EFFECT OF GENOTYPE X ENVIRONMENT INTERACTIONS ON YIELD AND GRAIN QUALITIES OF RICE (*Oryza sativa*, L.) IN MOROGORO REGION

BY

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A DISSERTATION SUBMITTED IN PARTIAL FULFILMENT OF THE REQUIREMENTS FOR THE DEGREE OF MASTER OF SCIENCE IN AGRICULTURE OF SOKOINE UNIVERSITY

2001

ABSTRACT

Three experiments were conducted in the 1999/2000 season at Lumemo (rainfed lowland), Tanganyika Agricultural Cooperation (TAC) (irrigated) and Sokoine University of Agriculture (SUA) Farm (upland). The aim of the study was to determine the relative contributions of the newly obtained genotypes, environments and their interaction to the variations of grain yield, yield components and grain quality characteristics. Ten genotypes obtained from SUA and Kilombero Agricultural Training and Research Institute (KATRIN) were used in the experiments which were laid down in a Randomized Complete Block Design (RCBD) with three replications. The plot size was 4m x2m in which the plants were spaced at 20cm x 20cm. Data collected included the agronomic and grain quality characteristics, which were subjected to the analysis of variance, Correlation, Path coefficient and Stability analyses. The analysis of variance revealed that there were significant variations in the genotypes tested for most of the traits tested. Although there was significant genotype x environment interactions for most of the traits tested, early maturing lines SSD1, SSD3 and SSD5 performed better in all three environments. However, the late maturing genotypes performed better under supplementary irrigation at TAC. The results from correlation and path coefficient analyses revealed that the number of panicles/plant and percent spikelet fertility could be important characters that influence grain yield. Since these two characters also showed high heritability estimates, they could be used as indirect selection criteria for grain yield during early generations of rice breeding. Similarly for grain quality, estimates of heritability and genetic advance were high for gel consistency.

From the results of this study, it can be provisionally concluded that early maturing genotypes may be grown in all three ecosystems in Morogoro region, while the late maturing genotypes are suitable in irrigated conditions or under rainfed with supplemental irrigation. Based on the overall performance and grain quality analysis, lines SSD1, SSD3 and SSD5 can be recommended for further evaluation in farmers fields.

DECLARATION

I, Nkori John Maregesi Kibanda do hereby declare to the Senate of the Sokoine University of Agriculture that this dissertation is my own original work and that it has neither been submitted nor being concurrently submitted for a degree award in any other Institution.

Signature.....

Date.....18.10.2001.....

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ACKNOWLEDGEMENT

I wish to acknowledge the TARP II of the Ministry of Agriculture and Food Security for providing financial assistance for my study.

I am greatly indebted to my supervisor, Dr. Luzi-Kihupi, A. for kindly accepting to supervise this study and for allowing me to draw upon her experience. Her patience, guidance, encouragement, diligence, brilliance advice and constructive criticism have enabled me to complete this study. Heartfelt and sincere appreciation is extended to Dr. Nchimbi-Msolla, S. for her concern during statistical analysis and reading the manuscript. Special appreciation are extended to my officer In charge, Dr. Mbapila, J.C. for his encouragement, care and support to my experimental plots.

Sincere thanks should go to course instructors for their course coverage whose contributions built a strong foundation and bearing to this study. I wish to thank other staff of Crop Science Department, in particular Professor Reuben, S.O.W.M., Dr. Misangu, R.N., Dr. Rwamugira, R. P. for their valuable encouragement and assistance in academics. I would like to express appreciation to Mr. Mwanjabe, A., Crop Science departmental field officer and Mr. Mkuya M. of the KATRIN institute for supervising and taking care of my experiments while I was away.

My appreciation would not be complete without mentioning the departmental secretarial staff, M/s Janeth, W. and Mrs. Ngetti, A. for their secretarial services.

I extend my heartfelt thanks to my parents whose wishful prayers made my stay at SUA hopeful.

Thanks are due to classmates, Letayo, E.A., Wanjara, R. M., Mlay, M.M., Kamwela, D.S. and Tesha, P. for their enjoyable company at SUA. However, the friendly companies from Mrosso, L., Banwo, O.O., Mhille, O.M., Mtwaenzi, H.H., Kakema, T.P. Zakayo, A. and Kashina, B. are hereby appreciated.

DEDICATION

To my parents, Maregesi Kibanda and Asteria Bhabuhae for sending me to school.

To my wife Rose Paul Maganga; my children, Asteria, Lucy and Emmanuel for their love, moral support and endurance, during my study leave.

TABLE OF CONTENTS

CHAPTER THREE

CHAPTER FIVE

CHAPTER SIX

LIST OF TABLES

Table **Page**

LIST OF APPENDICES

LIST OF ACRONYMS

AC	Amylose content
Al	Aluminium element
ARI	Agricultural Research Institute
^0C	Celsius centigrade
Ca	Calcium element
CO_2	Carbon dioxide gas
cm	Centimetre
Cu	Copper element
df	Degrees of Freedom
EMS	Error Mean Square
FAO	Food and Agricultural Organization of the United Nations.
Fe	Iron element
g	Gram
GC	Gel Consistency
GT	Gelatinization Temperature
IITA	International Institute of Tropical Agriculture
1N	One normality
IRRI	International Rice Research Institute
KATRIN	Kilombero Agricultural Training and Research Institute
kg	Kilogram
KI	Potassium Iodide

M	Mutant
MAC	Ministry of Agriculture and Cooperative
mm	Milimetre
Mn	Manganese element
Mo	Molybdenum element
MSTAT-C	Michigan State University Computer Software
N	Nitrogen element
NaOH	Sodium Hydoxide
nm	Nanometre
P	Phosphorous element
P≤	Statistical significance
P>	Non statistical significance
RCBD	Randomized Complete Block Design
Si	Silicon element
SSD	Single Seed Discent
SUA	Sokoine University of Agriculture
t/ha	Tons/hectare
TAC	Tanganyika Agricultural Cooperative
TARP II	Tanzania Agricultural Research Project Phase Two
TXD	Tanzania Cross Dakawa
USA	United States of America
Zn	Zinc element

CHAPTER ONE

1.0 INTRODUCTION:

Rice [*Oryza sativa* (L.)] belongs to the genus *Oryza* under the family *Gramineae.* The genus has at least 20 *species* of which *Oryza sativa* L. and *O.glaberrima* Steud. are the only cultivated species (Matsuo *et al.*, 1997). It is an important staple food crop that feeds over 51% of the world's population (Nguyen and Tran, 1998). The crop ranks second only after wheat in terms of nutrition (Grist, 1986), area of cultivation and production (FAO, 1997). More than 90% of the world rice supply is produced and consumed in Asia (IRRI, 1992a). Rice is also grown in the USA, Latin America, Mediterranean countries and Africa. It is estimated that an annual increase of 1.3 million tons of rice is necessary to meet the growing rice-eating world population (Grist, 1986).

From 1988/91 to 1997, Africa's rice area increased from 4.3-5% and 2.5-2.9% of the world's rice production. Rice yields rather decreased from 1.8-1.5t/ha in the same period (FAO, 1997a). Besides the slight increase in rice yield and production, the continent has remained one of the major rice importers in the world. In the period of 1988-1996, imports steadily increased from 2.6-4.1million tons (FAO, 1997b).

In Tanzania, rice has increasingly been an important staple food second to maize (Kihupi, 1984). The crop is grown in all regions of the country with varied levels of importance (Kanyeka, 1994). The country is, however, ranked second largest rice producer and consumer after Madagascar in East and Central Africa (Ching'ang'a,

1985). Rice production, area under rice cultivation and yields seemed to be equally constant throughout 1991/92-1996/97. Exceptional higher yield was noted in the season 1992/1993 (MAC, 1998). From the estimated harvestable area of 478 thousand hectares, the average yield was 1.56t/ha (FAO, 1997a). This yield is too low compared to that of Bangladesh (4.6 t/ha), Japan (6.4 t/ha), Korea (6.6 t/ha), USA (6.3 t/ha), and Indonesia (5.8 t/ha) (Yap, 1992 cited by Hossain, 1999). Consequently, just like other countries with food shortage Tanzania has constantly been importing rice from outside to offset the deficit. Since mid 1970s the country imported 60000 metric tons in 1994 and 65,000 metric tons of rice in 1996, depicting the rise of rice imports by 7.7% (FAO, 1996). Reasons for the heavy rice imports in Africa are not different from those in Tanzania. Kanyeka *et al.* (1994) documented that the rapid increase of rice demand in Tanzania in the last three decades, is associated with the increase in total population and changes in traditional food eating habits fuelled by rapid urbanization

Major rice producing regions in Tanzania are Mbeya, Shinyanga, Morogoro, Mwanza and Tabora regions. Morogoro region has been ranked second producer after Shinyanga for the past five years. The importance of Morogoro region as one of the largest rice producers is attributed to the existence of the large-scale rice farms and the numerous small-scale irrigation schemes. Morogoro region produced an average of 105 thousand metric tons from an estimated average area of 60 thousand hectares; with yields ranging between 1.36 t/ha - 2 t/ha (MAC, 1998).

The frequent fluctuation in rice production in Tanzania, and Morogoro region in particular has, however, been the main feature (MAC, 1998). Several authors have

outlined constraints that are responsible for fluctuation and even to steady declining levels in rice production in Tanzania (Ching'ang'a, 1985; Kihupi and Pillai, 1989; and Kanyeka, 1994). They include weeds, insects, diseases, and lack of improved varieties with acceptable qualities. Others were inadequate land preparation, inadequate soil and water management. With exception of desirable varieties with acceptable grain qualities, the rest of constraints greatly reduce the genotypic performance in different ways.

Among the above constraints, inadequate water and its management were relatively observed to affect rice crop performance more than the rest of constraints. O'Toole, (1982) noted that water is the predominant ecological factor affecting growth and yield of rice. The hydrological conditions interact strongly with edarphic, biotic, agronomic and other climatic factors. The variability of these interactive effects across and within locations and seasons illustrate the potential complexity of rice growing environments.

Morogoro region consists of three major growing ecosystems; namely upland, irrigated and upland. Each ecosystem has its own potential in rice production. However upland ecosystem produces the least while irrigated gives the most abundant rice production due to the their differential amount of water and the associated management.

From 1983 the National Rice Research Program relaunched a project for improving the undesirable agronomic traits of the traditional varieties. In Tanzania, grain quality appears to rank second to yield in importance. In local markets, the acceptable rice

grain qualities that fetch premium prices constitute the long, slender translucent grains that are highly aromatic; non sticky and fluffy cooking with intermediate amylose content and soft gel consistency (Kihupi, 1984).

In this way yield and grain quality were given priority in the project implementation. Using various breeding methods a number of progenies with different yields and grain qualities have consecutively been selected (Katrin, 1995 and 1996). In order to specify their performance and adaptation over a wide range of rice growing environments (ecosystems), the need to study the effect of genotype and environments and their interaction on yield and grain qualities becomes necessary.

Several studies on genotype x environment interaction on rice yield and to some extent on quality characteristics have been conducted elsewhere (Chartterjee and Maiti 1985; Oyedokun, 1985 and Kulkarni *et al.*, 1988). Limited work on G x E interactions have been done in Tanzania for rice yield and yield components under rainfed lowland and irrigated ecosystems (Kihupi and Doto, 1989). There is no information available on g x e interaction on grain qualities in Tanzania under upland growing environments. The experiments, which have been conducted in the country, are insufficient and not representative of all the available genotypes under the existing environmental conditions. Since new and promising breeding materials are still coming out, it is therefore necessary to test and evaluate them in the country's rice growing environments; upland, irrigated and rainfed lowland rice ecosystems. This will assist in selecting and recommending them on the bases of their yield performance and grain qualities across the existing ecosystems.

The present study is therefore, aimed at the following objectives:

1.1 Overall Objective

To investigate the response of the new breeding genotypes on the varying rice growing environments (upland and lowland conditions) and their interaction on yield and grain qualities of rice.

1.1.1 Specific Objectives:

i) To determine the relative contribution of newly obtained breeding genotypes, environments and their interactions on grain yield, yield components and quality characteristics.

ii) To evaluate the response and stability of the above said genotypes under the three different rice growing varied environments

iii) To determine the association between variables and study the path coefficient analysis of various components, their effects, and the contribution to grain yield.

CHAPTER TWO

2.0 LITERATURE REVIEW:

2.1 Origin and distribution.

2.1.1 Origin.

Rice is an ancient cultivated crop in the world. Through selections, it was later established under a variety of habitats before any organized sea borne expeditions (Carpenter, 1978). There are two cultivated species: *Oryza sativa* L and *O. glaberrima* Steud. The origin of *O. glaberrima* Steud was documented to be in West Africa (Porteres 1956 as cited by IITA, 1984). It was first grown in the Central Niger with other centres of diversity in Gambia, Casamance and Sokoto basins (Grist, 1986). In East Africa Carpenter (1978) also identified it in Zanzibar. *Oryza sativa* L., the common cultivated rice in the world has its origin in Asia, particularly in the South East Asia.

2.1.2 Distribution

Although the origin of *O. glaberrima* Steud was documented to be in West Africa, Carpenter (1978) did not clearly indicate its distribution from the centre of origin to Zanzibar. There are several postulations for the distribution of *O. sativa* L. from its center of origin. It is believed that *O. sativa* L. was probably introduced in Africa first in Madagascar by Malayo-Polynesia travellers from Java along the Southeast trade monsoon winds. Another route was from Asia into East Africa by the Sri-Lanka and India via Oman and then Northeast trade to Somalia and Zanzibar (Grist, 1986).

Three routes to Tropical West Africa were postulated. Porteres (1956 cited by IITA 1984) suggested that rice introduction to West Africa came from East Africa and/ or Asia into Senegal, Guinea-Bissau and Sierra Leone at around 1500AD. Nayar (1973) also suggested that Asian rice was introduced by Berbers across the Sahara soon after it was introduced in Egypt between the 9^{th}-10^{th}century AD. Carpenter (1978) further hypothesized that Asian rice was introduced into West Africa along the routes i.e. Zaire, Cameroon, Nigeria and Ghana. Since *O. sativa* L. was introduced in West Africa, *O. glaberrima* Steud was replaced by *O. sativa* L. from the 15^{th}century onwards (IITA, 1984).

2. 2 Taxonomy, Adaptation and Ecology.

2.2.1 Taxonomy.

The genus *Oryza* is classified under the tribe *Oryzae*, subfamily *Oryzoideae*, of the grass family *Poaceae (Gramineae)*. The genus has two cultivated species (*Oryza sativa* L. and *O. glaberrima* Steud.) and more than twenty wild species distributed throughout the tropics and subtropics (Lu, 1999). The genus was first described by Linnaeus, (1753) who recognized only one species; the *O. sativa* L. Within two centuries more than 100 species that were published by different authors (Voughan, 1959) arose great complexity to the genus (Lu, 1999). Many workers employed various criteria in attempting to serially classify the genus *Oryza.* (Chaterjee 1948; Sampath 1962; Sharma and Shastry 1965; Chang 1985; Wang *et al.*, 1992; Matsuo *et al.*, 1997 and Lu, 1999).

In every classification made there were persistent morphological, cytological and molecular variations among and between wild species of the same classification group and genome. Since there is no single classification system that has been generally accepted worldwide, Lu (1999) also proposed a taxonomic treatment to accomplish classification by considering all the deficiencies that were earlier encountered. The proposed taxonomic system intends to group up the species into three sections suggested by Sharma and Shastry (1965) but with certain modifications. They are Sect. Padia (with 3 series and 6 species); Sect. Oryza (3 series and 17 species) and Sect. Brachyantha (1 series and 1 species). This indicates that classification of the genus *Oryza* is still incomplete.

2.2.2 Adaptation.

It is not clear whether the cultivated species evolved from the wild or vice versa, and hence to their ecological adaptations (Grist, 1986). The fact that rice is a widely adapted crop, its ability is associated to the wide inherent genetic variations in the population of its progenitor, the evolutionary processes and the environments under which rice was subjected. The ancestors of *Oryza sativa* L.; the perennis and that of *O.glaberrima* Steud; the breviligulata form two series: perennis-sativa and breviligulata-glaberrima (Morishima, 1984). While the former is constituted with both annual and perennial forms; and characterized with wider genetic variations in the population, the latter only appears in annual form with narrow genetic base. Subsequently, the perennis-sativa have more intergrades than the other from which Japonica, Indica and Javanica groups originated.

Each of these groups has specific eco-regional adaptations as is to their rice varieties (Watanabe, 1997). In addition, Oka and Chang (1962) reported that adaptation was, a result of evolutionary process, under exposed certain environmental conditions. They also added that cultivation and breeding were only responsible to facilitate the adaptation advancement. As rice cultivation started long ago, rice plants in adverse environments had developed adaptive mechanisms either in physiological or morphological adjustments to suit the changing growing conditions (O'Toole, 1982). It is from this fact that there is rice, which is adapted to rainfed lowland, upland, deep wetland, tidal; be it toxic or non-toxic ecosystems (IRRI, 1992b).

2.2.3 Ecology

Though rice possesses roots of a dryland plant it can flourish in all types of soils with differential moisture (water) and fertility status. It may perform well under a wide range of climates extending from wet tropical to regions of semi-arid warm temperate climates (Grist, 1986). The existence of various varieties under these cosmopolitan growing conditions is a reflection of sufficient supply of basic requirements for the crop growth and development. Studies at IITA (1984) indicated that rice might perform in almost any conditions provided there is sufficient sunshine and water requirement for a particular variety. In addition to sunshine and water, soil fertility is also important for optimum performance of the rice crop (De Datta, 1981). Physical and chemical characteristics of the soil can deny nutritional elements from being absorbed by the plant. According to IITA (1984) physical characteristics of the soil could be unimportant if there would be sufficient moisture regime.

The redox potential and pH are among the important soil chemical factors affecting soil elements availability for plant uptake; and therefore they have direct bearing in determining and evaluating the fertility status and management of rice soils (Gupta and O'Toole, 1986).

Most rice soils have a range of pH 6.5-7.5; but the most suitable for most nutrient availability and less toxicity is pH 6.5 (Patrick and Reddy, 1978). Research conducted by Ponnamperuma (1978) indicated the possibility of increasing the availability of P, Si, and Mo; as well as the reduction in possible toxicities of Al, Mn, Fe, CO_2, organic acids; and the increased microbial release of nutrients when acid soils increase to near pH 6.5. Similarly IITA (1984) noted an increased availability of P, Ca, Fe, Mn, Cu, and Zn as alkaline soils were reduced to near pH 6.5 value.

Most of the zones of lowland rice soils have redox potential varying from +200mV to -300mV. The potential of upper few millimeters of the soil is higher ranging from 300mV to 500mV indicating oxidized layer (Ponnamperuma, 1972). In the absence of molecular oxygen (low redox potential) other compounds or elements are changed from oxidized to reduced forms and become unavailable. In contrast to upland conditions, lowland rice soils that are relatively richer in fertility status have variable redox potential. Ponnamperuma (1978) documented an increased availability of N, Si, Mn, Mo, and reduced availability of S, Cu, and Zn by lowering the redox potential to a range of +200mV to -300mV.

2.3 Economic importance and uses of Rice.

2.3.1 Economic importance of Rice.

The ancient Indian name of rice "dhana" meaning "Sustainer of the human race" indicates its age-old importance. To date rice is becoming an increasingly important staple food crop that feeds over 51% of the world's population (Nguyen and Tran, 1998). The crop ranks second only after wheat in terms of nutrition (Grist, 1986) and in area of cultivation and production (FAO, 1997). More than 90% of the world's supply is produced and consumed in Asia. In Africa rice is a strategic component food security and a crucial element in the staple food economies of several African countries (Zan *et al.*, 1984). The ever- increasing imports of rice in Africa, and Tanzania in particular reflect its growing importance as staple food in many African societies.

2.3.2 Uses of Rice.

Rice is basically grown for its grain. Various rices with different amylose-amylopectin ratios are used in specific rice products and grain in different regions of the world. Milled rice is mainly used as food. Its starch may be used for brewing. Waxy rices are also used for sweets, desserts and salad dressings. In Tanzania rice flour is mainly used for buns, brewing and bread making while broken rice is used for 'chapati.' Rice husks are for livestock bedding, farm mulching, and source of fuel. The intermediate amylose rices are used largely for fermented rice cakes in the Philippines and in canned soups in the United Stated of America. Rice straw and rice hulls are used as fertilizers. Bran and polish, and bran oil and other products provide

good quality proteins, source of vitamin B; and are rich in phytin, silica, dietary fibre, trypsin inhibitor and lectin (Juliano, 1985).

2.4. Effect of climatic conditions

Rice produced in areas between 49°N to 35°S, encompass a wide range of climatic and soil conditions. Regardless of the water supply and nutrients, genotypes vary greatly in their response to different climatic factors at various stages. Physiological variability in plant characters affected by these factors may limit rice varieties to adapt in a wide range of environments. The climatic factors that affect adaptability of rice varieties are temperature, solar radiation, rainfall (precipitation) and daylength.

2.4.1. Temperature

Yoshida (1978, 1973) found a temperature range of 25-35°C as optimum to most rice growth stages except at germination (18-40°C). Vergara (1976) noted that extreme temperatures outside the optimum critical values resulted into failure of seeds to germinate, delayed seeding to emergence, growth stunting, leaf discoloration, delayed and irregular flowering, incomplete panicle exertion, high spikelet sterility and irregular maturity. The critical low and high temperatures, normally below 20°C and above 30°C vary from one growth stage to another. Among the growth stages, Yoshida (1981) recorded optimum temperature for rice tillering (25-31°C), anthesis (30-33°C), and ripening (20-25°C). Low temperature ranges for initiation of panicle premordia (15°C) panicle differentiation (15-20°C) and its high critical temperature

(38°C) was also highlighted. However, these critical temperatures differ according to variety, duration of critical temperature, diurnal changes and physiological status.

Mandal and Chartterjee (1984) observed high reduction in the number of tillers per square meter at lower temperatures 13-20^{0}C under both cyclic and continuous submergence water. Other studies have indicated that fertility percentage is determined from young panicle initiation to flowering stage; and that lower temperatures (17-19^{0}C), usually below 20^{0}C after fertilization and grain filling disrupts translocation of photoassimilates (Choudhury and Ghildayal, 1970 and Matsushima, 1980). Sterility percentage depends on the variety, growth stage at which the rice plant is exposed and period of exposure to low temperature extremes. Apparently, Satake (1969) obtained sterility percentage after subjecting rice plant to temperatures below 20^{0}C at about reduction division stage. Also, varietal response was noted to such temperature differences. However, differences in day and night temperatures have counteracting effect. Yoshida (1981) reported that temperatures as low as 12^{0}C will not induce sterility if they last for 2 days, but will induce about 100% sterility if they last for 6 days at flowering.

Incomplete panicle exertion was, however, the outcome of low temperature after flowering (Vergara, 1976); and moisture stress (O'Toole and Namuco, 1983). Later, Yoshida (1981) indicated the significance of temperature on weight per grain; despite the 1000- grain weight of a variety being constant under different environments and cultural practices. Murata (1976) showed that 1000- grain weight of the test variety

varied from about 24 g when exposed to mean temperature 22^{0}C for 3 weeks after heading, and 21g at mean temperature of 28^{0}C in the same period in Japan. In the tropics where solar radiation is high, a daily mean temperature as high as 29^{0}C was not considered important.

A controlled experiment indicated that the optimum daily mean temperatures for grain filling range from 19-25^{0}C for IR20, an indica rice, and from 16-22^{0}C for Fujisaka 5, a japonica rice. This was suggested that indica varieties are better adapted to high temperatures while japonica rice required low temperature at ripening.

Differences in response to low temperature inducing sterility were found existing among varieties (Sasaki and Wada, 1973), whereas susceptible varieties Yukara and Shinei suffered about 80-100% spikelet sterility. Varietal differences also existed in high temperatures that exceeded 35^{0}C at anthesis usually in dry season crop. At 35^{0}C, N22, an upland rice variety from India, had greater than 80% spikelet fertility whereas BKN 6624-44-2, a lowland selection from Thailand, has about 10% spikelet sterility.

2.4.2. Wind

Observations made by Vergara (1976) indicated that strong winds were able to desiccate leaves and panicles, and give severe lodging ending up in giving high spikelet sterility percentage. Wind was able to cause shattering to some rice plants.

2.4.3 Solar radiation

This important environmental factor affects general adaptability and may pose limitation to a wide range of geographic adaptation of the genotype. Photosensitivity characteristics have been linked with maturity period. Observation by Chang and Vergara (1972) indicated that photoperiod insensitive varieties contrasted with late varieties as they do not have long growth duration and are not adaptable to deep-water areas. Apparently, early maturing and photoperiod insensitive genotypes permit year – round multiple cropping.

Solar radiation is responsible for photosynthesis and its requirements differ from one growth stage to another. The greatest effect of solar radiation on grain yield is at productive stage followed by ripening stage. It has been established that grain yields obtained during wet season are lower than those in the dry season. It is reasoned that in the wet season there is lower level of solar radiation received during the crop grain filling and ripening stages than is during dry season (De Datta, 1981 and Yoshida, 1981). Earlier observations made by Stansel (1975) revealed that solar radiation was becoming critical at panicle initiation until 10 days before maturity. Vergara (1976) noted that inadequate solar radiation could increase unfilled grains. The optimum requirement of 12-14 hours solar radiation was adequate to photoperiod sensitive cultivars to flower (Mackill *et al.*, 1996). To address this production constraint, breeding for insensitive to daylength becomes necessary.

2.4.4. Rainfall.

Variability in the amount and distribution of rainfall especially for rainfed rice which constitutes over 70% of rice grown in Tanzania is the most important factor limiting rice production (De Datta, 1981). Moisture stress environments have been exhaustively studied (Vergara, 1976; De Datta, 1981; O'Toole, 1982; O'Toole and De Datta, 1986 and Mackill *et al.*, 1996). According to O'Toole and De Datta, (1986), water deficit is among the factors contributing to low and unstable yields in rainfed lowland rice.

De Datta (1981) reported insufficient moisture regime at reproductive and ripening stages; and high relative humidity (90%) being responsible for yield reduction.

The effect of rainfall on grain yield depends on the duration and the stage of growth of rice. Shortage of rainfall at flowering can dramatically reduce rice yield by increasing the number of unfilled spikelets; and the effects on spikelet setting are irreversible (Hsiano, 1982). However, water deficit followed by crop recovery during vegetative growth had little or no effect on rice yield (Aragon *et al.* 1987). Ohashi *et al.* (2000) reported that water stress decreased biomass production, assimilate rates and export of assimilates. Plant height was found to be reduced in drought condition as a result of decreased gas exchange, nutrient uptake and its transportation, reduced photosynthesis and translocation of photoassimilates to different plant parts (O'Toole and Baldia, 1982).

Rice varieties differ in their panicle weights and 1000 grain weight but appreciable variations are more when moisture stress occurs in the late vegetative to milk stages. Although rice varieties vary in their panicle and 1000 grain weights, they become seriously susceptible when subjected to moisture stress environments from panicle initiation to near heading stage (Matsushima, 1980 and Nallathambi and Robinson, 1992). Mandal and Chatterjee (1984) also noted reduced number of filled grains per panicle due to moisture stress. On the other hand, Cruz *et al.* (1986) observed a reduction in rice growth, leaf area index and yield with vegetative phase water deficit. But results obtained by O'Toole and Padilla (1984) using two levels of water deficit imposed for 19 days during vegetative growth indicated to reduce grain yield by 15-27%. These contradictory results were concluded to be due to difference in water table depth in the midseason that influenced soil drying and consequently affected grain yield

2.5 Rice ecosystems

Rice is a semi-aquatic crop and within species/varieties, there exist differential moisture requirements for growth and development. By this phenomenon, rice cultivars have adapted differently across the growing environments (ecosystems). Worldwide rice environments are widely and variably classified dependent on moisture regime or topography. In Asia, rice environments are classified into irrigated, rainfed lowland, upland, deep wetland and tidal ecosystem (IRRI, 1992). In Africa, Buddenhagen (1978 and 1985) classified rice ecosystems and their respective enclosed subdivisions as: upland (dryland and hydromorphic), inland swamp (non-

toxic and toxic), flooded (riverine shallow, riverine deep, boliland/ dambos and mangrove/tidal swamp) and irrigated.

Rice genotypes vary in their adaptation and general performance under different growing environments due to their differential morphological and physiological characteristics. Kanyeka *et al.* (1995 and 1995) attempted to broadly document rice ecosystems with their quantitative distribution in Tanzania. They classified the ecosystems into lowland rice ecosystem (80%) under which rainfed lowland (74%) and irrigated (6%) were included. Under lowland rice ecosystem, water management may involve fields to be bunded, unbunded or left with freely moving water. The upland ecosystem (20%) was also indicated to include the dryland (12%) and hydromorphic (8%) ecosystems.

The levels at which rice ecosystems are scattered in the country differ from one region to another. Where other factors are constant, water is the main determinant in the rice production system. In contrast to upland culture, the irrigated ecosystem has the greatest potential in rice production. It is estimated that under farmers' conditions, upland culture may produce 0.4-0.5t/ha while irrigated culture is able to give up to 4.0t/ha. Rainfed ecosystem produces between yields the two ecosystems (Kanyeka *et al.*, 1995).

2.6. Production constraints.

There have been no significant increases in rice yields under farmers conditions in Tanzania. Apart from climatic weather, rice production is limited by several factors, which at a larger extent are aggravated by lack of application of improved agricultural technologies. These factors include weeds, lack of fertilizer application, poor water management, pests (insetpests, diseases and rodents) and lack of high yielding improved varieties with good and acceptable grain qualities (Kanyeka, 1994).

2.6.1. Weeds

Due to their high ability in competitiveness for light, nutrients and water, weeds tend to reduce rice yields drastically. They also result into reduction of rice market value due to contamination of weed seeds and debris. Weeds are found in all growing environments (ecosystems) but more severe where there is less time of standing water. However, Rao (1983) noted that the intensity of weed competition depends on type of weed species, severity and duration of infestation, the competing ability of the crop plants and climatic conditions. Sibuga *et al.* (1997) reported that weeds under areas with ample moisture and fertilization if not timely controlled may grow and compete vigorously against rice. Similarly, Akobundu and Fagade (1978) reported that higher level of amount of water is necessary to suppress the growth of weeds with rice.

De Datta (1981) noted that rice is very sensitive to weed competition and failure to control weeds would result into yield reduction at 34% in transplanted, 45% in direct seeded and 67% in rainfed lowland rice. In Tanzania, no yield loss figures due to weeds have been established under the existing ecosystems. Some important weeds in Tanzania include wild rice (*Oryza longistaminata, O. punctata* and *O. banthii)*; Barnyard grass (*Echinochloa erus-galli* and *E. colona*); Sedges (*Cyperus spp.*); Wandering Jews (*Commelina benghalensis);* Stargrass; (*Cynodon doctylon);* Guinea fowl (*Rottboellia conchichinensis*); '*Pyapya*' D*ersia hexandria.*

2.6.2. Insect Pests and Diseases

Pests are among important rice production constraints in Tanzania. Pests include insectpests, diseases, birds and rodents. Ching'ang'a (1985) estimated yield losses due to insect pests and diseases to be 20% in Tanzania, while in India, Rao (1983) reported annual yield loss of 30% by insect pests, 20% by diseases and 5% by others in India. Important insectpests in Tanzania as outlined by Ching'ang'a (1985) are stripped stem borer (*Chilo sp*); Pink stem borer (*Sesamia sp*), Stalk-eyed shootfly (*Diopsis macrophthalmia*) and African gall midge (*Orseolia oryzivora*). These pests may appear minor or devastating upon their occurrence in certain years/seasons if not early controlled. Other important pests include field rats (eg *Mastomys mastomys*) and birds (*Quelea quelea*) which damage the rice crop from when it is at milky to maturity stage (IITA, 1984).

Diseases of economic importance in Tanzania are the rice yellow mottle virus and the rice blast (*Pyricularia oryzae*) which attack the rice crop at any growth stage and may cause a complete loss.

These disease used to be not of an economic importance until later when Kanyeka (1994) reported that the intensification of cropping systems and introduction of new cultivars are factors that promoted these diseases to be important in Tanzania. To combat these diseases the integrated pest management approach in which the use of resistant varieties as a long-term solution has been advocated.

2.6.3. Lack of fertilizer application

With respect to the socio-economic factors, few rice farmers in Tanzania apply fertilizers. However, Acland (1971) reported that soils in Tanzania are rich in potassium except for nitrogen and phosphorous which are constantly removed from the soil through seasonal grown crops. In addition, the rare uses of fertilizers by farmers have been associated with the low nature of responsiveness of the Indica rice varieties to which applications of high nitrogen fertilizer results into severe lodging and susceptibility to fungal diseases.

Improved rice genotypes with short to semi dwarf stature are cultivated at a lesser extent by farmers in Morogoro region, despite that genotypes respond highly to nitrogen fertilizer up to 120kgN/ha for optimum yields. (Kanyeka, 1994) documented that farmers rice yields of improved cultivars range up to 4t/ha when fertilizer is applied under rainfed lowland rice. Nevertheless, under upland rice yields drop down to 0.5t/ha when soils are not fertilized.

2.6.4. Lack of high yielding improved varieties

Most farmers use numerous traditional low yielding varieties in Tanzania. Monyo and Kanyeka (1978) pointed out that farmers grow these varieties in extreme mixtures, which make them ripe unevenly. Ching'ang'a (1985) reported that the cultivars are both poor in yield and plant type; and lack disease and pest resistance.

For the improved variety to be adopted, desirable traits must be incorporated in it to suit farmers and consumers needs. Apart from genetic variability over environmental factors, De Datta (1981) outlined short plant stature with erect leaves and resistance to lodging; tillering ability and panicle number, early and sustainable growth vigor,; panicle and grain features as key factors for high grain yields. This means that improvement of these factors would lead to increased grain yields. Short plant stature has been associated with nitrogen responsiveness and high yielding ability. Trials of semi dwarf at high nitrogen levels had indicated the need for both short stature and resistance to lodging (IRRI, 1967). Crossess done at IRRI (1967) reported that the trait is controlled by highly heritable recessive genes located on the same locus and that several modifying genes are responsible for the minor variation in the trait. Further, when selecting for plant stature, IRRI (1968) found that the trait was polygenically (non-allelic to recessive) controlled.

Results from a diallel cross between parents differing in plant stature indicated that plant height is controlled by genes with additive effect and several loci that show dominance (Jennings *et al.*, 1979 and Singh and Sharma, 1982).

Singh and Sharma (1982) studied the inheritance of genetic parameters of 1,440 F_2 plants from crosses of tall Indica variety x semi-dwarf Jaya variety and 100 plants each with parental population. They found that the trait was controlled by a single gene pair, while 50% flowering, productive tillers, panicle length, grains per panicle, 100-grain weight and grain yield were controlled by polygenes.

Erect and relatively short leaves permit better light penetration into lower portion of the foliage canopy, contribute to efficient use of light and lessen susceptibility to lodging (Chang and Tagumpay, 1970). The highly heritable recessive genes located on the same locus and several modifying genes were also noted responsible for erect leaves, moderately high to high tillering; and moderately long basic vegetative phase (Chang *et al.*, 1969).

Lodging characteristics is primarily determined by plant height. Although resistance to lodging varies among rice genotypes, high application of nitrogen increases the incidences of lodging. Depending on the stage of growth and the ecosystem in which rice is grown, lodging tends to reduce grain yield and quality of rice. In Tanzania tall to semi-dwarf varieties are preferred by farmers since they are easily harvested by pricking single rice panicles at a time.

Under the prevailing environmental conditions in the tropics, a high tillering genotype has the inherent advantages of adapting to varying spacing or plant densities, compensating for missing hills or damaged tillers and rapidly attaining a favorable leaf area. The requisite for high yield is that very high proportions of the

tillers develop into fertile panicles. From a four – parent diallel set of extremely contrasting varieties, F1 and F2 data indicated that panicle number is largely controlled by additive gene effect and to a smaller but significant extent by dominant effect (Chang and Vergara, 1972).

Early and sustainable growth vigor is a desirable trait contributing to the faster development of a favorable leaf area which is necessary to an early maturing genotype (IRRI, 1966). Early vigor is important to direct seeded and transplanted rice crop as it decreases weed competition, compensates for missing plants and low seeding rate; and ensures that the crop attains its critical leaf area at flowering (Jennings *et al.*, 1979). Early vigor and late sustained vigor types differ in genes that control growth and hence differing in their harvest index (Chang and Vergara, 1972).

Panicle number per unit area and grain weight (or number of grains/panicle or panicle length) contributes directly to grain yield. In two dialled crosses, longer panicles were partially dominant to shorter panicles; and that larger number of spikelets/panicle were partially dominant to fewer spikelets; and are controlled by both additive and dominant effects (Li and Chang 1970).

Yield is a complex trait with many components that often correlate genotypically and phenotypically. Chandraratna and Sakai (1960) estimated that grain weight is controlled by ten additive genes with maternal effect in F_1 and F_2 generations. Among the yield components, grain yield was reported to have higher heritability (broad sense) than other components (IRRI 1965).

Li and Chang (1970) estimated highest heritability of 39-55% from panicle number. Kihupi and Doto (1989) evaluated rice grain yield and other characters and found that heritability estimates were higher for plant height (94.5%). It was followed by 1000-grain weight, number of filled grains/panicle, panicle length and days to 50% flowering and the least was for panicle number/plant. Later Luzi-Kihupi (1998) studied the genetics of 36 rice genotypes for yield and other components at two and three sites in Tanzania revealed that plant height, number of filled grains/panicle and 1000-grain weight were highly heritable characters.

Heritability (broad sense) studies as estimated by Singh and Sharma (1982) were high for flowering duration, plant height and 1000-grain weight, moderately high for panicle length, number of grains/panicle and productive tillers, and low for grain yield. Kaul and Bhan (1974) also noted high heritability on grain number/panilce, tillers/plant and culm length.

Estimates of expected genetic advance were high for plant height and grains/panicle; moderately high for flowering duration and low for productive tillers, panicle length, 100-grain weight and grain yield/plant. Estimates of expected genetic advance by Kihupi and Doto (1989) were highest for percent filled grains, followed by plant height. However, Johnson *et al.* (1955) reported that a high value of heritability does not necessarily mean an increase in genetic advance. They concluded that characters with high values of heritability and genetic advance were likely to respond better to selection than those with low heritability and low genetic advance.

Studies conducted by Kaul and Bhan (1974) showed that genetic variance were responsible in contributing to the variance of phenotypic traits; and that genetic variability appeared more considerably expressed than phenotypic variance. They observed that grain number/panicle, number of productive tillers/plant and culm length had high genetic variance. Kihupi and Doto (1989) also evaluated the genetics of rice yield components and reported that highest expected genetic advance was obtained from percent filled grains followed by plant height.

2.7. Simple, Genotypic and Phenotypic Correlations

Grain yield, a dependent variable upon other associated traits may not be improved without improvement of other associated dependent variables.

Estimation of inter-correlation between yield and yield components is necessary since yield increase would be achieved through efficient simultaneous selection of yield components than by synchronized selection of individual trait. Many workers (Saini and Gagneja, 1975; Gravois and McNew, 1993; Chandraratna, 1964; Chang and Vergara, 1972 and Luzi-Kihupi, 1998) have done correlation studies on rice. Moreover, Hill (1975) reported that correlations between important and unimportant characters may reveal that some of the unimportant traits are as useful as indicators of either important or both characters.

2.7.1. Yield and yield components

Saini and Gagneja (1975) noted that yield was significantly associated with days to heading, panicle length and spikelet/panicle. Days to 50% flowering had significant positive correlation with plant height and 1000-grain weight, panicle length and number of spikelets/panicle. They also reported that number of tillers/plant were negatively associated with all the characters including yield. Sarathe *et al.* (1969) earlier recorded significant association between yield with panicle length, tillers/plant and the 1000-grain weight. Panicle characters do not strictly cause or determine yield. Such traits simply permit yield to be divisible into yield components. However, Chang and Vergara (1972) observed that panicle number was negatively correlated with panicle length and with weight of a single panicle. In six F_2 populations of diallel crosses, phenotypic and genotypic correlation coefficients indicated that panicle length was positively correlated with plant height in all crosses and with long growth duration in four crosses. In addition, it was negatively correlated with panicle number in two crosses. Gravois and McNew (1993) also estimated correlations of 16 parents and 32 F_1 hybrids at 2 locations in USA. The results indicated that yield was positively correlated with panicle weight and negatively correlated with panicle number.

Luzi-Kihupi (1998) when evaluating rice genotypes for yield and other components in two sites revealed that yield per plant had a positive correlation with number of panicles per plant. The same trait was again positively correlated with panicle length, number of filled grains per panicle, 1000-grain weight and plant height. Negative correlation was noted on percent-unfilled grains and days to 50% flowering.

Gravois and McNew (1993) observed high genetic correlation between yield and panicle weight. Unfavorable genetic linkages have never prevented recombination of any important characters during rice improvement.

2.7.2. Path coefficient analysis.

Path coefficient analysis is defined as a standard partial regression coefficient that measures the *direct* influence of one variable upon another and permits the separation of the correlation coefficient into components of direct and indirect effects. Dewey and Lu (1959) stated that the use of the method requires a cause and effects situation among variables, and the direction must be assigned in the causal system based upon *a priori* grounds or experimental evidence. Rice crop whose yield is dependent upon several yield components requires an understanding of the factors that directly and indirectly influence yield. In any farming system these will permit selection and improvement of yield components for increased yield production.

Path coefficient analysis in rice conducted by Luzi-Kihupi (1998) identified number of filled grains per panicle, number of panicles per plant and 1000 grain weight to be important characters in influencing yield. Similar studies of correlation and path analysis were performed on sunflower (Singh *et al.*, 1985).

Although breeding for high yielding was earlier emphasized in Tanzania, such improved cultivars have failed to replace traditional cultivars and now are being cultivated at small scale due to their poor grain quality characteristics. Smallholder farmers extensively grow traditional cultivars such as Kahogo, Kula na Bwana and Supa (Kanyeka Z.L. personal communication, 2001). The reason is that these

traditional cultivars have excellent milling, eating and eating grain qualities. Grain quality is therefore an important consideration when consumers' acceptance is focussed beyond farmers' decision to adopt a variety.

Grain qualities are influenced by an array of attributes ranging from physical to biochemical characters. These include milling quality, grain appearance, cooking and eating qualities of rice.

2.8. Physical grain quality characters

Juliano (1987) pointed out the attributes of market quality as variety or grade, degree of milling (whiteness), impurities, colour and discoloured grains; head rice yield, translucency, chalkiness, grain size and shape mixtures.

2.8.1. Milling quality

Milling quality refers to ability of rice to resist breaking while being mechanically hulled (Unnevehr *et al.*, 1992). Milling quality affects market price, particularly head rice percentage. Factors that were enumerated by (Juliano, 1985 and Juliano and Betchel, 1985) to affect total rice milling yield and head rice yield included foreign materials content, chalky and immature grains, and damaged grain content. Others, which seriously affect the milling yield, are varieties, grain type, growing and harvesting conditions. Others are harvesting method, control of drying operations and of particular importance effects of moisture adsorption and desorption, as rice can easily be damaged by rapid drying or by rewetting of grains through moisture

adsorption. Upon milling, the uniformly translucent non-glutinous or opaque glutinous grain giveg higher head rice yield than those with chalky portions (Juliano, 1990). Also, van Ruiten (1985) pointed out that when grain length:breadth ratio of brown rice is high (slender), such grains tend to break easily upon milling. Jennings *et al.* (1979) also recorded adverse protein loss with increased degree of milling.

In marketing when all other factors are kept constant, grains with long size and slender to intermediate shapes tend to have high milling percentages and command high international market price (Juliano, 1985 and Juliano *et al.*, 1990).

2.8.2 Grain size and shape

Grain size and shape were found to vary among and within varieties, however, shape is less variable than grain length (Jennings *et al.*, 1979). Though not specified, both traits were largely reported to vary with the influence of the production environment (Unnevehr *et al.*, 1992).

Findings by de Rosario (1967) indicated that optimal width of the rice grain is attained earlier in 14 days after flowering and the length in 4 days. Thereafter each one develops to its full size or shape but length takes longer time than width. Processing factors like rice parboiling, aging or storage for 3-4 months after harvest were realized to improve the total and head rice. IRRI (1988) classified length of rice grains into four groups namely - extra long (6.61-7.50mm); medium (5.51-6.60mm) and short (less than 5.51mm). Similarly, shape of rice grain was determined on the

length/width ratio of brown rice. The classification fell into slender (greater than 3.0): medium (2.1-3.0); bold (1.1-2.0) and round (less than 1.1).

2.8.3. Chalkiness (Opacity).

Chalkiness, a trait that is genetically inherited and environmentally influenced is related to airspace of the endosperm (Hoseney, 1986). Chalky grains result in lower milling yields as its characteristic nature of chalkiness offer weaker points than are for translucent non-glutenous grains (Webb, 1985). With chalky grains, Sandya-Randi and Bhatacharya, (1989) found them possessing lower viscosity and lower amylose content. Low and high temperatures usually after flowering were reported to be important for increasing or decreasing/eliminating chalkiness.

In most cases soil fertility especially when excess under rainfed lowland rice was noted to influence the degree of chalkiness (Resurreccion *et al.*, 1977). Further, Webb *et al.* (1986) working with 28 rice varieties of diverse grain sizes (long, medium and short) varying in milling; cooking and processing characteristics demonstrated a low correlation to crushing strength hardiness. The chalkiness of rice grain disappears upon cooking and doesn't influence texture and taste of rices (Mackill *et al.*, 1996).

2.9. Cooking and eating quality

The cooking and eating qualities of rice are determined by the physiochemical properties of rice grains. The specific properties used to evaluate grain quality are gelatinization temperature, amylose content, and gel consistency.

2.9.1 Amylose content

Jennings *et al.* (1979) recorded amylopectin (branched fraction) and amylose (linear fraction) as main components of rice starch. Environmental factors especially low ambient temperatures during ripening were noted to increase amylose content (Ressurreccion *et al.*, 1977). Starches contain 20-30% amylose and 70-80% amylopectin. Ratios vary with botanical source of starch (Jane *et al.*1999). Amylose content of a rice variety can also vary by as much as 6% (Juliano, 1970). Such high variability in amylose content within a variety is dependent on the prevailing temperature during ripening. There is apparent increase of amylose content in indica varieties as temperature increases up to 29^0C. Nevertheless, after 29^0C amylose content decreases as temperature increases (Resurreccion, *et al.*, 1977). In addition, an amylose content decreases slightly with nitrogen fertilization but it is not affected by the stage at which nitrogen is applied (Paule, 1977 cited by Gomez, 1979).

Amylose content varies among varieties; and based on the amylose content, starch is categorized into glutinous (waxy) and non-glutinous (non-waxy). A grain with at most 2% amylose is categorized as glutinous (waxy). The non-glutinous rices are categorized into low amylose (8-20%), intermediate amylose (21-25%) and high amylose (more

than 25%) Jennings *et al.*, 1979). Amylose content was then considered the major factor responsible for cooked rice hardness, stickiness, colour, gloss and general acceptability (Mackill *et al.*, 1996). Based on cooking characteristics, Chatterjee and Maiti (1985) noted that waxy rices absorb little water during cooking than non-waxy rices and thus have low volume expansion. Non-waxy rices containing low amylose content tend to get moist, sticky and glossy when cooked; and they split and disintegrate when overcooked. Rices with high amylose cook dry, fluffy and become hard upon cooking; but resist disintegrating during boiling. Intermediate amylose rices that are generally preferred become fluffy when cooked and remain soft when cool (Chatterjee and Maiti, 1985).

2.9.2 Gelatinization temperature

Mackill *et al.* (1996) defined gelatinization temperature (GT) as a temperature at which the starch granules begin to swell irreversibly in hot water. Unnevehr *et al.* (1992) documented that GT was dependent upon variety and the production environment. Gelatinization temperatures may even vary by as much as 10°C with a variety depending on environmental factors. High air temperature after flowering raises GT; while low air temperature lowers it (Mackill *et al.* 1996). In addition, Fan *et al.* (1999) reported that GT in rice was dependent upon the varieties.

Gelatinization temperature is determined by the alkali spreading value (Little, 1958); and may indirectly indicate whether a variety has low amylose content despite that it cannot distinguish it into distinct classes. Gelatinization temperature was documented to vary due to the ratio of amylose to amylopectin, starch crystallinity, granule size,

distribution and the amount of minor constituents like phosphorus, lipids, protein and enzymes (Chattakanonda *et al.*, 2000). Gelatinization of starch significantly influences the starch properties of cooked rice and the use of flour as a food ingredient (Juliano, 1990 and Perez *et al.*, 1993). Differences in starch granules have resulted into classification of gelatinization temperature; and it ranges between 55-79 ^{0}C. The range is further divided into three groups: low (less than 70 ^{0}C), intermediate (70-74 ^{0}C) and high (above 74 ^{0}C).

Rices with high GT tend to require more water and time to cook than those possessing either low or intermediate GT (Chatterjee and Maiti, 1985). Experiments conducted by Juliano (1987) also revealed that low amylose content was associated with high GT. In contrast, glutinous starch exhibited low and some high GT too. Nevertheless, gelatinization temperature was reported to be highly heritable trait.

2.9.3 Gel consistency

Rice genotypes vary in the degree of gel consistency of starch. Their differences in gel consistency were observed to depend on variations in amylopectin fractions (Juliano and Perdon, 1975), which are environmentally influenced (Unnevehr *et al.*, 1992). Seetanum and De Datta (1973) observed that addition of nitrogenous fertilizer application at heading stage tend to result into largest increase of protein content in the rice grain sample; and consequently contribute to harder gel consistency.

Gel consistency test is used to separate varieties with high amylose content as per method developed by Cagampang *et al.* (1973) and is based on the consistency of rice paste.

Classification of rice gel consistency by Juliano and Villareal (1993) was documented into: soft gel (61-100mm), medium gel consistency (41-60mm) and hard gel consistency (25-40). This classification thus correlates with amylograph consistency or with increase in viscosity of rice paste on cooling from 50-94°C. Rices that have less than 24% amylose content were documented by Mackill *et al.* (1996) to possess soft gel consistency. Soft gel consistency, however, is generally preferred to hard gel consistency (Juliano, 1987). As opposed to low GT, some high GT rice also has tendencies of giving hard cooked rice and rice products due to presence of large amylopectin molecules (Perez *et al.*, 1979).

2.10. Genetics of rice grain quality characteristics.

Studies on the genetics of rice grain qualities are abundant and in some instances very contrasting. Mackill *at al.* (1996) reported the complexity of inheritance of grain length and shape based on the parental types. In contrast, they pointed out that grain length and shape may be highly heritable characters, which are little influenced by environments. Because of the early fixation of the trait, selection is effective in F_2 (or F_1 of multiple crosses). Some more genetic postulates on grain length were reported to vary from monogenic (Chao, 1928), digenic (Bollich, 1957), trigenic (Rumiah and Parthasarathy, 1933) to essentially polygenic (Mitra, 1962 and Mackill *et al.*, 1996) inheritance.

Chalkiness is quantitatively inherited and the exact mode was supposed to depend on the parental and environmental influences (Hoseney, 1986 and Chang and Somrith, 1979). According to them, other breeders' experience show that chalkiness is fixed earlier and therefore strict selection for chalkiness should begin from as early generations as possible.

The inheritance of amylose content is reported to be simple and may vary as much as 6% depending on the environmental conditions (Mackill *et al.*, 1996) from which temperature variation is the main factor (Resurreccion *et al.*, 1977). However, Chang and Somrith (1979) reported that the trait is largely controlled by multiple genes with additive effects. Maternal influences have been indicated to affect the levels of amylose levels. One gene with different alleles controls the inheritance of hard, medium and soft gel consistency (Tan *et al.*, 1991).

The inheritance of gelatinization temperature was documented to be simple involving one or two major genes (Shen *et al.*,1987). Although the heritability is high, gelatinization temperature may vary as much as 10^0C within a variety, depending on the environmental factors especially temperature fluctuations during ripening (Mackill *et al.*, 1996).

Gel consistency is a trait that was reported by Khush *et al.* (1979) to be controlled by one gene with different alleles for hard, medium and soft consistency and that its selection was suggested to start from F_4.

2.11. Correlation analysis on rice grain quality.

The expressions of grain qualities depend very much on the prevailing environmental conditions in which rice genotype is grown. Extensive evaluation over different world rice genotypes from different countries (environments) indicates that all grain qualities are dynamic and inconsistent in their expression.

Analysis by Juliano and Villareal (1993) on world rices revealed inconsistent correlations among grain physical and biochemical characteristics. Traits that were involved included grain length, width, amylose content, cooked rice hardiness gel consistency and alkali spreading value. For example, grain length had a negative correlation with width in Bhutan and USA, Malagasy, and Ivory Coast; and a positive correlation with amylose content and alkali spreading value (gelatinization temperature) in Brunei. Amylose content had a positive correlation with cooked rice hardiness and gel consistency in Bhutan; and with a positive correlation with alkali spreading value (gelatinization temperature) in Brunei. Gelatinization temperature as estimated by IRRI (1967) was reported to have positively correlated with cooking time. The trait, however, does not correlate with texture of cooking rice (IRRI, 1968).

In USA, amylose content indicated a positive correlation with length and alkali spreading value; and negative correlation with width, gel consistency and cooked rice hardiness. Observation made by Khush, (1994) reported that grain length had a negative association with chalkiness. Findings by Juliano and Villareal (1993) revealed the negative association between grain length and grain shape. Milling quality of chalky rices is affected through excessive breaking-up upon milling.

Studies by Champagne *et al.* (1990) and Marshall (1992) found negative correlation of the degree of milling of rice kernel with initial gelatinization and peak temperatures.

2.12. Genotype x Environment Interactions

The environments under which the crop is grown modify the phenotypic expression of the traits described above. When cultivars are compared in different environments their performance relative to each other may not be the same. Changes in relative performance of genotypes across environments are referred to as genotype x environment interactions (Fehr, 1987 and Allard and Bradshaw, 1964). Fehr (1987) defined genotype as the entire genetic makeup of an individual, while Chaudhary (1984) referred to environment as the sum total of the external conditions, which affect growth, and development of an organism. Allard and Bradshaw (1964) classified environmental variables into predictable (systematically fluctuating) and unpredictable (inconsistently fluctuating). Genotype x environment interactions are important to plant breeders in developing and recommending cultivars to suitable environments. Changes in rank among genotypes across environments may consequently limit the effectiveness of selection of superior genotypes.

In crop improvement, cauliflower, lettuce and *Nicotiana* varieties that were compared over a wide range of environments showed tendencies of inconsistent performances (Freeman and Crisp, 1979). Such interactions were however, earlier confirmed to reduce the correlation between genotype and phenotype, and consequently reducing the effectiveness of selection (Comstock and Moll, 1963).

A review made by several scientists on the early work on genotypes x environment interactions and their implications, revealed the need for the development of cultivars with respect to environment changes (Horner and Frey, 1957 Allard and Bradshaw, 1964, Baker *et al.,* 1981, and Mehta *et al.*, 1984;).

The impact of genotype x environment can be reduced by evaluating the lines in multiple locations. Allard and Bradshaw (1964) noted that lack of interaction of genotype across locations could optimize the use of resources within a single location in a tested environment. Genotype x location interaction led into developing genotypes for different locations through independent selections and testing programs (Horner and Frey, 1957). They then suggested a single year variety testing in the absence of significant genotype x year interaction. Fehr (1987) proposed the identification of genotype x year superior average performance over locations. Baker *et al.* (1981) evaluated genotype x environment interactions for forage yield of reed canarygrass clones. Among the order of interactions, genotypes x location x year was significant for yield.

Various attempts were made to reduce genotypic mean variance when varieties are grown at different environments. Among the methods to reduce the effect of genotype x environment interaction as suggested by Jensen (1952) is the use of multilines which allows the selection of genotypes that interact less across environments. There are several other methods that have been proposed to analyze genotype x environment interactions.

The analysis of variance has been widely used. This method requires the evaluation of genetic components of variation from comparable experiments grown in two or more locations. The implication of the presence of significant differences between the various estimates of the same components depicts the existence of genotypes x environment interactions. The relative magnitudes of variance of components were thus reported to contribute their effects on the stability of a group of genotypes (Sprague and Federer, 1951 and Johnson *et al.*, 1955). Young and Virmani (1990) reported a widely adapted rice variety IR36 as one of the outcomes of the efforts made to obtain a high yield and stable genotype.

Cluster analysis was also employed to estimate and assess genotypic sensitivity across environments, and grouped cultivars into clusters on the basis of similarities (Horner and Frey, 1957; Abou-El-Fittouh, 1969 and Ghaderi *et al., 1980*). Also, Abou-El-Fittouh (1969) added that the approach could be used even without necessarily finding out the responsible environmental factors. Pairwise analysis of variance was another method used (Plaisted and Peterson, 1959) to provide information of individual genotypes through a combined analysis in every pairwise combination of genotypes at locations in a given year. For each genotype, the mean of genotype-location variance isolated from a combination with all other genotypes measures genotype x location interaction.

However, the methods mentioned above were not able to provide information on the environment stability of individual genotypes (Fehr, 1987). Alternatively, regression analysis was then adopted. Although genotype stability performance exists, it was

observed to assist in determining genotypic suitability for the fluctuations in growing environments that will be encountered (Liang *et al.*, 1966). Eberhart and Russell (1966) modified an earlier regression analysis put forward by Yates and Cochran (1938) to a statistical linear regression model for the analysis and detecting stable/ unstable genotypes for wide or specific adaptation respectively. Tan *et al.* (1979) reaffirmed that differences in the relative responses of genotypes from one environment to another followed an orderly pattern that could be measured by regression.

A regression model developed by Eberhart and Russell (1966), classified varietal stability by regression coefficient (phenotypic response) "b" and deviation from regression "S^2d". Varietal stability was therefore considered stable when its phenotypic response was close to unity; and deviation from regression was close to zero. Yassin (1973) pointed out that significance of deviation from linearlity indicated the importance of unpredictable component of the genotype x environments interaction in the test materials than the relatively predictable component (linear response) e.g. diseases.

Few studies on genotype x environment have been made. Oyedokun (1985) conducted an experiment on genotype x environment interactions (locations and seasons) in upland rice and revealed presence of interactions for yield. Chamberlin and Insomphun (1982) also experimented on genotype x altitude environments and found severe low yields and high spikelet sterility as altitude increased.

Kihupi and Doto (1989) studied the genotypic and environmental variability of rice characters, and indicated interaction with environments for all traits except panicle number and yield per plant. Kulkarni *et al.* (1988) also evaluated the performance of 25 rice varieties and found genotype x environmental interaction with 50% flowering and plant height. Similar study conducted by Nei (1960) on rice revealed significant variety x year interaction on plant height, panicle length and panicle weight.
Nevertheless, De Datta, (1981) reported the importance of tillers as a yield component and that the widely grown cultivars in rainfed conditions have the ability to compensate tiller number with larger panicle size.

Gray (1982) evaluated 20 orchard grass clones for growth stage-forage yield at three locations for three years in the first experiment. Other 10 clones were evaluated at 3-plant spacings for three years in the second experiment. The outcome indicated significant genotype x environments for yield trait in both experiments. The first order interactions were all significant.

Other studies conducted were on cotton (Miller *et al.*, 1959), barley, oat and wheat (Liang *et al.*, 1966); groundnuts (Mercer-Quarshier, 1988); oilseed rape (Brandle and McVetty, 1988).and switch grass (Hopkins *et al.*, 1995)
Besides the observed variations on yield and its components, grain quality studies are also important in an understanding their performance under the existing and changing production environments in Tanzania. Although information on the rice grain qualities is inadequate, environmental conditions were reported to vary amylose content by up to

6% (Juliano, 1970) and protein up to 7% (Jennings *et al.*, 1979 and Chatterjee and Maiti, 1985).

High temperature and low light intensity from the required amount (Chatterjee and Maiti, 1985), and too early water drainage before harvest (Cheaney and Wyche, 1955) were reported to induce and increase opacity. Despite of protein variations due to genetic or environment, tropical brown rice was reported to have 80% energy (Juliano, 1966.) and 5-17% protein content (Juliano *et al.*, 1968). Further, Vellupillai and Pandey (1990) noted that excessive rice brokens during milling were associated with cracked (fissured) rice and conditions to which grains were subjected before the process. Immature and overripe grains, chalkiness and moisture content outside a range of 18-23% at harvest were factors noted to reduce head yield (Chatterjee and Maiti, 1985).

Quality studies have been made on other crops. Sheaffer *et al.* (1988) evaluated alfalfa cultivars for consistency of forage quality performance over time and environment, and tested the validity of sampling seeding-year stands for forage quality.

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 Experimental sites

The experiment was conducted at Lumemo-Ifakara (rainfed lowland), Tanganyika Agricultural Cooperation (TAC)-Ifakara (irrigated) and Sokoine University of Agriculture (SUA) Farm (upland) in Morogoro region in the 1999/2000 rainy season (March to August). Each of the sites had different soil characteristics. The respective soil characteristics of the three sites are presented in appendices i, ii and iii. The experiment consisted of 10 rice genotypes including the control (Table: 1) which were selected on the basis of their potential performance for future variety release. Sources of the seed materials were Sokoine University of Agriculture (SUA) Morogoro and The Agricultural Research and Training Institute (ARI) KATRIN, Ifakara.

3.2 Experimental design

Randomized complete blocks design (RCBD) with three replications was used, in which the plot size was 4m x 2m. The harvested net plot area was 3.5m x 1.5m.

3.3 Crop husbandry

Fields were disc ploughed and harrowed in early January 1999. Hand hoes were used for field leveling followed by experimental laying out in late February. Three to four seeds per hill were dibbled at a spacing of 20cm x 20cm. Seven days after emergence the seedlings were thinned to two seedlings per hill and gap filling was done

simultaneously. Nitrogen fertilizer at 80kg N/ha in the form of Urea (46%N) was equally split at three growth stages; viz. initial tillering, mid-tillering and at panicle initiation. Weeding was done where necessary. All the parameters were recorded according to the Standard Evaluation System of Rice (IRRI, 1988).

Table: 1b. Rice varieties evaluated in three different growing environments (Lumemo, TAC and SUA Farm).

Variety/Line	**Maturity Characteristics**	**Source**
SSD5	Early	SUA
SSD3	Early	SUA
Line 85	Late	KATRIN
M15A	Late	SUA
Supa (control)	Late	KATRIN
TXD 275	Late	KATRIN
Line 88	Late	KATRIN
TXD 220	Late	KATRIN
SSD1	Early	SUA
M55	Early	SUA

3.4 Data collected.

Data were collected from the net area of each plot excluding two boarder rows, replanted hills and plants that were adjacent to missing hills. Data collection and measurements were taken according to Gomez (1972), and Gomez and De Datta, (1972) as follows:

3.4.1 Days to 50% flowering

This was recorded when half of the plant population in each plot, had flowering. The number of days to 50% flowering was calculated from the date of planting to the date when 50% of the plants in a particular plot flowered.

3.4.2 Plant height

At maturity ten hills were randomly selected in each plot and height measured in centimeter. Measurements were taken from the soil surface to the tip of the tallest panicle in the hill and their mean value determined and recorded.

3.4.3. Panicle length

The length of ten centre panicles from randomly selected hills were measured in centimeters and their mean values determined and then recorded.

3.4.4. Number of productive tillers per square metre

The number of productive tillers per plot was determined by randomly placing a one-meter square quadrat in each plot. The number of productive tillers were each counted to get the total number of tillers per square meter.

3.4.5 Grain yields and yield components determination

Ten hills per plot were randomly selected; and their total number of panicles (P) from all sample hills was counted. Out of each sample hill the center or middle panicles were separated, threshed, and their grains bulked. Filled grains and unfilled grains were separated by use of seed separator, the salt-water (specific gravity 1.06) method. The filled grains (f) and unfilled grains (u) were counted and weight of unfilled grains (w) were determined. The rest of the panicles (excluding awns) of all sample hills were also threshed and the unfilled grains were separated from the filled grains. The unfilled grains (U) were counted and the filled grain weights (W) from each plot were recorded. The following formulae by Gomez (1972) were used to determine the yield components. Number of panicles/hill = P/4n;

Where: n= sampling units,

Number of filled grains/ panicle = f/w x W +w/P

Percent of unfilled grains = U + u / f (W+ w)/ w +U +u x 100

1000 grain weight = w/f x 100

The adjustments to 14 MC % of the weights of filled grains of center panicles and the rest of panicles were determined for their final filled grain weight (M) using the formula proposed by Gomez (1972) as follows:

100 grain weight = (100-M)/86 x w/f x 100

Where; the abbreviations are as indicated above.

3.3.6. Determination of grain yield/plot

The grain yield for each plot was harvested from the net area obtained by discarding two border rows from each side of the plot. The paddy was threshed, cleaned, dried and then weighed in kilograms. After weighing the grain yield from each plot, their respective moisture contents were determined. The grain weight per plot was adjusted to 14% moisture content before converting the grain yield to t/ha by a formula given by Gomez, (1972) as follows:

Adjusted grain weight =A x W.

Where; **A**= adjacent **coefficient** and **W**= weight of harvested grains.

However the computed **coefficient A = 100-M/86**

Where; **M** =percent moisture content of the grains

In plots with missing hills the formula proposed by Gomez (1972) was applied as follows:

Grain yield/plot = W x N/n,

Where; **W**= weight of grains from harvested hills,

N =Total number of hills in normal plots.

n = number of harvested hills and,

3.4.7. Grain appearance (Grain size, shape and opacity)

Ten milled whole grains were randomly selected from a sample of each genotype. Length and width of each grain from each genotype was measured and their respective means were established by using of a graphic (logarithmic) paper. Grain length describes the grain size of each genotype, while length-width 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 (IRRI, 1988) as shown below.

Size classification:

Code	Length (mm)	Grain type
1	Greater than 7.5	Extra long
3	6.61-7.50	Long
5	5.51-7.60	Medium
7	Less than 5.51	Short

Shape classification:

Code	Length: width ratio	Grain shape
1	Greater than 3.0	Slender
2	2.1-3.0	Medium
5	1.1-2.0	Bold
7	Less than 1.1	Round

Opacity of milled rice was visually rated in terms of chalky proportions of the grains. The assessment was done on the basis of chalkiness, whether the rice was white belly, white centre or white back.

Scale used for chalkiness (opacity) was adopted from the Standard Evaluation System for Rice (IRRI, 1988).

Opacity classification:

Code	% chalkiness	Description
0	0	None
1	Less 10	Small
5	11-20	Medium
9	More than 20	Large

3.4.8. Cooking and eating qualities:

The biochemical variables included: gelatinization temperature amylose content, gel consistency, and aroma content. The biochemical characteristics were determined according to Jennings *et al.* (1979) and IRRI (1988) respectively.

3.4.8.1. Gelatinization temperature (Alkali test)

Six whole milled rice grains were randomly selected in duplicate and placed in petri dishes. In each petri dish, 10 ml of 1.7 % Potassium hydroxide solution was added.

Samples in petri dishes were covered by lids and left undisturbed for 24 hours in a room temperature. The spreading rate of each kernel of each genotype was visually observed using numerical scale from the Standard Evaluation System for rice (IRRI, 1988):-

Classification of gelatinization temperature:

Code	Designation	Alkali digestion	Gelatinization temperature
1-2	Not affected but chalky swollen	Low	High
3	Swollen with collar incomplete and narrow	Low or Intermediate	High or Intermediate
4	Swollen with or collar complete and wide	Intermediate	Intermediate
5	Split or segmented with collar complete and wide	High	Intermediate
6-8	Dispersed merging with collar/Completely dispersed and cleared.		Low

3.4.8.2. Amylose content (AC).

The modified simplified assay (mannual procedure) of Juliano (1971) was used. The procedure was used to prepare a standard curve using a solution of purified potato amylose. A sample of each genotype was stored in the same room for 2 days to allow seeds to acquire equal moisture content. The samples were milled separately and

milled rice flour (100mg) was sieved by using 400 microns mesh screen and weighed in duplicate in 100ml volumetric flasks. Addition of 1ml of 95 % ethanol, washing down any sample adhering to the flask was followed by addition of 9ml of 1N Sodium hydroxide (NaOH). The suspension was heated in a boiling bath for 10 minutes to gelatinize the starch and then cooled for 1 hour at room temperature. Samples were diluted to volume with distilled water and mixed well. The samples were shaken and left to stand for 20 minutes and percent transmission was determined at 620nm in a spectrometer sp 600. A calibration curve was made with each set of unknown samples by plotting the absorbance of check milled rice samples against their known amylose content. The prepared Iodine solution consisted of 3ml 0.2% I_2 in 2% KI and 1ml 1N acetic acid diluted to 100ml. The amylose content of checked milled samples were obtained from 95% ethanol -defatted milled rice flour (reflux 18-24 hours) using standard mixtures of 70mg waxy rice flour (amylopectin). The 10mg amylose +60mg waxy rice, 20 mg amylose + 50 mg waxy rice, 25 mg amylose +45mg waxy rice, and 30mg amylose +40mg waxy rice were mixed in 100ml 0.009N NaOH. Results were expressed on dry weight basis.

Rating of amylose content of the materials was recorded according to the Standard Evaluation System for Rice (IRRI, 1988 and Juliano and Villareal, 1993) as follows:

Classification for amylose content

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

3.4.8.3.Gel consistency (GC).

Gel consistency was determined in the laboratory by a method developed by Cagampang *et al.* (1973). Rice flour weighing 100mg of each genotype was placed in a test tube (Pyrex) and wetted with 0.2ml 95% ethanol containing 0.025% thymol blue. The tube was shaken to suspend the starch and 2ml of 0.2N KOH was added and the mixture was dispersed by using the multi-shaker (Bairn and Tattock). Corks were then fitted to test tubes, placed for 8 minutes in the water bath for vigorous boiling to reflux. Later, samples were removed from water bath, left in room temperature for 5 minutes and cooled in an ice-water bath for 15 minutes.

Test tubes were then laid horizontally over ruled paper graduated in millimeters and the length of the gel was later measured from bottom of the test tube to gel length for 30-60 minutes.

Classification of gel consistency was recorded according to Standard Evaluation System for Rice (IRRI, 1988) as follows:

Classification of Gel consistency

Gel length (mm)	Gel description
Greater than 80	Soft
61-80	Medium soft
41-60	Medium
36-40	Medium hard
27-35	Hard

3.5 Statistical Analysis.

3.5.1. Analysis of Variance (ANOVA).

3.5.1.1. Single site analysis.

Recorded data was analyzed using MSTAT-C software (Michigan State University, 1990). Data were at first subjected to the standard analysis of variance for each location using the procedure described by Gomez and Gomez (1984) for a randomized complete block design (RCBD).

3.5.1.2. Combined analysis.

Similarly, combined analysis of variance was performed using MSTAT-C.

The statistical model was given by: $X_{ijk} = u + g_i + \varepsilon_j + g_{ij} + e_{ijk}$

Where: X_{ijk} = The measurement obtained for the unit in the i^{th} genotype of the k^{th} replicate of the j^{th} environment

μ = Overall mean.

g_I = The mean of the ith genotype.

ε_j = The mean of the jth environment.

g_{ij} = interaction effect of the ith genotype of the j^{th} environment.

e_{ijk} = random experimental error.

From the table of combined analysis below, different variance components were estimated using a method given by Al-Jibouri *et al.* (1958). The expected mean squares (EMS) were used to calculate the variance due to genotype, environment and genotype x environment.

The analysis of variance table from which the estimates of components of variance were calculated is given below.

Source of variance	df	Mean square	E(ms)
Environments (E)	n-1	M_1	$\sigma^2 + r\sigma^2_{GE} + g\sigma^2_{R/E} + rg\sigma^2_E$
Replications R/E	n(r-1)	M_2	$\sigma^2 + g\sigma^2_{R/E}$
Genotypes (G)	g-1	M_3	$\sigma^2 + r\sigma^2_{GE} + re\sigma^2_G$
GxE	(g-1) (n-1)	M_4	$\sigma^2 + r\sigma^2_{GE}$
Error [(R/E) x G]	n(r-1) (g-1)	M_5	σ^2

Where: $\delta^2 e$ =Plot error variance

$\delta^2 g$ =Genotypic variance among progenies

$\delta^2 l$ = Location (environment) variance

$\delta^2 gl$ =Genotype x Location (environment) variance

r = number of replications

n =number of environments

g =number of genotypes

The phenotypic variance (δ^2_{ph}) among genotype means tested in r-replicates and l-environments was later computed from the formula:

$$\delta^2_{ph} = \delta^2_g + (\delta^2_{lg}/l) + (\delta^2_e/lr).$$

Where: The numerators are the estimates of the respective variance components such that: δ^2_{ph} = phenotypic variance.

δ^2_g = genetic variance

δ^2_{gl} =variance due to genotypes and locations

δ^2_e = error variance

l = number of locations

r = number of replications

The estimates of phenotypic and genotypic variance were used to calculate the heritability (broad sense) using a formula proposed by Hanson *et al.* (1956) as follows:-

$\mathbf{h^2 = (\delta^2 g/\delta^2 ph) \times 100}$

where h^2 = heritability in the broad sense

$\delta^2 g$ = genetic variance

$\delta^2 ph$ = phenotypic variance

In addition, the expected genetic advance (EGA) was estimated using the formula proposed by Johnson *et al.* (1955) as follows:

Expected genetic advance, $\mathbf{GA = k\,(100\delta g)/\,\chi\,(\delta g)/\delta_{ph}}$

where: δg = genetic standard deviation,

χ = population mean,

δ_{ph} = phenotypic standard deviation.

The above formula indicates that the expected genetic advances from selection when expressed as a percent mean is the product of: -

(i) Selection differential measured in terms of phenotypic standard deviation. A constant value of 2.06 was used assuming that 5% of the lines saved.

(ii) The genetic coefficient of variation and ,

(iii) The square root of heritability ratio.

Covariance analysis was done using the MSTAT-C software from which estimates of genotypic ($\delta g_{1.\,2.}$) and phenotypic ($\delta ph_{1.\,2}$) covariance components between the two traits were derived. The expected components were estimated using the same procedure as for the variance components. The covariance components were used to compute genotypic and phenotypic correlations on a line basis between various characters by using the formula given by Robinson *et al.*, (1951) as indicated below:-

Genotypic correlation $r = (\delta g_{1.2.})/\sqrt{(\delta^2 g_1)(\delta^2 g_2)}$

Where: $\delta^2 g_{1.2}$ = the genetic covariance between the two traits.

$\delta^2 g_1$ = the genotypic variance of the first trait , and

$\delta^2 g_2$ = the genotypic variance of the second trait.

Phenotypic correlation $r = (\delta ph_{1.2})/\sqrt{(\delta^2 ph_1)(\delta^2 ph_1)}$

Where: $\delta ph_{1.2}$ = the phenotypic covariance of the two traits

$\delta^2 ph_1$ = the phenotypic variance of the first trait

$\delta^2 ph_2$ = the phenotypic variance of the second trait

3.5.1.3. Correlation and Path coefficient analyses.

Correlation coefficients and among yield and yield components, and grain qualities were done by using MSTAT-C software. Except for grain qualities that have no clearly dependent and independent attributes, path analyses was performed only on yield and yield components following the method outlined by Wright (1921) and adopted by Dewey and Lu (1959). Yield was assumed to be influenced by seven components:-

(1) Panicle length. (2) Panicle weight (3) Tillers/m^2

(4) % Spikelet fertility (5) Grain weight (6) Panicles/plant. .

(7) Filled grains/panicle

The method was basically employed to describe the relationship between correlation coefficients and path coefficients arranged in matrix notations was done using a method proposed by the following formulae:

$$r_{15} = P_{15} + r_{12} P_{25} + r_{13} P_{35} + r_{14} P_{45}$$

$$r_{25} = P_{25} + r_{12}P_{15} + r_{23}P_{35} + r_{24}P_{45}$$

$$r_{35} = P_{35} + r_{13}P_{15} + r_{23}P_{25} + r_{34}P_{45}$$

$$r_{45} = P_{45} + r_{14}P_{15} + r_{24}P_{25} + r_{34}P_{35}$$

$$1 = P^2x_5 + P^2_{15} + P^2_{25} + P^2_{35} + P^2_{45} + 2P_{15}r_{12}P_{25} + 2P_{15}r_{13}P_{35}$$

$$+2P_{15}r_{14}P_{45} + 2P_{25}r_{23}P_{35} + 2P_{25}r_{24}P_{45} + 2P_{35}r_{34}P_{35}$$

In path coefficient model; r_{ij} = simple correlation coefficients for measuring the mutual association of variables.

P_{ij} = path coefficients for measuring direct influence between variables

$r_{ij}Pij$ = indirect effects of variables upon another through the other variable.

P_x = the residual effect in the path analysis model.

Direct effects (Px_{iy}) were calculated from the standardized coefficient using the following formulae:

$$Px_{iy} = \frac{bx_i \,.\, Sx_i}{S_y}$$

Where,

Px_{iy} = direct effect of the independent variable x_i of the dependent variable y.

bx_i = regression coefficient of variable x_i

Sx_i = standard deviation of x_i

S_y = standard deviation of y

i = (1,2,3.....7).

3.5.1.4. Regression analysis

A linear regression analysis for variety performance assessed across environments was performed according to the method proposed by Eberhart and Russell (1966).

The Regression Model was given by: $Y_{ij} = \mu_i + \beta_i I_j + \delta_{ij}$

where: Y_{ij} = variety mean of the i^{th} variety at the j^{h} environment (I^{th} 1,2...v, j^{th}=1, 2..n).

μ_i = the i^{th} variety mean over all environments.

β_j = the regression coefficient that measures the response of the i^{th} variety to varying environments.

I_j = the environmental index obtained as the means of all varieties at the j^{th} environment, minus grand mean.

δ_{ij} (S^2d) = the deviation from regression of the i^{th} variety at the j^{th} environment

In addition to high mean yield, a desirable variety was hence considered stable when its regression coefficient (b), equaled a unit (b=1), with the deviation from regression equaled zero (S^2d =0) and at least high mean value of the grand mean.

CHAPTER FOUR

4.0 RESULTS.

4.1. Soils and climatic conditions.

Soil characteristics slightly varied across locations (environments). TAC and SUA sites had clay while Lumemo had sandy clay soil. Lumemo and SUA each had slightly acidic soils whereas TAC soils were medium acidic. Soils of Lumemo, however, had other characteristics similar to those at TAC. At these three sites, soils therefore had medium percentage organic matter, low percentage of total organic nitrogen, high available phosphorous, medium cation exchange capacity and very low exchangeable sodium. On the other hand, SUA site had medium percentage organic carbon, low percentage total nitrogen, medium available phosphorous, low cation exchange capacity and high exchangeable magnesium. (Appendix i, ii and iii).

Due to late onset of rainfall, planting was delayed in all locations until March. In terms of total rainfall, the highest rainfall was recorded during March and April. (Appendix iv and v), Initially Lumemo site was chosen for rainfed lowland while TAC was for irrigation and SUA for purely upland conditions.

Each location received ten rice genotypes for evaluation. However, at TAC and Lumemo rains which commenced in March were inadequate and did not sustain the crop to ripening stage. Since there was no irrigation at Lumemo, only four early maturing lines reached physiological maturity. SUA site that was supposed to be

rainfed upland seriously suffered inadequate soil moisture at seeding operation and at maximum tillering stage.

This condition therefore necessitated the application of supplementary irrigation three times a week for crop growth and development. At TAC, the irrigation did not take place from the early stage of crop growth; instead full irrigation was conducted when early maturing genotypes had reached booting and the late maturing genotypes had reached maximum tillering stage.

Temperatures varied between 19.6-35.2°C at Lumemo/TAC and 15.5^{0}C-35.2^{0}C at SUA during the season. Minimum temperatures lowered the ambient temperatures and consequently affected the performance of the rice genotypes. Generally, crop growth was good in the early stage and later retarded the rate of most of physiological activities from flowering to maturity. SUA site was more affected than TAC because of moisture and temperature differences. Early maturing lines were not affected and apart from adequate moisture, differences among them were due to variations in climatic factors in the locations (ecosystems).

Some disease incidences like leaf and panicle blast caused by (*Pyricularia grisea*), sheath rot (*Acrocylindrium oryzae*) and brown leaf spot (*Helminthospora oryza L.*) were observed from late vegetative to ripening phases at SUA and TAC. The diseases could be confused with low temperature effect, however, their severity was not high.

4.2. Yield and yield components

4.2.1. Days to 50% flowering

The genotypes significantly (P≤0.05) differed in attaining days to 50% flowering in all environments. At TAC and SUA entry, SSD 1 was the earliest while TXD 275 was the latest to flower (Tables 2 and 3).

There was significant (P≤0.05) difference in days to 50% flowering among genotypes when the two locations were combined (Table 4). The pooled results revealed that SSD1 flowered earliest while TXD 275 flowered latest. However, from the combined analysis of variance of data from SUA and TAC, significant (P≤0.01) variation of the trait was observed for location, genotypes and G x E components (Appendix vi)

4.2.2. Plant height.

Plant height exhibited significant (P≤0.05) difference among genotypes evaluated in all environments. At TAC variety Supa and M15A and TXD 220 were statistically the tallest while Line 88 and Line 85 were the shortest (Table 2). At SUA, SSD 5 was the tallest whereas Line 85 was the shortest in plant stature (Table 3). No lodging incidences in all environments were observed.

Results of combined analysis of variance over two locations indicated highly significant (P≤ 0.01) variation on plant height from which SSD 5 and SSD3 were the tallest while Line 85 had the shortest plant stature (Table 4).

The variation in plant height from the combined analysis of the two locations due to genotype, location, and genotype x environment interaction were highly significant (P≤ 0.01) (Appendix vi).

4.2.3. Panicle length

There were significant (P≤0.05) differences in panicle length among the genotypes tested in all environments.

At TAC site, variety Supa, TXD 275 and TXD 220 each with 24.67cm depicted the longest panicle length although not statistically different to M 55. Shortest panicle length was recorded from SSD 5 (Table 2). At SUA site, SSD 5 and SSD3 had statistically the longest panicle length. The shortest panicle length was recorded from TXD 220. (Table 3).

Combined analysis of means averaged over two sites showed significant (P≤0.05) variations in panicle length among the entries. Lines M55 and M15A each with 23.33cm had the longest panicle although they were not statistically different from SSD 1, SSD 3, SSD5 and Supa. Shortest panicle length was from Line 85 (Table 4).

In appendix vi, genotypes, location and genotype x environment interaction were also highly significant (P≤ 0.01) for this trait.

4.2.4. Panicle weight

There were significant (P≤ 0.05 differences in panicle weights among genotypes tested in all locations. Line 85 gave highest panicle weight whereas TXD 275 produced the lowest panicle weight from TAC, SUA and from the pooled results of the two locations (Tables 2,3 and 4).

The variations due to location and genotype x environment were non- significant for panicle weight (Appendix vi).

4.2.5. Productive tillers per square meter

Productive tiller number per square metre showed significant ($P \leq 0.05$) differences among genotypes at TAC and SUA site (Tables 2 and 3). At TAC, highest tillers per square metre were obtained from Line 85 though did not significantly differ from M55 (Table 2). From SUA and pooled analysis of the TAC and SUA locations, the highest tillers/m^2 were obtained from M15A. Lowest tillers per m^2 from all environments were obtained from TXD 220 (Tables 2, 3, and 4).

Highly significant ($P \leq 0.01$) variations due to environment, genotype and genotype x environment interaction (Appendix vi) for this trait were observed.

4.2.6. Number of panicles per plant

Significant ($P \leq 0.05$) differences of panicles per hill among genotypes was observed at TAC and SUA (Tables 2 and 3). Line 85 at TAC recorded highest number of panicles per plant (Table 2). At SUA and from pooled results, the highest number of panicles/plant was produced from Line 88 whereas the results from the pooled data indicated that Line 88 had the highest value, however it did not differ statistically from Line 85 (Table 3). Lowest number of panicles/plant recorded from variety Supa at all locations. (Table 2,3 and 4).

The variation on number of panicles per plant due to location and genotypes were highly significant (P≤0.01) while genotype x environment interaction was non-significant (Appendix vi).

4.2.7. Number of filled grain per panicle

Number of filled grains per panicle exhibited significant (P≤0.05) difference among genotypes in all locations (Tables 2 and 3). At TAC, SUA and pooled data over two environments, SSD1 had the highest number of filled grains/panicle (Tables 2, 3, and 4). While M15A gave the lowest number of filled grains per panicle at TAC and pooled results of TAC and SUA, TXD 220 recorded the lowest filled grains per panicle at SUA.

For this trait, genotype x environment interaction was non-significant. However, highly significant (P≤0.01) variation was observed for genotypes and location component (Appendix vi)

4.2.8. Percent spikelet fertility.

Significant (P≤ 0.05) differences in spikelet percent fertility were observed for TAC and SUA (Tables 2 and 3). The results from TAC and pooled data for TAC and SUA sites indicated SSD1 to have consistently produced the highest spikelet fertility, but did not significantly differ from SSD 5 and M 55 (Table 2 and 4). At SUA, M55 that statistically performed equally with SSD 1 recorded the highest spikelet fertility among the genotypes (Table 3). Lines TXD 275, M15A, and TXD 220 recorded the lowest fertility at TAC, SUA and pooled results of the two combined locations (Table2, 3 and

4). For this parameter, highly significant (P≤0.01) differences were observed for genotype and genotype x environment. On the other hand, location component was non-significant (Appendix vi)

4.2.9. 1000 grain weight

The genotypes significantly (P≤0.05) differed in their 1000 grain weight at TAC and SUA Farm sites (Tables 2 and 3). At the sites of TAC, SUA, and combined data over two locations, consistently gave the largest 1000-grain weight (Tables 2,3,and 4). Line TXD 220 gave the lowest 1000 grain weight at TAC whereas at SUA site Line SSD 1 produced the heaviest grain weight (Tables 2 and 3). In the combined analysis over two locations, TXD 275 recorded the lowest 1000-grain weight. However, lines SSD1, SSD5 and SSD3 statistically produced similar 1000 grain weight (Table 4).

The combined analysis revealed highly significant (P≤0.01) location and genotype differences while genotype x environment interaction for the trait was non-significant (Appendix vi).

Table 2: Yield and yield components of ten rice genotypes (n=30) at TAC (Supplementary irrigation).

Variety/lines	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	Panicle weight (g)	Tillers/ m^2	Panicles/ plant	Filled grains/ panicle	Percent spikelet fertility	1000 grain weight (g)	Grain yield (t/ha)
SSD 5	65.00f	122.00c	21.00e	22.00cf	103.30c	7.33cf	119.90b	85.95a	33.67b	4.08d
SSD 3	65.00f	123.00c	22.33d	25.33cd	120.00b	8.00d	141.20ab	79.13b	33.43b	4.30d
Line 85	85.67c	92.67e	22.67cd	30.00a	132,30a	10.33a	132.30b	71.13d	28.63e	6.63a
M15 A	75.67e	132.00a	23.67b	24.67d	120.70b	8.67e	104.10b	76.35b	29.40d	6.24b
Supa	80.67d	132.00a	24.67a	26.33bc	127.30ab	5.00h	120.50b	75.97bc	30.67c	4.92c
TXD 275	90.00a	96.33d	24.67a	20.67f	124.30ab	7.67de	114.30b	62.60e	28.00e	4.36d
Line 88	87.67b	91.67e	23.00c	28.00bcd	126.00ab	9.33b	212.10b	72.38cd	28.53e	5.12c
TXD 220	89.67a	129.70a	24.67a	22.33e	60.33d	6.33g	122.70b	65.71e	27.33f	4.26d
SSD 1	64.33f	120.70c	22.33d	23.00e	104.30c	7.33cf	192.10a	86.44a	34.60a	4.01d
M55	74.67e	126.7 b	24.33a	29.33ab	105.70c	7.00f	129.70b	83.51a	30.83c	3.34e
Mean	77.83	116.86	23.33	24.77	112.43	7.70	129.79	75.92	30.51	4.73
SE	0.42	0.76	0.16	0.50	2.79	0.17	18.78	1.24	0.22	0.13
% CV	2.93	3.58	3.68	10.98	13.61	11.96	25.07	8.94	3.98	14.76

Means within column followed by the same letter(s) are not significantly different from each other according to DMRT at 5% level

Table 3: Mean performance of ten rice genotypes (n=30) at SUA- (Rainfed upland condition).

Variety/lines	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	Panicle weight (g)	Tillers/ m^2	Panicles/ hill	Filled grains /panicle	Percent spikelet fertility	1000 grain weight (g)	Grain yield (t/ha)
SSD 5	67.67f	127.00a	23.67a	22.67ef	123.70d	5.67de	96.47b	86.67b	32.00b	3.31c
SSD 3	67.00fg	118.00b	23.33a	24.33bcde	147.30b	6.67c	98.97b	84.77b	32.33bc	4.39a
Line 85	104.00b	66.33g	16.67e	27.33a	115.30e	7.33b	73.77cd	60.80d	25.67f	2.12f
M15A	89.30e	107.70c	23.00a	23.00def	194.70a	6.67c	65.23ef	50.19f	27.33de	2.61e
Supa	100.70c	107.00c	21.00d	24.67cd	115.00e	5.33e	81.13c	65.13c	28.33d	1.89f
TXD 275	109.70a	72.67f	17.33e	19.33g	108.70f	7.00bc	70.20def	54.34e	25.33f	2.15f
Line 88	104.70b	75.00e	17.33e	25.00bc	150.00b	8.67a	72.77de	61.52d	27.33de	3.13cd
TXD220	104.00b	72.00f	16.67e	21.33f	49.67g	6.00d	63.37f	53.39e	26.33ef	0.72g
SSD 1	66.33g	106.70c	21.67c	23.67cde	114.30e	5.33e	108.50a	89.20a	34.33a	3.95b
M 55	90.33d	102.30d	22.33b	26.00ab	138.30c	5.33e	93.13b	89.30a	31.33c	2.91de
Mean	90.37	95.47	20.30	23.73	125.70	6.40	82.36	69.53	29.13	2.72
SE	0.29	0.44	0.22	0.58	1.86	0.14	2.51	0.81	0.38	0.122
% CV	1.76	2.54	5.91	13.35	8.11	8.01	16.72	6.42	7.20	24.52

Means within column followed by the same letter(s) are not significantly different from each other according to DMRT at 5% level

Table 4: Mean performance of ten rice genotypes (n=60) combined over two locations (TAC and SUA).

Variety/line	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	Panicle weight (g)	Tillers/ m^2	Panicles /hill	Filled grains /panicle	Percent spikelet fertility (%)	1000grain weight (g)	Grain Yield (t/ha)
SSD5	66.33e	124.50a	22.33a	22.33cd	113.50c	6.50cd	108.20bc	86.31a	33.47a	3.70cd
SSD3	66.00f	120.50ab	22.83a	24.83bc	133.70b	7.33bc	120.10b	81.95a	32.88ab	4.35ab
Line 85	94.83b	79.60f	19.67d	28.67a	123.80bc	8.83a	103.00bc	65.91bc	27.15c	4.54a
M15A	82.60d	119.80b	23.33a	23.83bc	157.70a	7.67b	84.65c	83.21bc	28.48dc	4.43ab
Supa	90.67c	119.50b	22.83a	25.50abc	121.20bc	5.17c	100.80bc	70.55b	29.50cd	3.40cdc
TXD 275	99.83a	85.50e	21.00bc	20.00d	116.50c	7.33bc	92.23bc	60.14c	26.67e	2.92ef
Line 88	96.17ab	83.33ef	20.17cd	25.20abc	138.00b	9.00a	96.95bc	66.95bc	28.07dc	4.29ab
TXD 220	96.83ab	100.80d	20.67cd	21.83cd	55.00d	6.17d	93.05bc	59.55c	26.83e	2.49f
SSD1	65.33f	113.70c	22.00ab	23.33bcd	109.30c	6.33d	150.30a	87.82a	34.47a	3.98abc
M55	82.50d	114.50c	23.33a	26.67ab	122.00bc	6.17d	111.40bc	86.40a	31.22bc	3.13def
Mean	84.43	106.17	21.82	24.25	119.07	7.05	106.07	72.89	29.87	3.72
SE	1.250	1.40	0.43	1.21	5.31	0.30	10.20	2.35	0.70	0.35
%CV	3.63	3.22	4.78	12.18	10.92	10.53	23.55	7.89	5.76	16.12

Means within column followed by the same letter(s) are not significantly different from each other according to DMRT at 5% level

4.2.10. Grain yield (t/ha).

The tested genotypes exhibited significant ($P \leq 0.05$) differences in yield performance in all environments. At SUA and the pooled results of SUA and TAC lowest yield was indicated from TXD 220; while lowest highest yield at TAC was recorded from M55 (Table 2 and 4). At TAC and pooled results of the two sites indicated that Line 85 gave the highest yield (Tables 2 and 4). The results also indicated that SSD 3 produced the highest yield at SUA whereas from the combined analysis, Line 85 gave the highest grain yield and did not differ statistically from grain yields obtained from SSD 3, M15A, Line 88 and SSD 1 (Tables 3 and 4).

The combined analysis exhibited highly significant ($P \leq 0.01$) environment, genotypes and genotype x environment interaction on yield performance (Appendix vi).

4.3. Grain quality

4.3.1. Grain length (size)

There were significant ($P \leq 0.05$) differences in grain length (size) at TAC and SUA sites. At TAC, the longest grain length was obtained from variety Supa and the shortest grain length was recorded from M15A (Table 5). At SUA and the combined data over two locations, SSD1 recorded the longest grain length.

Shortest grain length at TAC and in a combined data over two locations was recorded from TXD 275 and M15A respectively (Tables 6 and 7). For TAC, the grain sizes of three genotypes were very long, six genotypes were long and one entry had medium

grain sizes. At SUA grain sizes were categorized into two groups:-seven genotypes with medium and three genotypes possessing very long grain sizes.

The combined analysis of variance also revealed that there were no significant differences between environments, genotypes and genotype x environment interaction for the trait (Appendix viii).

4.3.2. Grain length: breadth ratio (Shape)

The genotypes did not show significant ($P>0.05$) differences among themselves for the grain shape at both locations (Tables 5 and 6). However, when combined the two locations, the trait indicated significant differences ($P\leq0.05$) among genotypes where Supa (control) recorded the largest shape whereas the smallest shape was obtained from SSD 3. All except two of the genotypes tested were intermediate (Table 7). Significant variations on grain shape due to location and genotype were observed when the TAC and SUA were combined. (Appendix viii)

4.3.3. Chalkiness (Opacity)

Chalkiness significantly ($P\leq0.05$) differed among genotypes in all the locations tested. At TAC, highest chalkiness was observed from TXD 275 while at SUA highest chalkiness was recorded from TXD 220 (Table 17 and 18). Supa recorded the lowest chalkiness from TAC, SUA and the combined data for the two sites (Tables 5, 6 and 7).

All entries tested contained small amount of chalkiness at TAC and SUA (Tables 5 and 6). After combining the data over two locations, chalkiness showed significant

($P \leq 0.05$) differences among the genotypes evaluated, where TXD 220 exhibited the highest chalkiness (Table 7). From the combined analysis, highly significant ($P \leq (0.01)$ differences were observed for environment and genotype components (Appendix viii), while genotype x environment interaction was non-significant.

4.3.4.Gelatinization temperature (GT)

Gelatinization temperature showed significant ($P \leq 0.05$) differences among genotypes tested at TAC, and combined results of the two locations. At TAC, highest GT was obtained from Line 88 (Table 5). When two locations were combined, SSD 1 produced highest GT (Table 7). Supa recorded lowest (GT) from TAC and from pooled results of the two combined locations. Genotypes tested were classified into high, high/intermediate and low GT types (Table 5 and 7). When two locations were combined, the variety Supa had the lowest GT while SSD1 produced highest GT. Five of genotypes evaluated, the other five had low and the other five had intermediate GT types (Table 7). Significant variation was observed for genotype, location and genotype x environment interaction components (Appendix viii).

4.3.5. Amylose content (AC).

Amylose content was significant ($P \leq 0.05$) at TAC, SUA and data for the combined analysis for the two locations. (Table 5, 6 and 7). At TAC, Supa had the highest amylose content while Line 85 exhibited the lowest amylose content. At SUA and data for two combined locations revealed that TXD 220 recorded the highest amylose content whereas SSD 1 had lowest amylose content. Variations of the trait due to

environments, genotypes and genotype x environment interaction were highly significant ($P \leq 0.05$) (Appendix viii).

4.3.6. Gel consistency (GC)

Significant ($P \leq 0.05$) difference on gel consistency among the tested genotypes was observed at TAC, SUA and from the pooled data of the two locations. (Tables 5, 6 and 7). From all the environments, the soft gel consistency was obtained from variety Supa and hard gel consistency was noted from SSD 5. Five genotypes had soft gel consistency and the other five showed medium gel consistency at TAC (Table 5).

Results at SUA also indicated that five genotypes were categorized into soft, one into medium soft, three into medium and one into hard gel consistency (Table 6).

From the combined analysis of two locations, five entries were grouped into soft GC, two into medium soft GC and three into medium GC. (Table 7). From appendix viii, highly significant differences were observed for environments, genotypes and genotype x environment interaction.

Table 5: Performance of ten rice genotypes (n=30) on physical and biochemical traits at TAC.

Variety/line	GL (mm)	Size	L/B ratio	Shape	Chalkiness	Opacity	GT	Description	AC	Description	GC	Description
SSD5	7.53ab	Very long	3.31	Slender	1.33cd	Small	4.67d	Intermediate	24.28e	Intermediate	53.67g	Medium
SSD3	6.70cde	Long	2.48	Intermediate	1.00cd	Small	4.67d	Intermediate	24.29e	Intermediate	59.33e	Medium
Line 85	6.93bcde	Long	2.87	Intermediate	3.00ab	Small	1.67e	High	23.33e	Intermediate	60.33e	Medium
M15A	6.20e	Long	2.58	Intermediate	2.33bc	Small	6.33abc	Low	30.51b	High	124.70b	Soft
Supa	7.77a	Very long	3.43	Slender	0.33d	Small	7.00a	Low	39.38a	High	141.30a	Soft
TXD 275	6.70cde	Long	2.95	Intermediate	4.33a	Small	6.33abc	Low	28.71c	High	104.30c	Soft
Line 88	6.40de	Medium	2.98	Intermediate	2.33bc	Small	6.00bc	Low	26.46d	High	97.67d	Soft
TXD 220	7.27abc	Long	2.65	Intermediate	3.67ab	Small	6.67ab	Low	37.81a	High	127.0b	Soft
SSD1	7.63ab	Very long	2.88	Intermediate	1.00cd	Small	4.67d	Intermediate	24.58e	Intermediate	58.00ef	Medium
M55	7.07abcd	Long	2.88	Intermediate	3.67ab	Small	5.67c	Intermediate	24.57e	Intermediate	55.33eg	Medium
Mean	7.02		2.90		1.76	Small	5.37		28.39		88.17	
SE	0.25				0.14	Small	0.28		0.57		0.99	
% CV	5.71		16.78		10.24	Small	9.07		3.50		1.95	

Means within column followed by the same letter(s) are not significantly different from each other according to DMRT at 5% level

Note: GL=Grain length; L/B= Grain length:breadth ratio; GT= Gelatinization temperature; AC= Amylose content; GC= Gel consistency

Table 6: Performance of rice ten genotypes (n=30) on physical and biochemical traits at SUA.

Variety/line	GL (mm)	Size	L:B ratio	Shape	Chalkiness	Opacity	GT	Description	AC	Description	GC	Description
SSD5	7.23ab	Long	2.97	Intermediate	0.67cd	Small	5.67	Low	25.03cd	High	58.33h	Medium
SSD3	6.53cde	Medium	2.63	Intermediate	1.00bcd	Small	6.00	Low	25.58bcd	High	60.00h	Medium
Line 85	6.60bcd	Medium	2.83	Intermediate	2.33abc	Small	6.33	Low	28.56b	High	74.67g	Medium soft
M15A	6.30de	Medium	2.87	Intermediate	2.67ab	Small	6.33	Low	28.26bc	High	130.00c	Soft
Supa	7.43a	Long	3.20	Slender	0.00d	None	7.00	Low	26.76bc	High	149.33a	Soft
TXD 275	5.00e	Short	2.40	Intermediate	3.00ab	Small	6.33	Low	25.47bcd	High	122.33d	Soft
Line 88	6.23de	Medium	2.68	Intermediate	0.67cd	Small	6.33	Low	26.92bc	High	104.33e	Soft
TXD 220	6.33cde	Medium	3.22	Slender	4.00a	Small	6.33	Low	32.19a	High	135.33b	Soft
SSD1	7.60a	Very long	2.89	Intermediate	0.67cd	Small	5.00	Intermediat	23.33d	Intermediate	59.33h	Medium
M55	7.00abc	Long	2.98	Intermediate	1.33bcd	Small	6.00	Low	26.82bc	High	97.33f	Hard
Mean	6.72		2.06		1.63		6.13		26.89		99.07	
SE	0.21				0.45				0.18		1.58	
% CV	5.36		18.26		14.94		7.43		6.88		2.76	

Means within column followed by the same letter(s) are not significantly different from each other according to DMRT at 5% level
Note: GL=Grain length; L/B= Grain length:breadth ratio; GT= Gelatinization temperature; AC= Amylose content; GC= Gel consistency

Table 7: Performance of rice genotypes (n=60) on physical and cooking and eating traits averaged combined over two locations (TAC and SUA).

Variety/line	GL (mm)	Size	LB ratio	Shape	Chalkiness	Opacity	GT	Description	AC	Description	GC	Description
SSD5	7.38ab	Long	3.14ab	Slender	1.00cd	Small	5.17e	Intermediate	24.66fg	Intermediat	56.00I	Medium
SSD3	6.62cde	Long	2.56b	Intermediate	1.00cd	Small	5.33de	Intermediate	24.93fg	Intermediat	59.67h	Medium
Line 85	6.77cde	Long	2.85ab	Intermediate	2.67b	Small	4.00f	Intermediate	25.95de	High	67.50g	Medium soft
M15A	6.25f	Medium	2.73ab	Intermediate	2.50b	Small	6.33bc	Low	29.39c	High	127.30c	Soft
Supa	7.60a	Very long	3.31a	Slender	0.17d	Small	7.00a	Low	33.06b	High	145.30a	Soft
TXD 275	6.30ef	Medium	2.68ab	Intermediate	3.67a	Small	6.33bc	Low	27.09d	High	113.30d	Soft
Line 88	6.32def	Medium	2.78ab	Intermediate	1.50c	Small	6.17bc	Low	26.69de	High	101.00e	Soft
TXD 220	6.80cd	Long	2.94ab	Intermediate	3.83a	Small	6.50ab	Low	35.00a	High	131.02b	Soft
SSD1	7.62a	Very long	2.88ab	Intermediate	0.83cd	Small	4.83e	Intermediate	23.95g	Intermediat	58.67hi	Medium
M55	7.03bc	Long	2.93ab	Intermediate	2.50b	Small	5.83cd	Intermediate	25.73d-g	High	76.17f	Medium soft
Mean	6.87		2.88		1.97		5.75		27.65		93.62	
SE	0.16		0.21		0.14		0.19		0.61		0.93	
% CV	5.54		17.54		14.04		8.20		5.38		2.44	

Means within column followed by the same letter(s) are not significantly different from each other according to DMRT at 5% level
Note: GL=Grain length; L/B= Grain length:breadth ratio; GT= Gelatinization temperature; AC= Amylose content; GC= Gel consistency

4.4. Estimates of variance components and genetic parameters.

4.4.1. Yield and yield components variances.

Variance components and genetic parameters for yield and some yield components of ten rice genotypes combined from two environments (TAC and SUA) are shown on table 8. The genotypic variances were lower than phenotypic variances for grain yields, panicle length and number of panicles/plant. For the other traits, the reverse was true. The genotype x environment interaction variance was not important for panicle weight, 1000-grain weight and number of filled grains/panicle.

The heritability estimates were higher for all the traits except grain yields, panicle length and number of tillers/m^2.

Expected genetic advance was generally low for all the variables. Yield and panicle length recorded the lowest expected genetic advance estimates.

4.4.2. Grain quality variances.

Table 9 shows the variance components for grain quality characters of ten genotypes combined over two environments. The genetic variance was higher than location and genotype x environment interaction variances for all the characters except chalkiness, amylose content and gelatinization temperature. There were no environmental influences on the performance of amylose content. While environmental variance component was unimportant for grain shape, the genotype x environment was however very important for amylose content and gelatinization temperature.

Highest heritability estimate was obtained for gel consistency followed by grain length; whereas lowest heritability value was observed on chalkiness. Further, the expected genetic advance was highest for gel consistency and lowest for grain shape.

Table 8:Variance components of some yield components of ten rice genotypes (n=60) grown at TAC and SUA.

Character	δ^2g	δ^2l	δ^2gl	δ^2e	δ^2ph	h^2	EGA (% of mean)
Yield	-	1.88	1.20	1.20	0.00	-	-
Plant height	234.67	215.03	131.16	11.69	302.20	77.7	32.94
Panicle length	-	3.94	6.32	1.00	3.34	-	-
Tillers/m^2	497.69	44.06	355.87	169.04	703.80	10.7	32.46
Panicle weight	6.12	-	-	8.72	7.57	80.8	18.90
Percent fertility	106.91	238.0	39.50	33.10	132.18	80.9	49.95
1000grain weight	8.29	1.11	-	2.96	8.78	94.4	19.29
Panicles/plant	1.26	0.94	0.29	0.56	1.50	84	49.98
Filled grains/plant	279.60	1117.51	-	623.95	383.59	72.9	27.72
50% flowering	159.93	66.60	33.84	9.38	178.41	89.6	29.97

δ^2g =genetic variance

δ^2l =location (environment) variance

δ^2gl =genotype location variance

δ^2e =error variance

δ^2_{ph} =phenotypic variance

h^2 =heritability

EGA = Expected genetic advance.

Table 9: Variance components for grain quality characters of ten rice genotypes (n=60) grown at TAC and SUA.

Character	$\delta^2 g$	$\delta^2 l$	$\delta^2 gl$	$\delta^2 e$	$\delta^2 ph$	h^2	EGA (% of mean)
Grain length	0.25	0.03	0.01	0.15	0.28	89.3	14.17
Grain length : breadth ratio	0.02	-	-	0.26	0.06	33.3	5.34
Chalkiness	0.02	0.12	0.01	0.07	0.17	11.8	36.4
Amylose content	7.66	-	11.55	2.21	13.80	55.5	15.36
Gelatinization temperature	0.26	0.18	0.99	0.22	0.82	35.4	17.68
Gel consistency	1123.72	51.61	70.92	5.21	1160.05	96.9	72.60

$\delta^2 g$ =genetic variance $\delta^2 e$ =error variance

$\delta^2 l$ =location (environment) variance δ^2_{ph} =phenotypic variance

$\delta^2 gl$ =genotype location variance h^2 =heritability

EGA = expected genetic advance

4.5. Correlation analysis.

5.5.1. Simple Correlation for yield and yield attributes.

Associations among yield and yield components at TAC are presented on table 10. Yield was found to have a positive and significant ($P \leq 0.05$) correlation with panicle weight, tillers/m^2 and panicles/plant. The other correlations with grain yield were not significant. The 1000-grain weight, which is one of the yield components, was negatively correlated with days to flowering, panicle length and positively correlated with percent spikelet fertility and filled grains/plant. Percent spikelet fertility was negatively correlated with days to days to 50% flowering and panicle length.

Correlation coefficients of yield and yield components at SUA are presented on table 11. Grain yield was positively correlated with all the traits except days to 50% flowering and panicles/plant. On the other hand, days to 50% flowering were negatively correlated with all the traits except number of panicles/square metre. Plant height and panicle length were positively correlated with all the traits except with the number of panicles/plant. Two important yield components viz. Percent filled grains and number of panicles/plant were negatively correlated. Grain weight, which is another important yield component, was negatively correlated with panicle length. However, it was positively correlated with percent spikelet fertility.

Correlation of yields and yield components as combined over two locations (TAC and SUA Farm) are presented on table 12. When the data was combined for two sites grain yield was positively correlated with all the traits except days to 50% flowering. The highest correlation was between the grain yield and panicle weight followed by

grain yield and percent filled grains/panicle. Plant height was positively correlated with all the traits tested except number of panicles/plant. The other important correlations were all positive; and those that were negative were non-significant as indicated in table12.

4.5.2. Genotypic and Phenotypic Correlation of yield and yield components.

Genotypic and phenotypic correlations for the data combined over two locations are presented on table 13. Grain yield had less important genotypic correlations with other characters. However, the phenotypic level was positively correlated with panicle length, panicle weight, percent spikelet fertility and 1000-grain weight.

Just like with simple correlations, days to 50% flowering was negatively correlated with all the traits at both genotypic and phenotypic levels. Similarly, 1000-grain weight was positively correlated with all the traits except with days to 50% flowering. (Table 13). The genotypic and phenotypic correlations between panicle length and percent spikelet fertility, panicle weight were highly significant where genotypic were higher than phenotypic levels. Likewise, there was significant genotypic correlation between number of panicles with 1000-grain weight. The rest, which were significant, had phenotypic levels being more important than genotypic level.

4.5.3. Simple correlation for physical and biochemical characteristics of the genotypes.

Simple correlations of physical and biochemical characters of individual and combined locations are shown on tables 14, 15, and 16.

At TAC, grain length was negatively correlated with grain shape and chalkiness. Amylose content was highly and positively correlated with gel consistency and negatively correlated with gelatinization temperature. High and negative correlation was exhibited between gelatinization temperature with gel consistency (Table 14).

At SUA, grain length was negatively correlated with chalkiness and amylose content. The trait, however, was positively correlated with gelatinization temperature. Chalkiness was negatively correlated with gel consistency and with gelatinization temperature (Table 15).

A combined analysis for TAC and SUA revealed that amylose was negatively correlated with gelatinization temperature and positively correlated with gel consistency. Similarly, grain length was negatively correlated with grain shape, chalkiness and gel consistency. Apart from significant negative correlation between gel consistency and gelatinization temperature, no correlations were significant (Table 16).

4.5.4. Genotypic and phenotypic correlation of grain quality characters.

The genotypic and phenotypic correlations among the grain quality characteristics showed a similar trend with simple correlations. The respective genotypic and phenotypic correlations were close in magnitude and similar in sign. (Table 17).

Amylose content was genotypically and phenotypically positively correlated with grain length and gel consistency; and phenotypically correlated with grain shape. The trait was however, negatively correlated with gelatinization temperature at both genotypic and phenotypic levels. Grain length was negative and highly correlated with grain shape and chalkiness.

Table 10: Simple correlation coefficients among yields and yield components of ten (n=30) rice genotypes at TAC.

Variables	1	2	3	4	5	6	7	8	9	10
1.Days to 50% flowering	1.000									
2.Plant height	-0.45*	1.00								
3.Panicle length	0.45*	0.21	1.00							
4.Panicle weight	0.09	-0.15	-0.15	1.00						
5.Tillers/m^2	-0.04	-0.42*	-0.22	0.41*	1.00					
6.Percent fertility	-0.59**	0.28	-0.44*	0.36	0.14	1.00				
7.1000 grain weight	-0.82**	0.35*	-0.49**	-0.02	0.07	0.67**	1.00			
8.No. Panicles/plant	0.06	-0.64*	-0.40*	0.26	0.34	-0.12	-0.22	1.00		
9.Filled grains/panicle	-0.37*	0.05	0.17	0.20	-0.20	0.37*	0.42*	0.09	1.00	
10.Yield	0.30	-0.25	0.06	0.39*	0.41*	-0.12	0.24	0.43*	-0.11	1.00

* Significant at 5% level ** Significant at 1% level

Table 11: Simple correlation coefficients among yields and yield attributes of ten rice genotypes (n=30) components at SUA.

Variables	1	2	3	4	5	6	7	8	9	10
1.Days to 50%	1.00									
2. Plant height	-0.84**	1.00								
3. Panicle length	-0.78**	0.93**	1.000							
4. Panicle weight	-0.07	0.04	0.064	1.00						
5.Tillers/m^2	-0.25	0.41*	0.489**	0.18*	1.00					
6.Percent fertility	-0.76**	0.60**	0.584**	0.19*	0.05	1.00				
7.1000grain weight	-0.82*	0.72**	0.622**	0.18*	0.16	0.79**	1.00			
8.No.Panicles/plant	0.41*	-0.52**	-0.479**	0.05	0.26	-0.47**	-0.50**	1.00		
9.Filledgrains/panicle	-0.70	0.56**	0.544**	0.245*	-0.01	0.79**	0.72**	-0.40*	1.00	
10.Yield	-0.72**	0.54**	0.586**	0.23**	0.51**	0.63**	0.62**	-0.08	0.59**	1.00

* Significant at 5% level ** Significant at 1% level

Table 12: Simple correlation coefficients among yield and yield components averaged over two locations (TAC and SUA).

Variables	1	2	3	4	5	6	7	8	9	10
1.Days to 50%	1.00									
2.Plant height	-0.77**	1.00								
3.Panicle length	-0.61**	0.79**	1.00							
4.Panicle weight	-0.06	0.03	0.67**	1.00						
5.Tillers/m^2	-0.09	0.01	0.15	-0.23	1.00					
6.Percent spikelet fertility	-0.72**	0.54**	0.39**	0.28*	0.03	1.00				
7.1000-grain weight	-0.62**	0.60**	0.41**	0.12	0.08	0.76**	1.00			
8.No. Panicles/plant	0.02	-0.23	-0.06	0.22	-0.21	-0.15	0.31*	1.00		
9.Filled grains/panicle	-0.57	0.48**	0.46**	0.24	0.16	0.51*	0.51**	0.25	1.00	
10.Yield	-0.50**	0.46**	0.61**	0.33**	0.20	0.38**	0.33**	0.47**	0.50**	1.00

* Significant at 5% level ** Significant at 1% level

Table 13: Genotypic (top) and phenotypic (bottom) correlation coefficients of some yield components of rice genotypes (n=60) combined from TAC and SUA.

Plant characters	1	2	3	4	5	6	7	8
1. Days to 50% flowering	1.000							
2. Panicle length	-0.32*	1.00						
	(-0.35**)							
3. Panicle weight	-0.04	0.38**	1.00					
	(-0.04)	(0.42**)						
4. Tillers/m^2	-0.22	0.22	0.09	1.00				
	(-0.21)	(0.22)	(-0.09)					
5. Percent spikelet fertility	-0.41**	0. 69**	0. 36*	0.03	1.00			
	(-0.53**)	(0.50**)	(0.26**)	(0.11)				
6. 1000-grain weight	-0.63**	0.74**	0.18	0.09	0.30*	1.00		
	(-0.91**)	(0.89**)	(0.21)	(0.08)	(0.31*)			
7. No. of panicles/plant	-0.74**	-0.24	0.17	0.22	0.19	0.38*	1.00	
	(-0.82**)	-(0.33)	(0.17)	(0.23)	(0.18)	(0.33)*		
8. Yield	0.00	0.00	0.00	0.00	0.00	0.00	0.000	1.00
	(-0.75**)	(0.40**)	(0.63)**)	(0.06)	(0.28*)	(0.29*)	(0.61)**)	

*** Significant at 5% level ** Significant at 1% level**

Table 14: Simple correlations of physical and biochemical traits of ten rice genotypes at TAC.

Trait.	1	2	3	4	5	6
1.Grain length	1.00					
2.Grain length:breadth ratio	-0.42**	1.00				
3.Chalkiness	-0.36*	-0.22	1.00			
4.Gelatinization temperature	0.01	-0.07	-0.01	1.00		
5.Gel consistency	-0.09	0.05	0.06	-0.70**	1.00	
6.Amylose content	0.22	0.14	-0.03	-0.66**	0.90**	1.00

* Significant at 5% level ** Significant at 1% level

Table 15: Simple correlations of physical, cooking and eating grain qualities of some rice genotypes at SUA.

Trait.	1	2	3	4	5	6
1.Grain length	1.00					
2.Grain length:breadth ratio	0.22	1.00				
3.Chalkiness	-0.54**	0.07	1.00			
4.Gelatinization temperature	0.32*	-0.12	-0.25	1.00		
5.Gel consistency	-0.29	0.13	0.33*	-0.62**	1.00	
6.Amylose content	-0.35*	0.15	0.47**	-0.39*	0.47**	1.00

* Significant at 5% level ** Significant at 1% level

Table 16: Simple correlations of physical, cooking and eating grain qualities of ten (n=60) rice genotypes as combined over two locations (TAC and SUA).

Trait.	1	2	3	4	5	6
1.Grain length	1.00					
2.Grain length:breadth ratio	-0.33**	1.00				
3.Chalkiness	-0.37**	-0.06	1.00			
4.Gelatinization temperature	0.16	-0.06	0.01	1.00		
5.Gel consistency	-0.23*	0.08	0.15	-0.64**	1.00	
6.Amylose content	0.06	0.14	0.15	-0.52**	0.67**	1.00

* Significant at 5% level ** Significant at 1% level

Table 17: Genotypic (top) and phenotypic (bottom) correlation of some rice grain qualities from ten rice genotypes (n =60) combined from TAC and SUA.

	Grain length	Shape	Chalkiness	Gelatinization temperature	Gel consistency	Amylose content
Grain length	1.00					
Shape	-0.28*	1.00				
	(-0.27*)					
Chalkiness	-0.37**	-0.13	1.00			
	(-0.39**)	(-0.13)				
Gelatinization temperature	0.21	-0.25	0.13	1.00		
	(0.24)	(-0.24)	(0.12)			
Gel consistency	0.58**	0.21	0.17	0.19	1.00	
	(0.65**)	(0.22)	(0.21)	(0.20)		
Amylose content	0.58**	0.23	-0.05	-0.43**	0.57**	1.00
	(0.50**)	(0.25*)	(-0.04)	(-0.48**)	0.62**	

* Significant at 5% level ** Significant at 1% level

4.6. Path coefficient analysis

Results indicating direct and the indirect effects of various characters of rice from these environments are shown in table 18. Path coefficient analysis of the data revealed that panicle length and number of panicles/plant significantly exhibited positive direct effect on grain yield. All traits indirectly contributed to grain yield via panicle length except numbers of panicles/plant, tillers/m^2, and percent spikelet/panicle. The number of panicles/plant also contributed positively and directly to yield. The rest of characters contributed to yield through number of panicles/plant except for panicle length, percent spikelet fertility and 1000-grain weight and tillers/m^2. The percent spikelet fertility, which was non-significant, exhibited high direct effect on yield increase through other traits except panicles/plant. The rest of the traits exerted both weak direct and indirect influences on grain yield.

Table:18: Direct (along the diagonal) and indirect effects of various characters from results combined over two locations (TAC and SUA).

	PL	PW	TM	%SF	GW	PP	FG
PL	**0.566**	0.010	-0.004	0.055	0.057	-0.035	-0.035
PW	0.040	**0.137**	-0.007	0.239	0.016	0.119	-0.018
TM	0.082	0.031	**-0.031**	0.004	0.010	0.085	0.016
%SF	0.221	0.038	-0.001	**0.540**	0.105	-0.081	-0.038
GW	0.233	0.016	-0.002	0.107	**0.138**	-0.109	-0.038
PP	-0.036	0.030	-0.005	-0.021	-0.028	**0.548**	-0.018
FG	0.261	0.033	0.006	0.071	0.071	0.133	**-0.075**

Residual effects (factors) (PX_8) = 0.546

Key

PL= Panicle length (cm)

PW= Panicle weight (g)

TM= Tillers/m^2

% SF= Percent spikelet fertility

GW= Grain weight (g)

PP= Panicles / plant

FG= Filled grains/panicle

4.7. Stability analysis

4.7.1. Stability analysis of some yield attributes

The combined analysis of variance for three locations showed that there were significant varietal differences, environmental effects and genotypes x environmental interaction for days to 50% flowering, plant height and panicle length (Table 19). Results from regression coefficient and the deviation from regression (i.e. b and S^2d) indicate that most of the entries performed significantly ($P \leq 0.05$) stable for all the traits across environments, except M55 for days to 50% flowering.

The genotypes performed non-significantly ($P > 0.05$) different in plant height across all environments. Similarly panicle length did not significantly ($P > 0.05$) differ among the entries evaluated (Table 19).

Table 19: Estimates of stability parameters for 50% flowering, plant height and panicle length of four early maturing rice genotypes averaged over three combined locations (Lumemo, TAC and SUA).

Line	Mean 50% flowering	b	S^2d	Mean plant height	b	S^2d	Mean panicle length	b	S^2d
SSD5	64.33	0.89	2.21	119.8	0.59	0.43	22.33	1.00	0.87
SSD3	64.00	0.75	1.73	117.2	0.99	1.90	22.11	1.00	0.00
SSD1	64.44	0.65	1.96	111.8	1.29	0.31	21.56	0.50	1.73
M55	81.67	0.62*	0.11	115.6	1.42	0.87	24.00	-1.00	-5.19
Mean	68.361			116.028			22.50		
LSD(0.05)	1.816			3.297			1.288		

* Significant at 5% level

4.7.2. Stability analysis of some grain quality traits.

Results on estimates of stability of parameters for chalkiness, amylose content and gel consistent of four rice genotypes are shown in table 20. Significant ($P \leq 0.05$) differences were shown in chalkiness and gel consistency. The stability analysis of these traits assumed the existence of linear relationship between genotypes and environments. For chalkiness, SSD5 had a coefficient of regression (b_i=0.294) and that significantly ($P \leq 0.05$) differed from unit. For gel consistency the respective deviation from regression was S^2d =3.351 and S^2d=4.427 for SSD5 and SSD1. These values were significantly ($P \leq 0.05$) different from zero. SSD1 further depicted to have a regression coefficient (b_i=0.881) which was significantly ($P \leq 0.05$) different from

unit. There was no significant difference in stability performance in amylose content among the varieties tested.

Table 20: Estimates of stability of parameters for chalkiness, amylose content. and gel consistent of four rice genotypes combined over three environments.

Line	Chalkiness			Amylose			Gel		
		b	S^2d	content	b	S^2d	consistency	b	S^2d
SSD5	4.44	1.122*	3.400	24.50	0.369	1.234	49.11	0.915	5.351*
SSD3	4.67	0.694	1.627	24.66	0.656	1.596	51.00	1.061	3.084
SSD1	4.11	0.793	1.853	22.09	2.625	1.513	50.89	0.881*	4.427*
M55	5.78	1.481*	0.966	25.75	0.313	0.299	77.67	1.117	1.739
Mean	4.75			24.25			57.17		
LSD(0.05)	0.71			2.56			1.57		

* Significant at 5% level, and ** Significant at 1% level.

CHAPTER FIVE.

5.0. DISCUSSION

When crop cultivars are compared over a range of environments, their performance relative to each other may not be the same. Changes in relative performance of such genotypes across environments referred to as genotype x environment interaction may consequently limit the effectiveness of selection of superior genotypes (Fehr, 1984).

The presence of genotype x environment interaction implies the behavior of genotypes with respect to the environments under which they are evaluated. The resulting effect may be either due to the alterations to the order of genotypes from one environment to the next or changes in the absolute differences between genotypes, which leave the rank order unchanged. When genotype x environment interaction is less important, the condition may occur either when the environments are similar or when the genetic make-up of a trait is highly heritable (Allard and Bradshaw, 1964 and Kaul and Bhan, 1974).

However, genotype x environment interaction is important to plant breeders in developing cultivars to specific environment(s).

The two sites, under which the genotypes were evaluated, differed in climatic, irrigation water regimes and in soil (P availability) chemical characteristics. According to Allard and Bradshaw (1964) climatic factors are unpredictable while irrigation water and soil characteristics are predictable environmental variables. Most

of the soil variables were similar except the available P, which was higher at TAC and low at SUA site. Although the pH ranges were different between the two sites, the values were, however, near to the acceptable level (pH 6.5), which according to Patrick and Reddy (1978) and Ponnamperuma (1978) these were suitable for most nutrients availability. Nevertheless, IITA (1984) reported that the soil physical characteristics could be unimportant if there would be sufficient moisture. Temperatures varied between locations and the range at TAC was 19.5-32.5^{0}C while at SUA site was 15.5-32.5^{0}C. In both locations, temperature was progressively dropping as the rice growth stages were advancing.

It may be realized that the main factors that attributed to distinctness of environmental differences between the two locations were weather (temperature and the amount of rainfall amount), irrigation water regimes and soil chemical characteristics (P availability). These factors must have differentially affected the growth and performance of the genotypes in the two sites.

From the study, it was indicated that genotypes, environments and genotype x environmental interaction attributed to the differences in the number of days to 50% flowering that also determines maturity. Genetic variation among genotypes for days to flower has also been reported by other workers (De Datta, 1981 and Yoshida, 1981). Results also suggested that besides the presence of genetic differences, flowering duration among genotypes perhaps varied due to differences in environments by which low temperature could be one of the main factor attributed to

slow the flowering physiological activities. Similar results on genotypic sensitivity to temperature below 30-33^{0}C for anthesis and 20-25^{0}C for ripening have been reported (Yoshida, 1981 and Vergara, 1976).

Soil moisture differences between TAC and SUA was probably another factor that affected the flowering duration in reducing the plant growth and development by reducing the manufacture of photosynthates and their translocation in the plant. O'Toole (1982) also reported the variability in genotypic sensitivity responses due to differences in soil moisture regimes.

The significance of genotype x environment interaction on days to 50% flowering suggested that some genotypes were poorly adapted to moisture stress and low temperature. These conditions may have retarded the growth and development of the rice plant. Low soil moisture (Ohashi, *et al.*, 2000) and low temperature regimes (Yoshida, 1981) were observed to differentially decrease the growth and development a rice plant and consequently varying their flowering duration. Genetic x environment interactions on days to 50% flowering in rice have also been reported by other workers (Kihupi and Doto, 1989 and Kulkarni *et al.*, 1988).

The variation in plant height in this study was exhibited to be due to genotype, location and genotypes x environment interaction. The genetic variability of plant height is in agreement with earlier rice study report by IITA in 1984. The importance of location differences in the variation of plant height was probably due to the effect of low ambient temperatures and soil moisture differences particularly on late

maturing genotypes. The two environments contained varied levels of the two environmental factors above such that plant height of genotypes became more reduced at SUA than at TAC. This could be due to the effects of low temperature and insufficient soil moisture. The effect of low temperature and insufficient soil moisture on the reduction of plant height due to decreased photosynthates production and translocation to plant parts have been documented by several workers (Vergara, 1976, O'Toole and Baldia, 1982 and Ohashi *et al.*, 2000,).

The same reasons could have attributed to the significance of genotype x environment interaction on plant height. Yoshida (1981) reported the importance of low temperature in the reduction of plant height; while moisture content was indicated to cause the same effect to the rice plant (Vergara, 1976 and O'Toole and Baldia, 1982). Similar results on the effect of genotype x environment interaction on plant height variations were earlier reported (Nei, 1960.Oyedokun, 1985 and Kulkarni, *et al.*, 1988)

Just like the other variables above, panicle length and panicle weight differences were partly indicated to be genetically dependent. This finding conforms the results reported by Mackill *et al.* (1996) that there is a wide variation in panicle length and panicle weight among genotypes. Location x genotype interaction was also observed to be significant. Thus the result indicated that the contribution to the variations in these traits was perhaps due to differences in weather factors and reduced soil moisture which denied the rice plants the optimum nutrition for panicle length and

panicle weight development. Highly reduced panicle length and panicle weights due to differences of these factors were more pronounced at SUA than at TAC site. The effect of low temperature below 25-35^{0}C on panicle length (Yoshida, 1973) and moisture stress on panicle weight (Nallathambi and Robinson, 1992 and Chatterjee and Maiti, 1985) have earlier been studied.

Results obtained from number of productive tillers/m^2 indicated significant differences due to genotypes, location and genotype x environment interaction. Genetic variations on number of tillers/m^2 have also been reported in other rice studies (Vergara, 1976; De Datta, 1981 and IITA, 1984). Water regime and soil moisture differences between environments could have caused the observed variations. Based on the differences of initial rainfall in the early tillering stage at these locations, there was higher water depth at TAC than at SUA due to water impoundment, which influenced subsequent greater suppression of tiller production at the former site. Effects of water depths on the reduction of plant tillers have been studied (De Datta, 1981). The differences in soil water regimes were, therefore responsible for the variations of tillering ability of the genotypes tested in these locations. Genotype x environment interaction in tillers/m^2 has documented in rice (Kihupi and Doto, 1989).

The importance of genotype, location and genotype x environment interaction was observed for percent spikelet fertility. Rice genetic variability in filled grains/panicle and percent spikelet fertility has been earlier reported by Vergara (1976); Yoshida

(1981) and Mackill *et al.* (1996). The climatic variable especially the low temperature and soil moisture differences could have differentially reduced the photosynthetic activities of the plant and consequently affecting the grain filling potential of most genotypes evaluated. Also, in Tanzania the fertility of late planted crop, whose flowering stage coincides with the cold temperatures in June/July is highly affected. This is one of the reasons that in all the rice farms in Usangu plains (Such as Mbarali and Kapunga) double cropping is not feasible (KATRIN Report, 1978 and 1979). Low temperatures below maximum/minimum 32/20^{0}C have been reported to reduce percent spikelet fertility (Choudhury and Ghildayal, 1970 and Matsushima, 1980). Similarly, the effect of moisture stress on the reduction of the number of filled grains and percent spikelet fertility from panicle initiation to flowering have been studied by several rice researchers (Hsiao, 1982; De Datta, 1981; O'Toole and De Datta, 1986).

The significant location and genotype x environment interaction in percent spikelet fertility among genotypes suggests the existence of different environment factors between the locations for the response of percent spikelet fertility. Soil moisture and low temperature regimes were probably responsible for the percent fertility differences between the two locations. Matsushima, (1980) reported that percent spikelet fertility, which is determined from panicle initiation to full flowering is significantly affected by unfavorable conditions like water, nutrients and space deficiency. The scientisr also pointed out that lower temperature (17-19^{0}C) is another factor responsible in reducing the grain filling. Other workres (Chamberlin and

Insomphun, 1982 and Kihupi and Doto, 1984) have noted the presence of genotype x environment interaction in percent spikelet fertility in rice.

For 1000-grain weight, variations due to genotype x environment was not important as compared to genotype and locations differences. Genetic differences among the genotypes on the trait have also been recorded (Mackill *et al.*, 1996). Similarly, the differences could be attributed due to differences in climatic and soil factors. Low temperature, being the probable growing environmental factor had variably retarded production of photosynthates and finally bringing about differences in the 1000-grain weight.

In Tanzania the spikelet fertility of late planted crop, whose flowering stage coincides with the cold temperatures in June/July is highly affected. This is one of the main reasons that in all rice farms in Usangu plain (such as Mbarali and Kapunga) double cropping is not feasible (Annual Rice Research, 1978 and 1979). The argument conforms to findings reported by Choudhury and Ghildayal, (1970) who noted that the optimum maximum/minimum temperature 32/20^{0}C is adequate for greater 1000-grain weight and other yield components; and below these temperatures, lighter grains are obtained. Moisture stress, which occurred at SUA, could have been the cause of lighter grains at this site than at TAC. Matsushima (1980) pointed out that a higher grain weight can be obtained when crops are not stressed by nutrient availability near heading.

Rice yields are influenced by a number of interrelated diverse environmental and biological factors whose effects are difficult to separate (De Datta, 1981). Genotype x environment interaction was important to grain yield due to differences in environments under which the genotypes were tested. From the results, genotype x environment interaction indicated that some of genotypes were poorly adapted to these environments. As mentioned earlier, environmental variations attributed to these variations could be due to climatic and soil water regimes. The factors responsible in limiting rice production like climatic factors are unpredictable while soil water regimes are predictable. Several rice workers have reported the importance of climatic factors and soil moisture regimes in yield reduction (Sasaki and Wada, 1973; Matsushima, 1980; Yoshida, 1981; Hsiano, 1982; Chatterjee and Maiti, 1985; O'Toole and De Datta, 1986 and Ohashi *et al.*, 2000;). Other workers (Oyedokun, 1985; Chamberlin and Insomphun, 1982 and Kihupi and Doto, 1989) have reported significant genotype x environment interaction on yields.

The study further revealed that in areas of marginal rainfall and cool temperature regimes, the use of early maturing genotypes is ideal to avoid the stress that would affect their growth and development. The late maturing genotypes appeared to be appreciably affected by these factors.

According to Fehr (1987), when unpredictable environmental factors are involved it becomes difficult to rely on results obtained for the development of genotypes for different locations through independent selection and testing program. The

significance of genotype x environment interaction implies that in order to reduce the environment variance, further evaluation of the traits in several seasons/years, increasing either number of replications or testing environments would be necessary. Rice breeders particularly for rainfed lowland rice have been assigning low priority to grain quality in rice improvement. The developed varieties have apparently suffered rejection by farmers due to their unacceptable marketing, milling, cooking, eating, and nutritional qualities. This emphasizes the fact that grain quality should be a priority in rice breeding programs. However, Mackill *et al.* (1996) reported that grain quality is also affected by environmental factors.

From this study, genotypes varied in their grain lengths (sizes) in each location and pooled data over two locations. The importance of genotypic variance from the combined analysis suggested the genetic differences in grain length among the genotypes tested. The existences of genetic variations among genotypes have been reported (Jennings *et al.*, 1979 and Mackill *et al.*, 1996). The differential responses of genotypes in grain size over locations also indicated that environmental factors were not the same. One of the most important factors that contributed to the variation of grain sizes was perhaps the difference in irrigation water regime.

Significant difference on grain shape was only observed when data over two locations were pooled together, suggesting the importance of the overall effect of environmental factors between the growing environments. Although irrigation regimes were different, it is further suggested that the genotypes utilized the available

soil moisture for optimal development of grain length and width at the shortest time possible. The results, therefore, indicated that grain shape requires short duration to be subjected to soil moisture content to attain its full shape and hence it is less variable. The faster rate of grain shape attainment was reported to complete in 14 days after flowering (de Rosario, 1967), and was further documented by Unnevehr *et al.* (1992) to be less variable as compared to grain size.

Considering both grain length (size) and length: breadth ratio (shape) revealed that genotypes at TAC were very long, long and medium, whereas their shapes were intermediate and slender. At SUA, most genotypes tested were long to medium grain sizes, and slender to intermediate shaped grains. The relatively less variability of grain shape was indicated in the results from the variance components where location, genotype and genotypes x environment interaction were not important among genotypes. This could be due to its genetic characteristic nature of grain shape being fixed in the early generations; implying that it is less affected by no-heritable factors. Early generations genetic fixation of rice grain shape has been reported by Mackill *et al.* (1996).

From the results, chalkiness levels were very low and varied among the genotypes. The variance components depicted that chalkiness variations were due to differences in genotype and location. Hoseney (1986) reported differences in chalkiness and that chalkiness was genetically controlled. Variations in chalkiness levels would be attributed mainly by the location differences in low temperature after flowering in

both locations. However, differences for irrigation water regimes could be another factor, which contributed to the differences in chalkiness levels. Several workers reported that chalkiness is influenced by several environmental factors; and amongst, are low temperature and water management differences (Chatterjee and Maiti, 1985, Cheaney and Wyche, 1955; and Villupillai and Pandey, 1990). In addition, Resurrection *et al.* (1977) emphasized that the influence of low temperature after flowering was found to reduce chalkiness and vice versa.

The importance of genotype on the variations of gelatinization temperature suggested that the variability of the trait could be due to the genetic differences among the genotypes. Genetic variations among rice genotypes on gelatinization temperature have been documented (Fan *et al.*, 1999). The inconsistency of the performance of genotypes indicated the differences in the environmental factors, which contributed to the changes of gelatinization temperature across locations. Location variance component promoted variations in gelatinization temperature through the effect of low temperatures during flowering. This is in agreement with results reported by Mackill *et al.* (1996), that temperature variations influence gelatinization temperature of a variety. Yoshida (1981) also reported that temperature below 30-33^{0}C after flowering lowers gelatinization temperature of a variety and vice versa

The significant differences among genotypes in each individual site indicated that genotypes tested were genetically different in amylose content. Jennings *et al.* (1979) indicated the presence of genetic variation in amylose content among rice genotypes.

From the present results, higher amylose content at TAC than at SUA resulted from temperature difference between TAC than at SUA sites. Since temperatures at TAC and SUA were below 29^0C during ripening, the change in the amount amylose content of indica varieties was directly proportional to temperature changes. Similar results have been reported by Resurreccion *et al.* (1977), who noted that in indica rice variety the amylose content increases with mean temperature up to 29^0C above which the amount decreases.

Gel consistency varied within and between locations tested. Nevertheless, differences in gel consistency were dependent upon location, genotype and genotype x environment interaction. Differences in weather condition and soil water between the locations might have resulted in the variation of amylopectin fractions. Gel consistency has also been reported to vary among genotypes due to amylopectin fractions, which are environmentally influenced (Unnevehr *et al.*, 1992 and Juliano and Perdon, 1975).

The partitioning of the variance into components allows an estimation of relative importance of the various determinants of the phenotype, in particular the role of heredity versus environment. The relative importance of a source of variation is the variance due to the source, as a proportion of the total phenotypic variance. The relative magnitude of these components determines the genetic properties of the population. When the genotypic variance is high, the heritability is simultaneously high with little environmental influence. As such, in plant breeding, heritability,

which is the relative importance of heredity that determines the phenotypic value, is of greatest importance.

High heritability estimates were observed in all the traits except in yield, panicle length and tillers/m^2. This suggests that yield, panicle length and tillers/m^2 are greatly influenced by non-heritable characters and therefore selection for these characters in early generations may not be feasible. Low heritability estimates for grain yield and panicle length were recorded in earlier studies (Li and Chang, 1970, Singh and Sharma, 1982 and Kihupi and Doto, 1989). High heritability estimates were recorded for 1000-grain weight, number of panicles/plant, percent spikelet fertility, panicle weight, plant height and filled grains/panicle. This indicates that these traits are highly heritable and are not influenced by environmental factors. Therefore, selection for these traits may commence from the early generations of crop improvement. High heritability estimates studies were obtained on plant height (Singh and Sharma, 1982; Kaul and Bhan, 1989; and Kihupi and Doto, 1989), days to 50% flowering (Kihupi and Doto, 1989 and panicles/plant (Singh and Sharma, 1982).

Apart from high heritability estimates, Johnson *et al.* (1955) reported that practical values in crop improvement are realized when both genetic advance and heritability variables are simultaneously high. Knowledge of the genetic advance produced by applying selection pressure to a population is useful in designing an effective breeding program. According to Johnson *et al.*, (1955) the expected genetic advance is referred to as a proportionate change of the selected group of population of

genetically variable individuals through successive selection cycles over environment(s). This indicates that the earlier the expected genetic gain attainment the higher the character is genetically controlled; and vice versa to environmentally (non-heritable) controlled characters. Results indicated that among the traits, percent spikelet fertility and panicles/plant had relatively higher genetic advance. This implies that selection may be effective for the improvement of percent spikelet fertility and number of panicles/plant. In contrast, the low expected genetic advance on the number of panicles/plant was, however, reported by Kihupi and Doto (1989). It is, therefore, inferred from this study that rice breeders should consider percent spikelet fertility and number of panicles/plant as reliable selection criterion for yield improvement.

High heritability estimates for grain length, shape and gel consistency on the other hand depicts high heritability characteristics on these traits suggesting effectiveness of phenotypic selection for these traits in the early stages of the rice improvement program. Other rice workers reported highest heritability estimates on grain length (Rumiah and Parthasathy; 1923, Chao, 1928; Bollich 1957; and Mackill *et al.*, 1996); gel consistency (Tan *et al.*, 1991), and for amylose content (Mackill *et al.*, 1996). In addition to high heritability estimates of these traits, gel consistency was the only trait that recorded the highest expected genetic advance. The results suggested that selection for this trait may be achieved in the early generations of rice improvement. Nevertheless, according to Jenning *et al.* (1979) and Juliano (1985), gel consistency is difficult to measure. From simple correlation of each single site, and the pooled

data over two locations as well as the genotypic and phenotypic correlation it was indicated that amylose content was positively correlated with chalkiness and gel consistency. However, in this study the trait was negatively correlated with gelatinization temperature and its correlation with grain length was somehow inconsistent.

According to Jennings *et al.* (1979), amylose content is the trait that determines the eating quality of rice and no varieties are known to have high gelatinization temperature and high amylose content. Again, varieties with high gelatinization temperature appear to have low amylose content, which makes them cook soft. The negative correlation between amylose content and gel consistency value has therefore an important implication in the breeding for acceptable grain quality. Since local consumers in Tanzania prefer rices with intermediate to high amylose content, breedres can determine the gelatinization temperature by discarding all segregants with high gelatinization temperature. Since gelatinization temperature is easy to measure and is positively correlated with amylose content the genotypes that are retained will simultaneously bear intermediate to intermediately high amylose content. This may save time and reduce cost.

It has been established that final yield in rice is dependent upon other interrelated traits (De Datta, 1981 and Yoshida, 1981). Similar interrelationships on other crops have also been reported (Robinson *et al.*, 1951, Johnson *et al.*, 1958; and Seith *et al.*, 1977). Correlation coefficients between traits are helpful in understanding the

behavior of the traits that are of value in selection for the desired traits in any breeding program. Estimates of genotypic and phenotypic correlations among characters are useful in planning and evaluating efficient breeding program. In addition, correlations between important and unimportant characters may reveal that some of unimportant traits are as useful as indicators of either important or both characters (Hill, 1975). Their relative importance will therefore depend on economic, heritability and genetic and phenotypic correlations between themselves.

From simple and combined correlation coefficient analyses, yield was significant and positively correlated with all the traits except days to 50% flowering. This suggests that in order to increase yield efforts should be made to select for early maturing genotypes with high yield attributes. This contradicts with findings by De Datta (1981) which reported that under normal conditions early maturing (100 days) genotypes have low yields compared to late maturing genotypes. Weather conditions that prevailed late in the season and the different water regimes applied between the environments were factors that probably favored early maturing and discriminated against the late maturing genotypes. The reduced plant parts of the cultivars as a result of low temperature and soil water deficiency have been recorded (Vergara, 1976).

Simple correlations on grain quality at TAC `indicated that grain length was negatively correlated with grain shape, which suggests that conditions that favored longer grains were suitable for slender grains. Negative correlation between grain

size and grain shape was also reported by Juliano and Villareal (1993). Grain size with grain chalkiness at TAC and SUA were negatively associated, implying that selection against long grain size will result in obtaining chalky grains. As it was for the case of TAC, results for the combined analysis over two locations showed negative correlation between grain length with grain shape and chalkiness suggesting that factors for longer grains would enhance slender and translucent grains. Results by Khush (1994) also reported that rice genotypes with shorter grains were usually chalky.

The phenotypic correlation is however the outcome of the genetic and environmental effects. The environmental correlation is of little importance to the breeder when simultaneous selection for more than one metric character are attempted. In the genetic correlation estimates, sign and magnitude of the correlated response to selection may impair or enhance the achievement of breeding objectives. The complexity arises when the signs of phenotypic and genotypic component correlations are opposite (Chandraratna, 1964).

From the present study, the genotypic and phenotypic correlations in the two combined locations had similar signs though with different magnitudes. Although all the studied traits displayed positive genetic correlations with yield, percent spikelet fertility gave significant positive genetic correlation with panicle length and panicle weight. Similarly, panicles/plant indicated a significant positive genetic correlation with 1000-grain weight. This suggests that the variations of percent spikelet fertility,

panicle weight, panicles/plant and 1000-grain weight, which are important yield components, were dependent on genetic effects contrary to other traits, which were largely dependent upon environmental variables.

Studies on the significant positive correlation between yield and panicle length and tillers/m^2 (Saini and Gagneja, 1975), and with days to 50% flowering, number of filled grains/panicle, and panicle weight (Sarathe *et al.*, 1969) have been reported. Other workers (Gravois and McNew, 1993) had however obtained the significant correlation between yield and panicle weight.

The simple, genotypic and phenotypic correlations for grain quality have similar trend. The genotypic correlation was higher than the phenotypic one for grain length and the amylose content. From the result, positive genetic correlation was exhibited between amylose content and grain length implying that selecting grains with higher amylose content would simultaneously improving/selecting for grain length. Positive correlation between amylose content and grain length has been reported by Juliano and Villareal (1993).

Besides the correlation studies, path coefficient analysis singled out panicle length and number of panicles/plant as the most important traits to select for increased yield. The influence of panicle length to the contribution of yield was found indirectly influenced by percent fertility, 1000-grain weight and filled grains/panicle. This means that holding other factors constant, panicle length would directly increase

yield through indirect influence of percent fertility, 1000grain weight and filled grain/panicle. Although Yoshida (1981) advocated that panicle length is not important in increasing yield, studies by Saini and Gagneja (1975), Sarathe *et al.* (1969) and Kihupi (1984) reported panicle length, 1000-grain weight and percent spikelet fertility in exerting positive effect on yield.

Apart from panicle length, the number of panicles/plant had a significant positive direct contribution on grain length. The trait contributed through many characters except for panicle length, percent spikelet fertility and grain weight. A non-significant percent spikelet fertility was also nearly important in contributing to yield through panicles/plant and tillers/m^2. From this study therefore, it is important for breeders to emphasize in increasing panicle length, percent spikelet fertility and number of panicles/plant for increased yield in rice.

According to phenotypic correlations, all traits except days to 50% flowering were positively correlated with yield. However, path coefficient analysis indicated that panicle length and number of panicles/plant were important factors contributing to yield. The expected genetic advance, which is dependent upon the amount of genetic variability, indicated that the percent spikelet fertility and number of panicles/plant had both highest heritability and genetic advance estimates. The characters could be useful as selection criteria for yield. Although panicle length had direct influence on yield, its heritability estimates and expected genetic advance are low making it unsuitable for indirect selection for yield during early generations. By virtue of the

negative and non-significant correlation between panicles/plant and percent spikelet fertility from the combined analysis, and since each of these traits had a positive association with yield, rice breeders should therefore consider number of panicles/plant and percent spikelet fertility as indirect selection criterion for yield.

Yield stability is one of the most desirable properties if a genotype has to be released for wide cultivation. Rice breeders, therefore have always aimed to identify high yielding and stable genotypes. According to Young and Virmani (1990), a widely adapted rice variety IR 36 is one of the outcomes of such efforts.

Results for stability analysis indicated that except for line M55 on days to 50% flowering, regression coefficients (bi) for all the entries were non-significantly different from unit, suggesting the presence of stability performance among genotypes. The deviations from regressions (S^2di) did not significantly differ from zero across environments indicating that all individual genotypes were less responsive in all the traits to environmental changes. According to Eberhart and Russell (1966), a stable variety is the one whose phenotypic response is close to unit, and deviation from regression close to zero. From the results, SSD1, SSD3, and SSD5 were stable in all the traits while line M55 was an unstable genotype. From the results, SSD1, SSD3, and SSD5 performed stable in all the traits.

For rice grain qualities, regression coefficients and their deviations from regressions of lines SSD3 and SSD1 were not significantly different from unit and zero respectively. The results indicated that the two genotypes were stable for chalkiness

formation and less responsive to environmental changes. Out of four genotypes, SSD1 had significant regression coefficient from unit while lines SSD1 and SSD5 had significant deviation from regression from zero on gel consistency. The results implied that line SSD1 was both unstable and more affected by environmental changes, whereas SSD5 was less responsive to environmental changes on gel consistency. All genotypes were stable for amylose content across environments. According to Eberhart and Russell (1966), the line SSD3 was both stable and less responsive to environmental changes. The inconsistencies of stability of the grain quality characters could be influenced by genetic differences and the production environments as proposed by Jennings *et al.* (1979) that variations in grain qualities depend on genetic differences and production environments.

CHAPTER SIX

6.0 CONCLUSION AND RECOMMENDATIONS

6.1. CONCLUSION.

A study conducted in the 1999/2000 to evaluate the effect of genotype x environment interaction on rice yields, yield components and grain qualities of early and late maturing genotypes under three environments revealed the following facts:

The genetic variations were exhibited on days to 50% flowering, plant height, number of productive tillers/m^2, panicle length, panicle weight, percent spikelet fertility, 1000-grain weight, and grain weight.

Genetic variations were also observed on grain quality characters such as grain length, chalkiness, gelatinization temperature, amylose content and gel consistency.

Environments that influenced the performance of genotypes differed appreciably due to low temperature, rainfall differences and irrigation water regimes, which determined the extent of soil moisture regime during the growth period.

Genotype x environmental interaction was important to a number of traits. Characters that were influenced by G x E interactions were days to 50% flowering, plant height, panicle length, panicle weight, productive tillers/m^2, percent spikelet fertility, and grain yield. Genotype x environment interaction was not important to 1000-grain weight. Regardless of differences of maturity periods of the genotypes tested, none of

the environments had serious moisture stress from panicle initiation to near heading. This was attributed due supplemental or full irrigation regime after rainfall ended.

From the study, high heritability estimates were obtained for 1000-grain weight, number of panicles/plant and percent spikelet fertility, grain length, shape and gel consistency. Grain yield, panicle length and tillers/m^2 had low heritability estimates. Percent spikelet fertility and panicles/plant had both high heritability and high expected genetic advance.

From the simple correlation coefficient analysis, yield was significantly and positively associated with all the traits except with days to 50% flowering. Results suggest that in order to increase yield, breeding efforts should be done to select for early maturing genotypes with high yielding attributes.

Path coefficient indicated that panicle length, number of panicles/plant and percent spikelet fertility are important traits to select in order to increase yield potential in rice. However, based on the correlation coefficients, heritability and genetic advance estimates, panicles/plant and percent spikelet fertility could be used as indirect selection criteria for increased yield.

The negative correlation between amylose content and gelatinization temperature implies that high gelatinization temperature segregants, which have low amylose content, can be discarded during early generation since consumers in Tanzania do not prefer low amylose rices.

Results from stability analysis indicated that except for line M55, all the early maturing genotypes SSD1, SSD3 and SSD5 were stable for days to 50% flowering, plant height and panicle length.

However, SSD3 was the only genotype that was stable in chalkiness, amylose content and gel consistency. Of special interest and importance, all genotypes were stable for amylose content.

In view of the results obtained regarding the overall performance and stability analysis, SSD1, SSD3 and SSD5 could be recommended for further testing.

6.2.RECOMMENDATIONS.

Based on the results obtained, early maturing genotypes may be provisionally recommended for areas with marginal rainfall. Lines SSD1, SSD3 and SSD5 can therefore be recommended for further testing in the region.

From the results obtained, the breeder may therefore consider using number of panicles/plant and percent spikelet fertility as indirect selection criteria for grain yields.

Significant genotype x environment interactions observed for the two sites, emphasizes the necessity of evaluating breeding lines over several environments for specific or wide recommendations of the newly obtained genotypes from the rice breeding program.

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8.0 APPENDICES.

Appendix i: Physical and chemical characteristics of the experimental soils at Lumemo.

Parameter	Value	Comments[a]
Particle size distribution		
Sand	43.2	
Silt	22.2	
Clay	34.6	
Textural class	Sandy Clay	
PH in water (1:25)	6.4	Slightly acidic
Organic Carbon (%)	1.76	Medium
Total N (%)	0.09	Very low
Available P Brayl (mg/kg)	47.5	High
CEC cmol (+)/kg	17.6	Medium
Exchangeable bases cmol (+) /kg		
Ca	8.51	Very high
Mg	1.76	High
K	0.81	Very high
Na	0.02	Very low

According to Landon (1991) [a]

Appendix ii: Physical and chemical characteristics of the experimental soils at TAC.

Parameter	Value	Comment[a]
Particle size distribution		
Sand	22.1	
Silt	22.2	
Clay	49.2	
Textural class		Clay
PH in water (1:25)	6.05	Medium acid
Organic Carbon (%)	1.59	Medium
Total N (%)	0.11	Low
Available P Brayl (mg/kg)	28.65	High
CEC cmol (+)/kg	17.35	Medium
Exchangeable bases cmol (+) /kg		
Ca	7.38	Medium
Mg	2.44	Medium
K	0.54	Medium
Na	0.03	Very low

[a] According to Landon (1991)

Appendix iii. Physical and chemical characteristics of the experimental soils at SUA Farm.

Parameter	Value	Comments [a]
Particle size distribution: -		
Sand	35.10	
Silt	8.50	
Clay	56.40	
Textural class	C	
PH in water (1:2.5)	6.10	Slightly acidic
PH in KCl (1:2.5)	4.60	
Organic carbon (%)	1.66	Medium
Total N (%)	0.17	Low
Available P Bray1 (mg/kg	4.80	Low
CEC cmol (+) /kg	9.20	Low
Exchangeable bases (cmol (+) /kg): -		
Ca	7.60	Medium
Mg	3.60	High
K	1.10	Medium
Na	0.50	Medium
Base saturation	141	

According to Landon (1991) [a]

Appendix iv: Weather conditions during the 1999/2000 rainy season at Lumemo and TAC.

Month	Max. Temperature (^{0}C)	Min. Temperature (^{0}C)	Rainfall (mm)
January	31.5	23.3	76.8
February	30.02	23.4	66.9
March	28.8	23.1	287.1
April	29.2	23.1	202.5
May	28.5	22.5	50.6
June	28.3	21.7	28.4
July	27.1	19.6	4.0

Source: Meteorological station near Lumemo and TAC.

Appendix v: Weather conditions during the study at SUA Farm.

Month	Max. Temp, ^0C	Minim Temp (^0C)	Total Rainfall (mm)	Month	Max Temp (^0C)	Day Length (Hrs/day)	Radiation (MJ/m^2)
Nov.1999	32.8	19.8	35.7	70	6.5	8.7	20.2
Dec.	31.6	18.6	60.9	72	5.4	7.7	19.5
Jan 2000	33.1	21.4	68.8	68	7.6	9.1	22.6
Feb.	35.2	22.0	37.9	65	8.7	9.4	22.0
Mar	30.6	20.7	207.4	78	4.3	6.1	17.3
Apr.	30.8	20.6	110.6	80	3.6	6.9	17.2
May	29.3	19.0	32.5	78	2.9	6.4	14.6
Jun.	27.4	17.4	47.8	76	3.1	6.7	0.6
July	25.0	15.5	21.4	52	2.6	6.4	0.5

Source: Meteorological station near SUA

Appendix vi: Mean squares from combined analysis of variance (ANOVA) for different characters of ten rice genotypes averaged over two locations.

Source of variance	Df	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	Panicle weight (g)	Tillers/ m^2	Panicles/ Plant	Filled grains/ panicle	Percent fertility (%)	1000grain weight (g)	Yield (t/ha)
Environment (E)	1	2112.27**	6869.40**	138.08**	16.02	2640.07**	25.35**	33744.07**	549.34	32.86**	60.44**
Replications (R/E)	4	50.46	100.33	3.47	23.68	250.77	1.00	434.76	192.20	0.84	0.51
Genotypes (G)	9	9634.40**	16319.00**	97.82**	38.27**	4222.79**	8.965**	2085.42**	793.08**	51.44**	3.05**
GXE	9	998.07**	3646.60**	180.48**	1.57	1236.66**	1.42	407.84	151.61	1.68	3.97**
Error	36	337.53	421.00	39.20	8.720	169.04	0.52	623.95	33.10	2.96	0.36

* Significant at 5% level ** Significant at 1% level

Appendix vii: Mean squares from combined analysis of variance (ANOVA) for different characters of four rice genotypes averaged from three locations.

Source of variations	Df	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	Panicle weight (g)	Tillers/ m^2	Panicles /plant	Filled grains/ panicle	Percent fertility (%)	1000 grain weight (g)	Yield tons/ ha
Environments (E)	2	195.19**	460.03**	0.75	0.75	3415.03**	5.44*	13164.69**	122.99	18.98**	0.35
Replications (R/E)	6	4.03	31.86	3.17	33.83	122.75	0.64	1052.39	76.77	1.27	0.21
Genotypes (G)	3	709.36**	96.47**	9.96**	22.33	496.69*	1.44	896.68	31.28	28.88**	1.62**
GXE	6	36.86**	179.81**	6.38*	4.75	172.25	0.52	3507.42	24.17	1.86	0.21
Error	18	3.36	11.08	1.69	13.94	118.57	0.60	1319.21	17.18	1.04	0.26

* Significant at 5% level ** Significant at 1% level

Appendix viii: Combined analysis of variance (ANOVA) for different physical and biochemical characters of some rice genotypes over two locations (TAC and SUA).

Source of variance	Df	Grain length	Grain length:breadth ratio	Chalkiness	Gelatinization temperature	Amylose content	Gel consistency
Location/Environment (E)	1	0.66*	0.02	3.86*	12.25**	12.92**	2057.25**
Replications	4	0.24	0.13	0.22	0.42	0.97	37.42
Genotypes	9	0.90*	0.48	8.37*	4.69**	21.39**	1687.74**
GxE	9	0.28	0.08	1.12*	1.14*	8.58**	115.55**
Error	36	0.15	0.19	0.15	0.27	2.95	56.97

* Significant at 5% level ** Significant at 1% level

Appendix ix: Mean squares from combined analysis of variance (ANOVA) for different physical and biochemical characters/traits of some rice genotypes over three locations (Lumemo, TAC and SUA).

Source of variations	Df	Grain length	Grain length:breadth ratio	Chalkiness	Gelatinization temperature	Amylose content	Gel consistency
Location/(Environment) (E)	2	1.04	0.03	6.67**	8.82*	33.56**	1782.15**
Replications (R/E)	6	0.35	0.20	0.77	0.33	1.22	21.13
Genotypes (G)	3	1.65	0.30	9.36**	4.94**	82.81**	6960.27**
GxE	6	0.16	0.18	1.15	3.19**	36.87**	217.97**
Error	18	-0.15	0.26	0.66	0.22	2.22	5.21

* Significant at 5% level ** Significant at 1% level