genetic variation and interrelationships of yield and yield components is very important, but integration of the study of G x E interaction will assist in determining how environment influence variation in yield and yield components. Several studies on G x E interactions on rice have been conducted in Tanzania (Kihupi, 1984; Kibanda, 2001). However, there is scanty information on G x E interactions and stability analysis of rice genotypes in Mwanza region under lowland rain fed ecosystem. Breeding rice genotypes with broad adaptability will ease the effect of genotype x environment on subsequent performance of rice genotypes.

Among the available options to overcome the yield gap problem and low rice productivity is exploiting genetic variability which exists among rice genotypes for grain yield and yield components that will provide basis for selection to improve productivity of rice in Tanzania. Moreover, there is inadequate knowledge of interrelationship among various agronomic traits which frequently end up in less optimal result in plant breeding for polygenic trait such as yield. Path coefficient analysis will help in partitioning correlations into direct and indirect effects of the yield and its components.

1.3 Objectives

1.3.1 Overall objective

The overall objective of the study was to assess the genotypic and phenotypic variability for yield and yield components, their interrelationships, magnitude of genotypes x environment interaction and stability analysis for the given lowland rice genotypes to facilitate more efficient selection for plant breeding programme under lowland rain fed rice ecosystem.

1.3.2 Specific objectives

(i) To estimate phenotypic and genotypic variability and heritability for yield and yield contributing characters.

(ii) To determine the extent and magnitude of genotype x environment interaction and stability analysis for selected important characters.

(iii) To assess magnitude of phenotypic and genotypic correlation between yield and its components under lowland conditions.

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Rice Description

Rice is a monocot plant which belongs to family *Gramineae*. Of the 24 rice species known to date, two are cultivated namely *O. sativa* L. and *O. glabberima* Steud. The cultivated rice is a diploid species having 24 chromosomes (2n=2x=24) in AA genome. The most common cultivated species *O. sativa* is further classified into sub species namely, indica, japonica and javanica. The 22 wild species in the genus *Oryza* have been proven to contain genes for resistance to biotic and abiotic stresses (Smith and Dilday, 2003).

2.2 Economic Importance of Rice

Rice is a predominant staple food for 17 countries in Asia and Pacific, nine countries in North and South America and eight countries in Africa (FAO, 2004). It provides 20% of the world`s dietary energy supply. Rice is rich in carbohydrates and proteins and is used mainly for human food consumed in the form of whole grains. It is also a good source of thiamine, riboflavin, niacin and dietary fibre.

The importance of rice has been increasing simultaneously with urbanization and population growth in Tanzania. It ranks second important crop after maize. In major rice growing areas such as Kahama, Shinyanga rural, Mvomero and Kyela rural farmers generate incomes sufficient to alleviate rural poverty since it serves as both food and cash crop (Mghase *et al*., 2010). The income generated from rice cultivation and postharvest activities provides cash to cover the expenses of clothing, housing, education and other

social activities of the majority of people in rural areas. It is estimated that rice is grown by 16% of Tanzanian farmers (Minot, 2010).

2.3 Rice Production Constraints in Tanzania

Demand for rice in Tanzania has been growing with per capital consumption of about 25-30 kg (Kibanda, 2008). Factors contributing to low yield include, use of genetically low yielding varieties, drought, low soil fertility, prevalence of insect pests and diseases, birds, short supply of fertilizer and weed infestation (URT, 2009b; Mghase *et al*., 2010). Among the weeds that affect rice fields, *Oryza longistaminata and O. punctata* have been identified as production constraint in southern Tanzania. A study based on farmers perception and preferences conducted in Tabora region revealed that the major rice production constraints were lack of improved varieties, diseases susceptibility, seed unavailability, drought and high input prices (Bucheyegi *et al*., 2011). Apart from the above constraints, salinity was reported as one of the challenging factor for irrigated lowland rice in the north-coast of Tanzania (Kashenge-Killenga *et al*., 2012).

Many lowland rice ecologies face severe water shortage, parasitic weeds and to some extent, devastating diseases such as rice yellow mottle virus, rice blast and bacterial leaf blight (URT, 2009b). In disease affected areas, rice yellow mottle virus was reported to cause yield losses of up to 50% to total crop failure (Luzi-Kihupi *et al*, 2000).

2.4 Genetic Variability

The term ‘variations’ refer to the measurable differences in individuals for a particular trait and may partly be due to genotypic (heritable) and partly to environmental (non-heritable) effects. The genetic variability is the real measure for variability concealed in a population, since it is a result of additive and non-additive gene effects. Genetic

variability for agronomic traits is a key component for broadening gene pool of rice (Selvaraj *et al*., 2011). On the other hand, the genotypic coefficient of variation provides a measure to compare genetic variability present in various quantitative characters (Akinwale *et al*., 2011). The success of breeding program depends upon the amount of genetic variability present in the population and the extent to which the desirable traits are heritable. The nature and magnitude of genetic variation varies with genotype and environment and, is an essential element for selection and improvement of the crop. The presence of large amount of variability might be due to diverse source of materials as well as environmental influence affecting the phenotypes (Ovung *et al*., 2012).

Several studies have been conducted to examine the extent of genetic variability for yield and agronomic parameters in rice. Ashfaq *et al*. (2012) observed high genetic diversity for various rice traits and their association with yield. The results reported highest genetic variability in plant height, number of spikelets per panicle, panicle length, days to heading, days to maturity, number of tillers per plant and flag leaf area. The use of readily available germplasm is an important strategy for incorporating genetic variability into rice breeding programme, which can potentially generate new cultivar with broadened genetic base and allow useful allelic combination (Mc Couch, 2005). Nevertheless, Yadav *et al*. (2008) and Osman *et al*. (2012) reported that phenotypic coefficients of variation were slightly higher than the genotypic coefficients of variation for yield and its related traits studied in upland rice reflecting high genetic influence. In agricultural investigations, the knowledge of genetic variability is very important for development of high yielding varieties (Singh *et al*., 2011). According to Patel *et al*. (2012) significant genotypic variation was reported for days to 50% flowering, plant height, panicle length, total number of tillers per plant, number of filled spikelets per panicle, biological yield per square meter and harvest index.

Natarajan *et al*. (2005) revealed that the improvement in grain yield will be efficient, if the selection is based on the biological yield, the number of productive tillers per square metre and the number of filled grains per panicle under tropical conditions. An attempt was made to study variability and genetic parameter analysis and observed that the phenotypic variance was higher than the corresponding genotypic variance (Singh *et al*., 2011). A critical analysis of genetic variability is a pre-requisite for initiating any crop improvement programme and for adopting appropriate selection techniques (Babu *et al.*, 2012). The extent of genetic variation in a population often relates to its breeding system. Promising genotypes which exhibit adequate genetic variation for main components: number of panicles, number of grains per panicle and grain weight (Xing and Zhang, 2010) are best options for improving grain yield.

2.5 Genotype x Environment Interaction

The term environment relates to sets of climatic, soils, biotic (pests and diseases) and management conditions in individual trial carried out at a given location in one year or over several years (Annicchiarico, 2002). The performance of rice cultivars are likely to vary with changing environments. When cultivars are tested in terms of seed yield at the multi-environmental trials, great differences are commonly observed in yield performance over environments. This differential yield response of cultivars from one environment to another is called genotype x environment (G x E) interaction (Allard, 1960; Vargas et al., 1998). G x E interactions have been extensively studied (Kang, 2002; Karasu *et al*., 2009; Annicchiarico, 2002; Elberhart and Russel, 1966). Understanding of the nature and magnitude of G x E will help the breeders to overcome constraints encountered when developing or evaluating genotypes in different environments. These constraints are the basis for defining breeding strategies that would contribute to higher and more stable

grain yield for the variable rainfed lowland environments, thereby reducing farmers risk and uncertainly while increasing productivity.

Previous studies on rain fed lowland rice by Rasyad *et al*. (2012) reported significant genotype and genotype x environment interaction for five rice cultivars evaluated in three environments implying that genotypes and genotype x environment interaction accounted for great contribution to these traits than environment. Most cultivated rice cultivars having high yield potential are erratic in term of performance when exposed to varied growing conditions. This could be attributed to genotype x environment interaction caused by differences in genotypic adaptation.

Rice ecology in Tanzania is diverse (Kanyeka *et al*., 1995) so breeding rice genotypes for diverse environment requires consideration of a particular environment. Ecologies are characteristically unique and development of a stable variety suitable in one area, will not necessarily give desirable results across environments. Adaptability of a variety over diverse environments is usually tested by its degree of interaction with different growing environments. For example, as soil type and weather varies from one area to another, there is possibility of variation in environments; therefore, yield performance of the cultivars might be influenced by the environments and to some degree by genotype by environment (G x E) interaction (Rasyad *et al*., 2012).

Ideally, varieties that show low G x E interaction and have high stable yields are desirable for crop breeders and farmers, because that indicates that the environments have less effect on the performance of genotypes and their yields are largely due to their genetic composition. Genotype x environment interaction may result in alternative arrangement of genotypes ranks. Kang (2002) reported that crossover interaction has

stronger implication for breeding for specific adaptation. But if there is absence of crossovers, the performance of a genotype remains consistent in all the environments. A non-crossover interaction is desirable which reflects the heterogeneity of genotypic differences across environments (Asad *et al*., 2009). However, crossover G x E interactions can be a significant barrier to selection strategies that aim to improve broad adaptation. Heritability and G x E components are negatively related. The larger the G x E component, the smaller the heritability estimates (Kang, 2002). Effective identification of superior genotypes is generally complicated by the presence of G x E interactions, whereby cultivar relative yields vary across different environments.

Testing genotypes over different location differing in unpredictable environmental variation is a suitable approach for selecting stable genotypes (Eberhart and Russell, 1966). A variety of statistical procedures are available to analyse results of multi-environment trials which include the combined analysis (Aremu *et al*., 2007), regression coefficient and deviation from regression (Elberhart and Russel, 1966), modified regression of G X E based on environmental index (Perkins and Jinks, 1968) and AMMI (Gauch, 1992). However, the regression technique is a standard procedure that has been used. In this technique, genotype response to a given environment is considered. According to Eberhart and Russel (1966) stability parameters like regression coefficient (b), deviation from regression (S^2d) of the genotypes is estimated following linear regression model. Genotypes giving b-value close to unity are considered to be adapted to all environments, while those showing b-value greater than or less than unity would show specific adaptation to rich or poor environment, respectively, and the genotypes showing low and non-significant S^2d are considered to possess stability of performance over the range of environments.

2.6 Heritability of Yield and Yield Components

Grain yield is a complex quantitative character, controlled by many genes interacting with environment and is the product of many factors called yield components (Khan *et al*., 2009). Its inheritance is controlled by additive and non-additive genes. Genetic variation is due to additive effects and some is due to dominance effects. The additive (VA) and non-additive genetic variance (VD) together are known as the genotypic or genetic variance, which is abbreviated as VG.

But, the heritability (narrow sense) of a trait is defined as the proportion of the total phenotypic variation that is due to heritable (additive genetic) that is VA/VP = h^2. Heritability is the proportion of variability that can be passed on from parent to offspring. This is a breeding value since breeders select genotypes mainly based on additive gene effects. Heritability of a trait is important in determining a cultivar's response to selection. Breeding for yield component to increase grain yield would be more effective if the components involved are highly heritable and genetically independent (Akinwale *et al*., 2011). In addition, the knowledge of heritability in the selection based improvement indicates the extent of transmissibility of a character in future generations (Sabesan *et al*., 2009).

Osman *et al*. (2012) observed high heritability estimation with high genetic advance for plant height, number of tillers per plant, 1000 grain weight and high heritability with low genetic advance for 50% flowering and days to maturity while Selvaraj *et al*. (2011) identified high heritability coupled with high genetic advance and high genotypic coefficient of variation for number of tillers per plant followed by number of productive tillers per plant, plant height and grain yield per plant. According to Panse (1957), if a character is governed by non-additive gene action, it may give high heritability but low

genetic advance, whereas, if it is governed by additive gene action, high heritability along with high genetic advance provide good scope for further improvement. It is pertinent to note that high heritability alone does not guarantee large gain from selection unless sufficient genetic advance (GA) attributed to additive gene action is present (Tiawari *et al*., 2011; Akinwale *et al*., 2011).

2.7 Correlation Coefficient Analysis

Grain yield, being a quantitative trait is a complex character of any crop. Various morphological and physiological plant characters contribute to yield. These yield contributing components are interrelated with each other showing a complex chain of relationship. Genetic correlations provide useful information to plant breeders for developing selection schemes. Genetic correlations among yield and yield components and other agronomic characters have been extensively studied. Tahir *et al*. (1988) and Zahid *et al*. (2006) reported that plant height was found to be negatively correlated with number of grains per panicle, number of tillers per plant and paddy yield.

When two character show negative phenotypic and genotypic correlations it would be difficult to exercise selection for these characters (Newell and Eberhart, 1961). Yadav *et al*. (2011) shared similar views. Negative correlation coefficient of plant height with paddy yield indicates that tallness in rice reduces the paddy yield due to high accumulation of photosynthates in vegetative parts as compared to reproductive parts (i.e. seed formation and grain filling) and lodging susceptibility. In a study by Idris *et al*. (2012) the genotypic correlation coefficients were higher than the phenotypic correlation coefficients demonstrating that, the observed relationships among the various characters were due to genetic causes. Complete knowledge on interrelationship of plant character like grain yield with other yield related characters is of greater importance to the breeder

for making improvement in complex quantitative character like grain yield for which direct selection is not much effective.

Akinwale *et al*. (2011) observed that grain yield exhibited significant positive correlation with the number of tillers per plant, panicle weight and number of grains per panicle. In addition, there is a positive correlation between panicle size and number of fertile grains per panicle. Luzi-Kihupi (1998) indicated that plants with large panicles tend to have high number of fertile grains. Chakraborty *et al*. (2010) after conducting correlation analysis revealed ($P \leq 0.01$) significant positive genotypic correlation of yield per plant with plant height, panicles per plant ($r=0.53$), panicle length ($r=0.53$), effective grains per panicle ($r=0.57$) and harvest index ($r=0.86$).

2.8 Path Coefficient Analysis

Selection for improvement of yield should not be based on yield alone but other components contributing to grain yield should also be considered. Interrelationship and relative contribution of each component towards yield is clearly described through path analysis. The path coefficient analysis which was initially developed by Wright (1921) and described by Dewey and Lu (1959) allows partitioning of correlation coefficient into direct and indirect effects of various traits towards dependent variable and thus helps in assessing the cause-effect relationship as well as effective selection. It is used in plant breeding programs to determine the nature of the relationships between yield and yield components that are useful as selection criteria to improve the crop yield. If the cause and effect relationship is well defined, it is possible to present the whole system of variables in the form of a diagram, known as path-diagram. In agriculture, path analysis has been used by plant breeders to assist in identifying traits that are useful as selection criteria to improve crop yield (Dewey and Lu, 1959). Rice yield can be effectively increased by

understanding the direct and indirect effects of yield components that provides the basis for its successful breeding program (Choudhry *et al*., 1986). In path analysis, one of the variables under study is taken as dependent variable (effect) which is assumed to be influenced by the other characters called independent characters or predictor variables (causes). Rangare *et al*. (2012) undertook a study on path analysis for forty exotic and Indian rice germplasm with respect to 11 yield contributing characters. The association studies revealed that for improvement in grain yield, selection should be based on yield per plant, number of tillers per plant, numbers of spikelets per panicle, panicle length and days to maturity as they are significantly associated with yield.

Pandey *et al*. (2012) findings revealed that path analysis identified harvest index, days to maturity, effective tillers per plant, 1000 grain weight, flag leaf area and panicle length as major direct contributors towards yield. Similarly, Osman *et al*. (2012) indicated that number of tillers per plant, number of filled grains per panicle, 1000 grain weight, panicle length and number of filled grains per panicle were the mostly directly related traits to yield. According to the study by Selvaraj *et al*. (2011), path-coefficient analysis revealed that grain weight exhibited maximum positive direct effect on grain yield per plant followed by filled grains per panicle, plant height, panicle length, number of tillers per plant and days to 50% flowering. These traits could be used as selection criteria for improved grain yield.

CHAPTER THREE

3.0 MATERIAL AND METHODS

3.1 Location and Duration

The experiment was conducted at the Lake Zone Agricultural Research and Development Institute, Ukiriguru, Misungwi district which lies between 02^{o} 42' South and 33^{o} 01' East at an altitude of 1207 m. The climate is sub humid tropical and rainfall are bimodal with annual average of 900 mm. The long rains usually start in March to May whereas short rains begin in October to December. Monthly temperature range is 26-30^{o}C (Appendix 3). The soil type was generally sand clay loam (Landon, 1991). Bukindo is located between 2^{o} 30' South and 32^{o} 00' East at 1132 m above sea level whereas Nansole is located at latitude 2^{o} 29' South and longitude 32^{o} 04' East with altitude of 1102 m above sea level.

3.2 Materials

The experimental material of this study was composed of sixteen genotypes including eleven (11) locally improved genotypes from Sokoine University of Agriculture (SUA), one (1) from KATRIN, three (3) introductions from AfricaRice Centre and a local check, Kalamata.

Table 1: Names for the rice varieties/genotypes used in the study

S/N	Genotypes	Source
1	NERICA L-4	Africa Rice
2	NERICA L-8	Africa Rice
3	NERICA L-52	Africa Rice
4	SUA 1-13-12-3	SUA
5	SUPA M 101-22	SUA
6	SUA 2-2-3-1	SUA
7	SUPA BC	SUA
8	SARO 5	KATRIN
9	Mwangaza	SUA
10	SUA 12-2-3-2	SUA
11	SUA 8-2-2-3	SUA
12	Salama M-57	SUA
13	SSD 1	SUA
14	SSD 3	SUA
15	SSD 5	SUA
16	Kalamata (local check)	Mwanza

3.3 Methods and Experimental Design

The experimental design used was randomized complete block design (RCBD) with three replications at three sites namely, Ukiriguru, Nansole and Bukindo. The plot size was 4.0 x 2.0 m in which plants were spaced 20 cm x 20 cm apart. Seeds of 16 genotypes were sown on 11 November, 2011 and transplanted on 02 December, 2011 using one seedling per hill.

3.4 Soil Analysis

Prior to planting, soil samples from experimental sites were collected for analysis of pH, texture, exchangeable bases, organic carbon, available phosphorus and nitrogen content and carbon nitrogen ratio. Soil analyses were conducted at Lake Zone Agricultural Research and Development Institute Soil Laboratory, Ukiriguru, Mwanza (Appendix 2).

3.5 Agronomic Practices

The experimental fields were ploughed, levelled and cleared of weeds. The crop was grown in bunded lowland rain fed conditions with suitable agronomic practices. Potassium and phosphorus fertilizers were applied as basal at a rate of 65 kg P ha^{-1} and 54 kg Kha^{-1} respectively. Top dressing with urea (46%N) was applied at the rate of 60 kg Nha^{-1} in two splits at initial tillering stage and panicle initiation stage (Kanyeka *et al*., 2007). Weeds were controlled manually and was done twice. All other standard agronomic practices were done accordingly.

3.6 Data Collection

Data collection was done according to Standard Evaluation System for Rice (SES) (IRRI, 2002) and as described by Gomez (1972). The data collected included 50% days to flowering, plant height, number of panicles per hill, number of panicles per square metre,

panicle weight (g), panicle length (cm), 1000 grain weight (g), grain number per panicle, percent filled grains per panicle, grain yield per plant and total grain yield per $2m^2$.

3.6.1 Days to 50% flowering and plant height

Days to 50% flowering were recorded by counting the number of days from sowing to when 50% of the plants in each particular plot had flowered. Plant height at physiological maturity was measured by using a metre rule as length from the ground to the tip of the tallest panicle.

3.6.2 Number of panicle per plant and number of panicles per square metre

Number of panicles per plant was recorded by counting all the number of panicles per plant from a sample of selected ten (10) plants and their sum averaged to obtain number of panicles per plant. The number of panicles per square metre was determined by counting all panicles in 1 m x 1 m area in the centre of each plot.

3.6.3 Panicle length and Panicle weight

From the 10 randomly selected plants, panicle length of the main tiller was measured in centimetres from the basal node of the panicle to the tip of the panicle. Dried and threshed sample of 10 panicles harvested from randomly selected plants was weighed using a sensitive balance. The average panicle weight was recorded.

3.6.4 1000 grain weight

Weight of 1000 grains was obtained by weighing samples of 1000 filled grains (w) and counting the number of filled grains (f). The following model was used to calculate the weight. 1000 grain weight = w/f * 100. The weight was adjusted to 14% moisture content.

3.6.5 Number of filled grains per panicle

Number of grains per panicle was determined by randomly selecting 10 panicles per plot. Filled grains were separated using a seed separator, the salt water (specific gravity of 1.06) method. Count the total number of panicles (P). The number of filled grains (f) and the weight of unfilled grain (w) were determined. Filled grain weight (W) from panicles in each plot was recorded.

$$\text{Number of filled grains per panicle} = \frac{f}{w} x \frac{W + w}{P}$$

3.6.6 Percent filled grains per panicle

A percent filled grain was determined by selecting a sample of panicles which were separated, threshed and their grains bulked. Filled grains were separated using a seed separator, the salt water (specific gravity of 1.06) method. The number of filled grains (f) and unfilled grains (u) and the weight of unfilled grain (w) were determined. The unfilled grains (U) were counted and the filled grain weight (W) from 10 panicles in each plot was recorded. Number of filled grains per panicle = U+u/f (W+w)/w+U+u x100.

3.6.7 Yield per plant and grain yield

Individual 10 plants per treatment were selected, their panicles threshed and grains weighed and adjusted at 14% MC and means of 10 plants expressed as grain yield per plant. Grain yield was determined by harvesting 1m² in each plot. The panicles were threshed, winnowed and grains weighed. The moisture was adjusted at 14% MC and yield was then expressed in grain yield kg/plot.

3.7 Data Analysis

3.7.1 Single site analysis

Analysis of variance (ANOVA) for RCBD was done using Gen-stat (14.2 edition) statistical package for each single sites following the procedures as described by Gomez and Gomez (1984). Random model was used in analysis of variance. The statistical model for each environment on analyzed variable was:

$Rijk= \mu+\beta i+rj+Eijk$……………………………………………………………………..(1)

Where:

Rijk= measurement for i^{th} genotype of j^{th} replicate in k^{th} plot

μ = overall mean

βi = i^{th} treatment effect

rj = block effect (replications) and

Eijk = random experimental error

3.7.2 Combined analysis of variance

Table 2 below shows the combined analysis of variance structure where the analysis of variance was pooled over three locations. The components of variance were computed following method proposed by Al-jibouri *et al.* (1958). The observed expected mean square obtained in combined analysis of variance table was used to separate genotype effects, environments and their interactions. The following model was used for combined analysis of variance:

$Yijk =\mu+\beta i+Ej+ki\ (EJ) +\beta iEj+\epsilon ijk$…………………………………………………..(2)

Where:

Yijk = response for i^{th} genotype in replication in j^{th} location in k^{th} plot

μ = overall mean

βi = the effect of the i^{th} genotype

Ej = the effect of the j^{th} location

Ki (Ej) = effect of i^{th} replicate /block in j^{th} location

βiEj = the interaction effect of i^{th} genotype and j^{th} location and

Eijk = random experimental error

Table 2: Combined analysis of variance for evaluating the effect of genotype x environment interaction

Source of variation	DF	Mean Square	Expected mean squares	F-value
Environments (e)	e-1	MI	$\delta^2 e + \delta r^2$ G x E $+\delta^2 g + rg\delta^2 E$	M1/M3
Replicates within E(Rj/e)	e(r-1)	M2	$\delta^2 e + \delta^2 r/E$	M2/M5
Genotype (g)	g-1	M3	$\delta^2_e + \delta^2_{G \times E} + re\delta^2_g$	M3/M4
G x E	(g-1)(e-1)	M4	$\delta^2_e + r\delta^2_{G \times E}$	M4/M5
Plot residuals	e(r-1)(g-1)	M5	δ^2_e	-

Assumptions all effects are random

Where:

$\delta^2 e$ = component of variance due to error term

$\delta^2 g$ = component of variance due to genotypes

$\delta^2 E$ = component of variance due to environment (location)

δ^2 G XE = component of variance due to genotype x environment interaction

r = number of replications

e = number of environments (locations)

g = number of genotypes

3.7.3 Computation of heritability (broad sense) and Expected Genetic Advance

Phenotypic variance among genotypes tested in r replications and l locations were computed by using a formula suggested by (Robinson et al., 1949);

$\delta^2 ph = \delta^2 g + (\delta^2 lg/l) + (\delta^2 e/lr)$……..(3)

Where:

δ^2ph = phenotypic variance

δ^2g = genotypic variance

δ^2lg = variance due to genotype and location interaction

δ^2e = error variance

l =number of locations and

r = number of replications

Genetic variance was calculated by the following formula

$$\text{Genetic variance} = \frac{EMSg - EMSe}{r} \qquad \ldots(4)$$

Where:

EMSg = Expected mean square of genotypes

EMSe = Expected error mean square

r = replication (number of replications)

The letters in the formula are estimates of respective variance components (Table 11). Broad sense heritability (h^{2}) was calculated using phenotypic variance and genotypic variances as the ratio of the genetic variance to the phenotypic variance and expressed in percentage using the following formula (Hanson *et al*., 1956).

$$H^2 = [\delta^2g / \delta^2ph] \times 100 \qquad \ldots(5)$$

Where:

h^2= broad sense heritability (%),

δ^2g = genotypic variance and

δ^2ph = phenotypic variance

3.7.4 Genetic advance

In order to determine the expected gain, genetic advance was computed according to the method suggested by Johnson *et al*. (1955).

GA= k (100δg)/χ (δg)/δph ……(6)

Where:

δg =genetic standard deviation

χ=population mean

δph=phenotypic standard deviation

k= selection differential measured on basis of phenotypic standard deviation (k). This was taken as 2.06 assuming 5% of superior genotypes were selected.

3.7.5 Phenotypic and genotypic variations

Phenotypic and genotypic coefficient of variation was computed following methods outlined by Singh and Chaudhary (1979).

Phenotypic coefficient of variation (PCV) = (δp/X) x 100……...(7)

Genotypic coefficient of variation (GCV) = (δg/X) x 100……(8)

Where:

δp = phenotypic standard deviation

δg= genotypic standard deviation and

X = Grand mean.

3.7.6 Covariance analysis

Covariance analysis was performed following the procedure outlined by Steel and Torrie (1984). The estimate of covariance components between two traits and phenotypic covariance components were derived in the same manner as variance components. To estimate simple correlations between two variables x and y, Karl Pearson's coefficient of

correlation was used. It is based on the variance and covariance of the variables and ranges between1 and +1.

3.7.6.1 Phenotypic correlation

The phenotypic (P) correlations between two characters; X and Y were calculated using the formula of Kwon and Torrie (1964).

$$P = \frac{COVp\ (X, Y)}{\sqrt{Vp\ (X).\ Vp\ (Y)}} \quad \text{.....(9)}$$

CovP(x, y) = Mean product of xy^{th} traits.

VP(x) and VP(y) = Mean squares for x^{th} and y^{th} traits, respectively.

3.7.6.2 Genotypic correlation

Genotypic correlations between two characters between X and Y was calculated using a formula:

$$G = \frac{COVg = (X, Y)}{\sqrt{Vg\ (X).\ Vg\ (Y)}} \quad \text{.....(10)}$$

Where:

Cov (x, y) are covariances of X and Y associated with genetic effects

Vg(x) and Vg(y) are genetic variances of X and Y, respectively

Genetic correlations were tested for their statistical significance by using the methodology developed by Lothrop *et al*. (1985).

3.7.6.3 Path coefficient analysis

Path Analysis was conducted following the procedure developed by Wright (1921) and adopted by Dewey and Lu (1959). Grain yield was considered as dependent variable and

was assumed to be influenced by days to 50% flowering, plant height, panicle number per plant, 1000 grain weight, percent filled grain per panicle and grain yield per plant. The formula in matrix form was used to solve sets of simultaneous equation of causal and effect relationship using a model arranged in matrix notation as follows below:

1. $r_{17} = P_{17} + r_{12}P_{27} + r_{13}P_{37} + r_{14}P_{47} + r_{15}P_{57} + r_{16}P_{67}$
2. $r_{27} = r_{12}P_{17} + P_{27} + r_{23}P_{37} + r_{24}P_{47} + r_{25}P_{57} + r_{26}P_{67}$
3. $r_{37} = r_{13}P_{17} + r_{23}P_{27} + P_{37} + r_{34}P_{47} + r_{35}P_{57} + r_{36}P_{67}$
4. $r_{47} = r_{14}P_{17} + r_{24}P_{27} + r_{34}P_{37} + P_{47} + r_{45}P_{57} + r_{46}P_{67}$
5. $r_{57} = r_{15}P_{17} + r_{25}P_{27} + r_{35}P_{37} + r_{45}P_{47} + P_{57} + r_{56}P_{67}$
6. $r_{67} = r_{16}P_{17} + r_{26}P_{27} + r_{36}P_{37} + r_{46}P_{47} + r_{56}P_{57} + P_{67}$
7. $I = P^2X_7 + P^2_{27} + P^2_{37} + P^2_{47} + P^2_{57} + 2P_{17}r_{12}P_{27} + 2P_{17}\ r_{13}P_{37} + 2P_{17}r_{14}P_{47} + 2P_{17}r_{15}P_{57} + 2P_{17}r_{16}P_{67} + 2P_{27}r_{23}P_{37} + 2P_{27}r_{24}P_{47} + 2P_{27}r_{25}P_{57} + 2P_{27}r26P_{67} + 2P_{37}r_{34}P_{47} + 2P_{37}r_{35}P_{57} + 2P_{37}r_{36}P_{67} + 2P_{47}r45P_{57} + 2P_{47}r_{46}P_{67} + 2P_{57}r_{56}P_{67}$

In the path model:

rij = simple correlation coefficients for measuring the mutual association of two variables

Pij = path coefficient for measuring direct influence between variables with yield

Rijpij = indirect effect of variables upon another through the other variable

Px = the residual effects in the path analysis model

I and j = (1, 2, 3...6)

3.7.6.4 Stability Analysis

The performance of genotypes across the three environments was assessed by performing the linear regression analysis. This was done according to the method of Eberhart and Russell (1966) which employs the following model:

$Yij = \mu i + \beta i\, Ij + \delta ij$ ……(11)

Where: Yij = mean of i^{th} genotype in j^{th} environment ($i= 1, 2.. g; j =1,2.. n$),

Ij = environmental index of j^{th} environment as the means of all genotypes, that is j^{th} environment mean (over all genotypes) minus the grand mean.

μi = mean of i^{th} genotype over all environments.

βi = regression coefficient which measures the response of i^{th} genotype to the varying environments.

δij (S^2d) = deviation from regression of i^{th} genotype at j^{th} environment, i.e.,

$\delta ij = Yij – Ij\, Y$.

In addition, performance of genotypes giving (b=1) value close to unity are considered to be adapted to all environments, while those showing b-value greater than or less than unity would show specific adaptation to rich or poor environment, respectively, and the genotypes showing low and non-significant S^2d values are considered to possess stability of performance over the range of environments.

CHAPTER FOUR

4.0 RESULTS

4.1 General Profile of the Study Area

The weather conditions during the cropping season at Ukiriguru, Nansole and Bukindo are presented in Appendix 3. Weather and climatic conditions varied over locations. At Nansole, rainfall distribution recorded the highest throughout the growing season and was relatively high compared to other sites. The experiments were established under rainfed lowland bunded conditions. Ukiriguru had pH of 5.72 with slightly acidic sand clay loam soils. The soil had high percentage of organic matter, low total N and relatively high available P (Appendix 2). At Ukiriguru, the mean maximum temperature was 31.5^{o}C in March 2012 while minimum temperature was 18.4^{o}C in April 2012. Maximum monthly rainfall was 192.4 mm in April 2012 while the minimum monthly rainfall was 12.4 mm in January 2012. The average monthly rainfall during the whole period of growing season was 91.3 mm per month. However, this site was supplemented with irrigation during drought season.

During earlier stages of crop growth and prior to flowering, all the experimental sites were affected by drought in the months of January through February. During this time growth of genotypes coincided with moisture stress which accounted for delay in flowering. At Nansole site, the soils were generally characterized by slightly acidic loam sand clay type. The temperature varied between 26.4-30.1^{o}C and 18.5-18.9^{o}C. Mean maximum rainfall was 282.6 mm in April while minimum was 35.8 mm in March (Appendix 3). The average rainfall during the entire growing period was 138 mm per month. At Bukindo, the area was characterized by clay soils with high water retention capacity, but with low organic carbon content, carbon nitrogen ratio, available P and

moderate Calcium and Magnesium. The average rainfall for entire growing period was 105.2 mm.

4.2 Analysis of Variance

The results showed significant differences among genotypes for all characters studied at all the sites (Appendix 5). There were no significant differences among the locations studied (Appendix v) while significant ($P \leq 0.05$) G x E interaction was observed for days to flowering and number of grains per panicle. Highly significant ($P \leq 0.05$) G x E was recorded for plant height, number of panicles per square metre, panicle length, percent filled grains per panicle, grain yield per plant and grain yield. The characters which showed non significant G x E were panicle weight and 1000 grain weight.

4.3 Growth Parameters and Yield and Yield Components

4.3.1 Days to 50% flowering

Genotypes differed significantly in reaching 50% days to flowering in all tested environments (Tables 3, 4, 5). Genotypes SUA 8-2-2-3 and SUA 12-2-3-2 consistently flowered earlier across environments and were statistically similar to Mwangaza. Pooled results over three environments indicated that genotypes mostly delayed in flowering at Ukiriguru and were earliest to flower at Bukindo. Genotype Mwangaza consistently flowered earliest whereas Kalamata delayed to flower at each location and across environments (Table 6).

Table 3: Agronomic and growth parameters of selected rice genotypes tested at Ukiriguru

Genotypes	Days to 50% Flowering	Plant Height (cm)	Number of Panicle/ plant	Panicles /m²	Panicle Weight (g)	Panicle Length (cm)	1000 Grain Weight (g)	Number Of filled Grains/ Panicle	% Filled Grain/ Panicle	Yield/ Plant (g)	Grain Yield (kg/ha)
NERICA L-4	99 d	64.37 a	16.53 gh	382.3 h	2.4 a	20.933 bcd	24.43 b	98.5 a	84 cde	30.39 cd	5422 efgh
NERICA L-8	117 fg	77.33 b	17.1 h	409 i	4.167 efg	22.467defg	29.7 c	157.1 e	79.67bcde	46.22 g	7781 i
NERICA L-52	104 e	69.8 ab	16.4 gh	406 hi	2.233 a	21 bcd	25.07 b	102.4 ab	81 bcde	20.73 ab	4440 cdef
SUA 1-13-12-3	116.67f	75.6 b	13.17 f	325.7 g	3.7 bcde	19.467 ab	31.73 cde	131.8 cde	84 cde	37.33 def	5877 gh
SUPA M 101-22	120 gh	108.77de	9.3 abcd	187 d	4.733 h	21.433 cde	35.1 g	154.7 de	77.67 bcd	30.57 cde	5130 defgh
SUA 2-2-3-1	121 h	68.53 ab	10.83 ab	260 f	3.533 bc	20.9 bcd	24.7 b	148.7cde	81.67bcde	24.13 abc	3840 bcd
SUPA BC	116 f	76.9 b	12.9 ef	280 f	3.6 bcd	20.167 abc	30.5 cde	126.3 abcd	82.67bcde	35.03 de	5553 fgh
SARO 5	120 gh	76.2 b	13.8 fg	277.3 f	4.367 fgh	18.767 a	30.13 cd	132.7 cde	88.33 e	38.8 efg	6296 h
Mwangaza	84 a	116.1 e	9.5 bcd	174.3 cd	4.8 h	23.567 fg	34.33 fg	139.8 cde	88 e	44.93 fg	4463 defg
SUA 12-2-3-2	90 b	109.07de	6.8 ab	219. bcd	3.933 bcdef	21.4 cd	31.1 cde	135.1 cde	74.33 ab	25.85 bc	4005 bcde
SUA 8-2-2-3	95.67 c	103.43 d	7.17 abc	155.3 abc	4.167 efg	21 bcd	30.17 cd	153.8 de	77.33 bcd	16.2 a	2359 a
Salama M-57	89 b	110.93 de	6.73 ab	147 a	4.1 defg	21.833cdef	32.53 ef	148.6 cde	83 bcde	21.67 ab	5021 defgh
SSD 1	96.3 cd	108.27 de	7.8 abc	187 d	4.467 gh	23.2 efg	31 cde	141.2 cde	86 de	24.01 abc	3796 bcd
SSD 3	96 c	88.03 c	8.17abcd	172.3 bcd	3.433 b	18.667 a	34.53 fg	124.6 abc	82.67bcde	18.4 ab	2642 ab
SSD 5	96 cd	70.07 ab	10.13cde	183.3 d	3.967 cdefg	21.6 cde	21.9 a	134.3 cde	76.67 bc	25.6 bc	3787 abcd
Kalamata	127 i	116.97 e	6.4 a	147.7 ab	3.833 bcde	24 g	32.1 de	130.4 bcde	67 a	22.17 abc	3032 abc
Grand mean	105.4	90.02	10.8	244.6	3.84	21.2	29.94	135	80.88	28.88	4590
s.e (±)	0.894	2.728	0.808	8.17	0.1725	0.4828	0.572	7.84	2.493	2.76	469.4
c.v (%)	1	3.7	9.2	3.3	4.5	2.8	2.3	7.1	3.8	9.6	10.2

*Numbers bearing the same letter (s) in a column are not statistically different at P≤0.05 by Turkeys test

4.3.2 Plant height (cm)

Plant height portrayed significant (P≤0.05) difference among genotypes at the three sites. Generally, genotypes were tallest at Nansole and shortest at Ukiriguru. Kalamata was the tallest at Ukiriguru, Salama M-57 at Nansole and Mwangaza was the tallest at Bukindo while NERICA L-4 consistently revealed the shortest plant stature both at Ukiriguru and Nansole while SUA 2-2-3-1 recorded shortest plant height at Bukindo (Table 3, 4, 5). Combined analysis indicated that Mwangaza was the tallest in plant height while NERICA L-4 was the shortest (Table 6).

4.3.3 Number of panicles per plant

Number of panicles per plant registered significant difference (P≤0.05) among genotypes for the tested environments. Genotype NERICA L-8 produced the highest number of panicles per plant at Ukiriguru and Bukindo while NERICA L-4 had the highest number of panicle per plant at Nansole (Tables 3, 4 and 5). Genotype NERICA L-8 consistently had highest number of panicles per plant in combined analysis whereas the lowest numbers of panicles per plant were shown by Kalamata (Table 6).

4.3.4 Number of productive panicles per square metre

The number of panicles per square metre recorded significant (P≤0.05) differences among genotypes in all tested environments (Tables 3, 4 and 5). NERICA L-8 had the highest number of panicles per square metre whereas Kalamata had the lowest number of panicles per square metre in each site and in combined analysis (Table 6). Ukiriguru showed the highest number of panicles per square metre while Bukindo gave the lowest.

4.3.5 Panicle weight (g)

Genotypes recorded significant differences (P≤0.05) for panicle weight in all the tested environments. However, Mwangaza produced the heaviest panicle at Ukiriguru, SSD 1 at Nansole and Salama M-57 at Bukindo (Tables 3, 4 and 5). Pooled results averages over three sites indicated that SSD 1 had the heaviest panicles though they were not statistically different from Salama M-57, SARO 5, SUPA M 101-22, Mwangaza and NERICA L-8 while NERICA L-52 gave the lightest panicle (Table 6).

4.3.6 Panicle length (cm)

Genotypes differed significantly (P≤0.05) in panicle length at all three environments. The longest panicles were recorded at Nansole for Kalamata while the shortest was recorded for SSD 3 at Ukiriguru (Tables 3, 4 and 5). Results from combined analysis of variance pooled over three environments indicated that Kalamata consistently produced the longest panicles which were statistically significant from the rest of the genotypes while SSD 3 had shortest panicles in each location.

4.3.7 1000 grain weight (g)

Significant differences (P≤0.05) among the genotypes were observed in 1000 grain weight in all environments. From combined analysis and a single sites analysis results, the heaviest 1000 grain weight was recorded for SUPA M 101-22 which was statistically similar with Mwangaza, Salama M-57 and Kalamata while SSD 5 had the lightest 1000 grains which were also statistically similar with NERICA L-4.

Table 4: Agronomic and growth parameters of selected rice genotypes tested at Nansole.

Genotypes	Days to 50% Flowering	Plant Height (cm)	Number of Panicles/ Plant	Panicles /m²	Panicle Weight (g)	Panicle Length (cm)	1000 Grain Weight (g)	Number Of filled Grains /Panicle	% Filled Grains/ Panicle	Yield/ Plant (g)	Grain Yield (kg/ha)
NERICA L-4	95 b	66.83 a	21.2 f	403.3 f	2.333 a	20.93 abc	24.23 a	109.67 ab	80 cde	30 d	5050 ef
NERICA L-8	114 d	75.8 cd	19.93 f	402 f	4.4 bcd	22.2 bcd	29.43 bcd	166 f	80.5 cde	45 f	8072 i
NERICA L-52	104 c	71.73abcd	15.33 e	392 f	2.2 a	21.13 abc	25.6 ab	93.47 a	83.67 efg	22.57 ab	4659 de
SUA 1-13-12-3	117 d	75.6 cd	13 de	280 e	3.9 bc	20.3 ab	31.6 cde	135.67 de	81.67 cdef	31.43 d	5038 def
SUPA M 101-22	120 de	104.8 f	9.23 abcd	167 bc	4.5 cd	21.53 bc	34.27 e	146.73 e	83.33 defg	30.67 d	4638 d
SUA 2-2-3-1	118 de	68.57 ab	11.67 bcde	264.7 e	3.433 abc	20.6 abc	24.23 a	138 de	86.33 gh	24.57 bc	3716 c
SUPA BC	116 d	75.07 bcd	12 bcde	260.3 e	3.933 bc	20.6 abc	30.53 cde	136.77 de	82.33 defg	31.9 d	5251 f
SARO 5	115.33 d	76.77 d	12.43 cde	268.3 e	4.367 bcd	20.3 ab	30.57 cde	142.33 de	89 h	38.57 e	5739 g
Mwangaza	80 a	119.87 h	8.6 abc	166.3 bc	4.5 cd	22.27 bcd	33.27 de	140 de	86.33 gh	38.7 e	3723 c
SUA 12-2-3-2	92.33 b	118.2 gh	7.67 a	201.3 d	4.033 bc	22.63 cd	31.93 cde	141.67 de	79.33 cd	36.23 e	6474 h
SUA 8-2-2-3	92 b	105.07 f	7.47 a	161 bc	4.2 bcd	21.33 abc	31.13 cde	150.13 ef	77.67 bc	20.87 a	2549 a
Salama M-57	82.67 a	121.33 h	8.53 ab	152 ab	4.4 bcd	22.63 cd	33.07 de	143.17 de	85.67 fgh	22.4 ab	4833 de
SSD 1	99.33 bc	119.9 h	9.47 abcd	163.3 bc	5.333 d	21.17abc	28.8 bc	129.53 cd	83.33 defg	25 bc	3745 c
SSD 3	94 b	88.47 e	8.9 abc	173.3 bc	3.2 ab	19.23 a	33.57 e	117.63 bc	83.67 efg	21.97 ab	3224 b
SSD 5	96.33 bc	69.87abc	9.53 abcd	180.3 cd	4.2 bcd	22.2 bcd	22.53 a	137 de	74.67 b	26.53 c	3597 bc
Kalamata	125 e	112.4abc	5.8 a	135.7 a	3.7 bc	23.77 d	32.47 cde	137 de	67.33 a	21 a	2176 a
Grand mean	103.8	91.89	11.3	235.7	3.915	21.43	29.83	135.3	81.55	29.21	4530
s.e (±)	2.061	1.804	1.029	7.16	0.4194	0.711	1.099	4.375	1.098	1.088	134.4
c.v (%)	2.4	2.4	11.2	3	10.7	3.3	4.5	4	1.6	3.7	3

*****Numbers bearing the same letter (s) in a column are not statistically different at P≤0.05 by Turkeys test

4.3.8 Number of filled grains per panicle

Number of filled grains per panicle registered significant ($P \leq 0.05$) variation among genotypes in all tested environments (Appendix 5). Genotype SUPA M 101-22 gave the highest number of filled grains per panicle at Ukiriguru site, SUA 8-2-2-3 at Nansole and SUA 12-2-3-2 had highest percentage of filled grains at Bukindo while NERICA L-4 consistently showed the lowest number of filled grains at three sites (Tables 3, 4, 5 and 6). Genotype SUA 8-2-2-3 recorded the highest number of filled grains per panicle in combined analysis but it was statistically similar with Salama M-57, SUA 12-2-3-2, Mwangaza, SARO 5 and SUA 2-2-3-1 whereas the lowest number of filled grains per panicle was registered by NERICA L-52.

4.3.9 Percent filled grains/panicle

Significant differences ($P \leq 0.05$) were observed in percent filled grains per panicle among genotypes in all locations (Appendix 5). Genotype SARO 5 consistently exhibited highest percent filled grains per panicle both at Ukiriguru and Nansole (Table 3 and 4). However at Bukindo the highest percent filled grains per panicle was recorded for NERICA L-52 (Table 5). Similarly, genotype Kalamata consistently showed lowest filled grain percentage at all sites. Combined analysis results averages pooled over three sites indicated SARO 5 gave highest filled grains per panicle whereas the lowest percentage of filled grains per panicle was exhibited by Kalamata (Table 6).

Table 5: Agronomic and growth parameters of selected rice genotypes tested at Bukindo

Genotypes	Days to 50% Flowering	Plant height (cm)	Number of Panicles/ Plant	Panicle /m²	Panicle weight (g)	Panicle Length (cm)	1000 Grain Weight (g)	Number Of filled Grains /Panicle	% Filled Grains /Panicle	Yield/ Plant (g)	Yield (kg/ha)
NERICA L-4	96.3 cd	68.77 a	17.57 f	381.7 c	2.383 a	20.30 ab	24.23 a	93.0 a	81.00 bc	27.60 abc	5279 cd
NERICA L-8	115.3 e	75.93 a	18.93 f	343.0 c	4.417 fgh	21.77 bcdef	27.03 ab	160.0 d	82.00 bc	44.37 e	7930 e
NERICA L-52	102.0 d	69.00 a	15.00 e	379.7 c	2.367 a	21.93 cdef	23.86 a	96.4 a	86.33 c	21.67 a	4806 bcd
SUA 1-13-12-3	115.0 e	74.13 a	12.92 de	267.7 b	3.833 de	20.57 abc	32.00 bcd	136.0 c	78.67 bc	30.43 bcd	4630 bcd
SUPA M 101-22	118.7 e	106.33 c	8.77 bc	164.3 a	4.433 gh	21.60 bcde	33.83 d	139.0 c	83.00 bc	31.03 bcd	4669 bcd
SUA 2-2-3-1	115.3 e	68.70 a	11.67 d	264.3 b	3.430 bc	20.73 abcd	27.27 abc	139.0 c	83.67 bc	24.97 abc	3689 abc
SUPA BC	115.3 e	74.67 a	10.93 cd	243.3 b	4.167 efg	21.03 bcde	30.77 bcd	139.3 c	80.33 bc	32.80 cd	5123 cd
SARO 5	113.7 e	75.93 a	12.00 d	276.0 b	4.333 fgh	21.73 bcdef	32.93 d	136.3 c	83.00 bc	37.83 de	5879 d
Mwangaza	80 a	119.67 e	8.20 b	159.7 a	4.400 fgh	21.93 cdef	33.57 d	138.7 c	79.67 bc	37.83 de	3734 abc
SUA 12-2-3-2	91.7 bc	117.00 de	7.40 ab	177.7 a	4.067 def	22.63 ef	32.17 bcd	143.4 cd	80.33 bc	31.20 bcd	5103 cd
SUA 8-2-2-3	90.7 bc	105.63 c	7.17 ab	165.0 a	4.233 fgh	21.93 cdef	32.83 d	141.7 c	80.67 bc	22.20 a	2652 a
Salama M-57	86.7 ab	114.83 cde	6.97 ab	141.0 a	4.533 h	22.43 ef	32.33 cd	141.0 c	84.00 bc	23.53 ab	4901 cd
SSD 1	95.3 cd	114.00 cde	7.60 ab	162.0 a	4.333 fgh	22.43 ef	31.98 bcd	138.7 c	79.33 bc	26.60 abc	3781 abc
SSD 3	94.3 c	87.80 b	7.30 ab	159.0 a	3.133 b	19.23 a	33.80 d	115.3 b	80.67 bc	21.43 a	3100 ab
SSD 5	95.3 cd	68.73 a	9.07 bc	175.3 a	4.233 fgh	22.27 def	22.33 a	135.0 c	78.00 b	26.33 abc	3538 abc
Kalamata	126.0 f	107.83 cd	5.80 a	134.3 a	3.780 cd	23.33 f	32.63 d	137.0 c	68.33 a	21.00 a	2152 a
Grand mean	103.23	90.56	10.46	224.6	3.88	21.617	30.22	133.11	80.56	28.83	4435
s.e (±)	2.3	3.137	0.763	18.87	0.0453	0.5348	1.722	5.755	2.614	2.645	574.8
c.v (%)	2.2	3.5	7.3	8.4	1.2	2.5	5.7	4.3	3.2	9.2	13

*Numbers bearing the same letter (s) in a column are not statistically different at P≤0.05 by Turkeys test

4.3.10 Grain Yield per plant

Grain yield per plant differed significantly ($P \leq 0.05$) among genotypes in all environments (Appendix 5). Except for Ukiriguru where the lowest grain yield per plant was shown by SUA 8-2-2-3, Kalamata produced the lowest grain yield per plant at Nansole and Bukindo sites. Pooled data over three sites indicated the genotype; NERICA L-8 constantly gave the highest grain yield per plant across environments while SSD 3 had the lowest grain yield per plant but was not statistically different with Kalamata, Salama M-57, and SUA 8-2-2-3 and NERICA L-52 (Table 6).

4.3.11 Grain yield

All genotypes revealed significant differences ($P \leq 0.05$) in yield performance in all experimented environments (Appendix 5). Except for Bukindo where Kalamata had the lowest grain yield, genotype SUA 8-2-2-3 steadily produced the lowest grain yield at Ukiriguru and Nansole. Genotype NERICA L-8 consistently yielded highest in all tested environments and at individual single sites while the lowest grain yield was exhibited by Kalamata (Tables 3, 4, 5 and 6).

Table 6: Agronomic and growth parameters of selected rice genotypes (combined analysis)

Genotypes	Days To 50% Flowering	Plant Height (cm)	Number of Panicles / Plant	Panicles/ m²	Panicle weight (g)	Panicle Length (cm)	1000 Grain Weight (g)	Number Of filled Grains/ Panicle	% Filled Grains /Panicle	Yield/ Plant (g)	Grain Yield (kg/ha)
NERICA L-4	96.8 e	66.66 a	18.43 g	389.1 g	2.372 a	20.72 bc	24.30 ab	100.4 a	81.67 cde	29.33 de	5250 ef
NERICA L-8	115.4g	76.36 b	18.66 g	384.7 g	4.328efgh	22.14 de	28.72 c	161 f	80.72 cde	45.20 h	7927 g
NERICA L-52	103.3 f	70.18 a	15.58 f	392.6 g	2.267 a	21.36 cd	24.8 b	97.4 a	83.67 ef	21.66 ab	4635 de
SUA 1-13-12-3	116.2gh	75.11 b	13.03 e	291.1 f	3.811 cd	20.11 b	31.78 def	134.5 c	81.44 cde	33.07 ef	5181 e
SUPA M 101-22	119.6 h	106.63 d	9.10cd	172.8 c	4.556 gh	21.52 cd	34.40 g	146.8 de	81.33 cde	30.76 ef	4812 e
SUA 2-2-3-1	119.6 h	68.60 a	11.39e	263.0 e	3.466bc	20.74 bc	25.40 b	141.9 cde	83.89 ef	24.56 bc	3748 c
SUPA BC	115.8 g	75.54b	11.94 e	261.2 e	3.9 cde	20.60 bc	30.60 cd	134.1 c	81.78 cde	33.24 f	5309 ef
SARO 5	116.3gh	76.30 b	12.74 e	273.9 ef	4.356 fgh	20.27 b	31.21 d	137.1 cde	86.78 f	38.57 g	5971 f
Mwangaza	81.4a a	118.54 f	8.77 bcd	166.8 bc	4.567 gh	22.59 e	33.72 efg	139.5 cde	84.67 ef	40.49 g	3973 cd
SUA 12-2-3-2	91.3 c	114.76 ef	7.29 ab	199.6 d	4.011def	22.22 de	31.73 de	140.1 cde	78.00 bc	31.09 ef	5194 e
SUA 8-2-2-3	92.8 cd	104.71 d	7.27 ab	160.4 bc	4.200 defg	21.42 cd	31.38 d	148.5 e	78.56 bcd	19.76 a	2520 a
Salama M-57	86.1 b	115.70 ef	7.41abc	146.7 ab	4.344 efgh	22.30 de	32.64 defg	144.2cde	84.22 ef	22.53 abc	4919 e
SSD 1	97.0 e	114.06 ef	8.29 bcd	170.8 c	4.711 h	22.27 de	30.59cd	136.5 cd	82.89 ef	25.20bc	3774 c
SSD 3	94.4 cde	88.10 c	8.12 bcd	168.2 c	3.256 b	19.04a	33.97 fg	119.2 b	82.33 de	20.60 a	2989 ab
SSD 5	95.9 de	69.56 a	9.58 d	179.7 cd	4.133 defg	22.02 de	22.26 a	135.4cd	76.44 b	26.16 cd	3640 bc
Kalamata	126.0 i	112.40 e	6.02 a	139.2 a	3.771 cd	23.70 f	32.40 defg	134.8c	67.56 a	21.39 ab	2454 a
Grand mean	104.16	90.83	10.851	235	3.878	21.440	30	134.47	81	28.97	4519
s.e (±)	2.071	2.937	1.0249	12.57	0.2707	0.6167	1.325	7.163	2.447	2.295	435.4
c.v (%)	2.0	3.2	9.4	5.3	7.0	2.9	4.4	5.3	3.0	7.9	9.6

* The numbers bearing the same letter (s) in the same column are not statistically significant at $P \leq 0.05$ by Turkey test

4.4 Estimates of Genetic Components for Yield and Its Components in Rice

Estimates of variance components are presented in Table 7. Results from this study indicated that the genotypic variance was generally greater in magnitude than the environment variance. However, the magnitude of variation between phenotypic and genotypic coefficients of variation was small. Grain yield registered maximum genotypic coefficient of variation, followed by the number of panicles per square metre and number of panicles per plant while the least was exhibited by panicle length. Generally, all genotypes showed high broad sense heritability for all characters accompanied by high expected genetic advance. Panicle weight exhibited highest heritability and the lowest was shown by grain yield while the highest genetic advance was shown by number of filled grains per panicle. The lowest expected genetic gain was recorded by grain yield.

Table 7: Estimates of genetic components for yield and its components in rice from combined analysis

Character	δ^2g	δ^2l	δ^2gl	δ^2e	δ^2ph	h^2	GA	PCV	GCV
FL	170.21	57.2	30.61	8.72	183.27	93.9	26.1	13.2	13
PHT	376.3	8.65	125.98	22.7	420.8	89.4	12.6	22.5	21.2
PN	210.8	17.4	146	10.2	270.7	77.8	26.3	37.67	35.9
PPM	19.97	4.63	14.22	15.18	26.7	71.0	7.5	38.4	38.1
PW	71.09	0.135	3.41	6.7	72.96	97.4	17.4	25.2	22.4
PL	11.93	1.4	3.78	1.37	13.34	89.4	6.72	5.37	4.7
GWT	28.2	7.2	15.7	4.6	33.9	83.1	9.96	12.9	11.8
GNPP	242.6	27.4	83.13	50.26	275.8	87.9	30	12.6	11.9
PFGPP	266.3	24.5	57.4	62.2	292.3	91.1	32	5.48	5.17
GYPP	79.19	4.13	47.4	48	93	77.3	15.3	26.43	24.7
GY	2.928	1.73	5.434	1.845	4.944	59.2	2.71	42.3	37.9

δ^2g = component of variance due to genotypes; δ^2l = component of variance due to environment (location); δ^2gl = component of variance due to genotype x environment interaction; δ^2e = component of variance due to error term; δ^2ph = component of variance due to phenotype; h^2 = Heritability (broad sense); GA= Genetic advance; PCV = Phenotypic coefficient of variation; δ^2 GCV = Genotypic coefficient of variation; FL =Days to 50% flowering, PHT = Plant height, PN= Panicle number per hill, PW= Panicle weight, PL=Panicle length, WGT= 1000 grain weight, GNPP=Grain number per panicle, PFGPP=Percent filled grains per panicle, GYPP= Grain yield per panicle, GY= Grain yield (kg/ha).

4.4.1 Simple correlation coefficients (r)

Table 8 indicates the simple correlations coefficients for yield and yield components at Ukiriguru site. The highest simple correlation with grain yield was recorded for grain yield per plant, followed by number of panicles per square metre, number of panicles per plant, percent filled grains per panicle and days to 50% flowering. Grain yield per plant was strongly and positively correlated with number of panicle per plant, percent filled grain and panicle weight. On the contrary, plant height, panicle length and 1000 grain weight were inversely correlated with grain yield. Other characters such as panicle weight and number of grains per panicle showed weak correlation with grain yield.

Table 8: Simple correlation coefficients for agronomic and growth parameter at Ukiriguru

	FL	PHT	PN	PW	PL	GWT	GNPP	PFGPP	GYPP	GY
FL										
PHT	-0.285									
PN	0.312*	-0.778**								
PW	-0.027	0.629**	-0.504**							
PL	-0.120	0.560**	-0.285	0.320*						
GWT	-0.046	0.740**	-0.479**	0.579**	0.081					
GNPP	0.086	0.436**	-0.398**	0.767**	0.267	0.388**				
PFGPP	-0.229	-0.244	0.322*	0.051	-0.263	0.045	-0.118			
GYPP	0.211	-0.134	0.502**	0.313*	0.101	0.150	0.120	0.363*		
GY	0.332*	-0.330*	0.661**	0.062	-0.042	-0.020	0.056	0.347*	0.801**	
PPM	0.301*	-0.729**	0.932**	-0.593**	-0.236	-0.467**	-0.406**	0.233	0.413**	0.648**

* Significant at the 0.05 level; ** Significant at the 0.01 level. FL=50% flowering, PHT=Plant height, PN=Panicle number, PW=Panicle weight, PL=Panicle length, GWT=1000 grain weight GNPP=Grain number/panicle, PFGPP=Percent filled grain/panicle, GYPP=Grain yield/plant, GY=Grain yield, PPM= Panicles per square meter

Simple correlation coefficients of grain yield and yield components for Nansole site are presented in Table 9. At Nansole, grain yield was positively correlated with all characters except plant height, panicle weight, panicle length and 1000 grain weight which were negatively correlated. The highest positive association with grain yield was depicted by

grain yield per plant, followed by number of panicles per plant. Panicle weight had positive but weak correlation with grain yield. Other characters which had relative positive contribution with grain yield were as shown in Table 9.

Table 9: Simple correlation coefficients for agronomic and growth parameter at Nansole

	FL	PHT	PN	PW	PL	GWT	GNPP	PFGPP	GYPP	GY
FL										
PHT	-0.400**									
PN	0.182	-0.660**								
PW	-0.011	0.538**	-0.327*							
PL	-0.136	0.450**	-0.334*	0.048						
GNPP	0.147	0.275	-0.229	0.608**	0.375**	0.389**				
PFGPP	-0.184	-0.090	0.180	0.065	-0.474**	0.097	-0.062			
GYPP	0.100	-0.124	0.412**	0.266	0.051	0.122	0.445**	0.279		
GY	0.120	-0.257	0.597**	0.053	-0.006	-0.012	0.266	0.321*	0.776**	
PPM	0.236	-0.729**	0.922**	-0.531**	-0.249	-0.495**	-0.291*	0.191	0.383**	0.617**

* Significant at the 0.05 level; ** Significant at the 0.01 level FL=50% flowering, PHT=Plant height, PN=Panicle number, PW=Panicle weight, PL=Panicle length, GWT=1000 grain weigh GNPP=Grain number/panicle, PFGPP =Percent filled grain/panicle, GYPP=Grain yield/plant, GY=Grain yield, PPM= Panicles per square meter

Estimates of simple correlations for Bukindo site are presented in Table 10. Grain yield was positively correlated with all characters except plant height and panicle length. Highest simple correlation with yield was registered for grain yield per plant, followed by number of panicle per plant and panicle per square metre. The correlation between panicle weight and 1000 grain weight with grain yield was negative but non significant.

Simple correlations coefficients for combined analysis pooled over three environments are presented in Table 11. Correlation with grain yield was positive and significant for all

the characters except plant height and panicle length. The highest simple correlations with grain yield in combined analysis were displayed by grain yield per plant (r=0.774**), followed by number of panicle per plant (r=0.645**) and numbers of panicles per square metre (r=0.625**). Grain yield per plant had strong and positive association with number of panicles per plant, number of grains per panicle, percent filled grains per panicle. Furthermore, number of filled grains per panicle was strong and positively associated with panicle weight, panicle length and 1000 grain weight.

Table 10: Simple correlation coefficients for agronomic and growth parameter at Bukindo

	FL	PHT	PN	PW	PL	GWT	GNPP	PFGPP	GYPP	GY
FL										
PHT	-0.39**									
PN	0.276	-0.714**								
PW	-0.020	0.500**	-0.417**							
PL	-0.042	0.474**	-0.313*	0.448**						
GWT	-0.015	0.649**	-0.567**	0.467**	0.109					
GNPP	0.175	0.367*	-0.260	0.862**	0.364*	0.375**				
PFGPP	-0.239	-0.230	0.336*	-0.129	-0.182	-0.168	-0.141			
GYPP	0.146	-0.085	0.434**	0.423**	0.046	0.084	0.427**	0.161		
GY	0.177	-0.313*	0.687**	0.080	-0.077	0.222	0.122	0.420**	0.757**	
PPM	0.251	-0.738**	0.932**	-0.586**	-0.338*	-0.596**	-0.414**	0.397**	0.275	0.602**

* Significant at the 0.05 level; ** Significant at the 0.01 level. FL=50% flowering, PHT=Plant height, PN=Panicle number, PW=Panicle weight, PL=Panicle length, GWT=1000 grain weigh GNPP=Grain number/panicle, PFGPP=Percent filled grain/panicle, GYPP=Grain yield/plant, GY=Grain yield, PPM= Panicles per square meter

Table 11: Simple correlation coefficients for agronomic and growth parameter (combined analysis)

CHARACTER	FL	PHT	PN	PW	PL	GWT	GNPP	PFGPP	GYPP	GY
FL										
PHT	-0.367**									
PN	0.254**	-0.707**								
PW	-0.022	0.553**	-0.401**							
PL	-0.117	0.491**	-0.309**	0.249**						
GWT	-0.039	0.660**	-0.519**	0.421**	0.127					
GNPP	0.136	0.357**	-0.286**	0.730**	0.314**	0.380**				
PFGPP	-0.213*	-0.181*	0.276**	0.011	-0.308**	-0.005	-0.102			
GYPP	0.16	-0.118	0.446**	0.319**	0.061	0.122	0.306**	0.285**		
GY	0.215**	-0.301**	0.645**	0.061	-0.053	-0.086	0.148	0.356**	0.774**	
PPM	0.271**	-0.729**	0.923**	-0.564**	-0.278**	-0.514**	-0.362**	0.262**	0.364**	0.625**

*Significant at the 0.05 level; ** Significant at the 0.01 level, FL=50% flowering, PHT=Plant height, PN=Panicle number, PW=Panicle weight, PL=Panicle length, GWT=1000 grain weigh GNPP=Grain number/panicle, PFGPP=Percent filled grain/panicle, GYPP=Grain yield/plant, GY=Grain yield, PPM= Panicles per square metre

4.4.2 Phenotypic and genotypic correlations

Phenotypic and genotypic correlations at Ukiriguru site are shown in Table 12. Generally, the magnitude of genotypic correlations was higher than the corresponding phenotypic correlations. Grain yield had positive and significant correlation with days to 50% flowering, days to maturity, number of panicles per plant, panicle weight, number of grains per panicle, percent filled grains per panicle and grain yield per plant both at genotypic and phenotypic levels. Maximum positive and significant correlation with grain yield was observed for grain yield per plant, number of panicles per plant, percent filled grain per panicle, days to 50% flowering, days to maturity. Just like simple correlations, plant height had negative significant correlation with grain yield both at genotypic and phenotypic levels whereas panicle length has negative but less contribution towards grain yield (Table 12).

Table 12: Phenotypic (P) and genotypic (G) correlations for rice agronomic and growth parameters at Ukiriguru.

		FL	PHT	PN	PW	PL	GWT	GNPP	PFGPP	GYPP	GY
FL											
PHT	P	-0.285									
	G	-0.296									
PN	P	0.312*	-0.778**								
	G	0.321*	-0.781**								
PW	P	-0.027	0.629**	-0.504**							
	G	-0.031	0.629**	-0.507**							
PL	P	-0.120	0.560**	-0.285	0.320*						
	G	-0.140	0.568**	-0.293	0.322*						
GWT	P	-0.046	0.740**	-0.479**	0.579**	0.081					
	G	-0.036	0.726**	-0.470**	0.575**	0.068					
GNPP	P	0.086	0.436**	-0.398**	0.767**	0.267	0.388**				
	G	0.086	0.433**	-0.398**	0.767**	0.264	0.387**				
PFGPP	P	-0.229	-0.244	0.322*	0.051	-0.263	0.045	-0.118			
	G	-0.228	-0.243	0.318*	0.049	-0.257	0.045	-0.120			
GYPP	P	0.211	-0.134	0.502**	0.313*	0.101	0.150	0.120	0.363*		
	G	0.225	-0.146	0.510**	0.308*	0.075	0.158	0.121	0.363*		
GY	P	0.332*	-0.330*	0.661**	0.062	-0.042	-0.020	0.056	0.347*	0.801**	
	G	0.345*	-0.340*	0.669**	0.058	-0.067	-0.011	0.058	0.348*	0.805**	
PPM	P	0.301*	-0.729**	0.932**	-0.593**	-0.236	-0.467**	-0.406**	0.233	0.413**	0.648**
	G	0.313*	-0.733**	0.933**	-0.593**	-0.251	-0.454**	-0.403**	0.231	0.422**	0.655**

*Significant at the 0.05 level; ** Significant at the 0.01 level, FL=50% flowering, PHT=Plant height, PN=Panicle number, PW=Panicle weight, PL=Panicle length, GWT=1000 grain weight, GNPP=Grain number/panicle, PFGPP=Percent filled grain/panicle, GYPP=Grain yield/plant, GY=Grain yield, PPM= Panicles per square meter

Phenotypic and genotypic correlations studied at Nansole are presented in the Table 13. The genotypic correlations were slightly higher than the phenotypic correlations except for plant height, panicle length which were negative and non significantly correlated with grain yield at both levels. Days to 50% flowering, numbers of panicle per plant, panicle weight, number of grains per panicle, percent filled grains per panicle and grain yield per plant had positive and strong correlations with grain yield. A maximum correlation with grain yield was depicted by grain yield per plant, number of panicles per square metre and number of panicles per plant.

Table 13: Phenotypic (P) and genotypic (G) correlations for agronomic and growth parameters at Nansole

		FL	PHT	PN	PW	PL	GWT	GNPP	PFGPP	GYPP	GY
FL											
PHT	P	-0.400**									
	G	-0.401**									
PN	P	0.182	-0.660**								
	G	0.181	-0.663**								
PW	P	-0.011	0.538**	-0.327*							
	G	-0.012	0.537**	-0.332*							
PL	P	-0.136	0.450**	-0.334*	0.048						
	G	-0.136	0.451**	-0.332*	0.051						
GNPP	P	0.147	0.275	-0.229	0.608**	0.375**	0.389**				
	G	0.146	0.275	-0.233	0.607**	0.378**	0.393**				
PFGPP	P	-0.184	-0.090	0.180	0.065	-0.474**	0.097	-0.062			
	G	-0.184	-0.090	0.180	0.065	-0.474**	0.097	-0.062			
GYPP	P	0.100	-0.124	0.412**	0.266	0.051	0.122	0.445**	0.279		
	G	0.100	-0.124	0.413**	0.267	0.051	0.121	0.446**	0.279		
GY	P	0.120	-0.257	0.597**	0.053	-0.006	-0.012	0.266	0.321*	0.776**	
	G	0.120	-0.257	0.598**	0.054	-0.006	-0.012	0.267	0.321*	0.776**	
PPM	P	0.236	-0.729**	0.922**	-0.531**	-0.249	-0.495**	-0.291*	0.191	0.383**	0.617**
	G	0.236	-0.729**	0.924**	-0.533**	-0.249	-0.496**	-0.291*	0.191	0.383**	0.617**

*Significant at the 0.05 level; ** Significant at the 0.01 level, FL=50% flowering, PHT=Plant height, PN=Panicle number, PW=Panicle weight, PL=Panicle length, GWT=1000 grain weigh GNPP=Grain number/panicle, PFGPP=Percent filled grain/panicle, GYPP=Grain yield/plant, GY=Grain yield, PPM= Panicles per square meter

Phenotypic and genotypic correlations among all pairs of characters at Bukindo are shown in Table 14. The genotypic correlations in general were slightly higher than correspondent phenotypic correlations. The maximum correlation with grain yield was revealed by grain yield per plant and number of panicles per plant at both levels. Plant height and panicle length had negative and significant correlation with grain yield. The percent filled grain per panicle was strong and positive associated with grain yield whereas number of filled grains per panicle had positive but non significant correlations with grain yield at both levels.

Table 14: Phenotypic (P) and genotypic correlation (G) coefficients for agronomic parameter at Bukindo

		FL	PHT	PN	PW	PL	GWT	GNPP	PFGPP	GYPP	GY
FL											
PHT	P	-0.398**									
	G	-0.399**									
PN	P	0.276	-0.714**								
	G	0.276	-0.716**								
PW	P	-0.020	0.500**	-0.417**							
	G	-0.019	0.503**	-0.416**							
PL	P	-0.042	0.474**	-0.313*	0.448**						
	G	-0.042	0.474**	-0.314*	0.448**						
GWT	P	-0.015	0.649**	-0.567**	0.467**	0.109					
	G	-0.018	0.649**	-0.575**	0.475**	0.108					
GNPP	P	0.175	0.367*	-0.260	0.862**	0.364*	0.375**				
	G	0.174	0.366*	-0.261	0.863**	0.364*	0.375**				
PFGPP	P	-0.239	-0.230	0.336*	-0.129	-0.182	-0.168	-0.141			
	G	-0.239	-0.230	0.337*	-0.129	-0.182	-0.168	-0.140			
GYPP	P	0.146	-0.085	0.434**	0.423**	0.046	0.084	0.427**	0.161		
	G	0.145	-0.087	0.433**	0.427**	0.045	0.079	0.427**	0.162		
GY	P	0.177	-0.313*	0.687**	0.080	-0.077	-0.222	0.122	0.420**	0.757**	
	G	0.176	-0.314*	0.687**	0.080	-0.077	-0.226	0.122	0.421**	0.757**	
PPM	P	0.251	-0.738**	0.932**	-0.586**	-0.338*	-0.596**	-0.414**	0.397**	0.275	0.602**
	G	0.251	-0.740**	0.932**	-0.586**	-0.338*	-0.603**	-0.415**	0.397**	0.274	0.602**

*Significant at the 0.05 level; ** Significant at the 0.01 level, FL=50% flowering, PHT=Plant height, PN=Panicle number, PW=Panicle weight, PL=Panicle length, GWT=1000 grain weight, GNPP=Grain number/panicle, PFGPP=Percent filled grain/panicle, GYPP=Grain yield/plant, GY=Grain yield, PPM=Panicles per square meter

Phenotypic and genotypic correlations of all characters results pooled over three sites are presented in Table 15. Grain yield was significantly and positively associated with grain yield per plant, number of panicles per plant, number of panicles per square metre, days to 50 % maturity and days to maturity both at genotypic and phenotypic levels. Genotypic and phenotypic correlations had similar trend, but very close and similar value were observed for numbers of panicles per plant, percent filled grain per panicle, grain yield per plant and days to 50% flowering. However, plant height as well as panicle length were negatively correlated with grain yield both at phenotypic and genotypic levels. Grain yield had negative and significant correlation with plant height both at genotypic and phenotypic levels whereas it showed positive and non significant correlation with panicle weight and 1000 grain weight.

Table 15: Phenotypic (P) and genotypic (G) correlations for rice grain yield and its components in combined analysis (n=192)

		FL	PHT	PN	PW	PL	GWT	GNPP	PFGPP	GYPP	GY
FL											
PHT	P	-0.367**									
	G	-0.367**									
PN	P	0.254**	-0.707**								
	G	0.253**	-0.707**								
PW	P	-0.022	0.553**	-0.401**							
	G	-0.02	0.554**	-0.402**							
PL	P	-0.117	0.491**	-0.309**	0.249**						
	G	-0.111	0.493**	-0.306**	0.251**						
GWT	P	-0.039	0.660**	-0.519**	0.421**	0.127					
	G	-0.037	0.661**	-0.518**	0.424**	0.123					
GNPP	P	0.136	0.357**	-0.286**	0.730**	0.314**	0.380**				
	G	0.134	0.358**	-0.289**	0.732**	0.322**	0.383**				
PFGPP	P	-0.213*	-0.181*	0.276**	0.011	-0.308**	-0.005	-0.102			
	G	-0.215*	-0.18*	0.274**	0.01	-0.307**	-0.003	-0.104			
GYPP	P	0.16	-0.118	0.446**	0.319**	0.061	0.122	0.306**	0.285**		
	G	0.16	-0.118	0.448**	0.321**	0.06	0.12	0.307**	0.286**		
GY	P	0.215**	-0.301**	0.645**	0.061	-0.053	0.086	0.148	0.356**	0.774**	
	G	0.213**	-0.301**	0.645**	0.063	-0.049	0.086	0.147	0.356**	0.775**	
PPM	P	0.271**	-0.729**	0.923**	-0.564**	-0.278**	-0.514**	-0.362**	0.262**	0.364**	0.625**
	G	0.267**	-0.731**	0.924**	-0.565**	-0.271**	-0.515**	-0.368**	0.261**	0.366**	0.624**

* Significant at 0.05 level; **Significant at 0.01 level, P=Phenotypic correlation, G=Genotypic correlation FL=50% flowering;
PHT=Plant height, PN=Panicle number, PW=Panicle weight, PL=Panicle length, GWT=1000 grain weigh GNPP=Grain number/panicle,
PFGPP=Percent filled grain/panicle, GYPP=Grain yield/plant, GY=Grain yield, PPM= Panicle per square meter

4.5 Path analysis

4.5.1 Path analysis (Ukiriguru, Nansole and Bukindo)

Path analyses at Ukiriguru site are presented in Table 16 and Fig. 1. Grain yield had positive and direct effect with all characters. Grain yield per plant had the maximum and positive degree of direct effects on grain yield, followed by number of panicle per plant, 50% days to flowering, plant height, percent filled grain per panicle and 1000 grain weight. Positive and direct effect of grain yield per plant with grain yield was lessened by negative and indirect effect of plant height. Similarly the positive and direct effect of number of panicle per plant (p=0.4044) on grain yield was lowered by its indirect effect of plant height and 1000 grain weight. Significant and positive direct effect of per cent filled per panicle on grain yield was attributed to 1000 grain weight and number of panicles per plant and grain yield per plant.

Table 16: Path analysis of six selected variables showing direct (along Diagonal) and indirect effects on grain yield at Ukiriguru

Predictor variable	FL	PHT	PN	GWT	PFGPP	GYPP
FL	**0.1351**	-0.0399	0.0434	-0.0048	-0.0306	0.0303
PHT	-0.0291	**0.0983**	-0.0767	0.0714	-0.0239	-0.0143
PN	0.1298	-0.3156	**0.4044**	-0.1896	0.1296	0.2051
GWT	-0.0008	0.0157	-0.0101	**0.0216**	0.001	0.0034
PFGPP	-0.0155	-0.0166	0.0219	0.0031	**0.0682**	0.0246
GYPP	0.1246	-0.0809	0.2819	0.0875	0.2	**0.5556**
GY	0.3442	-0.3391	0.6646	-0.0108	0.3443	0.8047
Residual effects (Px7)						**0.4978**

FL=50% flowering, PHT=Plant height, PN=Panicle number, GWT=1000 grain weight, PFGPP= Percent filled grains/panicle, GYPP=Grain yield/plant and GY=Grain yield

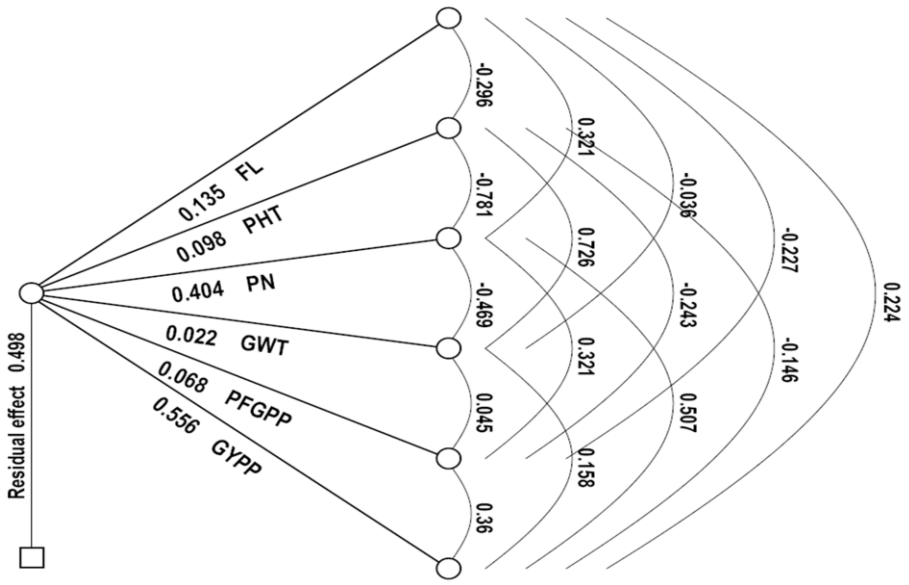

Figure 1: Path diagram for relationship between yield and six yield contributing predictor variables namely days to 50% flowering (FL), plant height (PHT), panicle number (PN), 1000 grain weight (GWT), % filled grains per panicle (PFGPP) and grain yield per plant (GYPP). Single headed arrows indicating direct effects measured by Path coefficients (pij) and double header arrows depict simple correlation coefficients (rij) at Ukiriguru

Table 17 and Fig. 2 show the results from path analysis for Nansole site which indicated that all characters had positive and direct effects on grain yield except days to 50% flowering. Direct effect of number of panicles per plant on grain yield was due to indirect correlation with 50% days to flowering, percent filled grains per plant and grain yield per plant but lowered by the indirect correlation with plant height and 1000 grain weight. The positive direct effect of percent filled grains per panicle on grain yield was positively contributed by number of panicles per plant, 1000 grain weight and grain yield per plant and was negatively associated with 50% days to flowering and plant height.

Table 17: Path analysis of six selected variables showing direct (along the Diagonal) and indirect effects on grain yield at Nansole

Predictor variable	1	2	3	4	5	6
FL	**-0.0288**	-0.0115	0.0052	-0.0018	-0.0053	0.0029
PHT	-0.0215	**0.0536**	-0.0354	0.0333	-0.0048	-0.0067
PN	0.0786	-0.2856	**0.4327**	-0.2244	0.0778	0.1781
GWT	-0.0065	0.0643	-0.0538	**0.1037**	0.01	0.0126
PFGPP	-0.0158	-0.0077	0.0154	0.0083	**0.0858**	0.0239
GYPP	0.0564	-0.0701	0.2326	0.0688	0.1575	**0.565**
GY	0.12	-0.257	0.5968	-0.0122	0.321	0.7759
Residual effects (Px7)						**0.5361**

FL=50% flowering, PHT= Plant height, PN= Panicle number, GWT= 1000 grain weight, PFGPP= Percent filled grains/panicle, GYPP= Grain yield/plant and GY=Grain yield

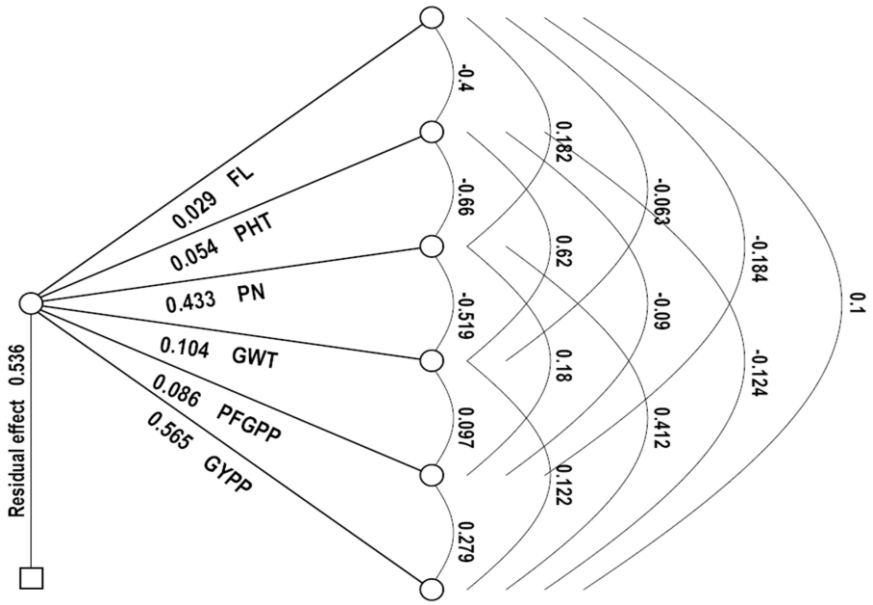

Figure 2: Path diagram for relationship between yield and six yield contributing predictor variables namely days to 50% flowering (FL), plant height (PHT), panicle number (PN), 1000 grain weight (GWT), % filled grains per panicle (PFGPP) and grain yield per plant (GYPP). Single headed arrows indicating direct effects measured by Path coefficients (pij) and double header arrows depict simple correlation coefficients (rij) at Nansole.

Path coefficient analysis at Bukindo site is shown in Table 18 and in Fig. 3. Except for 1000 grain weight, all selected variables had positive and direct effect on grain yield. As noted in the other study areas, grain yield per plant consistently had the highest direct

effects on grain yield, followed by number of panicles per plant, plant height , percent filled grain per panicle and the lowest was displayed by days to 50% flowering. Maximum direct interaction of grain yield per plant with grain yield was positively contributed through percent filled grains per panicle and number of panicles per plant, 1000 grain weight and days to 50% flowering. Conversely, grain yield per plant was indirectly correlated with plant height. The direct effects of number of panicles per plant were positively contributed by days to 50% flowering, 1000 grain weight, percent filled grains per panicle, grain yield per plant but the relationship was lessened through indirect correlation with plant height.

Table 18: Path analysis of six selected variables showing direct (along the diagonal) and indirect effects on grain yield at Bukindo

Predictor variable	1	2	3	4	5	6
FL	**0.1325**	-0.0527	0.0366	-0.002	-0.0316	0.0193
PHT	-0.0909	**0.2286**	-0.1632	0.1483	-0.0527	-0.0194
PN	0.1138	-0.2939	**0.4116**	-0.2335	0.1383	0.1786
GWT	0.0021	-0.0899	0.0787	**-0.1386**	0.0233	-0.0117
PFGPP	-0.0608	-0.0586	0.0855	-0.0428	**0.2545**	0.0411
GYPP	0.08	-0.0467	0.2383	0.0461	0.0886	**0.549**
GY	0.1767	-0.3132	0.6874	-0.2225	0.4203	0.7569
Residual effects (Px7)						**0.4603**

FL=50% flowering, PHT=Plant height, PN=Panicle number, GWT=1000 grain weight, PFGPP= Percent filled grains/panicle, GYPP=Grain yield/plant and GY=Grain yield

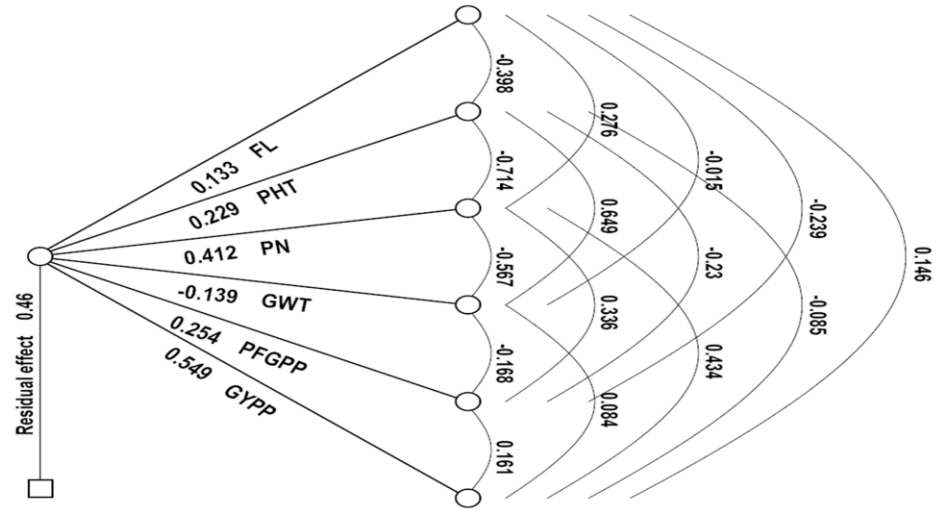

Figure 3: Path diagram for relationship between yield and six yield contributing predictor variables namely days to 50% flowering (FL), plant height (PHT), panicle number (PN), 1000 grain weight (GWT), % filled grains per panicle (PFGPP) and grain yield per plant (GYPP). Single headed arrows indicating direct effects measured by Path coefficients (pij) and double header arrows depict simple correlation coefficients (rij) at Bukindo.

On partitioning correlations into components of direct and indirect effects for pooled data over three sites, all characters except 1000 grain weight had positive and direct effects on grain yield as shown in Table 19 and Fig. 4. Grain yield per plant had highest direct effect on yield (0.551), followed by number of panicle per plant (0.426), plant height and percent filled grains per panicle. Direct effect of number of panicle per plant on grain yield were due to positive correlation with days to 50% flowering; percent filled grain per panicle, grain yield per plant but negatively correlated with plant height and 1000 grain weight. Although 1000 grain weight had negative direct effect on yield, it was positively correlated with grain yield per plant and plant height. Percent filled grain per panicle had direct positive correlation on grain yield but indirectly positively correlated with panicle number per plant, grain yield per plant but negatively correlated with 1000 grain weight, plant height and days to 50% flowering.

Table 19: Path analysis of six selected variables showing direct (along the Diagonal) and indirect effects on grain yield in combined analysis

Predictor variable	1	2	3	4	5	6
1 Days to 50% flowering	**0.092**	-0.0337	0.0234	0.0036	-0.0196	0.0147
2 Plant height	-0.0479	**0.1306**	-0.093	0.0862	-0.0236	-0.0154
3 Panicle number/plant	0.1083	-0.3014	**0.4264**	0.2213	0.1175	0.1903
4 1000 grain weight	0.0005	-0.0091	0.0072	**-0.0138**	0.0001	-0.0017
5 % filled grain/panicle	-0.0265	-0.0225	0.0342	0.0006	**0.1243**	0.0355
6 Grain yield/plant	0.0882	-0.0651	0.2459	0.0671	0.1572	**0.5511**
7 Grain yield	0.2148	-0.3012	0.6448	-0.0681	0.3559	0.7745
Residual effect (Px7)						

1= 50% flowering, 2=Plant height, 3=Panicle number, 4=1000 grain weight, 5= Percent filled grains/panicle, 6=Grain yield/plant

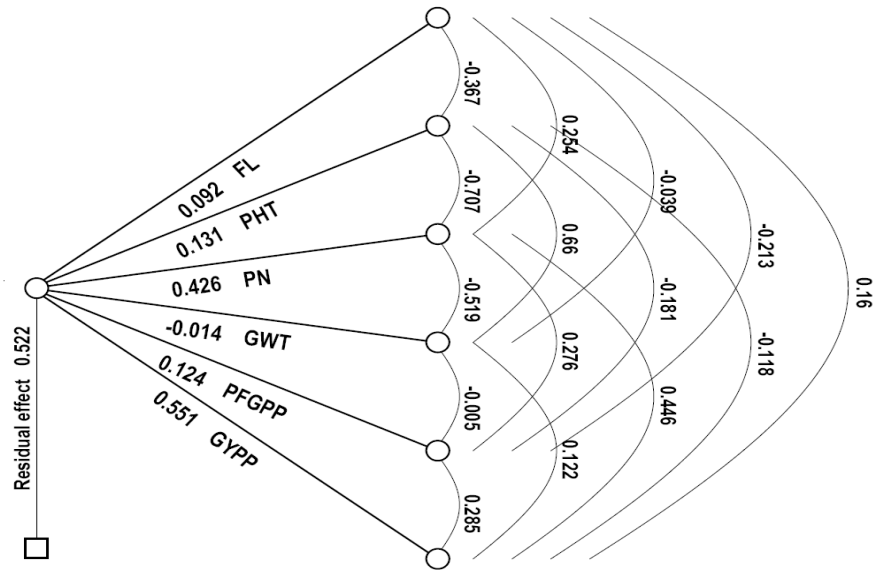

Figure 4: Path diagram for relationship between yield and six yield contributing predictor variables namely days to 50% flowering (FL), plant height (PHT), panicle number (PN), 1000 grain weight (GWT), % filled grains per panicle (PFGPP) and grain yield per plant (GYPP). Single headed arrows indicating direct effects measured by Path coefficients (pij) and double header arrows depict simple correlation coefficients (rij) for combined analysis.

4.6.1 Stability of selected yield components

The joint regression analysis results for regression coefficient (βi) and deviation from regression (S2di) indicated that some genotypes performance was significantly (P≤0.05)

stable for all characters across environments. For panicle weight, genotypes NERICA L-8, SUA 1-13-12-1, SUPA BC, Salama M-57, SSD 1, SUA 12-2-3-2 and SSD 5 had regression coefficient greater than unity and non significant deviation from regression whereas NERICA L-4, NERICA L-52, SUPA M 101-22, SUA 2-2-3-1, SARO 5, Mwangaza, SUA 8-2-2-3, SSD 3 and Kalamata had regression coefficient less than unity.

SUA 2-2-3-1, SUPA BC, Salama M-57 and SSD 3, NERICA L-8 had regression greater than unit and non significant deviation from regression while SUA 12-2-3-2 had coefficient of regression which significantly ($P \leq 0.05$) differed from unity for percent filled grains per panicle. The rest of genotypes had no significant difference in stability performance for the trait (Table 23).

Genotypes SUPA BC, SUPA M101-22, SUA 12-2-3-2, SUA 8-2-2-3, SSD 5 and NERICA L-52 showed regression coefficient greater than unit with deviation from regression (S^2d) approaching to zero. On the other hand, NERICA L-4, NERICA L-8, Salama M-57, SSD 1, SSD 3 had regression greater than unit with non-significant deviation from regression. The remaining genotypes did not show significant differences in stability performance for percent filled grains per panicle.

Adaptability and stability analysis revealed that genotypes namely NERICA L-4, NERICA L-52, SSD 3, and SSD 5 had significant stable performance for grain yield per plant. The rest of the genotypes were not significantly stable for this character.

Table 20: Mean performance and stability parameters for panicle weight and percent filled grains per panicle

Genotypes	Mean of Panicles weight	βi	S²di	Mean % filled Grains /Panicle	βi	S²di
NERICA L-4	2.37	-0.88	-0.02	81.66	-1.8	4.83
NERICA L-8	4.32	3.19	-0.01	80.72	1.08	0.03
NERICA L-52	2.26	-0.35	-0.01	83.67	-1.63	10.69
SUA 1-13-12-3	3.81	2.6	-0.02	81.44	-1.99	10.1
SUPA M 101-22	4.55	-3.2	0	81.33	-1.63	16.7
SUA 2-2-3-1	3.46	-1.36	-0.02	83.88	3.37	2.99
SUPA BC	3.9	4.69	0.08	81.77	1.61	-0.32
SARO 5	4.35	0.02	-0.02	86.77	-1.24	5.38
Mwangaza	4.56	-4.15	0.01	84.66	-1.26	22.58
SUA 12-2-3-2	4.01	1.39	-0.03	78	0.34	18.44
SUA 8-2-2-3	4.2	0.48	-0.01	78.55	-2.47	1.45
Salama M-57	4.34	4.18	0.03	84.22	-1.04	-0.68
SSD 1	4.71	1.37	0.21	82.88	-1.76	16.4
SSD 3	3.25	-3.2	0	82.33	-1.78	-1.46
SSD 5	4.13	3.2	-0.01	76.44	-3.3	-2.13
Kalamata	3.77	-1.76	-0.02	67.55	-0.77	-1.51
Mean	3.87			80.97		
LSD (0.05)	0.43			4.29		

(Bi) = regression co-efficient; S^2di =deviation from regression

Table 21: Mean performance and stability parameters for number of panicles per plant and grain yield per plant.

Genotypes	Mean of Panicles number /Plant	βi	S²di	Mean Grain Yield /Plant	βi	S²di
NERICA L-4	18.43	4.67	3.73	29.33	3.49	1.78
NERICA L-8	18.65	1.52	2.92	45.197	0.34	0.03
NERICA L-52	15.57	0.2	0.68	21.65	3.55	-1.14
SUA 1-13-12-3	13.02	0.47	-0.34	33.067	-5.03	23.89
SUPA M 101-22	9.1	0.5	-0.29	30.75	-0.49	-1.64
SUA 2-2-3-1	11.38	0.43	0.09	24.55	-0.16	-1.4
SUPA BC	11.94	1.03	1.19	33.24	-5.01	1.3
SARO 5	12.74	0.26	1.37	38.56	0.12	-1.63
Mwangaza	8.76	0.5	0.48	40.489	-5.62	25.55
SUA 12-2-3-2	7.28	0.42	-0.04	31.093	9.98	17.86
SUA 8-2-2-3	7.267	0.37	-0.36	9.75	3.09	17.26
Salama M-57	7.411	1.98	0.12	22.53	-1.03	-0.06
SSD 1	8.28	2.29	-0.17	25.202	-1.5	1.49
SSD 3	8.12	1.86	-0.34	20.6	4.9	3.59
SSD 5	9.57	0.62	0.14	26.15	1.38	-1.42
Kalamata	6.022	-0.01	-0.15	21.38	-1.32	-0.98
Mean	10.851			28.974		
LSD (0.05)	1.7			3.63		

(Bi) = regression co-efficient; S^2di =deviation from regression

CHAPTER FIVE

5.0 DISCUSSION

5.1 General

Highly significant genotypic differences which were observed among genotypes for all characters investigated revealed a wide range of genetic variability for all characters studied. Genotypes used in this study were from wide genetic sources, some were locally improved genotypes of Tanzania while others were introductions developed from interspecific hybridization between cultivated rice species, *O. sativa* and *O. glabberima* and a popular local check cultivated in Mwanza region. This could explain the genetic variation which was observed in the materials tested. According to Ovung *et al*. (2012), the presence of large amount of genetic variability might be due to diverse source of material as well as environmental influence. Similar genetic variations have been reported by Akinwale *et al.* (2011) and Singh *et al*. (2011) who observed significant genotypic variation for all characters studied in rice.

5.2 Days to 50% Flowering

Genotypes flowered relatively late at Ukiriguru than at Nansole and Bukindo sites. All genotypes revealed a wide range of variability in relation to days to flowering. The possible cause for differential response of genotypes for this character in varying environments could be due to water stress responsible for delayed flowering. Moisture stress affect physiological processes like transpiration, photosynthesis, respiration and translocation of assimilates in the plant (Turner, 1986). It delays the phenological development of the rice plant such as flowering. The variation in rainfall distribution prior to flowering could be the probable cause attributed to that delay. Days to 50% flowering is controlled by both genetic factors and environmental conditions (Sabouri and Nahvi,

2009). Genotype Mwangaza, Salama M-57, SUA 12-2-3-2, SUA 8-2-2-3 had relatively short duration to flowering. The genotype Mwangaza could possibly be selected for growing in areas with marginal rainfall pattern because of short growth duration and moderate grain yield.

Presence of early maturing genotypes is not only important for rice crop improvement but also for climate mitigation as drought escape mechanism for areas with marginal rainfall pattern. However, early flowering genotypes do not permit production of sufficient assimilates for production of large number of panicles and fully-filled grains and as the result the early maturing genotypes had relatively low grain yield. Variation among genotypes for days to flowering, particularly the medium and late flowering genotypes could be effective selection criteria for areas with bimodal rainfall like Mwanza. Late flowering could be advantageous if genotypes flower near the end of rain season when moisture is sufficient (Kihupi, 1984). The observed significant differences for genotype x environment interaction on days to 50% have been reported in Tanzania (Kihupi, 1984; Kibanda, 2001) and elsewhere (Kang, 2002; Aremu *et al*., 2007; Sreedhar *et al*., 2011).

5.3 Plant Height

Genotypes differed for plant height among the locations with Nansole exhibiting the tallest plants while Bukindo site had relatively taller plants than that of Ukiriguru site. At Nansole site, the area was suitable and well preferred location for growing of these genotypes because the genotypes seemed to be well adapted to this location. This may be due to favourable growing conditions as the location is characterized by good soils and higher monthly rainfalls mean (Appendix 2). Well distributed rainfall throughout the entire growing season probably stimulated vegetative growth resulting in an increase in plant height. Results from this study indicated the importance of selection of short to

intermediate plant height in order to increase grain yield in particular areas. Therefore selection of semi dwarf or intermediate plant type would be advantageous. According to Yoshida (1981) high yield gain in rice varieties with reduced plant height is associated with increase in lodging resistance of rice plant. Similar view was shared by Hairmansis *et al*. (2010).

The observed numeric difference in plant height among genotypes was due to the influence of genotype and genotype x environment interaction. Similar results were obtained by Nassir and Omolayo (2011) who reported plant height as the most important factor underlying the G x E interaction. According to Kibanda (2001) the significant genotype x environment were observed for plant height, panicle length, tillers/m^2 and spikelet fertility when he studied the influence of G x E on yield and grain quality in three ecologies of Morogoro, Tanzania.

5.4 Number of Panicles per Plant and Number Panicles per Square Metre

Just like other characters, the observed variation for number of panicles per plant and number panicles per square metre were due to genotype x environment interaction. Several workers have reported significant genotype x environment interaction on these traits (Nassir and Omolayo, 2011; Rasyad *et al*., 2011). The above traits are the main determinants of rice grain yield. High grain yield is associated with a large number of productive panicles per plant and per unit area. Soil moisture differences between the test sites were the probable cause of variation in number of panicles per plant. The high tillering capacity is considered as a desirable trait in rice production, since number of tillers per plant is closely related to number of panicles per plant. To some extent, yield potential of a rice variety may be characterized by tillering capacity (Wu, 1998). NERICA L-8 consistently yielded highest and had highest number of panicle per plant. The number

of panicle per plant played a major role in determining grain yield and that an increase in number of panicles per rice plant had subsequent effect on grain yield.

5.5 Panicle Weight and 1000 Grain Weight

Genetic variation which was observed for panicle weight and 1000 grain weight among genotypes in this study has also been reported by other workers (Akinwale *et al*., 2011; Osman *et al*., 2012). The revealed genetic variability indicated that the genotypes were genetically diverse and that variations were due to presence of inherent genetic differences among the genotypes. Three sites were composed of varied levels of environmental factors; however genotypes performance across environments did not vary considerably. Genotypes maintained high grain yield through compensatory effect of having large number of panicles per plant, number of filled grains per panicle and high percent filled grains per panicle but with lowered panicle weight and 1000 grain weight. This finding agrees with results reported by Laza *et al*. (2004) who concluded that rice cultivars with large panicles produced fewer tillers and hence fewer panicles than the cultivar with small panicles.

5.6 Panicle Length and Panicle Weight

Observed significant genotypic differences were due to genotype and genotype x environment interaction effects for the trait. Panicle length had a limited influence on the yield of tested genotypes. However, sites varied slightly for moisture levels and temperature regime as well as soil types. Seasonal climatic variables such as high fluctuations of day and night temperatures, changing rainfall patterns and day-length adversely affected panicle length (Yoshida, 1981). These environmental factors possibly contributed to this variation. Apart from panicle length, panicle weight had non significant genotype x environment interaction. The environmental factors had less effect

on panicle weight. In addition, panicle weight showed less importance on grain yield. For instance, genotypes with lowest panicle weight were NERICA L-4 and NERICA L-52, yet they had higher grain yield compared to other genotypes that showed highest panicle weight including SSD1, Mwangaza and SUPA M 101-22. Similar results were earlier reported by Feng *et al*. (2007) who observed similar variations. In this regard, having "heavy panicles" or improvement of panicle weight in rice would not necessarily lead to increase in grain yield due to competition.

5.7 Number of Filled Grains per Panicle and Percent Filled Grain per Panicle

The observed significant genotype x environment interaction for number of filled grains per panicle and percent filled grain per panicle emphasize the importance of these characters in the study. Rice displayed wide genetic variability for number of filled grains per panicle and percentage grain filling. Babu *et al*. (2012) recently reported genetic variation for number of filled grains per panicle. Similarly, Patel *et al*. (2012) reported significant variation for number of grains per panicle in rice. Results from the study revealed that plants with many panicles per plant tend to compensate for too few seeds per panicle. This may be assumed to be due to competition within a panicle. Most genotypes with many panicles per plant had moderate number of grains per panicle. Genotype NERICA L-8 gave highest number of filled grains per panicle. Number of filled grains per panicle contributed positively to grain yield. Genotype SARO 5 indicated the highest percentage of filled grains per panicle. The percentage of filled grains depend on the grain filling rate and grain filling duration of superior and inferior grains. However, Luzi-Kihupi (1998) studied interrelationship between yield and selected characters in rice and revealed that plants with large panicles tend to have high grain filling. The highest number of filled grains per panicle was recorded at Nansole since this site had favourable weather conditions while the lowest was registered at Bukindo.

Variation in moisture levels accounted for the variation in number of filled grains per panicle. Moisture stress had adverse effect on grain filling percentage. Water deficit could result in major reduction in grain dry matter in rice. Water stress was likely to be the possible cause of shortage of assimilates supply due to inhibition of photosynthetic processes (Yoshida, 1981).

5.8 Grain Yield and Grain Yield per Plant

The importance of genotype x environment interaction revealed on grain yield and grain yield per plant was previously reported by Rangare *et al*. (2011). Based on mean grain yield combined over the three locations, genotypes NERICA L-8, SARO 5, SUPA BC and NERICA L-4 are suitable to be selected for grain yield improvement as they had consistently maintained higher grain yield across locations indicating wider adaptability to varying environment. The consistent genotypes performance over varying locations indicated the necessity of growing genotypes with wide adaptability. The stable genotypes minimize farmers' risks associated with unfavourable climatic conditions. However, some extent of genotype x environment interaction observed indicated that some genotypes had specific adaptability to environments. The probable cause for grain yield variation could be due to variation in rainfall distribution among these three sites.

The results emphasize the importance of number of panicles per plant for grain yield improvement. Breeding strategy to improve grain yield per plant should also focus on developing dense panicles or plant with large number of panicles. As previously mentioned, there was reasonable difference in grain yield between the highest yielder, NERICA L-8 and the genotype with the lowest value, Kalamata. Improvement for number of panicles per plant could lead in tremendous increase in grain yield per plant. Wide variability displayed by grain yield might be due to diverse genetic variation of

tested materials. Xing and Zhang (2010) reported that rice varieties display tremendous levels of variation in yield owing to diversity of genetic constitution. Many characters interacted with each other to give grain yield. The variation revealed in individual characters contribution towards yield revealed the genetic divergence in the material. Grain yield per plant and number of panicles per plant were attributed to the major genetic variability among genotypes for grain yield.

5.9 Genetic Components of Variation and Heritability Estimates

From estimated genetic components for growth and agronomic parameters, the phenotypic coefficients of variations (PCV) of yield and yield components were comparatively higher than their corresponding genotypic coefficient of variation (GCV) which emphasises the presence of environmental influence on studied characters. The magnitudes of the genotypic variance (heritable) of these characters were higher than the environmental variance (non heritable), indicating that the genotypic component was the major contributor to total variance. Khan *et al.* (2009); Sadeghi (2011); Ashfaq *et al*. (2010); Osman *et al*. (2012) reported similar results. Similarly, Yadav *et al*. (2008) reported highest GCV for tillers per plant and number of spikelets per panicle. Thus selection of numbers of panicles per plant, percent filled grains per panicle and number of grains per panicle on the basis of the phenotypic value may still be effective.

High broad sense heritability coupled with high genetic gain was exhibited by days to 50% flowering, plant height, number of panicles per plant, 1000 grain weight, number of filled grains per panicle, percent filled grains per panicle. High broad sense heritability values depicted the predominance of non-additive gene action in the expression of these characters and that environmental influence on these characters was reasonably low. This result conforms to the findings of Ahmadikhah (2010) who observed high heritability

coupled with high genetic advance for all character except grain yield and panicle length (Subbaiah, 2011).

From the present study, grain yield and number of panicles per square metre had high broad sense heritability with low expected genetic advance. According to Panse (1957) if a character is governed by non-additive gene action, it may give high heritability but low genetic advance, whereas, if it is governed by additive gene action, high heritability along with high genetic advance provided good scope for further improvement. It is worth to emphasize that a very significant improvement is possible through selection of all these characters with high broad sense heritability coupled with adequate genetic advance. The magnitude of G x E was relatively low for studied characters; this led to high broad sense heritability for most of characters. Kang (2002) reported that the smaller the G x E component, the higher the heritability. Similarly, Kihupi (1984) studied the magnitude of G x E interaction for rice varieties at two sites in Morogoro and observed that genetic variance were higher than G X E interaction for all characters except for number of panicle per plant indicated that most of observed variation were due to genetic cause.

5.10 Correlations Coefficients and Path Analysis

Genotypic correlations were generally higher compared to the corresponding phenotypic correlations. Idris *et al*. (2012) observed similar findings suggesting that relationship were mainly due to genetic causes. In the present study, there was a slight numerical difference in magnitude between simple correlation and correlations at both genotypic and phenotypic levels. Combined analysis and single site correlations had similar pattern of behaviour of characters towards yield. However, panicle length and plant height were negatively correlated with grain yield both at genotypic and phenotypic levels.

Newell and Eberhart (1961) reported that when two characters show negative phenotypic and genotypic correlations it would be difficult to exercise selection for these characters. Yadav *et al*. (2011) shared similar views. Positive and significant correlation of number of panicles per plant with grain yield indicated the importance of this trait in determining grain yield. Selecting number of panicles per plant in rice breeding would result in increased grains yield. The inverse genotypic correlation between plant height and grain yield indicated that higher yields could be realized by breeding short statured plants in these environments. Negative correlation coefficient of plant height with paddy yield indicates that tallness in rice reduces the paddy yield due to high accumulation of photosynthates in vegetative parts as compared to reproductive parts (i.e. seed formation and grain filling) and lodging susceptibility (Yoshida, 1981). Likewise, number of grains per panicle, grain yield per plant, percent filled grain per panicle, panicle per square meter was positively and genotypically correlated with yield. Thus using number of panicles per plant and percent filled grains per panicles as selection criteria for improving grain yield will be effective.

Path analyses results from pooled data over three sites pointed out that number of panicles per plant was the most important character influencing grain yield. Similarly, at each single site analyses the number of panicles per plant constantly remained to be the most important variable influencing grain yield. All selected variables had positive and direct effect on grain yield except 1000 grain weight in combined analysis as well as at Bukindo site. The results from this study revealed that, in order to increase grain yield, more emphasis should be placed on increasing number of panicles per plant. Negligible and negative direct effect of 1000 grain weight on grain yield indicated the trait was less important in influencing grain yield of the tested genotypes. Generally, genotypes differed considerably for number of filled grains per panicle. Many panicles per plant tend to

compensate too few seeds per panicle. This may be assumed to be due to competition within a panicle. The results indicated that most genotypes with many panicles per plant had moderate number of filled grains per panicle. Tillering was importantly increasing panicle density, but it appears that the number of filled grains per panicle decreased when panicle density increased (Tran *et al*., 1999).

5.11 Stability of the Genotypes

To recommend stable cultivars for diverse ecologies in a country like Tanzania, multilocational testing of genotypes provides an opportunity to plant breeders to identify adaptability of genotypes to a particular environment and stability of genotypes over different environments (Sreedhar *et al*., 2011). Therefore, prediction of performance of genotypes based on stability parameters would be feasible and reliable. Results from stability analysis indicated that panicle weight had regression coefficient greater than unity and non significant deviation from regression for genotypes NERICA L-8, SUA 1-13-12-1, SUPA BC, Salama M-57, SSD 1, and SUA 12-2-3-2 suggesting that these genotypes were stable and adapted to favourable environments for that trait. Genotypes NERICA L-4, NERICA L-52, SUPA M101-22, SUA 2-2-3, SARO 5, Mwangaza, SUA 8-2-2-3, SSD 3 and Kalamata had regression significant from unity with non significant deviation from regression suggesting that these genotypes had average stability for suboptimal growing conditions.

Percent filled grain per panicle exhibited wide stability to favourable environments for SUA 2-2-3, SUPA BC, Salama M-57 and SSD 3 while SUA 12-2-3-2 which had stability over poor environment with respect to this character. For number of panicles per plant, all genotypes were stable and widely adapted to either over favourable or unfavourable environments except for SUPA BC which was stable across a wide range of environment

while Kalamata was unstable. Similarly for grain yield per plant NERICA L-4, NERICA L-8, SUPA BC, Salama M-57, SSD 1 and SSD 3 were identified as stably adapted to optimal growing conditions while the rest of the genotypes were unstable for the character. According to Eberhart and Russel (1966) a stable genotype is one with highest mean yield and whose regression coefficient is close to unity (b=1) and deviation from regression close to zero (S^2d). The study revealed that most of the genotypes were stably adapted to either poor or rich environments. Most genotypes registered minimal variance across varying environments. According to Sabaghnia *et al*. (2006) genotypes with minimal variance across different environments are considered stable. Since most genotypes had average stability over high yielding environment, they are responsive to rich growing environment such as application of inputs like fertilizer and irrigation.

CHAPTER SIX

6.0 CONCLUSIONS AND RECOMMENDATIONS

6.1 Conclusions

The study was conducted to assess genotypic and phenotypic variation, interrelations and influence of genotype x environment interaction and stability analysis for yield and yield components among lowland rice genotypes in rainfed lowland conditions in Mwanza region. The analysis of variance results revealed a wide range of genotypic variation existed amongst all genotypes for most of the traits studied. The genotypes tested indicated the richness of genetic diversity available in lowland rice genotypes. All genotypes had significant Genotype x Environment interaction for all characters except 1000 grain weight and panicle weight.

Stability analysis results suggested that most genotypes were stable adapted to either favourable or non favourable growing environments. Grain yield had positive and highly significant correlation with grain yield per plant, number of panicles per plant and percent filled grain per panicle. High heritability and high genetic advance observed for all those characters emphasizes the importance of using grain yield per plant, number of panicles per plant and percent filled grains per panicles as selection criteria for grain yield in early generation testing in plant breeding.

6.2 Recommendations

(i) Genotypes NERICA L-4, NERICA L-8, Salama M-57, SSD 1 and SSD 3 were stable and adaptable to favourable growing environment while NERICA L-52, SUA 1-13-12-3, SUPA M 101-22, SUA 2-2-3-1, SARO 5, SUA 12-2-3-2 and SSD 5 were stable and adapted to poor growing environments. These genotypes could be further tested in order to recommend varieties for specific environments.

(ii) Genotype NERICA L-8 was shown to be high yielding while SUPA BC was found to be stable across three locations therefore further testing of these genotypes is recommended in order to recommend them for wider cultivation in the Lake zone.

(iii) Since Genotype x Environment study was limited to few sites in only one season, it is recommended to test the genotypes in more locations over a number of years in order to partition genotype x environment variance further into genotype x location x year interaction.

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APPENDICES

Appendix 1: Physical and chemical characteristics of the experimental soils at Ukiriguru

Parameter	Value		Methods	Remarks
Soil separates				
Sand	64	68		
Silt	14	12	Hydrometer	
Clay	22	20		
Depth	0-30	30-50		
	Sand	Loam		
Texture	Clay loam	Sand clay		
pH in water (1:2.5)	5.72	6.4	Electrometrical	Slightly acidic
pH in KCL (1:25)	4.9	5.4	Electrometrical	
Organic carbon (%)	1.18	1.51	Walkley and Black	Low
Total N (%)	0.1	0.1	Micro Kjeldhl	Low
C/N ratio	9	8		Medium
Available P Bray 1 (mg/kg)	22.1	19.7	Bray 1	High
K	0.1	0.1	Flame photometer	Low
Ca	7.9	8.7	Atomic absorptionspectrophotometer	Medium
Mg	1.8	2.84	Atomic Absorptionspectrophotometer	High

Remarks according to Landon (1991)

Appendix 2: Physical and chemical characteristics of the experimental soils at Nansole

Parameter	Value		Methods	Remarks
Soil separates				
Sand	62	74		
Silt	11	5	Hydrometer	
Clay	27	21		
Depth	0-30	30-50		
	Loam	Sand		
Texture	sand clay	loam clay		
pH in water (1:2.5)	6.4	5.54	Electrometrical	Slightly acidic
pH in KCL (1:25)	5.4	4.7	Electrometrical	
Organic carbon (%)	1.51	0.69	Walkley and Black	Low
Total N (%)	0.1	0.1	Micro Kjeldhl	Low
C/N ratio	8	8		Medium
Available P Bray 1			Bray 1	
(mg/kg)	10.7	10		medium
K	0.1	0.1	Flame photometer	Low
			Atomic	
Ca	8. 7	6.7	absorptionspectrophotometer	Medium
			Atomic	
Mg	2.84	0.98	Absorptionspectrophotometer	High

Remarks according to Landon (1991)

Appendix 3: Physical and chemical characteristics of the experimental soils at Bukindo.

Parameter	Value		Methods	Remarks
Soil separates				
Sand	24.2	24.1		
Silt	22.1	26.2	Hydrometer	
Clay	53.7	49.7		
Depth	0-30	30-50		
Texture	Clay	Clay		
			Electrometrical	Slightly
pH in water (1:2.5)	6.4	6.2		acidic
pH in KCL (1:25)	4.6	4.3	Electrometrical	
Organic carbon (%)	0.58	0.32	Walkley and Black	Low
Total N (%)	0.1	0.2	Micro Kjeldhl	Low
C/N ratio	8	8		Medium
Available P Bray 1 (mg/kg)	9	9	Bray 1	Medium
K	0.1	0.1	Flame photometer	Low
			Atomic	
Ca	5.5	4.4	absorptionspectrophotometer	Medium
			Atomic	
Mg	1.82	1.78	Absorptionspectrophotometer	medium

Remarks according to Landon (1991)

Appendix 4: Meteorological data for 2011/2012 cropping season at Ukiriguru, Nansole and Bukindo, Mwanza

Year		2011			2012			
Site	Monthly Totals	NOV	DEC	JAN	FEB	MAR	APR	MAY
Ukiriguru	Total rainfall (mm)	124.5	171.9	12.4	44	36.5	192.4	57.9
	Rain days (No.)	10	13	2	4	3	8	6
	Max. air temp (°C)	26.7	27.5	29.7	30.5	30.1	28.2	28.9
	Min. air temp (°C)	18.7	18.6	18.5	18.9	18.9	18.4	18.6
	Relative humidity (%)	77.9	64	66.5	61	62	73	66.5
Nansole	Total rainfall (mm)	243.5	101.9	58.4	46.8	35.8	282.6	200.3
	Rain days (No.)	13	7	3	4	4	9	9
Bukindo	Max. air temp (°C)	26.4	26.9	28.8	29.9	30.1	27.6	27.8
	Min. air temp (°C)	18.5	18.5	18.6	18.7	18.9	18.5	18.6
	Relative humidity (%)	76.5	67.4	64.7	62.2	61	74.5	64.9

Source: Ukiriguru Meteorological station and Ukerewe district council

Appendix 5: ANOVA summary for variance components studied at each location and in combined analysis

SV	DF	FL	PHT	PN	PW	PL	GWT	GNPP	PFGPP	GYPP	GY	PPM
UKIRIGURU												
Replication	2	1.021	2.95	1.343	0.01021	0.6244	0.8827	133.12	24.188	6.112	103009	235.56
Genotype	15	578.11**	1146.69**	41.67**	1.5374**	7.2527**	46.146**	856.99**	88.217**	254.335**	6052349**	25848.48**
Error	30	1.199	11.16	0.9793	0.2976	0.3497	0.49	92.1	9.321	7.618	220311	66.76
Total	47	580.33	1161.24	43.9893	1.9371	8.2268	47.5187	1082.21	121.726	268.065	6375.66	26150.8
NANSOLE												
Replication	2	10.397	0.474	3.911	0.1015	0.0765	1.075	92.42	20.234	0.242	56073	65.81
Genotype	15	598.1**	81.43**	56.497**	1.956**	3.8845**	41.635**	847.01**	1399.635**	163.525**	6585415**	26031.31**
Error	30	6.374	1.807	1.587	0.1759	0.5051	1.811	28.71	4.881	1.185	18053	51.23
Total	47	568.368	83.711	61.995	2.2334	4.4661	44.521	968.14	1424.7	164.952	6659541	26148.35
BUKINDO												
Replication	2	2.646	15.078	0.7807	0.03281	0.0038	11.191	8.9	18.812	7.241	310993	924.9
Genotype	15	560.432**	1262.249**	47.0421**	1.4743**	3.1417**	45.866**	888.97**	46.21**	141.711**	5766125**	21710**
Error	30	5.29	9.839	0.5828	0.01423	0.286	2.965	33.13	6.835	6.997	330336	356
Total	47	568.368	1287.166	48.4056	1.521	3.4315	60.02	931	71.857	155.949	6407454	22990.9
Location	2	2.132	44.427	8.716	0.0676	1.41	2	67.55	12.283	2.065	292815	4818.1
COMBINED ANALYSIS												
Replication	2	2.132	19.724	2.275	0.09252	0.3433	4.542	181.35	1.689	10.489	325911	744.6
Error	4	5.965	9.266	1.88	0.02598	0.18	4.3	26.54	20.892	1.553	72082	240.8
Genotype	15	1721.837	3763.6	140.56	4.7	11.937	128.29	2426.7	177.557	527.963	17317018	72641.4
G x E	30	7.442*	22.486***	2.32**	0.11397	1.17***	2.678	83.13*	19.15***	15.804***	543435***	474.2***
Error	90	4.287	8.628	1.05	0.0733	0.38	1.755	51.31	5.988	5.267	189573	158
Total	143	1741.663	3848.4	154.526	4.98	15.077	139.023	2655.23	235.87	552.652	18414923	78,332