MULT ILOCATION PERFORMANCE EVALUATION OF EXOTIC HYBRID RICE (*Oryza sativa* L.) VARIETIES IN EASTERN ZONE OF TANZANIA

ALOYCE KASMIR

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ABSTRACT

Three exotic hybrid rice genotypes, HEU 022, HEU 188 and HEU 528 from China were tested to evaluate their stability and adaptability in the eastern agronomic zone of Tanzania. Three commonly grown varieties, SUPA, SARO 5 and TXD 88, were used as checks. A Randomized Complete Block Design (RCBD) experiment with three replications was carried out at four locations, ARI-Cholima, ARI-Katrin, Sokoine University of Agriculture (SUA) and Kilangali Rice Seed Farm all located in Morogoro Region during the March to August 2011 cropping season. Seeds were established in a nursery and transplanted to the main plots after 21 days of growth. All rice cultural practices such as weeding, fertilization and irrigation were done according to the site specifications. After harvest, small grain sample were taken for grain quality assessment which was conducted in the Department of Food Science and Technology Laboratory at SUA. The results showed high genetic divergence and phenotypic variability among the hybrids, with the maximum range of variation being on yield components and minimum on grain quality variables. Genotypes x Environment interactions were also high, especially for yield components. Overall, genotypic correlations showed linear positive correlation of grain yield with number of panicles per hill (P), percentage filled grains per panicle (FG) and number of grains per panicle (GP). Plant height (PH) was negatively correlated with grain yield. Grain length (GL) was positively correlated with length: breadth ratio (LBR) and aroma. In general, the tested hybrids exhibited outstanding performance in terms of yield compared to the check varieties at all locations. Grain quality did not differ significantly among the tested varieties, implying that these hybrids could get as good a market demand as the check varieties.

DECLARATION

I Aloyce Kasmir do hereby declare to the senate of Sokoine University of Agriculture that this is my own original work and that it has neither been submitted nor being concurrently submitted for degree award in any other institution.

_____ _____

Aloyce Kasmir Date

The above declaration is confirmed by

_____ _____

Prof. S. Nchimbi-Msolla Date

(Supervisor)

_____ _____

Prof. A.J.P. Tarimo Date

(Supervisor)

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I dedicate this work to my lovely parents, the late Kasmir Aloyce Mark and his beloved wife Adela Mathew Mhange and their descendants, without forgetting my lovely and beautiful wife Saada Aboubakar Kombo.

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LIST OF ABBREVIATIONS

ADB	-	Asian Development Bank
ANOVA	-	Analysis of a variance
ARI	-	Agricultural Research Institute
ASA	-	Agricultural Seed Agency
ASV	-	Alkali spread value
CMS	-	Cytoplasmic male-sterile
DNA	-	Deoxyribonucleic acid
F1	-	First-generation
F2	-	Second-generation
FAO	-	Food and Agriculture Organization
GDP	-	Gross domestic product
G x E	-	Genotype by environment
GEI	-	Genotype-environment interaction
GMOs	-	Genetically modified organisms
HCL	-	Hydrochloric acid
HYVs	-	High yielding varieties
IRRI	-	International Rice Research Institute
KATRIN	-	Kilombero Agricultural Training and Research Institute
KOH	-	Potassium hydroxide
LSD	-	Least significant difference
MAFC	-	Ministry of Agriculture, Food Security and Cooperatives
NaOH	-	Sodium hydroxide
NaCL	-	Sodium chloride

pH	-	Hydrogen ion concentration
QTL	-	Quantitative trait loci
RFLP	-	Restriction fragment length polymorphism
SSRs	-	Simple Sequence Repeats
SUA	-	Sokoine University of Agriculture
UNDP	-	United Nations Development Programme
WARDA	-	West Africa Rice Development Association
WUE	-	Water use efficiency

CHAPTER ONE

1.0 INTRODUCTION

1.1 Background Information

Rice (*Oryza sativa* L.) belongs to the family Poaceae which include annual grasses. It is generally classified into two subspecies, *indica* and *japonica*. Inter-subspecies heterosis has long been attempted, but it is difficult due to unharmonious genetic backgrounds between the two subspecies (Qian *et al.,* 1995, Fan *et al.,* 1999). In crop breeding, the use of hybrid vigour in the first-generation seeds (F1) is well known. However, until about 40 years ago, its application in rice was limited because of the self pollination character of this crop. In 1974, Chinese scientists successfully transferred the male sterility gene from wild rice to create the cytoplasmic genetic male-sterile (CMS) line and hybrid combination (Cheng *et al.,* 2007).

This discovery is believed to be one among very useful scientific achievements in twentieth century as far as crop production is concerned. In pitching the technology, FAO (2004) cites the case of China that was able to feed more than one billion people through its hybrid rice program. The program resulted in an increase in China's national average yield of rice from 3.5 to 6.2 tons per hectare. Hence, this can be an answer to the increasing demand for rice, which is expected to exceed production in many countries in Asia, Africa and Latin America. The use of hybrid rice has revealed better heterosis in unfavorable soil and climatic conditions - such as saline soils and uplands - than in favorable irrigated rice conditions. In Egypt,

hybrid rice performed well in saline conditions, where it yielded 35 percent more than inbred varieties (FAO, 2004).

1.2 Justification

Tanzania is one among many African countries that produce and consume rice as their major staple food but its production is low. The total area is about 1 million km^2, including some offshore islands. It consists of plains along the coast where rice is grown, a large central plateau separating the rift valleys, and highlands in the north and south; three percent of this land is arable. The country's economy is heavily dependent on agriculture, which accounts for 48% of the GDP, provides 85% of exports, and occupies 90% of the workforce (IRRI, 2007). However, apart from having enough land and suitable climatic condition for rice production, its production is still low and account almost non in country's exports irrespective of increased areas of production as illustrated in (Table 1).

Table 1: Rice production and export data

Basic statistics, Tanzania						
	1985	1990	1995	1998	1999	2000
Rice						
Area harvested (ha)	236 540	384 500	477 900	492 306	473 909	503 533
Yield (t/ha)	1.8	1.9	1.5	1.6	1.4	0.8
Production (t)	427 692	740 000	722 700	810 800	676 000	378 562
Rice imports (t)	53 192	34 000	65 000	108 500	46 700	na
Rice exports (t)	0	0	0	14 504	5 000	na
Paddy exports (t)	na	na	na	160	0	na

Source (IRRI 2007) Rice statistics- Info by country- Tanzania

The rice consumption in Africa is growing at 6 percent per year and nearly 50 percent of sub-Saharan rice consumption is imported, mainly from Asia. (Thin, 2010). As a human food, rice continues to gain popularity in many parts of the world where other coarse cereals, such as maize, sorghum and millet, or tubers and roots like potatoes, yams, and cassava have traditionally dominated. On the basis of mean grain yield, the rice crop produces more food energy and protein supply per hectare than wheat and maize. Hence, rice can support more people per unit of land area than the other two staples (Lu and Chang, 1980).

According to Kouassi *et al.* (2005), Africa produces only 2.7% of the world's rice and is the second-largest rice importing region in the world (6.5 Mt in 2003). This amount represents about 25% of the world rice importation (40 Mt). Rice production in Africa, with exception of Egypt, is significantly low (average of 2 t/ha), compared with other continents (Asia 3.8 t/ha, Latin America 3.0 t/ha and United States 7.0 t/ha).

The WARDA (2007) reported that, in the East Africa sub-region, rice consumption grew at a relatively high speed of 2.66% per year. On per capita consumption basis, Madagascar, Comoros and Tanzania noticeably stand out as the major rice-consuming nations in the word (WARDA, 2007). Thin (2010) has noted that some African countries, such as Mozambique and Tanzania, have the potential to bring millions of hectares of land into rice production but the author is also worried about a growing move by richer nations to sign long-term leases on farmland in Africa, aimed at boosting their own food security rather than Africa's. Meanwhile, there are

more than thirty cultivars which are grown throughout the country but their income contribution is very low to compensate the farmer's resources and efforts spent. Rice production needs to be increased to keep pace with the growing population; however, its productivity is affected by several biotic and abiotic stresses. The genetic diversity for these stresses is limited in the current rice cultivars (Nabeela *et al*., 2004). Therefore, genetic variability for agronomic traits is the key component of breeding programmes for broadening the gene pool of rice (Akwinwale *et al*., 2011).

In accordance with Pandey *et al.* (2009), there are only two effective ways to increase the yield potential of crops through plant breeding: morphological improvement and the use of heterosis. However, the potential is very limited when using morphological improvement alone and heterosis breeding will produce undesirable results if it is not combined with morphological improvement. For this, the presence of sufficient amount of genetic variability and diversity in a base population is essential.

In any crop, the germplasm serves as a valuable source of base population and provides scope for wide variability. Information on the nature and degree of genetic divergence would help the plant breeder in choosing the right parents for breeding programme (Vivekanandan and Subramanian, 1993). The crosses between parents with maximum genetic variability are generally the most responsive for genetic improvement (Arunachalam, 1981).

However, according to Zhang *et al.* (2005), a big challenge is the assembling process to combine all of the favorable alleles into a single cultivar and ensure their proper functioning. In this regard, it may be more advantageous to breed for hybrids than conventional pure line cultivars because it may take less effort to have two complementary sets of genes in two parental lines than stacking all of the genes in a single genetic background.

On relying to this fact, the importance of introducing hybrid rice in Tanzania should not only be focused in terms of their high yielding advantage but also to broaden the genetic base of this important crop by introgressing genes from diverse sources, which may be used to improve the quality of our landrace varieties. Therefore, in order to achieve the goal of "Green revolution" by increasing crop productivity as far as rice is concerned, there is a need of using the technology that the major rice producing countries are using and that is the use of hybrid rice. According to Cheng *et al.* (2007), hybrid rice technology has contributed significantly towards food security, environmental protection, and employment opportunities in China for the past 25 years. Hybrid rice with a higher yield advantage over inbred varieties has helped China to produce more than 300 million tones of paddy. Hybrid rice not only has a distinct yield advantage over inbred varieties but also is more responsive to fertilizer and can adapt to varying environments (Jumin *et al.*, 2000).

However, according to Jumin *et al.* (2000) in subsequent evaluation, hybrids need to be tested in replicated trials with a larger plot size. The performance of hybrids may be location specific. Therefore, it is necessary to conduct multilocation trials to

identify hybrids having wide adaptability and those that are specifically adapted to certain locations. Testing the performance of hybrids in farmers' fields along with local check varieties of the region is necessary before these hybrids are released for commercial cultivation.

1.3 Objectives

1.3.1 Overall objective

To identify suitable hybrid rice that would improve productivity and quality of rice in the country.

1.3.2 Specific objective

i. To evaluate hybrid rice varieties for wide and specific adaptability in the eastern zone of Tanzania.

ii. To evaluate grain cooking quality of the introduced hybrids.

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Formation of Hybrid rice

Hybrid rice is the commercial rice crop grown from F1 seeds of a cross between two genetically dissimilar parents. Rice (*Oryza sativa*) is generally classified into two sub-species, *indica* and *japonica*. Inter-subspecies heterosis has long been attempted, but it is difficult due to unharmonious genetic backgrounds between two sub-species (Qian *et al.*, 1995). Currently, hybrid rice technology mainly uses intra-subspecific heterosis, that is, indica x indica and japonica x japonica. Heterosis is a phenomenon in which F1 hybrids derived from diverse parents show superiority over their parents in vigor, yield, panicle size, number of spikelets per panicle, number of productive tillers, etc (Yang *et al.*, 2006, Cheng *et al.*, 2004).

Rice, being a highly selfpollinated crop, requires the use of a male sterility system to develop commercial rice hybrids. Male sterility (genetic or nongenetic) makes the pollen unviable so that rice spikelets are incapable of setting seeds through selfing. A male sterile line is used as a female parent and grown side by side with a pollen parent in an isolated plot to produce a bulk quantity of hybrid seed because of cross pollination with the adjoining fertile pollen parent. The seed set on male sterile plants is the hybrid seed that is used to grow the commercial hybrid crop. (Khush and Brar, 2008, Cheng *et al.*, 2007).

2.2 Importance of Hybrid rice

The need for hybrid rice has been felt because, yield levels of semidwarf varieties of the Green Revolution era have been plateaued, the demand for rice is increasing rapidly with the increase in population, especially in less developed countries, more and more rice has to be produced on less land and with fewer inputs. Hybrid rice varieties have already shown a 15–20% higher yield potential than inbred pureline rice varieties under farmers' field conditions in several countries and they have also shown ability to perform better under adverse conditions of drought and salinity (Cheng *et al.*, 2004).

Over the last decade, Food and Agriculture Organization of United Nations (FAO), the International Rice Research Institute (IRRI), the United Nations Development Programme (UNDP) and the Asian Development Bank (ADB) have provided strong and consistent support to improving national capacity in hybrid rice breeding which led to F1 seed production and research facilities in several countries. In 2001/02, it was estimated that about 800 000 ha of hybrid rice were planted in Bangladesh, India, Indonesia, Myanmar, the Philippines and Vietnam. At present, hybrid rice technology for large-scale production has a yield advantage of 15 to 20 percent, or more than 1 tonne of paddy per hectare, over the best bred varieties. Successful commercial hybrid rice production has enabled China to diversify agricultural production on millions of hectares of land. Although Chinese rice lands steadily decreased from 36.5 million ha in 1975 to 30.5 million ha in 2000 (0.6 percent per year), the country has been able to feed more than 1 billion people and raised her national average yield from 3.5 to 6.2 tonnes/ha (FAO, 2004).

2.3 Challenges of Hybrid rice

Hybrid rice production has been noted to have high production cost. Jumin *et al*. (2000) have found hybrid rice to have not only a distinct yield advantage over inbred varieties but also is more responsive to fertiliser and can adapt to varying environments. However, contrary to these advantages of hybrid rice cultivation, certain disadvantages have also been reported in China and other growing regions such as Bangladesh Muazzam *et al.* (2001) and India (Janaiah and Hossain, 2001). Janaiah (2000) have noted the coefficients for seed and fertilisers were of higher magnitude in case of hybrid rice, indicating that the marginal efficiency of these two inputs was higher for hybrid rice. This clearly shows that yields of hybrid rice respond more to these inputs. Therefore in order for a farmer to achieve full higher yielding advantage of hybrid rice, they should also spend more money to buy seeds and fertilizers.

In some cases, hybrid rice received poor consumer acceptability due to their grain quality (He Guiting and Flinn, 1987). The authors also reported that hybrid rice in China had a 15 per cent yield gain over the inbreeds, but that it got lower prices in the market because of poor grain quality compared with conventional HYVs. Hybrids were also found to have lower yields in Orissa and Tamil Nadu due to pests and disease attack compared with inbred varieties. The exhaustive survey undertaken by Janaiah (2000) in these areas covering 254 farmers spread over five major rice-growing states of India indicated that the pace of hybrid rice adoption is too slow due to many socio-economic factors, thereby affecting its profitability. This study revealed that there are additional costs and risks involved in the cultivation of

hybrid rice varieties compared with inbred varieties. In fact, farmers growing hybrid rice realised a lower net return (of 51 per cent) due to higher cost/tonne of production (21 per cent) and lower market realisation (price) due to its inferior quality perception among consumers and traders. It has been concluded that the higher costs incurred in hybrid rice cultivation are not commensurate with higher yield gains.

In fact, the quantity of seed required for hybrid rice cultivation is comparatively lower than inbred varieties. However, the price per kg of hybrid rice is much higher than that of inbred varieties, besides, they need to purchase seed for each and every cropping season unlike farmers who use varieties who quite often use their own seeds. Janaiah and Hossain (2001) observed the seed cost for hybrid rice cultivation to be three to four times higher than that of conventional varieties.

2.4 Multilocation Yield Trial

Among the objectives of multienvironment yield trials are the establishment of adaptation strategies for breeding programs and definition of domains for cultivar recommendations (Gómez-Becerra *et al*., 2006). According to Jumin *et al*. (2000) the major objective of multilocation yield trials is to identify the hybrids that have a wider adaptability or those that are specifically adapted to a particular location. Gómez-Becerra *et al*. (2006) defined high yield stability as a genotype's ability to perform consistently, whether at high or low yield levels, across a wide range of environments. Multi-environment trials must be established mainly to identify the best cultivars for a location and then determine if locations can be established as

mega-environments (Yan *et al*., 2000). The Multilocation yield trial exercise is essential as hybrids perform differently in different environments, this also provides an opportunity for breeders to see the performance of hybrids bred by them in other locations, even though these hybrids may fail to perform well in the location where they are developed. The concept of multilocation yield trials has really improved the efficiency of rice breeders and this is more so in hybrid rice breeding.

Wang *et al.* (1999) reported that, most economically important traits, such as yield, quality and tolerance to various abiotic stresses (drought, salinity, submergence etc.), are of a quantitative nature. Genetic differences affecting such traits (within and between populations) are controlled by a relatively large number of loci, each of which can make a small positive or negative contribution to the final phenotypic value of the traits. Such loci are termed "quantitative trait loci" (QTL). The genes governing such traits - known as polygenes or minor genes - also follow Mendelian inheritance but are greatly influenced by the environment.

2.5 Genotype by Environment Interactions

The term "GxE interaction" refers to instances where the joint effects of genetic and environmental risk factors are significantly greater (or significantly reduced, in the case of protective factors) than would be predicted from the sum of the separate effects (Baker, 1988). Crossa *et al.* (1991) defined genotype × environment interaction (G × E) as the response of each cultivar to variations in the environment. The phenotype of an individual is affected both by genotype (G) and environment (E). Most agronomically significant characters are inherited quantitatively and are

known to be affected by environmental factors. Selection based on the phenotype would be difficult for such traits (Hittalmani *et al*., 2003).

Genotype by environment (GxE) interactions is almost unanimously considered to be among the major factors limiting response to selection and, in general, the efficiency of breeding programs. GxE interactions become important when the rank of breeding lines changes in different environments. This change in rank has been defined as crossover GxE interaction (Baker, 1988). Roozeboom *et al*. (2008) defined the term environment as the sum of all external conditions affecting cultivar growth and development. Soil texture, pH, depth, organic matter, fertility, diseases, and insects contribute additional variability to the environment.

Experimental evidence from a number of crops in different geographical areas suggests that when different cultivars or breeding lines are tested in a sufficiently large environmental range, GxE interactions of the crossover type are of common occurrence (Baker, 1988). Sultan (2000); and Van Tienderen *et al*. (1996) have noted that, not all genotypes respond similarly to environmental signals, some of them exhibit different performance which is manifested as genotype x environment interaction (G x E). Phenotypic plasticity and GxE are of considerable interest from both ecological and evolutionary genetic perspectives. Hildebrand (1990) and Stroup *et al*. (1993) argued that, in the presence of GxE interactions of crossover type, breeders have traditionally selected lines which were, on the average, the highest yielding, discarding the top yielding lines at either extremes. They defined this breeders' attitude as "negative interpretation of GxE interactions". Such a

negative interpretation of GxE interactions is caused by the search for widely adapted lines to accommodate large scale centralized seed production (Davis, 1990). By contrast, a positive interpretation of GxE interactions as explained by Ceccarelli (1989) and Stroup *et al*. (1993). Ceccarelli (1994) recognizes the importance of specific adaptation and leads to the selection of lines specifically adapted to favorable environments, and of lines specifically adapted to unfavorable environments.

In many countries, before a cultivar is released for production, government authorities usually require at least 3 years of performance tests in different environments. There are two possibilities to develop cultivars with low G×E interaction: subdivide areas in relatively homogeneous regions where cultivars need specific adjustment, or generate high-stability materials adapted to a wide range of environments. The ideal cultivar would be the one with high seed yield and high stability when evaluated across different environments (Yan *et al.,* 2007).

A process of fitting cultivars to an environment instead of altering the environment (by adding fertilizer, water, pesticides, etc.) to fit cultivars has been defined as breeding for sustainability (Coffman and Smith., 1991). On the other hand, genotype stability is important since it indicates if a high-yielding genotype in one environment maintains its relative ranking across environments (Escobar *et al*., 2011). GxE interaction has been done in several cereal crops such as rice, maize and wheat. Broccoli and Burak (2004) working with maize, found significant genotype x environment interaction on yield after evaluating fourteen commercial popcorn

maize hybrids in three locations for two years with the aim of introducing this crop into a region of the Buenos Aires province, Argentina.

2.6 Genetics of Agronomic Traits

Yield is a complex character which mainly depends upon several component characters; direct selection for yield is not effective in rice. Therefore, it is essential to study the variability and association among the yield and its component characters, because these are less variable in environmental change (Nayak, 2008). Lack (2011) describes yield as a function of many factors including plant growth duration, speed, duration and the association of many critical processes during the plant development. It's components do not function independently and an increase in one component can lead to a decrease in another. The research conducted by Jones and Snyder (1987) and also by Miller *et al.* (1991) had revealed that increased number of panicles per unit area was the single most important yield component associated with rice yield; number of spikelets per panicle and percent filled grains per panicle being of secondary and tertiary importance. Kusutani *et al.* (2000) also reported that the genotypes, which produced higher number of effective tillers per hill and higher number of grains per panicle also showed higher grain yield in rice.

Generally, as the number of plants rises, the number of panicles per unit area rises as well, and the increase in the number of seeds per panicle results in a decrease in the weight of each seed. Therefore, a proper yield requires all the components to function harmoniously only with each other, unlike other cereals, rice yield is less likely to improve through increasing the grain size because of the grain growth is

physiologically restricted by the grain crust, and in most areas, the 1000 grain weight of rice is one of the most stable genetic characteristics (Lack, 2011). Grain weight depends on the photosynthetic materials particularly at the earlier stages of grain development and the capability of the growing grain (sink) to use the available assimilate (Modhej *et al*., 2008).

Understanding the kind, amount and heritability of genes influencing a particular trait(s) can be useful in determining the performance of offspring(s) resulting from a cross. Such information is critical in breeding programs where breeder seek to maximize specifically desirable traits like yield components. Based on RFLP map Benmousa *et al*. (2005) identified several QTLs for rice yield components. For total number of grains per panicle, a total of five QTLs were detected in four chromosomes viz; Chromosomes 3, 4, 10 and 11 where the QTL at chromosome 10 was found to cause a negative additive effect.

Zhuang *et al*. (1997) found out that the direction of additive effect of QTLs for related rice agronomic traits were in agreement with the results which suggested that pleiotropism rather than close linkage of different QTLs was the major reasons why QTLs for different traits were frequently detected in the same intervals. Mei *et al*. (2003) suggest that additive gene action is largely independent from non-additive gene action in the genetic control of quantitative traits of rice and that epistasis plays an important role in the genetic control of quantitative trait in rice. Yang *et al.* (2006) also identified a total of 23 and 24 QTLs, which control rice tiller number and plant height respectively, and these QTLs/genes apparently controlled these

traits at different development stages. The author also identified three genomic regions as putatively located QTL that showed opposite additive effects on tiller number and plant height. These findings concluded a possible genetic explanation for the negative correlations between the traits.

2.7 Grain Quality Traits

In rice production, grain quality is an increasingly important factor determining the income of farmers because in many rice growing countries including Tanzania, rice quality is a demand-driven aspect. Therefore, it is essential that newly developed varieties are of high quality. The market value of milled rice is based to a large extent on its physical appearance, aroma and cooking quality.

According to Traore (2005), rice quality is considered the second most important problem following yield although is rarely mentioned in Africa as a constraint. However, even varieties with high yield are rejected by consumers because of their poor cooking and nutritional quality. Amylose content, gelatinization temperature and gel consistency are the important starch properties that influence cooking and eating characteristics of rice (Shy-yong *et al*., 2006). However, historical and socio-cultural factors of a particular region determine what consumers consider as quality rice. In Tanzania for example, long grain and aromatic rice is mostly preferred. Shobha *et al*. (1996) reported that in the Middle East and India long grain and aromatic rice are mostly preferred whereas in the West the aroma is sometimes considered as contaminant. Japan, Australia, Korea, parts of China and Italy prefer soft and sticky rice.

2.8 Genetics of Grain Quality Traits

Amylose content of endosperm starch is an important characteristic of rice in determining eating and cooking quality. Amylose content in rice seed influences the degree of transparency which is a quality parameter of rice preferred by most rice consumers. Rice with very low amylose content (1-2%) are waxy, a characteristic which renders them sticky, firm and not to expand in volume. Intermediate amylose rices (< 30%) cook moist, tender and do not harden after cooking whereas rice with high amylose content (≥ 30) have high expansion volume, are non-sticky and harden after cooking (Rohilla *et al*., 2000).

Amylose content is genetically controlled by a major gene, the *Waxy (Wx)* gene Minoru and Yoshio (1998); Ge *et al*. (2005); Yan *et al*. (2007) and Liu *et al*. (2006). In addition, amylose content is also affected by several modifying genes and environmental factors such as temperature. They also found out that amylose content was affected by a minor and a major gene found on chromosomes 5 and 6 respectively. The major gene is an allele of *we,* and cause 91.9% of the total variation. The authors also suggested that alkali digestion gene *alk* (responsible for gelatinization temperature) should be in the same locus with *wx* gene because QTL analysis indicated a genetic linkage between *wx* and *alk.*

Zhou *et al*. (2003) reported that the waxy region had major effects on the four quality traits, viz; amylose content (AC), gel consistency (GC), gelatinization temperature (GT) and opacity; and these traits were simultaneously improved. Studies conducted by Lanceras *et al*. (2000), Li *et al*. (2003) and Zhang (2007) in

mapping genes of rice cooking and eating qualities revealed that chromosome 6 contains genes that control amylose content, gelatinization temperature and gel consistency.

Slightly different findings were obtained by Shy-yong *et al*. (2006). The authors were working with rice varieties containing the low amylose content and found that chromosome 6 contains QTLs responsible for amylose content and gelatinization temperature and the influence on gel consistency was due to epistatic effect. On the other hand Lin *et al*. (2005) found that amylose content and gel consistency of *japonica* rice were greatly controlled by the genetic main effects from the endosperm, cytoplasmic and maternal plant genes whereas Shi *et al*. (1997) found out that amylose content, gelatinization temperature GT and gel consistency of *indica* rice were affected by endosperm and cytoplasm. Gelatinization temperature is the range of temperature wherein at least 90% of the starch granules swell irreversibly in hot water with loss of crystalinity and birefringence (Dela-Cruz and Khush, 2000). Aroma is an important quality characteristic of high quality rice. The aroma is due to certain chemicals (volatile compounds) present in the endosperm and is influenced by both genetic and environment factors. Rice grown in areas where temperature is cooler during maturity develops more aroma. Goodwin *et al*. (1994) indicated that cultural, harvest and post harvest practices can affect rice aroma. Tufail (1996) crossed aromatic and non-aromatic rices and then test-cross them. The results indicate that aroma is recessive and monogenically inherited. Nakai *et al.* (2003) found out that in cross involving aromatic rice parents, all F1 progenes were aromatic but the F2 segregated into aromatic and non-aromatic

progenies. These results suggest that genes responsible for aroma were non-allelic in the parents.

Sha and Linscombe (2004) concluded that selection for aroma in early generation may slightly reduce the chance of recovering aromatic genotypes but nonetheless it is well compensated by eliminating a majority of non-aromatic ones from later generations. They also added that intracrossing among different aromatic breeding lines has the greatest chance to recover aroma.

On the other hand Loc *et al*. (2006) reported that aroma in rice is a quantitative character and that several genes are involved in the expression of the aroma trait in rice. Similar findings by Amarawathi *et al*. (2007) indicated that aroma is controlled by at least three genes located on chromosomes 3, 4 and 8. Other findings by Louis *et al*. (2005) indicate that the flavor or fragrance of basmati and jasmine rice is associated with the presence of 2-acetyl-1-pyrroline. A recessive gene (*fgr*) on chromosome 8 of rice has been linked to this important trait. Similar findings were also reported by (Dong *et al*. 2001; and Jain *et al*. 2002) indicating that aroma in rice was controlled by the single recessive gene located on chromosome 8. As far as the grain shape is concerned, grain appearance of milled rice is of great importance to consumers. According to Kaul (1970), a length:breadth ratio ranging from 2.5 to 3.0 has been considered widely acceptable as long as the length is more than 6mm.

2.9 Correlations

Yield is a complex character and is collectively influenced by various component characters that are subjected to much environmental variations. The efficiency of selection for yield based on component characters mainly depends upon the direction and magnitude of association between those component characters and yield. The relationship between rice *(Oryza sativa* L.) yield and its components has been studied extensively at the phenotypic level (Akbar *et al*., 1998).

An understanding of the nature and extent of association of the component characters with grain yield and amongst themselves is an essential prerequisite for formulating best breeding programs (Laxuman *et al*., 2011). Selvaraj *et al*. (2011) also insisted that, a complete knowledge on interrelationship of plant character like grain yield with other characters is of paramount importance to the breeder for making improvement in complex quantitative character like grain yield for which direct selection is not much effective.

The correlation between the characters may exist due to various reasons such as pleiotrophy, genetic linkage loci or block of loci governing variability for different characters located on the same chromosomes. The extent of observed relationship between the two characters is known as simple, total or phenotypic correlations. Environmental correlation is the measure of environmental influence on the covariance between the two characters (Laxuman *et al*., 2011). The knowledge of genetic variability, character association i.e. genotypic and phenotypic correlation between yield and its component characters is essential for yield improvement

through selection programe (Fraser and Eaton, 1983). In a hybridization program, understanding of the relationship between yield and its components is of paramount importance for making the best use of these relationships in selection (Sarawgi *et al.,* 1997).

Many quantitative characters are correlated with others. Characters are said to be correlated if they are statistically dependant and have the same or at least approximately conditional distribution shape, but differ in means. A correlated character may therefore be an aid to selection aimed at changing the character with which it is correlated. The degree of relationship between two individuals is measured by the coefficient of relationship i.e correlation coefficient (r) (Johanson and Rendel, 1972). Correlation between two or more positive characters will facilitate the selection because it will be followed by an increase in other properties. Conversely, if a negative correlation, it is difficult to obtain the expected character. If there is no correlation, then the selection becomes ineffective (Angelita *et al*., 2011). Correlation coefficient measures more exactly the closeness of linear relationship (Snedecor and Cochran, 1989). The correlation between two unrelated characters is 0 and correlation between two related characters is such that; $1> r >-1$. Correlation between identical or the same character is equal to 1 and is termed as complete or perfect correlation and the two variates are said to be statistically independent (Finney, 1972). Falconer and Mackay (1996) reported that, the degree of correlation expresses the extent to which the two characters are influenced by the same gene. The nature of the correlation can be either positive or negative. When a gene(s) increase both characters, there is positive correlation whereas a negative

correlation results from the action of gene(s) such that the effect is increasing on character while reducing the other.

However, the correlation coefficient between two characters does not necessarily imply a cause and effect relationship. The inter-relationship could be grasped best if a coefficient could be assigned to each path in the diagram designed to measure the direct influence on it (Selvaraj *et al*., 2011). Partitioning of total correlation into direct and indirect effect by path coefficient analysis helps in making the selection more effective (Priya and Joel, 2009). Plant breeders commonly select for yield components that indirectly increase yield (Gravois and McNew, 1993). Yield component breeding would be most effective if the components involved were highly heritable and positively correlated.

Grain yield has been reported by many authors to be influenced positively by productive tillers, this have been reported by Kumar (1992); Ram (1992); Sundaram and Palanisamy (1994); Rangare *et al*. (2011); Sharma and Choubey (1985); Dhanraj and Jagadish (1987); Prasad *et al*. (1988); Bai *et al*. (1992); Sürek and korkut (1998); Samonte *et al*. (1998); Kalaimani and Kadambavanasundram (1988); and (Vermaa and Srivastava, 2004). Baloch *et al*. (2006) concluded that, among yield components, productive tillers are very important because the final yield is mainly a function of the number of panicles bearing tillers per unit area.

It was also reported by Sarhadi *et al.* (2009) in Afghan native rice cultivar that number of productive tiller was not correlated with total grain per panicle, because

varieties with the largest number of panicles per plant had the lowest number of grains per panicle

Grain yield was also associated positively with 1000 grain weight, this has been observed by Kumar (1992); Mehetre *et al*. (1994); Samonte *et al*. (1998); Surek *et al*. (1998); Mehetre *et al*. (1994); Samonte *et al*. (1998); Sarawgi *et al*. (1997); Sharma and Choubey (1985); Dhanraj and Jagadish (1987); Prasad *et al*. (1988); Sürek and korkut (1998); Prasad *et al*. (2001); Samonte *et al*. (1998); Vermaa and Srivastava (2004); Mirza *et al.* (1992); Kennedy and Rangasamy (1998) and Zheng-jin *et al*. (2006) while Patil and Sarawgi (2005) reported 1000 grain weight to have the highest direct effect on rice yield followed by tillers/plant, percent filled grains per panicle and days to 50% flowering. Khan *et al*. (2009) noted 1000-grains weight was correlated positively and significantly with maximum characters among all characters. The results presented above are in agreement with the findings of Nandan *et al*. (2010) and were also evident by (Bidhan *et al*., 2001).

Number of grains per panicle and percentage filled grains per panicle were also proven to have positive correlation with grain yield by Samonte *et al*. (1998); Vermaa and Srivastava (2004); Sundaram and Palanisamy (1994); Sharma and Choubey (1985); Dhanraj and Jagadish (1987) and (Bai *et al*., 1992). In the study conducted by Angelita *et al*. (2011), grain yield was reported to have positive correlation with all of the characters but not significant, except for plant height. In other case, panicles per plant, panicle length, and grain weight found to have positive but non significant correlation with yield (Ramakrishnan *et al*., 2006).

However the findings of Iftikharuddaula *et al.* (2001); Rangare *et al*. (2011) and Prasad *et al*. (2001) reported grain yield to have negative association with days to maturity and plant height. The results of investigation conducted by Sabesan *et al*. (2009) indicated that, 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. This is also in confirmation with the findings of Radhidevi *et al*. (2002); Najeeb and Wani (2004); Sarkar *et al*. (2007); Anbanandan *et al*. (2009), and (Jayasudha and Sharma, 2010).

On the other hand, several studies have also been done for correlations among grain quality and its components to obtain information about the plant performance traits and their genetic association with one another and existence of some correlation were noted. Environment and some agronomic characteristics of rice such as temperature and flowering time can have significant effect on grain quality. Research conducted by Zhengxun *et al*. (2005) on effect of temperature on physicochemical properties of rice revealed that, with increasing temperature during the filling period, the gelatinization temperature and protein content increased and gel consistency grew long while amylose content decreased. Correlation analysis showed that daily mean temperature during the filling period has a negative correlation with alkali spreading value and amylose content. Mohapatra *et al*. (2006) and Yang *et al*. (2005) demonstrated that spikelets that anthesed earlier produce better quality rice grain. Khatun *et al*. (2003) and Vanaja and Babu (2003) reported a positive correlation between amylose content and gelatinization temperature. However, Chauhan *et al*. (1995) found a negative association between these two

traits. Vanaja and Babu (2003) documented a negative significant correlation between rice grain length and amylose content, absence of correlation between amylose content with grain breadth and length/breadth ratio. Khatun *et al*. (2003); Vanaja and Babu (2003) and Koutroubas, *et al*. (2004) observed a positive significant correlation of rice grain length with the length/breadth ratio and a negative correlation with grain breadth.

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 Materials

In this experiment, three exotic hybrid lines from China: HEU 022, HEU 528 and HEU 188 were tested at four different locations to compare with three commonly grown varieties TXD 88, TXD 306 (Saro 5) and SUPA. The seed of the test materials were obtainted from Agricultural Seed Agency (ASA) office located at Msamvu area in Morogoro municipality.

3.2 Location and Duration

The selected locations are Cholima-research located at latitude of 8°10 ' S and longitude of 37° 33 ' E at an elevation of 396 m a.s.l, with a sand clay soil (Appendix 1). The area has a bimodal rainfall with an average of 1000 mm per annum (Appendix 2). The experiment was also conducted at Kilangali rice seed farm located at latitude of 6°50 ' S and longitude of 36° 40 ' E at an elevation of 491.0 m a.s.l with a sand clay soil (Appendix 1) and a bimodal rainfall with an average of 1559 mm per annum (Appendix 2) in Kilosa district. Another location was Katrin rice research centre- Ifakara in Kilombero district located at latitude of 8° 10 ' S and longitude of 36° 40 ' E at an elevation of 251.0 m a.s.l with a clay soil (Appendix 1) and the area has a bimodal rainfall with an average of 1400 mm per annum (Appendix 2). The fourth location was Sokoine University of Agriculture (SUA) crop museum in Morogoro Municipality; the area is located at latitude of 6° 50 ' S and longitude of 37° 39 ' E at an elevation of 526 m a.s.l with a clay soil (Appendix

1) the location receives a bimodal rainfall with an average of 823 mm per annum (Appendix 2). In all locations, the climate is almost sub-humid tropical grassland with a bimodal rainfall; the long rains start in March and end in May whereas short rains are in December to February. The field experiment was conducted from March to August 2011 whereas the laboratory experiment for grain quality analysis was done at SUA Department of Food Science and Technology Laboratory in October 2011.

3.3 Soil Analysis

Soil samples from all the experimental sites were collected and analysed in the Department of Soil Science laboratory of Sokoine University of Agriculture for pH, exchangeable bases, soil texture, organic carbon, and nitrogen and phosphorus contents (Appendix 1).

3.4 Experimental Design

Experimental materials (Three hybrid and three check varieties) were planted in a randomized complete block design (RCBD) replicated three times in a 5m x 3m sized plots. Direct seeding practice was done at SUA and Cholima sites followed by thinning practice to leave one seedling per hill, however, at Katrin and Kilangali main field were highly flooded following heavy rainfall few days before planting which prevent the direct sowing, therefore transplanting practices were carried out in which 21 days old seedlings were planted at 20 x 20cm spacing interval with one seedling per hill.

3.5 Agronomic Practices

In all locations experimental plots were ploughed and harrowed in February, 2011. With exception of SUA site where plots were constructed in bunds due to nature of its mode of irrigation, which depends mainly in tap water. In the other three locations, plots were laid out on a flat field to allow for surface irrigation using water from the rivers.

In all locations, only fertilizer N in the form of Urea was applied. Application rate depended mainly on the experience of the particular area; at Kilangali, SUA and Cholima sites, a rate of 100 kg N/ha were used while at Katrin it was 80 kg N/ha. In all sites application was done in two splits; at tillering and booting stages.

Hand weeding was done at Kilangali, SUA and Katrin sites whereas at Cholima flooding method was used in which water was left to stay in the field soon after seedling emergence up to few days before harvesting. In terms of irrigation, tap water was used to flood bunded plots at SUA site to supplement rain water, at Kilangali and Katrin sites water from Kilangali and Lumemo rivers, respectively, were used for surface irrigation soon after the rainy season had ended whereas at Cholima site water from Wami river was used to flood the field almost throughout the cropping season (Plate 1).

3.6 Data Collection

Data were collected in two major groups which are grain yield and its related components from the field and grain quality variables in laboratory.

3.6.1 Field experiment

In this category, data for plant height, days to 50% flowering, number of productive tillers per hill (panicles per hill), panicle length, number of grain per panicle, percentage filled grains per panicle, 1000 grain weight and grain yield were collected. For plant height, 10 plants were randomly selected from each plot and measurements were taken using field ruler from soil surface to the tip of the tallest panicle and their results were divided by 10 to obtain an average plant height on that particular plot. From the same plants data for number of productive tillers and panicle length were also taken.

Plate 1: Flooded rice field at Cholima site.

Number of grains per panicle was obtained by counting the threshed grains from 10 randomly selected panicles using an Elmor C1 Seed Counter Machine. Their results were then divided by 10 for an average data. From this result the grains were then winnowed to obtain the number of an empty (unfilled) paddy and their difference

were divided by total number of grain to obtain data for percentage filled grains per panicle.

Grain weight that is 1000 grain weight was obtained by counting 1000 grains from each plot using an Elmor C1 Seed Counter Machine and then their weight was measured using an OHAUS Scount Pro weigh balance MODEL 60-220-502 AT.

Yield data were obtained by first removing plants in 1m of guard rows leaving a $3m^2$ harvest area for plot (Plate: 2). Panicles from this area were cut, threshed and winnowed before taking their weight using an OHAUS Scount Pro weigh balance MODEL 60-220-502 AT. Each time the grain weight was taken, their transformation to 14% moisture condition was also done.

Plate 2: Guard rows removed to leave a $3m^2$ harvest area per plot for yield data at SUA site.

3.6.2 Grain quality variables

Rice samples for quality assessment were obtained from the samples used to estimate grain yield/ha from each plot in all locations.

3.6.2.1 Determination of grain length, breadth and shape

Ten grains of the milled sample randomly picked from each plot were measured by using a vernier caliper for grain length (mm) and breadth (mm) and their means were calculated. Length-breadth was computed by simple arithmetic. Grain length describes the grain size of each genotype, while length-breadth ratio determines the grain shape. Grain size and shape were recorded and assessed according to the scale established by the Standard Evaluation System for rice (Khush *et al*., 1979; IRRI, 2002) (Tables 2 and 3).

Table 2: Rice grain size classification

Grain type		Length (mm)
Extra long	(E)	Over 7.50
Long	(L)	6.61-7.50
Medium	(M)	5.51-6.60
Short	(S)	Less than 5.51

Table 3: Rice grain shape classification

Grain type		Length: breadth ratio
Slender	(S)	Over 3.0
Intermediate	(I)	2.1 - 3.0
Bold	(B)	2.0-or less

3.6.2.2 Chemical qualities

Physicochemical analysis of rice grains were carried out in the Department of Food Science and Technology at the Sokoine University of Agriculture, Morogoro. Three variables were assessed in this category, which were amylose content, gelatinization temperature and aroma. These characteristics were determined according to Jennings *et al*. (1979), Khush *et al*. (1979) and IRRI (2002).

3.6.2.2.1 Gelatinization temperature

Six whole milled grains from each sample of each genotype were randomly selected in triplicates. The samples were then stored in plastic bags, then the grains were removed from the bags and spaced evenly in respective petri dishes. Then 10mls of 1.7% KOH was carefully added to each petri dish containing the kernels. The contents were kept overnight (24hrs) at room temperature. The alkali digestibility was determined by visual observation. Spreading rate was recorded as per numerical scale by the Standard Evaluation System for Rice (IRRI, 2002) (Table 4).

Table 4: Classification of gelatinization temperature

Code	Designation	Alkali digestion	Gelatinization temperature (^{0}C)	Classification
1-2	Not affected but chalky swollen	Low	>74	High
3	Swollen with collar incomplete and narrow	Low or intermediate	-	High or Intermediate
4	Swollen with collar complete and wide	Intermediate	70-74	Intermediate
5	Split or segmented with collar complete and wide	High	-	
6-8	Dispersed merging with collar completely dispersed and cleared		55-69	Low

3.6.2.2.2 Amylose content

This was done on the bases of simplified iodine colorimetric assay technique (Juliano, 1971). Twenty (20) lots of kernels from sample of each plot from all locations were stored in the same room for two days to attain equal moisture content. The samples were separately ground to fine powder using MD cylone mill (400 microns-mesh). Forty mg of potato starch was weighed into 100ml volumetric flask. 4mls of absolute methanol was added carefully and left to stand for 2.5 hours. Then 2.5mls of the methanol was pippeted out. Afterwards, 1.0ml of 95% ethanol and 9mls of 1.0N NaOH was added into the flask. The contents were then heated for ten minutes in a boiling water bath to gelatinize the starch. The samples were then cooled to room temperature and diluted by distilled water to 100ml standard amylose preparation by taking 1, 2, 3, 4 and 5.0mls of the aliquots of purified amylose solution of each standard rice sample solution in 150mls beaker with 50mls distilled water. Then 6.0mls of 0.05N HCl was added and titrated to pH 10.5 of each respective solution. Iodine solution 2.0mls was added to the contents of each beaker and beaker and made up to 100mls with distilled water and allowed to stand for 20 minutes.

The standard samples were read on the calorimeter within 30 minutes at 590nm wavelength against blank test. Transmittance values of purified potato amylase solutions (mg/ml) were plotted against standard rice sample on x20 dilutions. Scoring for amylose content was done according to the Standard Evaluation System for Rice (Juliano and Villareal, 1993 and IRRI, 2002) (Table 6).

Table 5: Classification of amylose content

Amylose type	Amylose content (%)
Waxy	0-2
Very low	3-9
Moderately low	10-14
Low	15-19
Intermediate	20-24
High	25-30

3.6.2.2.3 Aroma

This was done followed the cooking method developed at IRRI in 1971 (Graham, 2002). Five grams of milled rice for each genotype from all locations in three replicates were placed in 50ml test tubes and 20ml of distilled water was added. The tubes were covered by aluminium foil and then cooked in boiling water bath for about 10-15 minutes. The contents were then allowed to cool. Perforations were made on the aluminium foil cover and aroma was detected by a panel of 10 students for each sample. Scent scoring was according to IRRI standard evaluation system for rice (IRRI, 2002) (Table 7).

Table 6: Classification system for aroma (scent)

Scale	Aroma description
1	Non scented (NS)
2	Mild scented (MS)
3	Strongly scented (SS)

3.7 Data Analysis

3.7.1 Analysis of variance

Analysis of variance ANOVA and ANCOVA for single site and combined sites analysis among the traits to find out the differences between genotypes for variability was done using GenStat software 13th edition (SP2) using the procedures of Steel and Torrie (1980): Snedecor and Cochran (1989). Genotypic means were compared pairwisely by means of Fisher's unprotected test.

The ANOVA model for single site analysis was

$$Y_{ij} = \mu + R_j + G_i + E_{(a)} \quad \ldots\ldots\ldots\ldots\ldots\ldots (1)$$

Where

Y_{ij} = the measurement obtained for the unit in i^{th} genotype of the j^{th} replication

μ = experimental mean,

R_j = j^{th} replication,

G_i= i^{th} genotype effect and

E = Error

The statistical model used for combined sites analysis was;

$$Y_{ijl} = \mu + R_j + L_l + E_{(a)} + G_i + GL_{(il)} + E_{(b)} \ldots\ldots\ldots (2)$$

Where

Y_{ijl} = the measurement obtained for the unit in i^{th} genotype of the j^{th} replication of the l^{th} plot

μ = experimental mean

$R_{j(l)}$ = j^{th} replication within l^{th} location effect

L_l = l^{th} location effect

$E_{(a)}$ = Error a

G_i = i^{th} genotype effect

$GL_{(il)}$ = interaction effect of i^{th} genotype effect and l^{th} location

$E_{(b)}$ = Error b

From the analysis of a variance table of single sites (Table 8), phenotypic and genotypic variances were computed using the method adopted by Kaul and Bhan (1974). Then the combined analysis was done following the method outlined by Cochran and Cox (1957). From the analysis of a variance of the combined site the different variance components were calculated using the method prepared by Al-Jibouri *et al*. (1958) (Table 7).

Table 7: ANOVA table used to compute expected mean squares

Source of variation	Degree of freedom	Mean square expectation
Replication	r-1	
Genotype	g-1	$\sigma_e^2 + \sigma_g^2$
Error	(r-1) (g-1)	σ_e^2

Table 8: ANOVA table used to compute expected mean squares for combined sites

Source of variation	Degree of freedom	Mean square expectation
Location	l-1	
Replication	l(r-1)	
Genotype	g-1	$\sigma_e^2 + r\sigma_g^2 gl + rl\ \sigma_g^2$
Genotypes x Environment	(g-1) (l-1)	$\sigma_e^2 + r\sigma_g^2 gn$
Error	l(g-1) (r-1)	e

3.7.2 Correlations

In order to determine the association of the yield and yield components' traits at phenotypic ($\mathbf{r_p}$) and genotypic ($\mathbf{r_g}$) levels, correlation coefficients were computed according to the procedure suggested by Robinson *et al*., (1951) and Al-Jibouri *et al*. (1958) using variance and covariance components. The significance of the correlations was tested by *t*-test, with n-2 degrees of freedom.

$$\text{Phenotypic correlation } r_p = \frac{\sigma^2_p X.Y}{\sqrt{(\sigma^2_p X)(\sigma^2_p Y)}} \quad \ldots\ldots\ldots\ldots\ldots\ldots (3)$$

Where: $\sigma^2_p X.Y$ = phenotypic covariance of two variables (X and Y)

$\sigma^2_p X$ = phenotypic variance of variable X

$\sigma^2_p Y$ = phenotypic variance of variable Y

$$\text{Genotypic correlation } r_p = \frac{\sigma^2_g X.Y}{\sqrt{(\sigma^2_g X)(\sigma^2_g Y)}} \quad \ldots\ldots\ldots\ldots\ldots\ldots (4)$$

Where: $\sigma^2_g X.Y$ = genotypic covariance of two variables (X and Y)

$\sigma^2_g X$ = genotypic variance of variable X

$\sigma^2_g Y$ = genotypic variance of variable Y

CHAPTER FOUR

4.0 RESULTS

4.1 Seedling Emergence and Growth

Germination ability as determined by seedling emergence, was generally good at all locations and varieties with the exceptional of HUE 022, which showed only 80% crop emergence at the SUA and less than 20% at Kilangali, which led to the total abandonment of this hybrid from the experiment (Plate 4) thus remaining with only five (5) varieties to be tested at that site.

Overall growth of varieties was good but there were some differences among locations, Plants at Cholima were more vigorous and greener than those at Katrin, Kilangali or SUA locations. The SUA site was the poorest, especially with regard to plant vigour. This might have been contributed to by low moisture availability due to poor irrigation facilities and removal of top soil during bund construction. (Plate 3).

Plate 3: Rice plants in bunded plots at SUA site

Plate 4: Green patches show the weeds in the plots at which HEU 022 was supposed to be transplanted at Kilangali before harvest.

4.2 Plant Height

The ANOVA for plant height showed highly significant differences among varieties and locations. There were significant differences ($P \leq 0.001$) between the genotypes and plant height at all locations (Appendices 3-7), where the check variety SUPA, showed superiority over all the other varieties and locations, but there was no any variety that maintained its height at all locations (Table 9).

The mean values for individual variety performance at all locations have ranked SUPA as the tallest variety (130.5 cm) and SARO 5 as the shortest (88.1 cm) while all hybrid varieties were found to have intermediate height of 89.4 and 96.2 cm for HEU 528 and HEU 022, respectively. Comparing the sites Cholima had the tallest plants (113.2 cm) while Kilangali was the least (83.6 cm). There was high G x E interaction for this trait (Appendix 7).

Table 9: Mean plant height (cm) of six varieties at four sites in Morogoro Region

Variety	Cholima	Katrin	Kilangali	SUA	Mean
HEU 022	107.1 [b]	90.4 [b]	0.0	91.0 [bc]	96.2
HEU 188	105.5 [bc]	90.8 [b]	78.3 [bc]	85.9 [bc]	90.1
HEU 528	105.4 [bc]	87.9 [b]	77.1 [bc]	87.1 [bc]	89.4
SARO 5	105.8 [bc]	91.0 [b]	72.3 [c]	83.3 [c]	88.1
SUPA	156.4 [a]	127.2 [a]	108.0 [a]	130.3 [a]	130.5
TXD 88	99.8 [c]	94.5 [b]	82.2 [b]	96.9 [b]	93.4
Mean	113.4	96.9	83.6	95.7	
Prob	<.001	<.001	<.001	<.001	
CV (%)	3.0	3.8	4.4	6.5	
LSD (0.05)	6.24	6.71	6.94	11.27	

Means within a column with common letters are not significantly different at 5% level according to Fisher's unprotected test

4.3 Days to 50% Flowering

There were highly significant ($P \leq 0.001$) differences among varieties and locations with regard to days to 50% flowering (Appendices 3-7), in which HEU 022 and SUPA seemed to be the first and second earliest varieties, respectively although there were large variations across locations for the latest flowering variety (Table 10). The varietal mean values for all locations revealed that, HEU 022 was the earliest flowering variety and SARO 5 was the latest flowering one. Hybrids, HEU 188 and HEU 528 were found to have intermediate flowering time at all locations. All varieties were found to flower earlier at Cholima but there were high varietal variations in days to flowering at the other locations. The lowest value was recorded from HUE 022 at Cholima (71 days) while the highest value was recorded from the SARO 5 at Kilangali site (105 days). This trait also exhibited high G x E interaction (Appendix 7).

Table 10: Mean days to 50% flowering of six varieties at four sites in Morogoro Region

Variety	Cholima	Katrin	Kilangali	SUA	Mean
HEU 022	71 [d]	85 [e]	0.0	89 [f]	81
HEU 188	85 [ab]	97 [b]	97 [c]	101 [c]	95
HEU 528	85 [ab]	90 [c]	99 [b]	103 [b]	94
SARO 5	86 [a]	97 [b]	105 [a]	104 [a]	98
SUPA	75 [c]	88 [d]	93 [d]	93 [e]	87
TXD 88	84 [b]	99 [a]	99 [b]	97 [d]	95
Mean	81	93	99	98	
Prob	<.001	<.001	<.001	<.001	
CV (%)	0.8	0.6	0.5	0.3	
LSD	1.13	0.99	0.87	0.62	

Means within a column with common letters are not significantly different at 5% level according to Fisher's unprotected test

4.4 Yield Components and Grain Yield

4.4.1 Number of panicles per hill

Results from Appendices 3-7, on this trait revealed highly significant ($P \leq 0.001$) differences in almost all sites. In general all hybrids seemed to outperform the check varieties at all locations, except SUA where TXD 88 was the best. The variety SUPA had the least number of panicles per hill at all locations (Table 11). Individual varietal mean have ranked hybrid HUE 188 as the leading variety for having high number of panicles per hill whereas Katrin and SUA were sites with high average number of panicles per hill and the lowest value was recorded at Kilangali. The G x E interactions was highly significant in this trait (Appendix 7).

Table 11: Mean number of panicles per hill of six varieties at four sites in Morogoro Region

Variety	Cholima	Katrin	Kilangali	SUA	Mean
HEU 022	12 [b]	14 [b]	0.0	13 [b]	13
HEU 188	13 [a]	15 [a]	14 [a]	13 [b]	14
HEU 528	13 [a]	13 [c]	13 [b]	13 [b]	13
SARO 5	12 [b]	12 [d]	10 [c]	12 [c]	12
SUPA	6 [d]	7 [f]	5 [e]	6 [d]	6
TXD 88	9 [c]	10 [e]	9 [d]	14 [a]	11
Mean	11	12	10	12	
Prob	<.001	<.001	<.001	<.001	
CV (%)	4.6	0.6	0.7	0.9	
LSD	0.93	0.12	0.19	0.19	

Means within a column with common letters are not significantly different at 5% level according to Fisher's unprotected test

4.4.2 Panicle length

In this trait, significant ($P \leq 0.05$) differences were noted at Cholima and SUA at which genotype HEU 188 had the longest panicles followed by SUPA and HEU 258 whereas SARO 5 had shortest panicle at both sites (Appendices 3 and 6). Combined

results for locations revealed that HUE 188 had the longest panicles and TXD 88 had the shortest panicles. Upon location comparison, Cholima had longer panicles whereas Kilangali had the shortest panicles (Table 12). This trait was stable across all location (Appendix 7).

Table 12: Mean panicle length (cm) of six varieties at four sites in Morogoro Region

Variety	Cholima	Katrin	Kilangali	SUA	Mean
HEU 022	26.0 [ab]	22.5	0.0	25.1 [a]	24.5
HEU 188	27.5 [a]	24.1	23.6	25.6 [a]	25.2
HEU 528	27.0 [a]	24.1	23.2	24.7 [a]	24.8
SARO 5	23.9 [c]	22.9	20.9	22.7 [b]	22.6
SUPA	27.0 [a]	23.3	23.2	25.3 [a]	24.7
TXD 88	24.8 [bc]	24.3	22.3	24.6 [a]	24.0
Mean	26.0	23.5	22.6	24.7	
Prob	0.005	0.090	0.053	0.024	
CV (%)	3.6	3.3	4.3	3.6	
LSD	1.71	ns	ns	1.6	

Means within a column with common letters are not significantly different at 5% level according to Fisher's unprotected test

4.4.3 Number of grains per panicle

Results for this trait indicate that significant differences were noted only at Katrin site (Appendix 4), where TXD 88 was found with the highest number of grains while hybrid HEU 022 had the least (Table 13). However, when data were combined, significant differences were noted (Appendix 7). TXD 88 had more grains followed by the three hybrid varieties while SARO 5 had the least number of grains per panicles. In general, Cholima had more number of grains per panicle (165.6) and Kilangali had the least number of grains (116.7) respectively.

Table 13: Mean number of grains per panicle of six varieties at four sites in Morogoro Region

Variety	Cholima	Katrin	Kilangali	SUA	Mean
HEU 022	155.3	126.0 [b]	0.0	126.7	136
HEU 188	168.0	170.0 [a]	131.0	122.3	147.8
HEU 528	175.3	160.7 [a]	118.0	126.7	145.2
SARO 5	172.0	154.3 [a]	98.3	93.3	129.5
SUPA	141.0	155.0 [a]	112.3	118.3	131.7
TXD 88	182.0	172.7 [a]	123.7	132.7	152.8
Mean	165.6	156.4	116.7	120.0	
Prob	0.439	0.044	0.057	0.151	
CV (%)	15.3	9.9	9.6	13.9	
LSD	ns	28.27	ns	ns	

Means within a column with common letters are not significantly different at 5% level according to Fisher's unprotected test

4.4.4 Percentage filled grains per panicle

Results for this trait revealed significant differences among varieties but only at SUA site (Appendices 3-6). Variety performance across locations indicated that hybrid HUE 022 had more percentage filled grains per panicle and SARO 5 had less value (Table 14). When location means where observed, Cholima had the highest mean (82.4%) and the least was recorded at Kilangali (72.4 %). When all locations were pooled together, no significant differences were noted. However G x E interaction was noted (Appendix 7).

Table 14: Mean percentage filled grains per panicle of six varieties at four sites in Morogoro Region

Variety	Cholima	Katrin	Kilangali	SUA	Mean
HEU 022	87.8	77.8	0.0	77.8 [ab]	81.1
HEU 188	80.9	73.6	76.6	68.9 [c]	75.0
HEU 528	84.7	76.4	76.5	72.2 [bc]	77.5
SARO 5	85.5	75.7	64.3	72.8 [abc]	74.6
SUPA	77.5	76.6	71.5	78.2 [ab]	76.0
TXD 88	78.2	71.6	72.9	79.9 [a]	75.7
Mean	82.44	75.3	72.4	74.9	
Prob	0.053	0.200	0.133	0.043	
CV (%)	4.9	3.9	7.7	5.3	
LSD	ns	ns	ns	7.23	

Means within a column with common letters are not significantly different at 5% level according to Fisher's unprotected test

4.4.5 1000 grain weight

The results indicate that Cholima and Kilangali sites did not differ significantly in terms of this trait among varieties (Appendices 3-6). However, significant differences were noted at SUA where genotype HEU 022 had highest 1000 grain weight of all other genotypes (Table 15). At Katrin, 1000 grain weight varied significantly among genotypes. SUPA had the highest 1000 grain weight followed by TXD 88, HEU 528, SARO 5, HEU 022 and HEU 188 in descending order. When the results from sites were combined, hybrid HEU 022 and SUPA had more 1000 grain weights and hybrid HEU 188 had the lowest value. Overall site performance analysis showed that grains from Cholima were heaviest with a grand mean of 48.54g, while SUA had the lightest grains (30.1g). G x E interaction was highly exhibited in this trait (Appendix 7).

Table 15: Mean 1000 grain weight (gm) of six varieties at four sites in Morogoro Region

Variety	Cholima	Katrin	Kilangali	SUA	Mean
HEU 022	50.6	31.0 [b]	0.0	37.1 [a]	39.6
HEU 188	46.3	30.8 [b]	45.0	27.6 [b]	37.4
HEU 528	49.4	32.4 [ab]	45.2	28.1 [b]	38.8
SARO 5	46.9	32.4 [ab]	42.9	29.7 [b]	38.0
SUPA	51.1	34.8 [a]	45.1	29.7 [b]	40.2
TXD 88	46.8	34.2 [a]	41.2	28.2 [b]	37.6
Mean	48.5	32.6	43.9	30.1	
Prob	0.054	0.04	0.083	0.006	
CV (%)	4.2	4.5	4.0	8.0	
LSD	ns	2.64	ns	4.38	

Means within a column with common letters are not significantly different at 5% level according to Fisher's unprotected test

4.4.6 Grain yield per hectare

The ANOVA results for grain yield revealed significant differences within locations except SUA site (Appendices 3-6). Plants at Cholima had higher yields than in the other locations; lowest grain yield was recorded from the SUA site. Overall, all tested hybrids outperformed the check varieties in this parameter at all locations (Table 16).

When results from all sites were pooled, there were no significant differences among the five genotypes (Appendix 7), but they all differed significantly from the genotype SUPA genotype which was the least yielding (Table 16).

Table 16: Means grain yield (t/ha) of six genotypes grown at four sites in Morogoro Region

Variety	Cholima	Katrin	Kilangali	SUA	Mean
HEU 022	6.1 [bc]	5.9 [a]	0.0	4.5	5.5
HEU 188	7.5 [a]	5.6 [a]	6.9 [a]	3.5	5.9
HEU 528	7.1 [ab]	6.6 [a]	6.0 [b]	3.7	5.8
SARO 5	6.9 [ab]	5.6 [a]	5.8 [bc]	3.5	5.4
SUPA	5.2 [c]	4.1 [b]	4.5 [c]	3.5	4.3
TXD 88	6.4 [abc]	5.6 [a]	5.8 [b]	5.1	5.7
Mean	6.5	5.6	5.7	3.9	
Prob	0.028	0.027	0.002	0.466	
CV (%)	10.9	12.7	7.9	29.7	
LSD	1.29	1.29	0.84	ns	

Means within a column with common letters are not significantly different at 5% level according to Fisher's unprotected test

4.5 Correlation Analysis

Genotypic and phenotypic correlations for yield and yield components of rice varieties for combined data over four locations are presented in Table 17. Highly significant and positive genotypic and phenotypic correlations were found between 1000 grain weight ($P \leq 0.01$), number of panicles per hill ($P \leq 0.05$), percentage filled grains per panicle and number of grains per panicles with grain yield, while days to 50% flowering had significant negative phenotypic correlations with yield.

Percentage filled grains per panicle had also significant positive genotypic and phenotypic correlations with 1000 grain weight, and found to had positive significant phenotypic correlations with the number of grains per panicle, panicle

length and plant height. Grain yield significant and negatively correlated with days to 50% flowering.

Positive significant genotypic correlation were also observed between days to 50% flowering with number of panicles per hill, plant height with panicle length and 1000 grain weight with percentage filled grains. Days to 50% flowering had negative but significant correlations with all components except with number of panicles per hill.

Table 17: Genotypic (above) and phenotypic (below) correlations for grain yield and its components for combined sites

Trait		Plant height	50% flowering	Panicles/ hill	Panicle length	No. of grains/ panicle	Percentage Filled grains	1000 grains weight
50% flowering	r_g	-0.465**						
	r_p	-0.662**						
Panicles/hill	r_g	-0.606**	0.237*					
	r_p	-0.468**	0.120					
Panicle length	r_g	0.340**	-0.215	0.103				
	r_p	0.534**	-0.538**	0.141				
No. of grains/panicle	r_g	-0.160	0.149	0.194	0.144			
	r_p	0.265*	-0.456**	0.201	0.483**			
Percentage filled grains	r_g	0.090	-0.413**	0.166	0.140	0.033		
	r_p	0.364**	-0.636**	0.149	0.403**	0.413**		
1000 grains weight	r_g	0.162	-0.557**	-0.290*	0.140	-0.153	0.292*	
	r_p	0.233	-0.487**	-0.284*	0.215	0.015	0.322*	
Grain yield	r_g	-0.332**	-0.134	0.262	-0.135	0.379**	0.314*	0.389**
	r_p	-0.083	-0.335**	0.266*	0.095	0.499**	0.427**	0.416**

*Significant at 0.05 level **Significant at 0.01 level r_g = genotypic correlation r_p = phenotypic correlation

4.6 Grain Quality Variables

4.6.1 Grain length

The ANOVA results for grain length found to have significant different at all sites (Appendices 8-11). Cholima site was revealed to have longest grains in general for almost all variety compared with other sites; SUPA was the leading genotype for longer grains followed all three hybrid varieties and TXD 88 was the least. Shorter grains were found at Kilangali site (Table18). When the results from all four sites were pooled together, the same trend was found in which SUPA variety had the longest grains followed by all three hybrid variety and TXD 88 had the shortest grain.

Table 18: Mean grain length (mm) of six varieties at four sites in Morogoro Region

Variety	Cholima	Katrin	Kilangali	SUA	Mean
HEU 022	7.5 [c]	7.2 [d]	0.0	7.3 [bc]	7.3
HEU 188	7.9 [b]	7.7 [b]	7.5 [a]	7.7 [ab]	7.7
HEU 528	7.7 [bc]	7.5 [bc]	7.4 [a]	7.6 [b]	7.6
SARO 5	7.5 [c]	7.3 [cd]	7.3 [a]	7.2 [c]	7.3
SUPA	8.3 [a]	8.1 [a]	7.6 [a]	8.0 [a]	8.0
TXD 88	6.9 [d]	6.9 [e]	6.8 [b]	7.1 [c]	6.9
Mean	7.6	7.5	7.3	7.5	
Prob	<.001	<.001	0.020	0.003	
CV (%)	2.5	1.6	3.5	2.8	
LSD	0.34	0.22	0.48	0.39	

Means within a column with common letters are not significantly different at 5% level according to Fisher's unprotected test

4.6.2 Grain breadth

The results for this trait show significant different at Katrin, Kilingali and SUA (Appendices 8-11). However, the trend of their dimensions is almost the same in which genotype TXD 88 found to have thicker grains and HEU 528 thinnest in all locations. Same results were also found for the combined data (Table 19). Thicker grains were found at SUA site and Kilangali had thinnest although their differences were very minimal.

Table 19: Mean grain breadth (mm) of six varieties at four sites in Morogoro Region

Variety	Cholima	Katrin	Kilangali	SUA	Mean
HEU 022	2.7	2.7 [ab]	0.0	2.6 [bc]	2.7
HEU 188	2.4	2.4 [bc]	2.2 [c]	2.5 [cd]	2.4
HEU 528	2.4	2.4 [d]	2.3 [c]	2.4 [d]	2.4
SARO 5	2.5	2.5 [bc]	2.4 [b]	2.7 [ab]	2.5
SUPA	2.5	2.5 [bc]	2.5 [b]	2.6 [bc]	2.5
TXD 88	2.7	2.8 [a]	2.8 [a]	2.9 [a]	2.8
Mean	2.5	2.5	2.4	2.6	
Prob	0.058	<.001	<.001	0.002	
CV (%)	5.5	3.9	3.2	3.8	
LSD	ns	0.14	0.15	0.18	

Means within a column with common letters are not significantly different at 5% level according to Fisher's unprotected test

4.6.3 Length to breadth ratio

Results for length:breadth ratio reveal significant differences among varieties at all locations (Appendices 8-11). TXD 88 was found to have smallest value in all locations, the lowest value was noted in TXD 88 (2.5) at Katrin, Kilangali and SUA

while highest value found between HUE 188 (3.4) and Kilangali (Table 20). However, varietal mean values within locations were the same in all locations. Combined results revealed that hybrids HUE 188 and HUE 528 have largest ratio value which indicates that they have more slender grains than the rest (Table 20). Appendix 12 revealed G x E interaction for this trait.

Table 20: Mean Length: breadth ratio of six varieties at four sites in Morogoro Region

Variety	Cholima	Katrin	Kilangali	SUA	Mean
HEU 022	2.8 [cd]	2.7 [c]	0.0	2.8 [b]	2.8
HEU 188	3.3 [a]	3.2 [a]	3.4 [a]	3.2 [a]	3.3
HEU 528	3.3 [ab]	3.2 [a]	3.3 [ab]	3.2 [a]	3.3
SARO 5	3.0 [bc]	3.0 [b]	3.0 [b]	2.7 [bc]	2.9
SUPA	3.3 [ab]	3.2 [a]	3.0 [b]	3.1 [a]	3.2
TXD 88	3.3 [a]	2.5 [d]	2.5 [c]	2.5 [c]	2.7
Mean	3.0	3.0	3.0	2.9	
Prob	0.001	<.001	<.001	<.001	
CV (%)	5.5	2.4	4.5	4.5	
LSD	0.30	0.13	0.26	0.24	

Means within a column with common letters are not significantly different at 5% level according to Fisher's unprotected test

4.6.4 Amylose content

The results for this trait revealed significant differences in almost all four locations although all varieties were found in intermediate and high amylose content category (Appendices 8-11). HEU 022 seems to maintain its low amylose content compared with the rest in all locations while TXD 88 maintains its average high values but surprisingly HEU 528 found to have unstable amylose content by having the lowest 20.25% and highest values 29.56% at SUA and Cholima sites respectively (Table 21). When results from all locations were pooled together, TXD 88 was the leading genotype followed by SARO 5 in a high amylose content category while SUPA,

HEU 188, HEU 528 and HEU 022 fall under intermediate category in descending order (Table 21). Highest value of amylose content was recorded at Cholima and lowest value was observed at SUA site. G x E interaction was highly ($P \leq 0.001$) exhibited in amylose content of tested varieties (Appendix 12).

Table 21: Mean Amylose content of six varieties at four sites in Morogoro Region

Variety	Cholima	Katrin	Kilangali	SUA	Mean
HEU 022	22.4 [f]	21.4 [e]	0.0	20.1 [d]	21.2
HEU 188	28.2 [b]	22.5 [d]	23.8 [d]	22.2 [c]	24.2
HEU 528	29.6 [a]	26.3 [b]	20.5 [e]	20.3 [d]	24.2
SARO 5	27.4 [c]	25.4 [c]	24.3 [c]	23.2 [b]	25.0
SUPA	24.4 [e]	26.8 [a]	26.0 [b]	20.3 [d]	24.4
TXD 88	26.5 [d]	26.2 [b]	26.6 [a]	26.7 [a]	26.5
Mean	26.4	24.8	24.2	22.2	
Prob	<.001	<.001	<.001	<.001	
CV (%)	2.1	0.8	0.2	1.0	
LSD	0.39	0.37	0.09	0.42	

Means within a column with common letters are not significantly different at 5% level according to Fisher's unprotected test

4.6.5 Gelatinization temperature

Gelatinization temperature results have revealed highly significant difference (Appendices 8-11) in all location, hybrid variety HEU 188 maintained its leading position in all four locations, while there were variations of varieties with lower value within locations. Results for combined data also rank HEU 188 and TXD 88 as varieties with highest and lowest values for gelatinization temperature respectively. In general, all varieties were found to be under intermediate and high

category except SUPA at Katrin site where it seemed to be in low gelatinization temperature category (Table 22). Cholima site had the highest gelatinization temperature value than all locations and Kilangali had lowest. G x E interaction noted in this trait was highly significant ($P \leq 0.001$) (Appendix 12).

Table 22: Mean Gelatinization temperature (^{o}C) of six varieties at four sites in Morogoro Region

Variety	Cholima	Katrin	Kilangali	SUA	Mean
HEU 022	73.4 [b]	70.5 [c]	0.0	73.2 [b]	72.4
HEU 188	75.8 [a]	78.6 [a]	77.1 [a]	77.9 [a]	77.4
HEU 528	70.3 [c]	70.5 [c]	71.9 [b]	73.4 [b]	71.5
SARO 5	71.1 [c]	73.5 [b]	70.6 [b]	73.4 [b]	72.2
SUPA	71.2 [c]	57.9 [e]	70.7 [b]	70.6 [c]	67.6
TXD 88	74.2 [b]	64.3 [d]	64.0 [c]	60.8 [d]	65.8
Mean	72.7	69.2	70.86	71.6	
Prob	<.001	<.001	<.001	<.001	
CV (%)	0.7	0.6	2.1	1.9	
LSD	0.96	0.77	2.81	2.43	

Means within a column with common letters are not significantly different at 5% level according to Fisher's unprotected test

4.6.6 Aroma

ANOVA results for aroma revealed high significant ($P \leq 0.001$) differences in all locations (Appendices 8-11). In most cases SUPA variety was found to have high value of aroma and TXD 88 had the lowest value in all locations (Table 23). In general Cholima and Kilangali sites had promisingly good average performance followed Katrin and by finally SUA. When data from all locations were analyzed together; SUPA and TXD 88 were the only genotypes observed to be in scented and non scented categories respectively while all other four varieties were under slightly scented category (Table 23). G x E interaction was also highly noted in his traits (Appendix 12).

Table 23: Mean Aroma of six varieties at four sites in Morogoro Region

Variety	Cholima	Katrin	Kilangali	SUA	Mean
HEU 022	1.6 [f]	2.1 [b]	0.0	1.6 [d]	1.8
HEU 188	2.0 [b]	1.5 [d]	1.7 [c]	2.0 [a]	1.8
HEU 528	1.9 [d]	1.4 [e]	2.3 [a]	1.5 [e]	1.8
SARO 5	2.0 [c]	2.0 [c]	2.0 [b]	1.8 [c]	2.0
SUPA	2.5 [a]	2.4 [a]	2.0 [b]	1.9 [b]	2.2
TXD 88	1.6 [e]	1.4 [e]	1.2 [d]	1.3 [f]	1.4
Mean	1.9	1.8	1.9	1.7	
Prob	<.001	<.001	<.001	<.001	
CV (%)	0.9	0.9	5.0	0.8	
LSD	0.03	0.03	0.18	0.03	

Means within a column with common letters are not significantly different at 5% level according to Fisher's unprotected test

4.7 Correlations for Grain Quality

Genotypic and phenotypic correlation results for combined site was found to have highest values of positive significant correlations for both categories in pairs of grain length with length: breadth ratio followed by aroma with length: width ratio. Five pairs were found to have negative significant correlations in both categories which are grain breadth with length: breadth ratio, gelatinization temperature, grain length and aroma, and gelatinization temperature with amylose content. Pairs between length: breadth ratio and with gelatinization temperature and grain length with aroma had only positive genotypic significant correlation (Table 24).

Table 24: Genotypic (above) and phenotypic (below) correlations for grain quality for combined site

Trait		Grain length	Grain breadth	Length: breadth ratio	Gelatinization temperature	Amylose content
Grain breadth	r_g	-0.369**				
	r_p	-0.348**				
Length: Breadth ratio	r_g	0.770**	-0.873**			
	r_p	0.774**	-0.858**			
Gelatinization temperature	r_g	0.121	-0.444**	0.370**		
	r_p	0.106	-0.429**	0.349		
Amylose content	r_g	-0.135	0.198	-0.197	-0.513**	
	r_p	-0.038	-0.033	0.003	-0.356**	
Aroma	r_g	0.565**	-0.314**	0.497**	0.049	-0.201
	r_p	0.553	-0.254*	0.463**	0.026	0.014

*Significant at 0.05 level **Significant at 0.01 level r_g = genotypic correlation r_p = phenotypic correlation.

CHAPTER FIVE

5.0 DISCUSSION

5.1 Yield and Yield Components

Generally, all tested genotypes exhibited highly significant differences among the studied characters and across the tested environments which indicated differences in the genetic makeup of the materials used. This finding is in agreement with that of Surek and Baser (2003, 2005) who also found that rice genotypes differed significantly for yield component traits. All tested characters performed differently when tested at one site and another, and even when the results from all sites were pooled, significant differences were noted in almost all traits, implying that there were high GxE interactions. The differences in soil types, rainfall amount and distribution, temperatures and altitudes existed among locations, which affected greatly the performance of these traits. This observation is in agreement with that of Sultan (2000) and Van Tienderen *et al*. (1996) who have repoted that, not all genotypes respond similarly to environmental signals, however, is manifested as genotype-environment interaction (GEI). Baker, (1988) also stated that, GxE interactions become important when the rank of breeding lines changes in different environments. This change in rank has been defined as crossover GxE interaction.

The observed highly significant ($P \leq 0.001$) effects of location x genotype interaction for plant height, days to 50% flowering, number of panicles per hill, percentage filled grains per panicle and 1000 grains implies that the influence of genotypes on the performance of these traits depended on locations, and were also

affected by genetic variations existing among studied genotypes and thus indicating the existence of a scope for genetic improvement of the studied genotypes using these traits. On the other hand, highly significant ($P \leq 0.001$) differences between locations and 1000 grains weight and none significant differences amongst the genotypes within locations for this trait implies that the performance of this variable was influenced by locations and that the genotypes were homogeneous for this trait and it might be a stable variable. McDonald *et al.* (2004) in their study of historical evidence for climatic influences on maize observed that, variations in climate are widely recognized as central factors governing the competitive balance in mixed-species plant communities. None significant differences among the genotypes for panicle length, number of grains per panicle and grain yield across environments reveals homogeneity of the studied genotypes on these traits.

According to the results of this study, the genotype HUE 022, was found to be superior on days to 50% flowering, 1000 grains weight, and percentage filled grains per panicle while hybrids HEU 188 and HUE 528 performed very well on number of panicles per hill and number of grains per panicle, although their differences were not significant. All tested hybrids seem to outyield their check counterpart, this might be attributed by their high number of panicles per hill, number of grains per panicle and percentage filled grains. Kusutani *et al.* (2000) reported that the genotypes, which produced higher number of effective tillers per hill and higher number of grains per panicle also showed higher grain yield in rice. Generally, as the number of plants increases, the number of panicles per unit area increases as well, and the increase in the number of seeds per panicle resulted in a decrease in the

weight of individual seeds. The research conducted by Jones and Snyder (1987) and also by Miller *et al.* (1991) revealed that increased number of panicles per unit area was the single most important yield component associated with rice yield; and the number of spikelets per panicle and percent filled grains per panicle being of secondary and tertiary importance as yield components.

Highly significant ($P \leq 0.001$) differences that were observed amongst locations for days to 50% flowering indicate that the locations played a great role in determining the period taken by plants to reach maturity. However, apart from high significant difference for days to 50% flowering noted in all locations, their average means fall under short duration category. According to Khush, (1995) short duration varieties (105-115 days) are excellent in marginal areas because they grow rapidly during the vegetative phase and are thus more competitive with weeds. They reduce weed control costs and utilize less water. Plant traits such as small plants (small leaves and reduced tillering) or short growth duration are associated with low yield potential and high WUE because of reduced water use. In this study, hybrid variety HUE 022 and SUPA were the early flowering varieties; however flowering duration of SUPA is highly controlled by its photoperiodic sensitivity. Upon describing the characteristics of variety SUPA, Luzi-Kihupi and Zakayo (2001) explained that, it had excellent cooking and eating qualities but its yield potential was low. It is too tall and photoperiod sensitive.

In case of individual site performance in terms of grain yield, Cholima was found to have outstanding performance while SUA was the least. These observations could

be attributed to rainfall amount and distributions differences. SUA site had low amount of rainfall and inefficient irrigation facilities while Kilangali had high amount of rainfall (Appendix 1). This rainfall distribution might be one among the strong reasons as to why most genotypes at the SUA site were low in grain yield compared with the other sites. Soil analysis results also revealed very low Phosphorus content than all the other sites which might have also contributed to poor performance of the genotypes (Appendix 2). On the other hand, the Cholima site had more high yielding potential than the Kilangali site despite its high amount of rainfall. This might be due to two major reasons. Firstly, most water from Kilangali rainfall was lost as runoff and ended up in Wami river, which is the major source of irrigation water at Cholima site. Secondly, is the flood irrigation carried out at Cholima, plants at Cholima grew in a flooded field soon after seedling emergence up to their full maturity (Plate 1). This gave them full nutrient uptake and freedom from weed completion. De Datta (1973a) reported that the amount of rainfall received up to the reproductive growth stage was the most important variable contributing to differences in genotypic performance. This period represents the vegetative and panicle initiation growth stages. Ouk *et al.* (2007) has further discussed the contribution of water availability in the lowland rice as an important component of G x E interaction, especially when varieties exhibit differential response to this factor. It has been proven that, paddy grown under flooded fields has high yield potential than under aerobic soil condition. Aerobic rice has been defined by Bouman and Tuong (2001) as high-yielding rice grown under non-flooded conditions in nonpuddled and unsaturated (aerobic) soil. It is responsive to high inputs, can be rainfed or irrigated, and tolerates occasional flooding.

Experimentally, growing the high-yielding lowland rice varieties under aerobic conditions has shown great potential to save water, but with severe yield penalty (Peng and Bouma, 2007). In the early 1970s, De Datta *et al*. (1973a; 1973b) tested the lowland variety IR20 in aerobic soil under furrow irrigation at IRRI. Water saving was 55% compared with flooded conditions, but the yield fell from about 8 t/ha under flooded conditions to 3.4 t/ ha under aerobic conditions. Peng *et al*. (1999) found hybrid rice varieties to have a 9% higher yield potential than inbred varieties with comparable growth duration when grown under flood-irrigated conditions in the tropics.

Over all, the average yield in this study ranged from 7.5 t/ha in HEU 188 at Cholima to 3.5 t/ha in SARO 5 at SUA site. These results were in agreement with those reported by Kihupi *et al*. (1979) at SUA where a highest yield of 7.9 t/ha and lowest yield of 4.4 t/ha were reported.

In this study, the tested genotypes HEU 188 and HEU 528 were found to be superior at all locations over the check varieties although not statistically significant. This implies that, although these two hybrids are exotic materials they have high stability hence can be adopted to a wide range of environments as elaborated by Yan *et al.* (2007). Genotype stability is important since it indicates if it were high-yielding genotype in one environment it maintains its relative ranking across environments (Escobar *et al*., 2011). On the other hand, although hybrid HEU 022 did not maintain its yield performance in tested locations and also exhibited weak seedling emergence at SUA. This hybrid was also completely eliminated from the experiment

at the Kilangali site (Plate 4), due to poor seedling emergence, it was able to maintain its early flowering ability at all tested locations and was second as high yielding genotype at Katrin and SUA sites. It was also found to have high resistance on rice blast disease, second to the check variety TXD 88 at SUA which was the only disease manifested site in the experiment. This finding indicates the need for multilocation evaluation of introduced genotypes because if Kilangali was the only testing site this genotype (HEU 022) could have been completely discarded.

This site selectivity performance exhibited by hybrid HEU 022 describe well the emphasis of Hildebrand (1990) and Stroup *et al*. (1993) towards the importance G x E interactions, the authors argued that, in the presence of GxE interactions of crossover type, breeders have traditionally selected lines which were, on the average, the highest yielding, discarding the top yielding lines at either extremes. They defined this breeders' attitude as "negative interpretation of G x E interactions". By contrast, a positive interpretation of G x E interactions, Ceccarelli (1989); Stroup *et al*. (1993); and Ceccarelli (1994) recognized the importance of specific adaptation, which leads to the selection of lines, specifically adapted to favorable environments, and of lines specifically adapted to unfavorable environments.

5.2 Relationship among Traits

High significant positive genotypic and phenotypic correlations that were found between 1000 grain weight ($P \leq 0.01$), number of panicles per hill ($P \leq 0.05$), percentage filled grains per panicle and number of grains per panicles with grain

yield implied that these traits can be simultaneously improved and that the improvement of these traits would result into grain yield improvement because these traits were significantly and positively associated with grain yield at genotypic and phenotypic levels. The association of grain yield with above mentioned traits has been reported by various authors, number of panicle per hill (Ram 1992); Hairmanisis *et al*. (2010) and (Sundaram and Palanisamy 1994), number of grains per panicles (Sundaram and Palanisamy 1994), percentage filled grains per panicle (Mehetre *et al*. 1994 and Samonte *et al*. 1998) and 1000 grains per panicle (Surek *et al*.1998; Ram 1992; Mehetre *et al*. 1994 and (Samonte *et al*., 1998).

Highly significant positive genotypic and phenotypic correlations between percentage filled grains per panicle with 1000 grains weight, implies that percentage filled grains per panicle and 1000 grain weight can be simultaneously selected for improvement of the studied genotypes and that they can also be used concurrently in improving the genotypes studied. Percentage filled grains per panicle was found to have only positive significant phenotypic correlations with number of grains per panicle, panicle length and plant height. This implies that associations that exist between them are highly affected by external environment rather than genetic composition of the studied varieties.

Highly positive significant genotypic correlation that existed between days to 50% flowering with number of panicles per hill, imply that these traits could be selected together for simultaneous improvement. Highly significant positive genotypic and phenotypic correlations between 1000 grains weight with percentage filled grains as

also evidenced by Patil and Sarawgi (2005) indicates that these traits can be simultaneously selected for improvement of the studied genotypes and can also be used concurrently in improving the genotypes studied.

Significant positive genotypic and phenotypic correlations that existed between plant heights with panicle length imply that these variables can be selected together for improvement of the studied genotypes. Significant negative genotypic and phenotypic correlations between days to 50% flowering with plant height which was also noted by Prasad *et al.* (2001), percentage filled grains per panicle and 1000 grain weight depicts that these variables cannot be selected simultaneously for improvement of the studied genotypes. Significant negative correlations that existed between plant height with number of panicles per hill and grain yield at genotypic and phenotypic levels as also reported earlier by Iftikharuddaula *et al.* (2001) and Prasad *et al.* (2001) suggests that the variables are antagonistic.

The tendency of the same types of the genotypes to exhibit different performance when grown in different locations or same location but in different seasons has been noted in several experiments. Surek and Beser (2003) presented interesting results where the same experiment done in successive years yielded differently. In experiment done in 1995, plant height exhibited negative direct effect in contrast to positive direct effect observed in 1996 results. A reverse result was obtained on panicle length.

5.3 Grain Quality

Results from all four sites revealed significant genotypic variations in all the quality traits studied. However, as far as grain shape is concerned, shape categories of most genotypes were maintained across the locations. Such variation is linked to the differences in the genetic materials used. Grain length and grain breadth were the only grain quality traits which did not show G x E interactions, which implies that they are very stable traits which cannot be affected by external factors rather than genetic makeup.

Rice grain size and shape is critical in breeding new varieties, as each variety must fit an existing market class. All tested genotypes were found to range between medium to slender (2.1- >3 mm) grain shape and long to extra long grain (6.61- >7.5 mm) type which is acceptable in wide range of rice market worldwide including Tanzania. In Tanzania for example, long grain and aromatic rice is mostly preferred. Shobha *et al*. (1996) reported that in the Middle East and India long grain and aromatic rice are mostly preferred.

However, significant ($P \leq 0.05$) effect for location x genotype interaction for grain length:breadth ratio was noted for combined results. According to Kaul (1970), a length:breadth ratio ranging from 2.5 to 3.0 has been considered widely acceptable as long as the length is more than 6mm. This implies that all three exotic hybrid variety used in this study have acceptable grain shape, since they were between 2.7 and 3.3 mm and their grain length is more than 6 mm. Highly significant ($P \leq 0.001$) effect for location x genotype interaction for amylose implies that the influence of

genotypes on the performance of this traits depended on locations, and were also affected by genetic variations existed between studied genotypes and thus implies the existence of a scope for genetic improvement of the studied genotypes using this trait. The influence of locations on performance of the studied genotypes for amylose content was evidenced by lowest value for hybrid variety HUE 022 (20.1) and SUA whereas highest interaction found between HUE 528 (29.6) and Cholima.

According to Juliano and Hicks (1996), in order to meet required functional and sensory properties, rice cultivars are chosen based on specific amylose content because of the strong associations between amylose and desired properties. Since amylose content plays such a pivotal role in the properties of rice, it is used at early stages of breeding programs to select and discard breeding material. On the other hand, the cooking and eating quality of rice has been reported to be dependent on the amylose content (Juliano, 1972) while protein content is the determinent property for rice nutritional quality. All tested materials seems to fall under intermediate (20-24) to high (25-30) amylose type as they range between 20-29 in all locations. This range indicate that all tested genotypes have acceptable amylose content as reported earlier by Anonymous (1997) that rice having 20-25% amylose is highly acceptable as it gives soft and relatively sticky cooked rice. However, the different values for amylose content for the same cultivar have been reported in different publications, and the different methods used for measuring amylose found in different research papers suggest confusion about measuring amylose at the international level. Highly significant ($P \leq 0.001$) effect for location x genotype interaction for gelatinization temperature and aroma implies that the influence of genotypes on the performance

of these traits depended on locations, and was also affected by genetic variations which existed between studied genotypes and thus implies the existence of a scope for genetic improvement of the studied genotypes using these traits.

The influence of locations on performance of the studied genotypes for gelatinization temperature was evidenced by highest value for genotype HUE 188 (78.6) at Katrin whereas the lowest value was observed at Katrini for genotype SUPA (57.9 cm). The influence of locations x genotypes was also noted in aroma, the highest value was found at Cholima for SUPA (2.5) whereas the lowest value was exhibited at Kilangali for TXD 88 (1.2).

In case of aroma, with exception of SUPA genotype which maintains its good scented ability across the locations, genotypes HEU 528, HEU 188, and SARO 5 revealed to have strong variations between non scented and strong scented across the locations while HEU 022 and TXD 88 mainly were under non scented category. These results prove the findings of various authors who stated that the gene controlling aroma in rice is recessive and can be affected by environment. According to Tufail (1996), the aroma in rice is caused by certain chemicals (volatile compounds) present in the endosperm and is influenced by both genetic and environment factors. Rice grown where temperature is cooler during maturity develops more aroma. Goodwin *et al*. (1994) also pointed out that cultural, harvest and post harvest practices can affect rice aroma. Tufail (1996) following the results obtained after crossed aromatic and non-aromatic rices and then test-cross them, concluded that aroma is controlled by recessive gene and monogenically inherited.

Hence, their presence in genotypes should not be guaranteed. However, the results from combined data found that all genotypes with exception of SUPA and TXD 88 which fall under strong scented and non scented respectively, were found to have slightly scented characters. This indicates the market acceptability of all tested hybrids in terms of aroma.

Genotypic and phenotypic correlation results for combined site were found to have highest values of positive significant correlations for both categories in pairs of grain length with length: breadth ratio, this implies that grain length and length:breadth ratio can be simultaneously selected for improvement of the studied genotypes and that they can also be used concurrently in improving the genotypes studied. Khatun *et al*. (2003); Vanaja and Babu (2003) and Koutroubas *et al*. (2004) also observed a positive significant correlation of rice grain length with the length/breadth ratio. Highly significant positive genotypic and phenotypic correlations between length:breadth ratio and positive genotypic correlation between grain length with aroma indicates that as grain length increase length:breadth ratio is also increased and aroma is directly improved. This also implies that these traits can simultaneously be selected for genetic improvement.

Grain length and amylose content was documented by Vanaja and Babu, (2003) to have negative correlation between them which is in agreement with the results from this study. This indicates the difficulties of using them together for genetic improvement of the genotypes used. Pairs between length:breadth ratio with gelatinization temperature and grain length with aroma had only positive genotypic

significant correlation which indicates that they are mainly affected by genetic makeup rather than environment. Highly significant negative correlation in both phenotypic and genotypic correlation for gelatinization temperature with amylose content observed in this study indicates that any effort of reducing gelatinization temperature will also end up in increasing amylose content of the genotypes used. This is in agreement with the findings of Hussain *et al*. (1987) and (Chauhan *et al*., 1995).

Highly significant positive correlation was also revealed between grain length with length:breadth ratio which was also evidenced by Khatun *et al*. (2003); Vanaja and Babu (2003) and Koutroubas *et al*. (2004) indicating the possibility of these traits to be inherited simultaneously for genetic improvement for the studied genotypes. Highly significant negative genotypic and phenotypic correlations between grain length with grain breadth implies that these two traits are antagonistic and hence they can not be used together for genetic improvement. These findings were also witnessed by Khatun *et al*. (2003); Vanaja and Babu (2003) and (Koutroubas *et al*., 2004).

CHAPTER SIX

6.0 CONCLUSIONS AND RECOMMENDATIONS

6.1 Conclusions

Results from this study indicate that, all introduced hybrids have potential characters which can be used to improve rice production in the country. In terms of yield; hybrid HEU 188 and HEU 528 were outstanding in performance at all the four locations compared with the current most acceptable genotypes which were used as check varieties even though their differences were not statistically significant. Apart from the observed unsatisfactory germination performance in some locations, hybrid HEU 022 was found to be promising in terms of high productivity and early flowering observed at Katrin, SUA and Cholima sites. Those hybrids have been proved to have good tillering ability, number of grains per panicle and percentage filled grains per panicle, which contribute positively to grain yield.

Their amylose content, gelatinization temperature, aroma, grain shape and size results were not so different from that of check varieties, which would imply that they could access positive market acceptability the same as that of the check varieties.

The significant genotype x environment interaction observed also clearly points out the necessity of evaluating breeding materials over several environments in order to identify an ideal site. In the present study, although the genotype x environment interaction effect was significant for most of the traits, the magnitudes of the interaction component were generally small in relation to the size of the

corresponding genetic components for most of the traits except number of grains per panicle and grain yield. This indicates that sufficient genetic variability is present in the tested population.

6.2 Recommendations

i. Since the tested hybrids exhibited their yielding superiority over check varieties across various locations, they can be used to increase rice production performance in our country; therefore, I recommend these hybrids to be incorporated in national breeding program for testing and release.

ii. It has been reported that hybrids respond positively to inputs, especially fertilizers. Special attention should be paid in identifying suitable fertilizer rates which could lead to their full exploitation rather than using local recommendation rates as has been bone in this experiment.

iii. As the country is intending to widen rice production as a means of increasing food security, the hybrid technology seem to have a promising answer towards this goal, more hybrid multilocation trials should be conducted in all rice production zones.

iv. Special attention should also be paid on developing hybrid rice varieties using different inbred lines developed within the country.

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APPENDICES

Appendix 1: Monthly rainfall data (mm) for SUA. Cholima, Katrin and Kilangali sites for 2011

Month	J	F	M	A	M	J	J	A	S	O	N	D
SUA	52.8	73.7	135.9	194.2	58.8	5.3	0.4	5.8	45.0	23.2	37.0	191.1
CHOL	98.8	95.8	217.2	213.0	53.9	8.5	0.0	0.0	17.2	27.3	73.1	195.5
KATR	31.1	86.8	351.4	262.2	279.4	11.4	NA	NA	NA	NA	NA	NA
KLNG	169.8	138.1	344.2	403.8	134.9	5.3	0.9	3.2	53.6	25.8	54.7	225.3

Appendix 2: Soil physic-chemical properties for SUA. Cholima, Katrin and Kilangali sites

S/no	pH water	% N	% clay	% silt	% sand	Texture class	mg P/kg	% O.C	ppm Zn	ppm Cu
KATR	5.75	0.17	45	31	24	C	6.425	2.450	0.31	34.79
KLNG	6.11	0.15	47	9	44	SC	6.285	1.516	2.28	28.84
CHOL	6.63	0.13	39	11	50	SC	6.570	1.593	0.91	20.45
SUA	6.05	0.13	49	6.2	44	C	1.685	1.510	0.46	1.43

Appendix 3: ANOVA summary for investigated yield and yield component at Cholima site

Source of Variation	df	Plant height	50% flowering	Panicles/ hill	Panicle length	Grains/ panicle	%age filled grains	1000 grain weight	Grain yield
Replication	2	61.52	0.15	0.17	2.93	231.7	37.90	3.44	0.27
Genotypes	5	1354.35***	130.36***	5.10***	6.07**	672.6	52.52	13.51	2.08**
Error	10	11.78	0.38	0.48	0.88	638.0	16.12	2.04	0.51
LSD (5%)		6.24	1.13	1.26	1.71	45.95	7.30	3.72	1.30
CV (%)		3.0	0.8	8.7	3.6	15.3	4.9	4.2	10.9

,* = Significant at 1% and 0.1% probability levels respectively.

Appendix 4: ANOVA summary for investigated yield and yield component at Katrin site

Source of Variation	df	Plant height	50% flowering	Tillers/ hill	Panicle length	Grains/ panicle	%age filled grains	1000 grain weight	Grain yield
Replication	2	11.10	1.40	0.72	0.67	261.1	22.46	22.51	0.23
Genotypes	5	670.85***	102.49***	7.18***	1.55	838.9**	15.44	38.37	2.08
Error	10	13.62	0.30	1.34	0.59	241.4	8.56	2.41	0.50
$LSD_{(5\%)}$		6.71	0.99	2.11	1.39	28.27	5.32	4.38	1.29
$CV_{(\%)}$		3.8	0.6	13.5	3.3	9.9	3.9	8.0	12.7

,* = Significant at 1% and 0.1% probability levels respectively.

Appendix 5: ANOVA summary for investigated yield and yield component at Kilangali site

Source of Variation	df	Plant height	50% flowering	Tillers/ hill	Panicle length	Grains/ panicle	%age filled grains	1000 grain weight	Grain yield
Replication	2	33.03	0.16	0.28	1.58	496.1	98.37	1.21	2.16
Genotypes	4	596.01***	52.83***	10.14**	3.56	458.3	75.63	9.65	2.41**
Error	8	13.59	0.21	0.82	0.95	126.2	31.15	3.15	0.20
LSD (5%)		6.94	0.87	1.71	1.84	21.15	10.51	3.34	0.84
CV (%)		4.4	0.5	12.0	4.3	9.6	7.7	4.0	7.9

,* = Significant at 1% and 0.1% probability levels respectively.

Appendix 6: ANOVA summary for investigated yield and yield component at SUA site

Source of Variation	df	Plant height	50% flowering	Tillers/ hill	Panicle length	Grains/ panicle	%age filled grains	1000 grain weight	Grain yield
Replication	2	0.34**	0.39	1.85	2.89	27.2	6.70	2.64	1.53
Genotypes	5	923.75***	108.87***	11.86***	3.32**	581.2	55.21	7.99	1.39
Error	10	38.38	0.11	0.49	0.78	278.4	15.77	2.11	1.40
LSD (5%)		11.27	0.62	1.28	1.60	30.35	7.25	2.64	2.15
CV (%)		6.5	0.3	8.0	3.6	13.9	5.3	4.5	29.7

,* = Significant at 1% and 0.1% probability levels respectively.

Appendix 7: ANOVA summary for investigated yield and yield component for Combined sites

Source of Variation	df	Plant height	50% flowering	Panicles/ hill	Panicle length	Grain/ panicle	%age Filled grains	1000 Grain weight	Grain yield
Location	3	2689.63***	1169.76***	5.78***	38.88***	11222.2***	336.00***	1409.55***	20.17***
Replication	2	46.85	0.3759	1.78	2.57	178.9	19.83	5.83	0.13
Genotype	5	3197.64***	286.83***	24.22***	10.03***	1218.5**	32.18	22.78***	4.23***
Genotype x Environment	15	76.04***	32.38***	2.60***	1.25	413.6	50.50**	14.94***	4.23
Error	46	18.80	0.28	0.74	0.89	310.0	20.54	4.22***	0.73
$LSD_{(5\%)}$		7.13	0.88	1.41	1.55	12.6	5.9	3.38	1.40
$CV_{(\%)}$		4.5	0.6	10.5	3.9	28.94	7.449	5.3	15.8

Appendix 8: ANOVA summary for investigated grain quality variable at Cholima site

Source of Variation	df	Grain length	Grain breadth	Length Breadth ratio	Gelatinization temperature	Amylose content	Aroma
Replication	2	0.033	0.002	0.003	0.212	0.004	0.0002
Genotypes	5	0.644***	0.060	0.273***	13.512***	20.158***	0.324***
Error	10	0.035	0.019	0.028	0.279	0.047	0.0003
LSD (5%)		0.342	0.252	0.304	0.960	0.393	0.033
CV (%)		2.5	5.5	5.5	0.7	0.8	0.9

Appendix 9: ANOVA summary for investigated grain quality variable at Katrin site

Source of Variation	df	Grain length	Grain breadth	Length Breadth ratio	Gelatinization temperature	Amylose content	Aroma
Replication	2	0.016	0.0005	0.005	0.222	0.017	0.0001
Genotypes	5	0.531***	0.061***	0.239***	156.547***	15.107***	0.485***
Error	10	0.015	0.005	0.005	0.181	0.042	0.0003
LSD (5%)		0.220	0.135	0.128	0.773	0.372	0.0298
CV (%)		1.6	2.9	2.4	0.6	0.8	0.9

Appendix 10: ANOVA summary for investigated grain quality variable at Kilangali site

Source of Variation	df	Grain length	Grain breadth	Length Breadth ratio	Gelatinization temperature	Amylose content	Aroma
Replication	2	0.013	0.0004	0.0007	4.395	0.0024	0.0092
Genotypes	4	0.356*	0.1350***	0.3864***	65.374***	17.101***	0.4904
Error	8	0.065	0.0060	0.0185	2.233	0.0022	0.0088
LSD (5%)		0.480	0.1468	0.2561	2.813	0.0884	0.1764
CV (%)		3.5	3.2	4.5	2.1	0.2	5.0

Appendix 11: ANOVA summary for investigated grain quality variable at SUA site

Source of Variation	df	Grain length	Grain breadth	Length Breadth ratio	Gelatinization temperature	Amylose content	Aroma
Replication	2	0.060	0.00004	0.0061	1.941	0.0094	0.0007
Genotypes	5	0.358**	0.08593**	0.2508***	99.539***	19.485***	0.2048***
Error	10	0.045	0.00997	0.0171	1.787	0.0517	0.0002
LSD (5%)		0.387	0.1817	0.2384	2.432	0.4139	0.0255
CV (%)		2.8	3.8	4.5	1.9	1.0	0.8

Appendix 12: ANOVA summary for investigated grain quality variable for combined sites

Source of Variation	df	Grain length	Grain breadth	Length Breadth ratio	Gelatinization temperature	Amylose content	Aroma
Location	3	0.290***	0.0731***	0.0730**	37.189***	55.904***	0.143***
Replication	2	0.004	0.0012	0.0020	2.122	0.013	0.004
Genotype	5	1.677***	0.2826***	0.9823***	194.504***	24.962***	0.778***
Genotype x Environment	15	0.047	0.0110	0.0301**	42.464***	14.490***	0.2096***
Error	46	0.037	0.0086	0.0147	1.079	0.032	0.002
$LSD_{(5\%)}$		0.317	0.1528	0.1989	1.707	0.293	0.073
$CV_{(\%)}$		2.6	3.7	4.1	1.5	0.7	2.4