

**GENETIC VARIABILITY, HERITABILITY AND INTERRELATIONSHIPS
AMONG YIELD COMPONENTS OF RICE (*Oryza sativa* L.) EXOTIC
GENOTYPES IN ZANZIBAR.**

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**A DISSERTATION SUBMITTED IN PARTIAL FULFILMENT OF THE
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ABSTRACT

The experiments were conducted using 13 rice genotypes from International Rice Research Institute (IRRI) and commonly grown variety (SARO 5) as a check during April-June 2012 growing season at three rice irrigation schemes of Zanzibar. The aim was to estimate genetic variability, heritability and interrelationships among yield components of genotypes so as to identify potential lines for improvement and production. RCBD with three replications at each site was used. ANOVA showed significant differences for all studied characters indicating that genotypes constitute a lot of genetic variability. GCV were lower than PCV in all studied characters indicating considerable influence of environment on expression of the traits. Broad sense heritability was higher for panicle length, number of tillers per plant, plant height, 1000 grains weight, panicle weight and yield per hectare indicating heritable portion of variation; this suggesting that selection can be carried out on the basis of their phenotypic expression. The correlations that were consistently significant at all locations and in addition to the combined analysis were days to 50%flowering with days to maturity, number of primary branches per panicle with days to 50% flowering, and grain yield per plant with yield/ha suggesting that grain yield per plant should be considered during selection for yield. Path analysis revealed that number of tillers per plant showed positive direct effect on grain yield also had indirect effect via 1000 grains weight and panicle length. Number of grains per panicle had positive direct effect on grain yield also had indirect effect on yield via number of primary branches per panicle. Panicle length showed positive direct effect on grain yield also had indirect effect through number of primary branches. With

respect to yield genotype IR07M101 was stable and could be selected for production and further improvement.

DECLARATION

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

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DEDICATION

This work is dedicated to my beloved father the late Mr. Mohamed Shaali Khatib
may God rest his soul in peace.

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LIST OF ABBREVIATIONS AND SYMBOLS

ANOVA	Analysis of variance
CV	Coefficient of variation
DF	Degree of freedom
ECA	East and Central Africa
EMS	Expected mean squares
FAO	Food and Agriculture Organization
FL	50% days to flowering
G X E	Genotype by environment
GCV	Genotypic Coefficient of Variation
GWT	1000 grain weight
GY	Grain yield
GY	Genotype x Year interaction
GYPP	Grain yield per plant
IRRI	International Rice Research Institute
l.s.d	Least significant difference
m.a.s.l	meter above sea level
DMT	85% days to maturity
MS	Mean Squares
NGPP	Number of Grain per panicle
PCV	Phenotypic Coefficient of Variation
PHT	Plant height
PL	Panicle length
NP	Number of Panicles

PW	Panicle weight
RCBD	Randomized Complete Block Design
SE	Standard error
SS	Sum of Squares
SV	Source of Variation
USA	United States of America
ZATI	Zanzibar Agricultural Transformation Initiatives
WARDA	West Africa Rice development Agency

CHAPTER ONE

1.0 INTRODUCTION

1.1 Background

Rice (*Oryza sativa* L.) is grown extensively in tropic and sub-tropic regions of the world. It is a staple of more than 2.5 billion people and provides 20% of world's dietary supply, also employs over 1 billion people, who either work directly in rice production or related support activities (Tran, 2004). According to Jamal *et al.* (2009) the chief rice producing countries are China, India, Indonesia, Bangladesh, Vietnam, Thailand, Myanmar, Philippines, Brazil, Japan, USA, and Pakistan.

During the past three decades there has been a consistent increase in demand for rice, the demand exceeds production in many Africa countries. Africa's emergence as a big rice importer is explained by the fact that during the last decade rice has become the most growing food source in Sub-Saharan Africa (Solh, 2005). With the sub-regional population growth rate of 2-3% per year, rice production is not keeping up with increased demand, resulting in rice imports that are using valuable foreign exchange. Analysis of the rice consumption and importation statistics for the East and central Africa (ECA) countries as well as the changing consumption patterns of urban population, indicate that rice has a potential to be an important commercial crop in the sub-region (FAOSTAT, 2004). Tanzania is the second largest producer of rice in Eastern, Central and Southern Africa after Madagascar. It is a food crop for 60 percent of the people in Tanzania. The crop is grown in three agro- ecosystems namely rain fed low land (74%), rain fed up land (20%) and irrigated low land (6%)

(Kanyeka, 1994). According to Kibanda (2008) the annual per capita consumption of rice in Tanzania has drastically shifted due to consumer preference both in urban and rural areas. The annual per capita consumption of rice in Tanzania is about 25-30 kg/year. Rice is a very important food crop in Zanzibar and is mainly produced by small holders for home consumption. It is the most favourable food of Zanzibaris, and any deficit in market is reflected in food shortage.

1.2 Justification

Rice is an important food crop in Zanzibar as it forms 50% of the staple food consumed per capita in calorie basis followed by cassava 25%, fish 10% ,maize 5%, and others 10%. Consumption per capita is 125kg per year thus rice demand in Zanzibar stands at 120000 tons per year, Zanzibar Agricultural Transformation Initiatives (ZATI, 2010). The total area under rice cultivation is estimated at 11646 ha. Rice production in Zanzibar is far below the demand, with the productivity of 1 ton per ha compared to a potential of 3.5 tons per ha. (Khatib and Makame 2009). Despite the amount of rice demanded, the local production achieved is hardly 20 000 tons of rice per year which is less than 11% of the annual requirement (ZATI, 2010). Most farmers in Zanzibar grow traditional aromatic rice varieties which are low yielding, photoperiod sensitive and have some undesirable characteristics such as low tillering, late maturity and lodging. Many efforts have been done to increase rice production in Zanzibar; including introduction and evaluation of elite genotypes, still there is a wide gap between rice demand and production. Major problems constraining rice production in Zanzibar include lack of improved varieties with acceptable grain quality, weed infestation and unavailability of fertilizer.

Zanzibar has the potential to either meet its own demand or reduce the volume of importation of rice by increasing productivity. While some regions in sub-Saharan Africa have attained food production through increased area under cultivation (Juma and Mohammed 2009), this option seems to be not possible in the context of Zanzibar, since land is already a scarce resource. The only viable option to increase rice production in Zanzibar is through the application of improved production technologies.

The objectives of any breeding program are to produce high yielding better varieties. The pre requisites to achieve this goal are the presence of sufficient amount of genetic variability in which desirable lines are selected for further manipulation (Jamal *et al.*, 2009). Development of high yielding varieties requires a thorough knowledge of existing genetic variation for yield and its components (Mohd and Samullah 2006).

Yield is a complex quantitative character controlled by many genes interacting with the environment and is a product of yield components. Khan *et al.* (2009) reported that selection based on yield alone is often misleading, and therefore the knowledge about relationships between yield and its components is needed for an efficient selection strategy. Hence, any breeding program aiming at increasing yield should consider association between yield and its attributes through estimation of genotypic and phenotypic correlation, which is very important in formulating selection indices to aid in selection program. An understanding of the variability existing in a crop is necessary to formulate and accelerate conventional breeding program.

Therefore this study was aimed at evaluating the extent of genotypic and phenotypic variability, heritability, stability and interrelationships among yield components existing for different characters in 13 rice lines collected from International Rice Research Institute (IRRI).

1.3 Overall Objective

To investigate genetic variability of 13 introduced rice genotypes so as to identify potential lines for production and improvement in Zanzibar.

1.4 Specific Objectives

- i. To determine heritability, phenotypic and genotypic variation of important agronomic traits.
- ii. To evaluate the interrelationships among yield components of introduced rice genotypes
- iii. To determine adaptability and stability of introduced rice genotypes under three locations of Zanzibar.

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Importance of Rice

Rice is the staple food of 2.5 billion world's population which may escalate to 4.6 billion by the year 2050. It is the predominant food for 17 countries in the Asia and Pacific, 9 countries in North and South America and 8 countries in Africa. Rice provides 20% of the world dietary energy supply, while wheat supplies 19% and maize 5% (FAOSTAT, 2004). Over 90% of the world's total rice crop is produced in South and East Asia. In area and production, China is the leading country in the world. Africa accounts for 3% of global production. Global rice cultivation is estimated at 150 million ha. Rice yields recorded worldwide include 5.8 MT/ha in Japan, 5.6 MT/ha in China and 4.3 MT/ha Indonesia (FAO, 2007).

In 2009 world rice production was about 680 million tons with a projected record harvest of 710 million tons in 2010, alongside an increase in consumption of about 8 million tons (FAO, 2010).

In the years 2001-2005 rice production in Africa expanded at the rate of 60% per annum, with only 30% being attributed to increasing productivity (Fagade, 2008). According to (FAO, 2010), Africa cultivated about 9 million hectares of rice in 2006.

Tanzania is the second rice producer after Madagascar; rice is the second cultivated cereal food crop after maize. The crop is grown in three agro- ecosystems namely

rain fed lowland (74%), rain fed upland (20%) and irrigated lowland (6%) (Kanyeka, 1994). Drastic shift of consumer in both urban and rural areas from conventional foods to rice coupled with rapid urbanization has resulted into simultaneous increase in annual per capita consumption of rice in Tanzania of about 25-30kg/year (Kibanda, 2008).

Rice is the main staple food in Zanzibar and accounts for more than 50% of staple consumed. According to Khatib and Makame (2010) annual per capita of rice in Zanzibar is about 120kg, and total rice requirement is estimated at 120 000 tons out of which 80% is imported. In Zanzibar rice is cultivated on lowland under rain fed conditions. In Unguja rice is grown on large plains where in Pemba production is mainly in narrow flooded valleys and some on plains.

2.2 Description and Classification of Rice

Rice refers to species (*Oryza sativa L.* and *Oryza glaberrima Steud.*) of grass, native to tropical and sub tropical southern and Southeast Asia and to Africa, which together provide more than one fifth of the calories consumed by human (Crowford and Shen, 1998).

Rice is an annual plant, growing to 1-1.8 m tall, occasionally more, with long slender leaves 50 -100cm long and 2-2.5 cm broad. The small wind pollinated flowers are produced in branched arching to pendulous inflorescence 30- 50 cm long. The seed is grain (caryopsis 5-12mm long and 2-3mm thick).

The classification is as follows:

Kingdom : *Plantae*

Division: *Magnoliophyta*

Class: *Liliopsida*

Order: *Poales*

Family: *Poaceae*

Genus: *Oryza*

Cultivated Species:

Oryza glaberrima

Oryza stiva

([www.http://: en.wikipedia.org/wiki/rice.](http://en.wikipedia.org/wiki/rice))

2.3 Genotypic and Phenotypic Variation

The presence and magnitude of genetic variability in a gene pool is the pre-requisite of a breeding program. The knowledge of certain genetic parameters is essential for proper understanding and their manipulation in any crop improvement program.

Genetic parameters like genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance are useful biometrical tools for determination of genetic variability. The grain yield is a complex character, quantitative in nature and an integrated function of a number of component traits. Therefore, selection for yield per se may not be much rewarding unless other yield attributing traits are taken into consideration (Aditya *et al.*, 2011).

2.4 Phenotypic Variability

Phenotypic variance is a composite of two variables, genetic, environment and their interaction. It is a common practice in trials involving varieties and breeding lines to grow a series of genotype in a range of different environments. If all the genotypes respond similarly to the entire environment tested, their relative performance in other environments may be predicted with some confidence (Alake and Ariyo 2012). Khan *et al.* (2009) reported phenotypic coefficient of variability was higher than genotypic coefficient of variability for all quantitative characters studied in rice, this was also reported earlier by Zahid *et al.* (2006) and (Buu and Truong 1988). Idris *et al.* (2012) reported significant phenotypic variation for yield in kg/ha, followed by number of grain per panicle. Highest phenotypic coefficient of variation for number of grains per panicle followed by number of grains per panicle and number of tillers per plant was reported by Akhtar *et al.* (2011).

Akinwale *et al.* (2011) reported high phenotypic variance for days to heading, days to maturity, plant height, grain yield, and number of grains per panicle, panicle weight, and number of panicles per m² and panicle length. High phenotypic variance in rice was also reported earlier by Basak and Ganguli (1990) and Hasib and Kole (2004).

2.5 Genotypic Variability

Genetic variability is the measure of the tendency of individual genotype in population to vary from one another. Variability is different from genetic diversity, which is the amount of variation seen in a particular population. The variability of a

trait describes how much that trait tends to vary in response to environmental and genetic influence. Genetic variability for agronomic traits is the key component of breeding programs for broadening gene pool of rice, plant breeders commonly select for yield components which indirectly increase yield Akinwale *et al.* (2011). Many studies have been done to find genetic variability in rice, Jayasudha and Sharma, (2010) reported a high genotypic coefficient of variation for grain yield per plant, pollen fertility (%) and spikelet fertility (%). Highest values of genotypic variation were also reported in rice genotype by Idris *et al.* (2012), Sweta and Singh (2010) reported that number of grain per panicle and number of spike per panicle had genotypic variation in rice. High genetic variability for different quantitative characters in rice was also reported by Khan *et al.* (2009) and Ullah *et al.* (2011).

2.6 Heritability of Quantitative Trait

The broad sense heritability is the relative magnitude of genotypic and phenotypic variances for the traits and it is used as a predictive role in selection procedure (Allard, 1960). This gives an idea of the total variation ascribable to genotypic effects, which are exploitable portion of variation. It was found out earlier that genetic improvement of plants for quantitative traits requires reliable estimates of heritability in order to plan an efficient breeding program (Akinwale *et al.*, 2011).

It is difficult to judge whether the observed variability is highly heritable or not, the knowledge of heritability is essential for selection based improvement and it indicates the extent of transmissibility of a character in to future generations (Sabesan *et al.*, 2009). Heritability estimates provide the basis for selection on

phenotypic performance, the estimate of heritability and genetic advance should always be considered simultaneously as high heritability will not always be associated with high genetic advance (Johnson *et al.*, 1955). Therefore estimates of genetic advance help in understanding the type of gene action involved in the expression of various polygenic traits. High values of genetic advance are indicative of additive gene action where as low values are indicative of non-additive gene action (Singh and Marayanan 1993). Thus, the heritability estimates will be reliable if accompanied by high genetic advance.

Akinwale *et al.* (2011) observed high to medium heritability for days to heading, days to maturity, plant height, grains yield, number of grains per panicle, and number of panicles per meter square, but there was low broad sense heritability for number of tillers per plant and 1000 grains weight of rice. Kumar *et al.* (2009) found that there was high broad sense heritability for spikes per main panicle and 1000 grains weight but panicles per plant and grain yield per plant were found to have low heritability. High broad sense heritability for rice morphological traits was also reported by Khan *et al.* (2009). Plant height, days to flowering, panicles per plant, grain per panicle, 1000 grains weight exhibited high heritability in rice (Ullah *et al.*, 2011). Akhtar *et al.* (2011) reported highest heritability for number of grain per panicle, days to 50% maturity, plant height and paddy yield while lowest for number of tillers per plant.

2.7 Effect of Genotype and Environment Interaction on Heritable Traits

A genotype x environment interaction ($G \times E$) exists where the relative performance of genotype changes from environment to environment. Very often breeders

encounter situations where the relative ranking of varieties changes from location to location and /or from year to year. If $G \times E$ interactions are present, they are an important factor maintaining heritable variation of traits because no single genotype does best under all environmental circumstances. According to Collins *et al.* (1987) the effect of $G \times E$ interactions in breeding programs is to reduce correlations between phenotype and genotype resulting in invalid or biased conclusions about genetic variance.

Crop cultivars are grown in a wide range of environments hence there is effect of genotype x environment interaction which usually cause difficulty in comparing the performance of genotypes across environments and reduce the efficiency of genetic progress through selection (Negeve, 1993). Crop yield improvement is determined to a large extent by the effective functioning of the crop yield characters. Expression of these characters depends on the overall genetic and environmental factors (Berdahl and Backer 1997). Genotypic main effects (i.e. differences in mean yield between genotypes) provide the only relevant information when genotype \times environment ($G \times E$) interaction effects are absent or ignored. DeLacy *et al.* (1990) and Annicchiarico, (1997a) reported that differences between genotypes may vary widely among environments in the presence of $G \times E$ interaction effects. According to Kang (1998), $G \times E$ interactions are considered a hindrance to crop improvement. Bidinger *et al.* (1996) and Kang (1998) reported that major interaction can be expected when there is wide variation between genotypes for morphophysiological characters conferring resistance to or avoidance of one or more stresses (climatic, soil, biotic and management factors).

2.8 Yield Stability

Yield stability usually refers to a genotype's ability to perform consistently, whether at high or low yield levels across a wide range of environments, most stability measures relate to either of two contrasting concepts of stability: "static" and "dynamic" (Becker and Léon, 1988; Lin *et al.*, 1986).

A stable genotype tends to maintain a constant yield across environments, according to Falconer, (1989) and Dyke *et al.* (1995) the term "environmental sensitivity" has also been used in this respect, where greater sensitivity corresponds to lower stability. Dynamic stability implies for a stable genotype with a yield response in each environment that is always parallel to the mean response of the tested genotypes, i.e. zero $G \times E$ interaction.

The $G \times E$ effects contributing to yield stability can be either, exploited by breeding and growing genotypes that are stable according to the static concept (i.e. with a better response in unfavorable environments; or minimized, by using material that is stable according to the dynamic concept.

Simmonds (1991) reported that static stability may be more useful than dynamic in a wide range of situations, especially in developing countries. Due to the fact that location is a constant i.e. not variable factor, and yield consistency over time is the only relevant component of a genotype's yield stability. Barah *et al.* (1981), Lin and Binns (1988) proposed to evaluate yield stability with regard to genotype and year (GY) interaction effects within locations. Whatever the adaptation strategy, breeding

for high yield stability can be considered a useful target when the relevant G×E interaction variation is wide.

According to Eberhart and Russel (1966) a stable genotype across environments is the one which show high mean yield, regression coefficient (b-value) around unity and deviation from regression of zero.

2.9 Correlation of Rice Yield and its Components

Knowledge of correlation between grain yield and other characters is helpful in selection of suitable plant type. Phenotypic correlation measures the degree of association of two variables and is determined by genetic and environmental factor. The environmental factor is mainly responsible for the association of traits of low heritability such as grain yield. The genotypic correlation on the other hand, which represents the genetic portion of the phenotypic correlation, is the only one of inheritable nature and therefore, used to orient breeding programs (Falconer 1989). According to Oad *et al.* (2002) the correlation coefficient may also help to identify characters that have little or no importance in the selection programme. The existence of correlation may be attributed to the presence of linkage or pleiotropic effect of genes or physiological and development relationship or environmental effect or in combination of all. Many studies have been done to determine the association among yield components of rice. Javeed *et al.* (2010) observed that grain yield of rice was significantly correlated with its characters viz. number of productive tillers per plant, number of grains per panicle, 1000 grain weight, plant height, number of tillers per plant and number of grains per panicle. These variables

also showed positive correlation among themselves. Ullah *et al.* (2011) observed that grains per panicle, length of panicle were major characters contributing to grains yield per plant. Nayak *et al.* (2004) observed that number of grains per panicle had positive correlations with grain yield both at genotypic and phenotypic levels. Positive correlation was also observed for days to 50% flowering and 1000 grains weight. Plant height showed significant negative association with grain yield of rice.

Akinwale *et al.* (2011) reported that grain yield exhibited significant positive correlation with number of tillers per plant, panicle weight and number of grains per plant. The number of grains per plant showed significant positive correlation with days to 50% heading, days to maturity and panicle weight, but was correlated positively with days to heading and negatively correlated with plant height. Positive phenotypic and genotypic correlation coefficient was detected between grain yield and number of filled grain per panicle, panicle length and number of filled grain per panicle (Idris *et al.*, 2012).

According to Selvaraj *et al.* (2011) plant height, number of productive tillers per plant, panicle length, filled grains per panicle had significant positive association with grain yield. Sadegh (2011), observed positive significant association of grain with grain per panicle, days to maturity, number of productive tillers and days to flowering. Ullah *et al.* (2011) noted that grain yield was positively and significantly associated with panicle length and grains per panicle.

2.9.1 Path coefficient analysis

Yield is a complex character and is associated with a number of component characters which may be interrelated among them. Such inter-dependence of the contributing factors often affects their relationship with yield; thereby making correlation coefficients unreliable as selection indices (Blessing *et al.*, 2012).

Path analysis provides information on influence of each contributing factor to yield, directly as well as indirectly and also enables breeders to rank the genetic attributes according to their contributions (Dewey and Lu 1959). It helps not only to identify the cause and effect relationship between yield and its component characters but also the relative importance of each, as they affect the yield both directly and indirectly. Partitioning of the total correlation into directly and indirectly effects would provide actual information on the contribution of traits and thus form the basis for selection to improve yield (Blessing *et al.*, 2012).

The method is important in the assessment of compensation mechanisms operating among plant components which make improvement of one variable less rewarding because increment in yield will reach a certain level after which it declines because of sacrificial effects of other components (Marandu *et al.*, 2004). Many studies have been done to find the effect of yield components on rice yield. Khan *et al.* (2009), reported positive direct effect on grain yield for number of grains per panicle followed by plant height, days to maturity, days to heading, plant height, but number of tillers per plant had negative effect on grains yield. Nayak *et al.* (2004) observed that number of grains per panicle and harvest index had positive effects on yield of

rice. The result of path analysis obtained by (Sweta and Singh 2010) indicated that number of grains per panicle, and days to 50% flowering had maximum direct effect on grain yield per plant.

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 Study Areas

Experiments were conducted at Mwera, (Western District) 20m above sea level, 05° 54', 12.4'' E, 039° 14' 12.4'' S, Cheju (Central District) 35 m above sea level 05° 52' 10.5''E, 039° 15' 14'' S and Kibokwa 41m above sea level 05° 51', 11.7'' E, 039° 18', 44.2''S (North district) of Unguja during 2011/2012 growing season. These locations have sub-humid climate with bimodal rain fall, long rains (Masika) which start on last week of March to first week of June, short rains (Vuli) which normally start on mid September to November. Average temperature is 27-32°C. Generally all sites have clay loam soil. (Appendix 2) .Experiments was set in randomized complete block design (RCBD) with three replications in each location.

3.2 Experimental Materials

The materials studied were 13 exotic genotypes from International Rice Research Institute (IRRI) and one commonly grown variety, these are IR 09L325, IR09N505, IRRI 146, IR 05N359, IR 02A149, IR 08M110, IR 07M101, IR 06A107, IR 07A166, IR 07A167, IR 09A136, IR 03A550, IRRI 123 and SARO 5 was used as a check. These genotypes have potential grain yield up to 4-6 tons/ha, early maturing as shown in (Table 1) below.

3.3 Experimental Design

Each experiment was set in Randomized Complete Block Design (RCBD) with three replications. Two three weeks seedlings were planted per hill. Each plot planted

in a plot of 2.5m x 2 m, with 10 rows and one plants per hill, in a space of 20 cm x 20 cm.

3.4 Agronomic Practices

Fields were ploughed by using power tiller, then leveled by hand hoe, plots were cleaned to remove weeds. Water was drained from the plots before transplanting, then three weeks old seedling transplanted manually in rows. Water from river was used to irrigate the plot at Mwera site and for Kibokwa and Cheju water from bore hole was used. Phosphate fertilizer was used during transplanting at the rate of 30kg/h P₂O₅, top dressing of urea 46%N was applied at the rate of 60kgN/h in two splits, first application was done after three weeks (after first weeding) and the second was done during panicle initiation, and weeding was done by hands twice.

Table 1: Rice genotypes

ENTRY	DESIGNATION	PARENTAGE
1	IR 09L325	IR7 1700-247-1-1-2/SAMBHA MAHARUSI
2	IR09N505	IR66/IRR 146
3	IRRI 146	IRRI 134/IR 70479-45-2-3//IR 64680-81-2-2-2-1-3
4	IR 05N359	IR 72158-11-5-2-3/IR 72903-121-2-1-2
5	IR 02A149	IR 00A107/IRRI 116
6	IR 08M110	IR 75493-8-2-1-2-3/IR 65620-192-3-3-3-2
7	IR 07M101	IR 65192-4B-11-3/IR 64
8	IR 06A107	IR 74052-165-3-2/PUSA 1121
9	IR 07A166	IR 73013-95-1-3-2/IR 72862-27-3-2-3
10	IR 07A167	IR 73013-95-1-3-2/IR 72862-27-3-2-3
11	IR 09A136	IR 01A135/IRRI 123//IR 01A163
12	IR 03A550	IR 68427-15-2-3-1/IR 68068-99-1-3-3-3//IR 43
13	IRRI 123	IR 47761-27-1-3-6/IRRI 108
14	SARO 5	

3.5 Data Collection

3.5.1 Days to 50% flowering

Data on days to 50% flowering was recorded by counting the number of days from sowing to 50% flowering for each plot.

3.5.2 Days to maturity

Days to maturity was recognized when panicle color turn golden yellow, this was recorded by counting the days from planting to maturity.

3.5.3 Plant height (cm)

Plant height was taken during harvesting by using measuring tape in a random sample of 10 plants per plot and averaged to get plot value this was done by measuring height of a plant from ground level to tip of the panicle.

3.5.4 Number of primary branches per panicle

Number of primary branches per panicle was recorded by counting number of number of branches per panicle in a sample of ten panicles per plot and divided by ten to get average plot value.

3.5.5 Panicle length (cm)

Panicle length (cm) was measured using tape measure during harvesting in 10 plants per plot and averaged to get plot value.

3.5.6 Number of productive tillers per plant

Productive Tillers per plant was counted in a sample of 10 plants per plot and averaged to get plot value.

3.5.7 Number of grains per panicle

Number of grains per panicle was obtained by counting number of grains in each panicle in a sample of ten panicles from each plot and averaged to get plot value.

3.5.8 Panicle weight

Panicle weight was obtained from random sample of 10 plants per plot during harvesting, 10 panicles from each plot was threshed and dried to 14% moisture content and weighted and averaged to get panicle value.

3.5.9 1000 grain weight

Thousand grain weights were obtained by counting and weighing a sample of 1000 filled grains (14% moisture content) from each plot during harvesting.

3.5.10 Yield per meter square

Yield per meter square was measured by weighing grains (14% moisture content) obtained from an area of 1m² plot, and converted to yield per hectare basis

3.6 Data Analysis

Analysis of variance (ANOVA) was carried out to assess the genotypic and Environmental effect and their interactions using GenStat statistical software (Version 14.2).

The statistical Model for randomized complete block design was as follows.

For single site

$$Y_{ijk} = \mu + r_i + t_j + e_{ij} \dots \dots \dots (1)$$

Where μ = constant,

r_i = i^{th} replication effect,

t_j = j^{th} genotypic effect

e_{ij} = error effect.

3.6.1 Statistical model used for combined sites analysis was

$$Y_{ijkl} = \mu + R_{i(j)} + L_j + G_k + GL_{(jk)} + e_{ijkl} \dots \dots \dots (2)$$

Where

Y_{ijkl} = the measurement obtained for the unit in the k^{th} genotype of the i^{th} replication within j^{th} location of l^{th} plot,

μ = experimental mean,

$R_{i(j)}$ = the effect of the i^{th} replication within j^{th} location,

L_j = the effect of the j^{th} environment,

G_k = the effect of the k^{th} rice line,

$GL_{(jk)}$ = interaction effect of j^{th} environment and k^{th} genotype

and E = Error effect

3.7 Combined Analysis of Variance

Combined analysis of variance model for evaluating components of variance pooled over locations was estimated using the method given by Al- jibouri *et al.* (1958) as shown in the table 2.

Table 2: Combined analysis of variance

Source of variation	d.f	S S	MS	Expected Mean Squares
Environment	(L-1)			$\sigma^2_e + r \sigma^2_{Gl} + \sigma^2_g R/L + r g \sigma^2_l$
Replication (R/L)	L(L-1)			$\sigma^2_e + g \sigma^2_{R/L}$
Genotype	(g-1)			$\sigma^2_e + r \sigma^2_{GxE} + r l \sigma^2_G$
G×E	(g-1) (l-1)			$\sigma^2_e + r \sigma^2_{G \times E}$
Error (R/L)×G	L (r-) (g-)			σ^2_e

3.8 Genotypic and Phenotypic Correlation

The covariance component was used to compute genotypic and phenotypic correlation coefficients between any two selectable characters by using formula proposed by Robinson *et al.* (1951).

$$\text{Phenotypic correlation } r_{ph_{1.2}} = \sigma^2_{ph_{1.2}} / \sqrt{(\sigma^2_{ph_1})(\sigma^2_{ph_2})} \dots\dots\dots (3)$$

Where $\sigma^2_{ph_{1.2}}$ = phenotypic variance of the two variable

$\sigma^2_{ph_1}$ = phenotypic variance of the first variable

$\sigma^2_{ph_2}$ = phenotypic variance of the second variable

$$\text{Genotypic correlation } r_{g_{1.2}} = \sigma^2_{g_{1.2}} / \sqrt{(\sigma^2_{g_1})(\sigma^2_{g_2})} \dots\dots\dots (4)$$

Where $\sigma^2_{g_{1.2}}$ = genotypic covariance between two variable

$\sigma^2_{g_1}$ = genotypic variance of the first variable

$\sigma^2_{g_2}$ = genotypic variance of the second variable

The phenotypic variance (σ^2_{ph}) among genotype means tested in R replications within locations was computed by the formula following Robinson *et al.* (1949) as follow:-

$$\sigma^2_{ph} = \sigma^2_e + \sigma^2_{g \times E} + \sigma^2_g + \sigma^2_{R(L)} + \sigma^2_L \dots\dots\dots(5)$$

Where σ^2_{ph} =

σ^2_g = genotypic variance.

σ^2_p = phenotypic variance.

σ^2_{lg} = variance due to genotype x location

l = number of location

r = number of replication

3.9 Estimates of Broad Sense Heritability

Broad sense heritability (h_b^2) was calculated as the ratio component of genotypic variance to phenotypic variance using the formula $h_b^2 = \sigma^2_g / \sigma^2_p \times 100 \dots\dots\dots (5)$

h^2 = broad sense heritability (%),

σ^2_g = genotypic variance

σ^2_{ph} = phenotypic variance

3.10 Path Analysis

Path coefficient analysis was done to discern influences of variables on yield as described by Dewey and Lu (1959). Path diagram indicating the pattern of relationships as coined by Wright (1921). (1) Panicle length (2) Primary

branches/panicle (3) Number of grain/panicle (4) panicle weight (5) number of productive tillers per plant (5); (6) 1000 seed weight; (7) yield per ha. (X) Residue factors:

The complete path coefficient model was as follow:

$$r_{17} = P_{17} + r_{12}P_{27} + r_{13}P_{37} + r_{14}P_{47} + r_{15}P_{57} + r_{16}P_{67}$$

$$r_{27} = r_{12}P_{17} + P_{27} + r_{23}P_{37} + r_{24}P_{47} + r_{25}P_{57} + r_{26}P_{67}$$

$$r_{37} = r_{13}P_{17} + r_{23}P_{27} + P_{37} + r_{34}P_{47} + r_{35}P_{57} + r_{36}P_{67}$$

$$r_{47} = r_{14}P_{17} + r_{24}P_{27} + r_{34}P_{37} + P_{47} + r_{45}P_{57} + r_{46}P_{67}$$

$$r_{57} = r_{15}P_{17} + r_{25}P_{27} + r_{35}P_{37} + r_{45}P_{47} + P_{57} + r_{56}P_{67}$$

$$r_{67} = r_{16}P_{17} + r_{26}P_{27} + r_{36}P_{37} + r_{46}P_{47} + r_{56}P_{57} + P_{67}$$

$$1 = P^2X_7 + P^2_{17} + P^2_{27} + P^2_{37} + P^2_{47} + P^2_{57} + P^2_{67} + 2P_{17}r_{12}P_{27} + 2P_{17}r_{13}P_{37} + 2P_{17}r_{14}P_{47} + 2P_{17}r_{15}P_{57} + 2P_{17}r_{16}P_{67} + 2P_{27}r_{23}P_{37} + 2P_{27}r_{24}P_{47} + 2P_{27}r_{25}P_{57} + 2P_{27}r_{26}P_{67} + 2P_{37}r_{36}P_{67} + 2P_{47}r_{46}P_{67} + 2P_{57}r_{56}P_{67} \dots \dots \dots (6)$$

r_{ij} = simple correlation coefficients for measuring the mutual association of two variables

P_{ij} = path coefficient for measuring direct influence between variables with yield

R_{ij} = indirect effect of variables upon another through the other variable

P_x = the residual effects in the path analysis model

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

3.11 Stability Analysis

Stability of performance of genotypes over environments was analyzed using the linear regression model of Eberhart and Russell (1966) as follows:

$$Y_{ij} = \mu_i + \beta_i I_j + \delta_{ij}, (i= 1, g; j=1, n), \dots \dots \dots (7)$$

Where: Y_{ij} = mean of i^{th} genotype in j^{th} environment

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

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

β_i = regression coefficient which measures the response of i^{th} genotype to the varying environments. δ_{ij} (S^2_d) = deviation from regression of i^{th} genotype at j^{th} environment,

i.e., $\delta_{ij} = Y_{ij} - I_j \bar{Y}_i$.

CHAPTER FOUR

4.0 RESULTS

4.1 Results of ANOVA and Mean Effect of Genotypes

4.1.1 Analysis of variance for Mwera site

Results (Table 3) revealed that there was significant difference at ($p \leq 0.05$) among genotypes for the studied characters viz. plant height, days to 50% flowering, tillers per stand, days to maturity, number of primary branches per panicle, panicle weight, 1000 grain weight, grain yield per plant and grain yield per hectare.

Table 3: Anova Summary for Mwera site

S.V	D. f	50%F	DM	PL	NT/P	P H	PW	1000W	NG/P	NPB/P	GY/P	Y/ha
Rep	2	25.78	2.16	0.07	3.28	95.04	0.25	2.99	2.95	0.024	3.21	0.002
Geno	13	92.33 ***	78.31 ***	4.56 ***	11.43 *	109.88 *	1.21 **	9.28 ***	119.58***	1.663 ***	28.38 ***	2.06 ***
Error A	26	9.63	14.14	0.64	3.98	48.87	0.36	1.62	17.363	0.383	3.03	0.09
Total	41	36.64	33.90	1.85	6.31	70.47	0.62	4.11	49.071	0.771	11.08	0.09

* = significant at $p < 0.05$; ** = significant at $p < 0.01$; *** = significant at $p < 0.001$;

4.1.2 Mean performance summary for Mweru site

Mean performance (Table 4) showed that there was variation at ($p \leq 0.05$) among genotypes for the studied characters.

4.1.3 Plant height (cm)

The highest mean was observed in IRO7M101 (112.8 cm) followed by IR05N359 (107.5 cm) and the least mean was recorded in IRO5N505 (89.5 cm).

4.1.4 Days to 50% flowering

The latest to flower was genotype IR07A 167 (98.67days) followed by IR07A 166 (96.67days), IR09N505 (93.3days), SARO (92.67days), and the earliest genotype was IRRI 123 (80.67days), followed by IR 02A149 (81.67days) and IR09L325 (82.0days).

4.1.5 Days to maturity

Genotype IR07A 167 was the latest to mature (119days) followed by IR09N505 (113.3days), the earliest to mature was genotypes IRRI 123 and SARO 5 (100.7days).

4.1.6 Number of tillers per stand

Highest number of tillers was observed in genotypes IR09N505 (18.27) followed by IR 07A167 (16.23), and the least means observed were in genotypes SARO5 (11.77) followed by IR 07M101 (11.93).

4.1.7 Panicle length (cm)

Genotype IR 07A167 had highest mean panicle length (29.1cm) followed by IRRI 146 (26.6cm), IR03A550 (24.3cm), IRRI 123 (24.3cm) and SARO 5 had least mean of panicle length (18.9cm).

4.1.8 Number of primary branches per panicle

Genotype IR 07A166 had highest mean of number of primary branches per panicle (12.67) followed by IR 07A167 (12.00). SARO, IR03A550, and IR09A136 had 10.33 primary branches per panicle. Genotypes IR 02A149 and IRRI 123 had least number of branches per panicle (10.00).

4.1.9 Number of grains per panicle

Genotype IR07M101 had highest mean grain per panicle (103.33) followed by IR08M110 (102.00), IR03A550 (101.67) and lowest mean grain per panicle was found in genotype IR09N505 (80.33).

4.1.10 Panicle weight (g)

Highest mean performance for panicle weight was found in IR 08M110 (4.43g) followed by IR 03A 550 (3.76g), and lowest mean was IR 05N359 (2.03 g).

4.1.11 Thousand grain weight (g)

Genotype IR 02A149 had highest mean performance of thousand grain weight per panicle (30.23g) followed by IR07A166 (29.9g) and least mean thousand grain weight per panicle was observed in IR09N505 (24.03g).

4.1.12 Grain weight per plant (g)

Genotype IR 07A167 had highest mean performance of grain weight per stand (29.10g) followed by IR07M101 (28.27g), IR08M110 (28.27g) and the lowest mean grain weight per stand was recorded in SARO 5 (18.93g).

4.1.13 Yield (ton/ha)

Highest yield was recorded in IR 07A167 (7.26tons/ha) followed by IR 7M110 and (7.0 tons/ha), IR08M101 (7.0 tons/ha) and the lowest yield was found in IR 02A149 (4.66tons/ha).

Table 4: Mean performance for different growth variables - Mwera site

Genotype	P.HT (cm)	50% FL (days)	DM (days)	P.L (cm)	NT/P	NPB /P	PWT (g)	NG/ P	1000G W (g)	GY/P (g)	Y/ha
IR 09L325	103.3bcd	82.00a	102.0ab	19.77ab	12.67ab	11.00abc	2.96abc	97.00defg	26.20ab	19.77ab	5.01ab
IR09N505	89.5a	93.33def	113.3ef	22.29bc	18.27c	11.33bc	2.66abc	80.33a	24.03a	22.29bc	5.54bc
IRRI 146	100.4abcd	86.00abc	107.7abcd	26.6de	15.63ab	11.00abc	2.30ab	89.00bc	24.67ab	26.67de	6.67d
IR 05N359	107.5cd	89.33cd	110.7cde	22.47 bc	13.00ab	10.67ab	2.03a	89.00bcd	26.80b	26.67bc	5.53bc
IR 02A149	97.0abc	81.67a	104.3abc	21.30abc	14.63ab	10.00a	2.66abc	89.00efg	30.23c	26.67abc	4.66a
IR 08M110	92.1ab	88.67bcd	105.3abcd	21.30abc	14.63bc	11.00abc	4.43d	102.00gf	26.03ab	28.27e	7.06de
IR 07M101	112.8d	87.67bcd	106.0abcd	21.30abc	11.93a	11.00abc	3.03abc	103.33fg	25.33ab	28.27e	7.06de
IR 06A107	99.2abcd	88.67bcd	108.7bcde	23.57cd	14.37ab	11.00abc	2.80abc	94.33bcdef	25.20ab	23.57cd	5.89c
IR 07A166	100.1abcd	96.67ef	111.3cde	22.03abc	16.47bc	12.67d	2.33ab	94.33bcdef	29.90c	23.57abc	5.56bc
IR 07A167	102.5abcd	98.67f	119.0f	29.1 e	16.23bc	12.00cd	2.83abc	93.67bcde	27.17b	29.10e	7.26e
IR 09A136	100abcd	83.33ab	102.0ab	24.10cd	13.13ab	10.33ab	2.36ab	92.33bcde	27.07b	24.10cd	6.02c
IR 03A550	102.1abcd	83.33cd	107.3abcd	24.27cd	12.73ab	10.33ab	3.76cd	101.67bcde	25.63ab	24.27cd	6.07c
IRRI 123	97.6abc	80.67a	100.7a	24.27cd	14.33ab	10.00a	2.56ab	88.00b	25.63b	23.60cd	5.95c
SARO 5	107.4	92.67e	100.7de	18.93a	11.77a	10.33ab	3.36bc	97.00cdefg	27.03b	18.93a	4.71a
Grand Mean	100.8	88.57	107.74	25.72	14.37	10.90	2.86	94.38	26.58	23.84	5.91
CV	6.9	3.5	3.760	3.1	17.47	5.7	21.0	4.4	4.8	7.3	5.3
S.E ±	5.71	2.534	2.534	0.65	0.38	0.50	0.49	2.4	0.735	1.42	0.18

Means within the column having common letters are not significantly different from each other at $p < 0.05$ by Duncan's multiple range tests

P.HT = Plant height, 50% FL, D.M = Days to maturity, PL = Panicle length, NT/P = Number of tillers/ plant, NPB /P = Number of primary branches/panic, PWT = Panicle weight, NG/P = Number of grains /panicle, 1000gw = 1000 grain weight, GY/P = Grain yield/ plant, Y/ha = Yield/ha.

4.2 Analysis of Variance at Kibokwa Site

Results from analysis of variance revealed significant at ($p < 0.05$) for all of characters studied except for days to maturity, tillers per stand and number of branches per panicle (Table 5).

Table 5: ANOVA summary for Kibokwa site

	D. f	50%FL	DM	PL	NT/P	P HT	PWT	1000GW	NG/P	NPB/P	GY/P	Y/ha
Rep	2	1.81	1.167	0.22	1.35	8.502	0.38	0.17	292.31	2.66	2.48	0.001
Genotype	13	100.80 ***	5.78**	3.34**	0.98*	127.17 ***	1.140*	15.267***	474.29 ***	0.97*	24.84 ***	2.99*
Error A	26	1.32	5.78	0.82	0.66	11.64	0.49	1.59	125.13	0.51	0.60	0.03
Total	41	32.89	5.55	1.64	0.8	48.12	0.694	5.86	243.99	0.76	8.38	0.97

* = significant at $p < 0.05$; ** = significant at $p < 0.01$; *** = significant at $p < 0.001$;

PHT = Plant height, 50% FL, D.M = Days to maturity, P.L = Panicle length, NT/P = Number of tillers/ plant, NPB /P = Number of primary branches/panicle, PWT = Panicle weight, NG/ P = Number of grains /panicle, 1000GW = 1000 grain weight, GY/P = Grain yield/ plant, Y/ha = Yield/ha

4.2.1 Mean performance at Kibokwa site

Results of mean performance at Kibokwa site (Table 6) indicate that there were differences at ($p \leq 0.05$) among genotypes for studied characters.

4.2.2 Plant height (cm)

Highest mean plant height was observed in genotype IR07M101 (112.8 cm) followed by IR05N359 (107.5cm), SARO 5 (107.4cm) and least mean plant height was recorded in IR09N505 (89.5cm).

4.2.3 Days to 50% flowering

Latest genotype to flower was IR 07A167 (98.67days) followed by IR09N505 (93.3days).SARO 5 (92.67 days) IR 03A550 (90.6days) and the earliest to flower was IRRI 123 (80.67days).

4.2.4 Days to maturity

Earliest to mature was IRRI 123 (100.7days) followed by IR09A136 and IRO9L325 (102 days) and the latest to mature was IR 07A167 (119days).

4.2.5 Number of productive tillers per stand

The highest number of productive tillers were recorded for IR09N505 (18.27) followed IR07A166 (16.47) and the least number of productive tillers was obtained IR07M101 (11.93).

4.2.6 Panicle weight (g)

Highest mean weight of panicle weight was recorded for IR08M110 (4.43g), followed by IR03A550 (3.77g), SARO 5 (3.37g) and the lowest mean weight of grains/panicle was observed in genotype IR 05N359 (2.03g).

4.2.7 Thousand grains weight (g)

Highest mean Thousand grains weight was obtained in IR 02A149 (30.23g), followed by IR07A166 (29.9g), IR 07A167 (27.1g) and the lowest mean thousand grains weight was in IR09N505 (24.03).

4.2.8 Grain weight per plant (g)

Mean performance was highest in IR07A167 (29.1) followed by IR08M110 (28.2g), IRR1146 (26.6g) and least mean was in genotype SARO 5 (18.93).

4.2.9 Yield (t/ha)

Highest mean performance for yield (t/ha) was observed in IR 09L325 (5.5t/ha) followed by IR08M110 (5.05) and the lowest mean performance for yield was IR03A550 (1.89 t/ha).

Table 6: Mean performance of 14 genotypes for different growth variables- Kibokwa site

Genotype	PHT (cm)	50% FL (days)	D.M (days)	P L (days)	NT/S	NPB/P	PWT (g)	NG /P	1000GW (g)	GW/P (g)	Y/ha
IR 09L325	103.3bcd	82.00a	102.0ab	25.87bcd	12.67ab	11.00abc	2.967abc	97.00defg	26.20ab	19.77ab	5.00h
IR09N505	89.5a	93.33def	113.3ef	23.53a	18.27c	11.33bc	2.667abc	80.33a	24.03a	22.29bc	4.33ef
IRRI 146	100.4abcd	86.00abc	105.7abcd	23.63a	15.63abc	11.00abc	2.300ab	89.00bc	24.67ab	26.67de	4.33d
IR 05N359	107.5cd	89.33cd	110.7cde	26.73cde	13.00ab	10.67ab	2.033a	89.33bcd	26.80b	22.47bc	2.65bc
IR 02A149	97.0abc	81.67a	104.3abd	25.50bc	14.63abc	10.00a	2.667abc	98.33efg	30.23c	21.30abc	2.39b
IR 08M110	92.1ab	88.67bcd	105.3abcd	26.00bcd	16.13bc	11.00abc	4.433d	102.00fg	26.03ab	28.27e	5.05h
IR 07M101	112.8d	87.67bcd	106.0abcd	26.50cde	11.93a	11.00abc	3.033abc	103.33g	25.33ab	27.40e	4.75gh
IR 06A107	99.2abcd	88.67bcd	108.7bcde	26.53cde	14.37ab	11.00abc	2.800abc	94.33bcdef	25.20ab	23.57cd	4.46fg
IR 07A166	100.1abcd	96.67ef	111.3cde	27.17de	16.47bc	12.67d	2.333ab	95.00bcdef	29.90c	22.03abc	4.46fg
IR 07A167	102.5abcd	98.67f	119.0f	27.80e	16.23bc	12.00cd	2.833abc	93.67bcde	27.17b	29.10e	4.08de
IR 09A136	100.0abcd	83.33ab	102.0ab	25.47bc	13.13ab	10.33ab	2.367ab	92.33bcde	27.07b	24.10cd	2.84c
IR 03A550	102.1abcd	90.67cd	107.3abcde	24.50ab	12.73ab	10.33ab	3.767cd	101.67fg	25.63ab	24.27cd	1.89a
IRRI 123	97.6abc	80.67a	100.7a	25.33bc	14.33ab	10.00a	2.567ab	88.00b	26.83b	23.60cd	3.77d
SARO 5	107.4cd	92.67de	112.0de	25.47bc	14.33a	10.33ab	3.367bc	97.00cdefg	27.03b	18.93a	3.75d
G.Mean		88.57	107.74	25.72	14.38	10.90	2.86	94.38	26.58	23.84	3.8
C.V		3.5	3.5	3.1	3.4	5.7	21	4.4	4.8	3.1	5.2
S.E ±		1.84	23.07	0.6	1.6	0.5	0.49	3.4	1.04	1.4	0.16

Means within the column having common letters are not significantly different from each other at 5% level by Duncan's multiple range tests.

PHT = Plant height, 50% FL, DM = Days to maturity, P.L = Panicle length, NT/P = Number of tillers/ plant, NPB /P = Number of primary branches/panicle, P.WT = Panicle weight, NG/P = Number of grains /panicle, 1000GW = 1000 grain weight, GY/P = Grain yield/ plant, Y/ha = Yield/ha

4.3 Analysis of Variance (Cheju site)

Results (Table 7) showed significant differences at ($p \leq 0.05$) among genotypes for all studied characters viz., days to 50% flowering, days to maturity, plant height ,grains weight per plant, number primary branches per panicle, panicle weight,1000 grains weight and yield per ha.

Table 7: ANOVA summary for Cheju site

SOURCE	D. f	50%F	DM	PL	NT/P	P HT	PWT	1000W	NG/P	NPB/P	GY/P	Y/ha
OF VAR												
Rep	2	16.167	2.667	0.014	3.071	3.897	0.144	0.539	397.595	0.167	0.175 *	1.492
Genotype	13	65.907 ***	97.070 ***	5.25*	0.50*	88.898 ***	0.639 *	2.734 **	185.767***	0.498*	1.710 *	23.064 ***
Error A	26	7.885	5.256	2.952	0.533	0.132	0.222	2.512	98.262	0.372	0.05	1.166
Total	41	26.686	34.242	3.537	0.646	34.802	0.35	2.486	140.609	0.402	0.583	8.125

* = significant at $p < 0.05$; ** = significant at $p < 0.01$; *** = significant at $p < 0.001$

PHT = Plant height, 50% FL, DM = Days to maturity, PL = Panicle length, NT/P = Number of tillers/ plant, NPB /P = Number of primary branches/panicle, PWT = Panicle weight, NG/ P = Number of grains /panicle, 1000GW = 1000 grain weight, GY/P = Grain yield/ plant, Y/ha = Yield/ha

4.3.1 Mean performance for Cheju site

4.3.2 Plant height (cm)

There was significant difference at ($p \leq 0.05$) for the studied characters at Cheju site (Table 8).

Tallest plants were observed in genotype IR07M101 (112.8cm) followed by IR05N359 (107.5cm), IR09N505 (103.3cm) and shortest was genotype IR08M110 (92.1cm).

4.3.3 Days to 50% flowering

The latest genotype to flower was IR 07A167 (98.67days) followed by IR 07A166 (96.6days), IR09N505 (93.3days) and the earliest to flower was IRR1123 (80.67days).

4.3.4 Days to maturity

Latest genotype mature was IR07A167 (119.0days) followed by IR09N505 (113.3days), and the earliest mean was IRR1 123 (100.7days).

4.3.5 Number of productive tillers per stand

Highest mean Number of productive tillers per stand was recorded for genotype IR09N505 (18.27) followed by IR 07A166 (16.4), IR07A167 (16.2) and lowest mean Number of productive tillers per stand was recorded for SARO 5 (11.77).

4.3.6 Panicle weight (g)

Highest mean weight of grains/panicle was recorded for IR08M110 (4.43g), followed by IR03A550 (3.76g), SARO 5 (3.36g) and lowest mean weight of grains/panicle was in genotype IR 05N359 (2.03g).

4.3.7 Number of primary branches per panicle

Highest mean for number of primary branches per panicle was found in IR 07A166 (12.67) followed by IR07A167 (12.0), IR09N505 (11.3) and the lowest mean number of primary branches per panicle was IRRI 123 and IR02A149 (10.0).

4.3.8 Thousand grain weight (g)

Genotype IR 02A149 had highest mean performance thousand grain weight (30.23g) followed by IR 07A166 (29.9), IR 07A167 (27.1g) and genotype IR09N505 had lowest mean performance (24.03g).

4.3.9 Panicle length (cm)

Longest panicles were observed in genotype IR 07A167 (27.8) followed IR07A166 (27.17cm) and the shortest panicle was recorded IR09N505 (23.53cm).

4.3.10 Yield (ton/h)

Highest mean yield was obtained in IR 08M110 (4.96tons/ha) followed by IR 07M101(4.27tons/ha), IR 09L325 (4.14tons/ha) and the lowest yield was obtained by IR 03A550 (2.33tons/ha).

Table 8: Summary of Mean performance of 14 genotypes for different growth parameters - Cheju site

Genoty	PHT (cm)	50% F (Days)	DM (days)	PL (cm)	NPT/P	NPB/P	PWT (cm)	NG /P	1000GW (g)	GY/P (g)	Y./ha (Ton)
IR 09L325	103.3bcd	82.00a	102.0ab	25.87bcd	12.67ab	11.00abc	2.96abc	97.00defg	26.20ab	19.77ab	4.14e
IR09N505	103.3a	93.33def	113.3ef	23.53a	18.27c	11.33bc	2.66abc	80.33a	24.03a	22.29bc	3.90de
IRRI 146	100.4abcd	86.00abc	105.7abcd	23.63a	15.63abc	11.00abc	2.30ab	89.00bc	24.67ab	26.67de	3.52c
IR 05N359	107.5cd	89.33cd	110.7cde	26.73cde	13.00ab	10.67ab	2.03a	89.33bcd	26.80b	22.47bc	2.65ab
IR 02A149	97.0abc	81.67a	104.3abc	26.73bc	14.63abc	10.00a	2.66abc	98.33efg	30.23c	21.30abc	2.70ab
IR 08M110	92.1ab	88.67bcd	104.3abcd	26.00bcd	16.13bc	11.00abc	4.43d	102.00fg	26.03ab	21.30e	4.96f
IR 07M101	112.8d	87.67bcd	106.0abcd	26.50cde	11.93a	11.00abc	3.03abc	103.33g	25.33ab	27.40e	4.27e
IR 06A107	99.2abcd	88.67bcd	108.7abcde	26.50cde	14.37ab	11.00abc	3.03abc	94.33bcd	25.20ab	27.40cd	4.09e
IR 07A166	100.1abcd	96.67ef	111.3cde	27.17de	16.47bc	12.67d	2.80ab	95.00bcdef	29.90c	22.03abc	4.13e
IR 07A167	102.5abcd	98.67f	119.0f	27.80e	16.23bc	12.00cd	2.83abc	93.67bcde	27.17b	29.10e	3.94de
IR 09A136	100.0abcd	83.33ab	102.0ab	25.47bc	13.13ab	10.33ab	2.83ab	92.33bcde	27.07b	24.10cd	2.79b
IR 03A550	102.1abcd	90.67cd	107.3abcde	24.50ab	14.33ab	10.33ab	3.76cd	101.67fg	25.63ab	24.27cd	2.33a
IRRI 123	97.6abc	80.67a	100.7a	25.33bc	14.33ab	10.00a	2.56ab	88.00b	26.83b	23.60cd	3.60cd
SARO 5	107.4cd	92.67de	112.0de	25.47bc	11.77a	10.33a	3.36bc	97.00cdefg	27.03b	18.93a	3.49c
Grand Mean	100.8	88.75	107.74	25.72	14.38	10.9	2.86	94.38	26.58	23.84	3.61
CV	6.9	3.5	3.5	0.6	13.9	5.7	21	4.4	4.8	7.3	6.2
S.E ±	5.71	2.53	3.07	3.1	1.6	0.5	0.49	3.4	1.04	1.42	0.18

Means within the column having common letters are not significantly different from each other at $p < 0.05$ by Duncan's multiple range tests

PHT = Plant height, 50% FL, DM = Days to maturity, PL = Panicle length, NT/P = Number of tillers/ plant, NPB /P = Number of primary branches/panicle, PWT= Panicle weight, NG/P = Number of grains /panicle, 1000GW = 1000 grain weight, GY/P = Grain yield/ plant, Y/ha = Yield/ha

4.4 Combined analysis

4.4.1 ANOVA for combined sites

Results of ANOVA from data pooled over all three locations (Table 9) indicated highly significant differences among the environments. There were highly significant differences among the genotypes for all variables. While G×E interactions showed significant effect for days to 50% flowering, days to maturity, number of tillers per plant, 1000 grain weight, grain yield per plant and yield per hectare.

Table 9: ANOVA Summary for combined sites

S.V	D. f	50%F	D.M	P.L	NT/P	PHT	PWT	1000GW	NG/P	NPB/P	GY/P	Y/ha
Rep	2	21.55	2.45	0.63	1.305	18.812	0.722	1.41	466.79	1.02	1.789	0.07
Envir	2	122.38***	600.50 ***	177.95 ***	611.94 ***	377.17***	2.80 ***	343.08 ***	387.91 * **	3.71 **	1036.50***	68.77 ***
Geno	13	232.79***	114.59 ***	8.57 ***	6.67***	265.81 ***	2.08 ***	11.56 ***	585.30 ***	2.45 ***	50.20 ***	4.68 ***
Geno×En	26	13.12 **	33.28 ***	2.28	3.12 *	30.069**	0.459	7.85 *	97.16**	0.33	13.0 ***	1.04 ***
Error	82	6.515	8.07	1.419	1.79	24.563	0.34	1.87	81.85	0.44	1.65	0.06
Total	125	33.51	33.78	5.15	12.33	110.636	0.59	9.57	148.45	0.69	25.63	0.845

* = significant at $p < .05$; ** = significant at $p < 0.01$; *** = significant at $p < 0.001$;

PHT = Plant height, 50% FL, D.M = Days to maturity, P.L = Panicle length, NT/P = Number of tillers/ plant, NPB /P = Number of primary branches/panicle, PW T= Panicle weight, NG/P = Number of grains /panicle, 1000gw = 1000 grain weight, GY/P = Grain yield/ plant, Y/ha = Yield/ha

4.4.2 Mean performance combined over all three locations

There were significant differences at $p \leq 0.05$ for studied characters over all three locations (Table 10).

4.4.3 Plant height (cm)

Tallest plants were observed for genotype IR05N359 (97.21) followed by 4.4.5IR07M101 (97.12cm) and the shortest genotypes was IR09N505 (81.69 cm).

4.4.4 Days to 50% flowering

The latest genotype to flower over all location was genotype IR07A167 (97.56 days) followed by IR07A166 (96.11days) and the earliest was IR 09L325 (81.11days)

4.4.5 Days to maturity

The latest genotype to mature over all three locations was IR07A167 (119.3 days) followed by IR07A166 (115.4 days) and the earliest genotype was IR09L325 (98.6 days).

4.4.6 Number of productive tillers per plant

Highest mean productive tillers per plant was found in genotype IR09N505 (11.64) followed by IR07A167 (11.18) and lowest mean of productive tillers per plant was found in genotype IR03A550 (9.02).

4.4.7 Panicle weight

Highest mean panicle weight over all three locations was found in genotype IR08M110 (4.48 g) followed by SARO 5 (3.44g) and the lowest mean panicle weight was observe in genotype IRRI 123(2.58).

4.4.8 Number of primary branches per panicle

Highest mean number of primary branches per panicle was recorded for genotype IR07A166 (11.67) followed by IR07A167 (11.33) and lowest mean number of primary branches per panicle was recorded for IRRI 123 (9.67).

4.4.9 Thousand grain weight (g)

The highest mean performance for thousand grain weight over all three locations was recorded for genotype SAR0 5 (25.68g) followed by IR07A167 (24.99g) and the lowest mean thousand grain weight was recorded for IRRI 146 (21.87g).

4.4.10 Panicle length (cm)

Longest panicle length was recorded for genotype IR07A167 (25.23cm) followed by IR05N359 (24.98cm) and shortest panicle length was recorded for IRRI146 (22.27cm).

4.4.11 Yield (ton/ha)

Highest mean yield was obtained in genotype IR8M110 (5.69 ton/ha) followed by IR07M101 (5.28 ton/ha) and lowest mean yield over all locations was recorded for IR02A149 (3.25 ha).

Table 10: Mean performance for studied variables over all three locations

Genoty	P.HT (cm)	50% F (days)	D.M (days)	P.L (cm)	NT/P	NPB /PN	PWT	NG/P	1000GW (g)	GY/P (g)	Y/ha (ton)
IR 09L325	92.67 cd	81.11a	98.6a	23.50 abc	9.22 ab	10.67 cd	3.16ab	108.78 f	24.09 bcd	18.76 cd	4.71e
IR09N505	81.69a	88.89e	110.9f	22.90 ab	11.64e	10.67 cd	2.91ab	82.33a	22.06 a	18.60cd	4.62de
IRRI 146	84.92 ab	83.33 abc	105.6cd	22.27a	10.54bcde	10.44 bc	3.43ab	94.67bcde	21.87 a	18.52 cd	4.66de
IR 05N359	97.21d	87.89 de	110.3ef	24.98 de	9.55abc	10.67cd	3.06ab	92.11bc	23.87 bc	15.60b	3.61b
IR 02A149	83.19a	81.56a	103.2bc	22.49 a	9.98abcd	10.11 abc	2.92ab	91.00f	25.02cde	14.30a	3.25a
IR 08M110	81.86 a	84.78bc	104.8bcd	24.56 cde	9.71cde	10.78 cd	4.48c	108.22	25.47de	22.81g	5.69g
IR 07M101	97.12d	85.56cd	107.2 de	23.91 bcd	9.08ab	10.67 cd	3.44b	104.89f	24.50bcde	21.12f	5.28f
IR 06A107	93.00cd	87.44de	110.1f	23.29 abc	9.56 abc	10.78 cd	2.97b	90.33abc	23.43b	19.30de	4.81e
IR 07A166	93.24cd	96.11f	115.4 g	24.82 de	10.82cde	11.67e	2.73a	89.22 abc	24.04bcd	18.81cd	4.71e
IR 07A167	95.71d	97.56f	119.3h	25.23 e	11.18de	11.33 de	2.71a	91.44abc	24.99cde	20.43ef	5.10f
IR 09A136	88.98bc	82.44ab	105.6cd	23.50 abc	9.26ab	10.44bc	2.92ab	97.78 cde	23.80 bc	16.22b	3.88c
IR 03A550	88.19bc	87.89de	110.1cd	22.40 a	9.02 a	10.22 abc	3.43b	96.22cde	24.82bcde	16.22b	3.43ab
IRRI 123	88.60bc	81.33a	102.3b	24.13 bcde	10.00 abcd	9.67a	2.58a	86.56 ab	24.67bcde	17.64b	4.44d
SARO 5	92.86cd	87.56de	110.7f	23.39 abc	9.14ab	9.89ab	3.44b	102.22def	25.68e	15.86 b	3.98c
Grand Mean	89.95	86.67	108.15	23.67	9.98	10.57	3.16	95.41	24.16	18.16	4.44
CV	5.5	2.9	2.8	5.0	13.4	6.3	18.6	9.04	5.7	7.1	5.6
S.E ±	4.95	2.55	3.06	1.19	1.34	0.66	0.58	9.04	1.36	1.28	0.24

Means within the column having common letters are not significantly different from each other at 5% level by Duncan's multiple range tests

PHT = Plant height, 50% FL, D.M = Days to maturity, P.L = Panicle length, NT/P = Number of tillers/ plant, NPB /P = Number of primary branches/panicle, PW T= Panicle weight, NG/P = Number of grains /panicle, 1000GW = 1000grain weight, GY/P = Grain yield/ plant, Y/ha = Yield/ha

4.4.12 Mean performance for genotypes combined over all three locations

4.4.13 Location means for the studied variables

Table 11 indicates that Mwera site had highest number (88.57 days) mean days to 50% flowering followed by Kibokwa site (86.19 days) and the least mean (85.26days) recorded at Cheju site. For days to maturity highest mean was (109.38 days) at Cheju followed by (107.74 days) at Mwera and the least mean for days to maturity was obtained at Kibokwa (107.33 days).

Highest mean for panicle length was (25.72cm) at Mwera followed by (23.69 cm) at Kibokwa and lowest mean was (21.60 cm) at Cheju. Means for tillers per stand was the same at Mwera and Kibokwa (14.38 tillers) and the least mean for this variable was 7.50 tillers at Cheju. Highest mean for plant height was (100.84 cm) at Mwera followed by 85.40cm at Kibokwa and the least mean was (83.60cm) at Cheju. Mean for panicle weight was highest at Mwera (3.86 g) and lowest mean was (3.26g) at Cheju. For 1000 grains weight highest mean of (26.58 g) was obtained at Mwera followed by (24.90g) at Kibokwa and the least mean was (21.01g) at Cheju site. Location mean for number of grains per panicle showed that Kibokwa had highest mean (98.83grains) followed by (94.38grains) at Mwera and the least mean was (93.02grains) at Cheju. There was little variations across location for mean primary branches per panicle, however, the highest mean was (10.90) at Mwera followed by (10.47) at Cheju and the least was (10.33) at Kibokwa. Mean yield was highest at Mwera (5.91ton/ha) followed by 3.80ton /ha at Kibokwa and the least mean for this variable was 3.61t/ha at Cheju.

Table 11: Location means for studied variable

Location	50%F	D.M	P.L	NT/P	P H	PWT	1000GW	N.G/P	NPB/P	GY/P	Y/h
Mwera	88.57	107.74	25.72	14.38	100.84	3.86	26.58	94.38	10.90	23.84	5.91
Kibokwa	86.19	107.33	23.69	14.38	85.40	3.35	24.90	98.83	10.33	15.99	3.80
Cheju	85.26	109.38	21.60	7.50	83.60	3.26	21.01	93.02	10.47	14.64	3.61
Mean	86.67	24.16	23.67	9.98	89.95	3.16	24.16	95.41	10.57	18.16	4.44
SE ±	1.47	1.76	0.68	0.77	2.86	0.34	0.79	5.22	0.54	0.743	0.14
LSD(0.05)	4.14	4.97	1.93	2.179	8.05	0.95	2.22	14.69	1.08	2.09	0.40
VC %	2.9	2.8	5.0	13.4	5.5	18.6	5.7	9.5	6.30	7.1	5.6

PHP = Plant height, 50% FL, D.M = Days to maturity, PL = Panicle length, NT/P = Number of tillers/ plant, NPB /P = Number of primary branches/panicle, PWT = Panicle weight, NG/ P = Number of grains /panicle, 1000GW = 1000 grain weight, GY/P = Grain yield/ plant, Y/ha = Yield/ha

4.4.14 Interaction (combination) means

4.4.15 Combination means for G×E interaction for days to 50% flowering.

Combination means of G×E interaction for days to 50% flowering are shown in (Table 12). Genotype IR07A167 was the consistently the latest to flower across locations, however, no genotype that was consistently the earliest. Other genotypes showed various ranking for this variable.

Table 12: Combination means of G×E interaction for days to 50% flowering

Genotypes	Mwera	Rank	Kibokwa	Rank	Cheju	Rank
IR 09L325	82.00	9	80.67	12	80.67	10
IR09N505	93.33	2	90.00	4	83.33	7
IRRI 146	86.00	7	82.33	10	81.67	9
IR 05N359	89.33	5	88.67	5	85.67	4
IR 02A149	81.67	10	81.33	11	81.67	9
IR 08M110	88.67	6	82.67	9	83.00	8
IR 07M101	88.67	6	85.33	7	83.67	6
IR 06A107	88.67	6	85.00	8	88.67	3
IR 07A166	88.67	6	97.33	2	94.33	2
IR 07A167	96.67	1	97.67	1	96.33	1
IR 09A136	83.33	8	80.67	13	83.33	7
IR 03A550	90.67	4	90.67	3	84.00	5
IRRI 123	80.67	11	80.00	14	83.33	7
SARO 5	92.67	3	86.00	6	84.00	5
Mean	87.85		86.31		85.26	

S.E within table \pm 2.30
LSD (0.05) within table \pm 4.58

4.5.16 Combination means of G×E interaction for days to maturity

The latest genotype to mature across all three environments was IR07A167, the genotype showed similar ranking across all three locations (Table 13). While for early maturity there was no genotype showed consistent ranking across locations

Table 13: Combination of G×E interaction for days to maturity

Genotypes	Mwera	Rank	Kibokwa	Rank	Cheju	Rank
IR 09L325	102.00	12	95.00	13	98.67	12
IR09N505	113.33	2	110.00	7	109.33	6
IRRI 146	105.67	9	101.67	11	109.33	6
IR 05N359	110.67	5	110.67	4	109.67	5
IR 02A149	104.33	11	100.67	11	104.67	10
IR 08M110	105.33	10	101.00	10	108.00	8
IR 07M101	106.00	8	110.67	5	105.00	9
IR 06A107	108.67	6	107.33	9	114.33	3
IR 07A166	111.33	4	115.67	2	119.33	2
IR 07A167	119.00	1	119.33	1	119.67	1
IR 09A136	102.00	12	110.67	6	104.00	11
IR 03A550	107.33	7	112.00	3	111.00	4
IRRI 123	100.67	13	98.00	12	108.33	7
SARO 5	112.00	3	110.00	8	110.00	5
Mean	107.73		107.33		109.38	
S.E within table ± 2.50						
LSD (0.05) within table ± 4.98						

4.5.17 Combination means of G×E interaction for 1000 grains weight

The combined data for 1000 grains weight are shown in (Table 14) indicated that there was no genotype that showed consistently heaviest 1000 grains weight across locations. Although genotype IR08M110 ranked the second heaviest genotype at Kibokwa and Cheju.

Table 14: Combination means of G×E interaction for 1000 grains weight

Genotypes	Mwera	Rank	Kibokwa	Rank	Cheju	Rank
IR 09L325	26.20	7	26.00	6	20.07	13
IR09N505	24.03	14	21.33	11	20.80	7
IRRI 146	24.67	13	20.93	12	20.00	11
IR 05N359	26.80	8	24.60	9	20.20	9
IR 02A149	30.23	1	23.83	10	21.00	12

IR 08M110	26.03	11	28.13	2	22.23	2
IR 07M101	25.33	10	26.13	4	22.03	3
IR 06A107	25.20	12	26.13	4	20.30	8
IR 07A166	29.90	2	24.80	8	19.90	14
IR 07A167	27.17	3	25.17	7	22.63	1
IR 09A136	27.07	4	26.03	5	20.10	10
IR 03A550	25.63	9	26.90	3	21.93	4
IRRI 123	26.83	6	26.03	5	21.13	6
SARO 5	27.03	5	28.20	1	21.80	5
Mean	26.58		25.30		21.00	
S.E within table \pm 1.11						
LSD(0.05) within table \pm 2.24						

4.5.18 Combination means of G×E interaction for grain yield per plant

Data for G×E interaction for grain yield per plant showed rank changes for means yield per plant across locations (Table 15) However genotype IR 08M110 had ranked first yielding genotype across Kibokwa and Cheju sites and ranked the second at Mwera

Genotypes	Mwera	Rank	Kibokwa	Rank	Cheju	Rank
IR 09L325	19.77	12	19.97	2	16.53	4
IR09N505	22.29	9	17.40	6	16.10	6
IRRI 146	26.67	4	15.20	8	13.70	8
IR 05N359	13.70	14	13.13	14	11.20	11
IR 02A149	21.30	11	11.53	12	10.07	13

IR 08M110	28.27	2	20.17	1	20.00	1
IR 07M101	27.40	3	19.03	3	16.93	2
IR 06A107	23.57	8	17.90	4	16.43	5
IR 07A166	22.03	10	17.87	5	16.53	4
IR 07A167	29.10	1	16.37	7	15.83	3
IR 09A136	24.10	6	13.67	11	10.90	12
IR 03A550	24.27	5	11.50	13	12.90	10
IRRI 123	23.60	7	15.07	10	14.27	7
SARO 5	18.93	13	15.10	9	13.53	9
Mean	23.21		15.99		14.63	

S.E of mean within table \pm 1.05

LSD (0.05) within table \pm 2.09

Table 15: Combination table of G×E interaction for grain yield (grams /plant)

4.5.19 Combination of G×E interaction for grain yield (ton/h)

Combination means of G×E interaction for grain yield/h (Table 16) showed that there was no consistence in yield rank across locations. While genotype IR 08M110 was the first high yielding genotype at Cheju and Kibokwa and ranked the second at Mwera

Genotypes	Mwera	Rank	Kibokwa	Rank	Cheju	Rank
IR 09L325	5.01	12	5.00	2	4.14	3
IR09N505	5.54	11	4.33	4	3.99	6

IRRI 146	6.67	4	3.80	8	3.52	10
IR 05N359	5.53	10	2.65	9	2.65	8
IR 02A149	4.66	14	2.39	10	2.70	13
IR 08M110	7.06	2	5.05	1	4.96	1
IR 07M101	6.84	3	4.75	3	4.27	2
IR 06A107	5.89	8	4.46	4	4.09	5
IR 07A166	5.56	9	4.46	4	4.13	4
IR 07A167	7.26	1	4.08	5	3.94	7
IR 09A136	6.02	6	2.84	11	2.79	12
IR 03A550	6.07	5	1.89	12	2.33	14
IRRI 123	5.95	7	3.77	6	3.60	9
SARO 5	4.71	13	3.75	7	3.49	11
Mean	5.91		3.80		3.61	

S.E of means within table 0.20

LDS (0.05) within table \pm 0.40

Table 16: Combination table means of G×E interaction for grain yield ton/h

4.6 Genotypic and Phenotypic Correlations at Mwera Site

Grain yield per stand had positive and significant correlation with yield per hectare, both genotypically ($r_g = 0.920^{**}$) and phenotypically ($r_p = 0.919^{**}$), (Table 17) days to maturity had positive genotypic ($r_g = 0.820^{**}$) and phenotypic correlations ($r_p = 0.822^{**}$) with days to 50% flowering, number of primary branches per panicle had significant positive genotypic correlation with days to maturity ($r_g = 0.586^{**}$) and phenotypic ($r_p = 0.607^{**}$), panicle length had both genotypic ($r_g = 0.411^{**}$) and phenotypic ($r_p = 0.387^*$) correlations with 1000 grain weight, had significant genotypic and phenotypic negative correlations with yield per hectare ($r_g = -0.352^*$) and ($r_p = -0.370^*$) respectively. Plant height and number of tillers per stand had

significant negative genotypic correlation ($r_g = -0.481^{**}$) and phenotypic correlation ($r_p = -0.454^{**}$).

Table 17: Estimates of Genotypic (top) and Phenotypic Correlations (bottom) at Mwera site

Control Variables	DF	DM	PL	NT/P	PHT	PWT	1000GW	NGP/P	NPB/P	GRY/P	Y/H
DF	1										
DF	1										
DM	0.820**	1									
DM	0.822**	1									
PL	0.229*	0.209*	1								
PL	0.206*	0.202*	1								
TPS	0.199	0.199	0.057	1							
TPS	0.240*	0.215*	0.103	1							
PHT	-0.010	0.048	0.266*	-0.481**	1						
PHT	-0.037	0.039	0.243*	-0.454**	1						
GWP	0.113	0.020	-0.023	0.035	-0.114	1					
GWP	0.082	0.008	-0.058	0.093	-0.137	1					
TGW	-0.030	-0.006	0.411**	0.110	0.150	-0.248*	1				
TGW	-0.059	-0.016	0.387*	0.152	0.116	-0.304*	1				
NGPP	-0.023	-0.134	0.231*	-0.366*	0.281*	0.426**	0.279*	1			
NGPP	-0.057	-0.149	0.201*	-0.335*	0.255*	0.397*	0.248*	1			
NPB/P	0.611**	0.586**	0.400**	0.390*	0.034	-0.029	0.022	0.143	1		
NPB/P	0.657**	0.607**	0.447**	0.356*	0.060	-0.006	0.065	-0.109	1		
PW	0.143	0.123	0.115	0.227*	-0.106	0.288*	-0.324*	0.195	0.209*	1	
PW	0.143	0.123	0.114	0.231*	-0.113	0.278*	-0.327*	0.196	0.218*	1	
YPH	0.187	0.077	0.118	0.200*	-0.047	0.214*	-0.352*	0.135	0.180	0.920**	1
YPH	0.179	0.073	0.108	0.219	-0.058	0.204*	-0.370*	0.124	0.195	0.919**	1

** Correlation is significant at $p < 0.01$

* Correlation is significant at $p < 0.05$

DF = Days to 50% flowering, DM=Days to maturity, PL= Panicle length, NT/P= Number of Tillers /plant, PHT = Plant height. PWT= Panicle weight, 1000GW = 1000 Grains weight, NPB/P= Number of primary branches / panicle, Y/H = Yield per h. GRY/plant = Grain yield per plant.

4.6.1 Genotypic and Phenotypic correlations at Kibokwa site

Results of genotypic and phenotypic correlations between pairs of traits at Kibokwa site are shown in (Table 18). Grain yield per stand had positive and significant correlations with yield per hectare at both genotypic ($r_g = 0.951^{**}$) and phenotypic ($r_p = 0.943^{**}$) level, days to maturity and days to 50% flowering had significant positive genotypic and phenotypic correlations ($r_g = 0.778^{**}$) and ($r_p = 0.786^{**}$) respectively, plant height had positive significant genotypic correlation with days to flowering ($r_g = 0.467^{**}$) and positive significant phenotypic correlation ($r_p = 0.458^{**}$), panicle length had positive significant genotypic correlation with days to 50% flowering ($r_g = 0.317^*$) and phenotypic correlation ($r_p = 0.350^*$), number of primary branches per panicle had positive significant genotypic ($r_g = 0.406^{**}$) and phenotypic ($r_p = 0.422^{**}$) correlation with days to flowering, plant height also had positive significant genotypic correlation ($r_g = 0.454^{**}$) and phenotypic correlation ($r_p = 0.431^{**}$) with days to maturity.

Table 18: Estimates of Genotypic (top) and phenotypic Correlations (bottom) - Kibokwa Site

	DF	DM	PL	TPS	PHT	PWT	TGW	NG/P	NPB/P	GRY/P	YPH
DF	1										
DF	1										
DM	0.778**	1									
DM	0.786**	1									
PL	0.317*	0.285*	1								
PL	0.350*	0.360*	1.								
TPS	0.242*	0.059	0.065	1							
TPS	0.264	0.118	0.038	1							
PHT	0.467**	0.454**	0.425**	-0.035	1						
PHT	0.458**	0.431**	0.465**	-0.017	1						
GWP	-0.246*	-0.181	0.172	-0.160	-0.127	1					
GWP	-0.224*	-0.087	0.100	-0.200*	-0.103	1					
TGW	-0.209*	-0.073	-0.076	-0.222*	0.182	0.014	1				
TGW	-0.305*	-0.275*	-0.011	-0.180	0.129	0.161	1				
NG/P	-0.395*	-0.268*	0.128	-0.174	0.011	0.375*	0.461**	1			
NG/P	-0.361*	-0.238*	0.149	-0.197	0.050	0.302*	0.560**	1			
NPB/p	0.406**	0.299*	0.285*	0.250*	0.354*	0.058	-0.186	0.020	1		
NPB/P	0.422**	0.410**	0.193	0.227**	0.364*	0.040	-0.085	-0.074	1		
GRY/PL	0.058	-0.105	0.259*	-0.058	0.207*	0.170	0.119	0.335*	0.100	1	
GRY/PL	0.112	0.008	0.233*	-0.110	0.276*	0.075	0.302*	0.322*	0.005	1	
YPH	0.058	-0.148	0.224*	0.043	0.189	0.127	0.061	0.259*	0.097	0.951**	1
YPH	0.104	-0.051	0.186	0.003	0.244	0.050	0.219*	0.227*	0.031	0.943**	1

** Correlation is significant at $p < 0.01$

* Correlation is significant at $p < 0.05$

DF = Days to 50% flowering, DM=Days to maturity, PL= Panicle length, NT/P=Number of Tillers /plant, PHT = Plant height, NG/P = Number of grains per panicle, PWT= Panicle weight, TGW = 1000 Grains weight, NPB/P =Number of Primary Branches per Panicle/ panicle, YPH = Yield per ha, GRY/P = Grain yield per plant.

4.6.2 Genotypic and phenotypic correlations at Cheju site

Results of genotypic and phenotypic correlations between pairs of traits are shown in (Table 19) Grain yield per stand had positive significant genotypic and phenotypic correlations with yield ($r_g = 0.912^{**}$) and ($r_p = 0.909^{**}$) respectively, days to maturity had positive significant genotypic and phenotypic correlations with days to flowering ($r_g = 0.745^{**}$) and ($r_p = 0.710^{**}$) respectively, plant height had significant positive correlation with days to flowering both at genotypic and phenotypic level ($r_g = 0.504^{**}$), ($r_p = 0.457^{**}$) respectively. Tillers per stand had positive significant genotypic and phenotypic correlations with 1000 grains weight ($r_g = 0.467^{**}$), ($r_p = 0.492^{**}$) respectively, yield per hectare had significant positive genotypic and phenotypic correlations with grain yield per stand ($r_g = 0.912^{**}$) and ($r_p = 0.909^{**}$) respectively.

Table 19: Genotypic (top) and phenotypic correlations (bottom) at Cheju site

	DF	DM	PL	TPS	PHT	PWT	TGW	NG/P	NPB/P	GY/P	Y/H
DF	1										
DF	1										
DM	0.745**	1									
DM	0.710**	1									
PL	0.326*	0.284*	1								
PL	0.282*	0.230*	1								
TPS	0.147	0.177	0.178	1							
TPS	0.137	0.201*	0.186	1							
PHT	0.504**	0.299*	0.248*	0.041	1						
PHT	0.457**	0.231*	0.205*	0.056	1						
PW	-0.322*	-0.141	-0.177	0.174	-0.284*	1					
PW	-0.270*	-0.090	-0.146	0.143	-0.255*	1					
TGW	-0.083	0.084	0.088	0.467**	-0.029	0.163	1				
TGW	-0.169	0.002	0.040	0.492**	-0.093	0.200*	1				
NG/P	-0.227*	-0.038	0.014	-0.247*	-0.146	-0.279	0.079	1			
NG/P	-0.156	0.040	0.063	-0.279*	-0.100	-0.304	0.126	1			
NPB/P	0.278*	0.237*	0.116	0.178	0.138	0.096	-0.005	0.169	1		
NPB/P	0.315*	0.304*	0.147	0.191	0.181	0.062	0.033	0.129	1		
PW	0.218*	0.132	0.228*	0.217*	0.073	0.125	0.152	0.158	0.335*	1	
PW	0.276*	0.203*	0.271*	0.212*	0.120	0.100	0.198	0.126	0.320*	1	
Y/H	0.184	0.092	0.245*	0.272*	0.076	0.178	0.085	0.155	0.349*	0.912**	1
Y/H	0.257	0.188	0.307*	0.277*	0.143	0.138	0.149	0.102	0.335*	0.909**	1

** Correlation is significant at $p < 0.01$

* Correlation is significant at $p < 0.05$

DFL= Days to 50% flowering, DM=Days to maturity, PL= Panicle length, NT/P= Number of Tillers

/plant, PHT = Plant height, PWT= Panicle Weight, NG/P = Number of grain/ panicle, TGW = 1000

Grains weight , NPB/P= Number of Primary Branches Per panicle, Y/H = Yield per ha. GRY/P =

Grain yield per plant

4.6.3 Combined Genotypic and Phenotypic correlations

Data were analyzed for all three sites and genotypic and phenotypic correlations over the locations among yield components were assessed and are presented in (Table 20).

Grain yield per ha had significant positive genotypic correlations ($r_g = 0.730^{**}$) and phenotypic correlation ($r_p = 0.729^{**}$) with number of tillers per stand, number of spikes per panicle had significant genotypic ($r_g = 0.326^*$) and ($r_p = 0.316^*$) phenotypic correlations with yield, plant height also had significant genotypic correlations ($r_g = 0.250^*$) and significant phenotypic ($r_p = 0.619^{**}$) correlations with yield. 1000 grains weight had significant genotypic correlation with yield/ ha ($r_g =$

0.427^{**}) and phenotypic ($r_p = 0.460^{**}$), grain weight per panicle had positive genotypic and phenotypic correlations with yield ($r_g = 0.936^{**}$) and ($r_g = 0.967^{**}$) respectively.

Days to maturity had significant positive genotypic and phenotypic correlations with days to 50% flowering, ($r_g = 0.775^{**}$) and ($r_p = 0.713^{**}$); panicle length had positive genotypic and phenotypic correlations with days to 50% flowering, ($r_g = 0.283^*$) and ($r_g = 0.353^*$) respectively. Number of branches per panicle also had positive and significant genotypic and phenotypic correlations with days to 50% flowering ($r_g = 0.442^{**}$) and ($r_p = 0.517^{**}$) respectively. Tillers per plant had positive phenotypic significant correlation with plant height ($r_p = 0.584^{**}$) but there was no significant genotypic correlations. Thousand grains weight had significant positive phenotypic correlation with tillers per plant ($r_p = 0.572^{**}$) but had negative non significant genotypic correlations. Primary branches per panicle had positive significant genotypic and phenotypic correlation with tillers per plant, ($r_g = 0.352^*$) and ($r_p = 0.369^*$), grains yield per plant had significant positive phenotypic and genotypic correlations with tillers per plant ($r = 0.394^*$) and, ($r = 0.753^{**}$) respectively, thousand grains weight had positive significant phenotypic correlation with plant height ($r = 0.486^{**}$) but there was no significant genotypic correlation.

The associations that were consistently significant over all location were days to 50% flowering with days to maturity, panicle length with days to 50% flowering, plant height with days to 50% flowering, number of primary branches per panicle with days to 50% flowering, panicle length with plant height, number of primary branches

per panicle with panicle length, yield per ha with panicle length, 1000 grain weight with yield/ha and grain yield per plant with yield per ha.

Table 20: Genotypic (top) and Phenotypic Correlations (bottom) over all three sites

	DFL	DMT	PL	TPS	PHT	PWT	TGW	NG/P	NPB/P	GY/P
DFL	1									
DFL	1									
DMT	0.775**	1								
DMT	0.713**	1								
PL	0.283*	0.251*	1							
PL	0.353*	0.074	1							
TPS	0.169	0.160	0.046	1						
TPS	0.305*	0.030	0.623**	1						
PHT	0.274*	0.274*	0.262*	0.068	1					
PHT	0.340*	0.103	0.627**	0.584**	1					
PW	-0.137	-0.119	-0.021	-0.106	-0.217*	1				
PW	-0.166	-0.073	-0.165	-0.238*	-0.291*	1				
TGW	-0.125	-0.036	0.122*	-0.118	0.002	-0.005	1			
TGW	0.056	-0.163	0.604**	0.572**	0.486**	-0.144	1			
NG/P	-0.138	-0.049	0.027	-0.064	-0.041	-0.072	0.073	1		
NG/P	-0.137	-0.004	-0.049	-0.130	-0.084	-0.061	0.000	1		
NPB/P	0.442**	0.384*	0.227*	0.352*	0.225*	0.005	-0.114	0.063	1	
NPB/P	0.517**	0.415**	0.322*	0.369*	0.332*	-0.055	0.118	0.018	1	
GY/P	0.151	0.078	0.171	0.394*	0.219*	0.088	-0.143	0.117	0.262*	1
GY/P	0.294*	-0.005	0.639**	0.753**	0.626**	-0.107	0.514**	-0.099	0.326*	1
Y/H	0.147	0.028	0.596**	0.730**	0.250*	-0.104	0.427**	0.099	0.326*	0.936**
Y/H	0.290*	-0.029	0.606**	0.729**	0.619**	-0.114	0.460**	-0.010	0.316*	0.967**

** Correlation is significant at $p \leq 0.01$

* Correlation is significant at $p \leq 0.05$

DF = Days to 50% flowering, DM = Days to maturity, PL= Panicle length, NT/P= Tillers /plant, PHT = Plant height, PWT= Panicle weight, TGW = 1000 Grains weight, NG/P = Number of grains /panicle, NPB/P=Number of Primary Branches Per panicle / panicle, YH = Yield per ha. GY/P= Grain weight per plant

4.7 Genotypic and phenotypic variances

Highest genotypic variance was observed on plant height (64.13) followed by yield / plant (20.230) (Table 20). On the other hand, highest phenotypic variance was observed in number of grain per panicle (147.38) followed by plant height (117.48). The lowest phenotypic (0.71) and genotypic (0.17) variances were recorded for panicle weight. The highest environmental variance was (3.77) on number of grains per panicle and the lowest was (0.23) found on number of primary branches per panicle, weight of and yield/hectare, Results indicated low value of environmental variance on the studied characters, while phenotypic variances were higher than genotypic variances for all traits.

4.7.1 Genotypic and phenotypic coefficient of variation

Results indicated relatively high genotypic coefficients of variation for days to 50% flowering (36.66), tillers/plant (31.46), yield per ha (26.68) and yield per plant (24.96). For the phenotypic coefficients of variation highest value was on tillers per plant (36.21) followed by yield per hectare (31.45). Phenotypic coefficients of variation were higher than genotypic coefficient of variation for studied characters except days to 50% flowering

4.7.2 Broad sense heritability

Results (Table 21) showed that high heritability were obtained for yield per plant (75.59%) followed by tillers per plant (75.51%), yield /ha (72.0), panicle length (58.47%), and thousand grains weight (56.75%). Genetic advance was highest for

grain yield/h (59.77) followed by number of tillers per plant (56.32), the lowest was for number of filled grains per panicle (1.62).

Table 21: Genetic parameters of various yield component traits

Character	M S	δg^2	δp^2	δe^2	GCV%	PCV%	$h^2 B\%$	G.A%
50%F	115.59	10.05	35.12	1.60	3.66	6.84	28.63	4.03
D.M	124.35	11.10	35.53	1.58	3.13	5.6	31.24	3.60
PL	30.19	3.10	5.31	0.47	7.45	9.74	58.47	11.74
T/P	91.98	9.86	13.06	0.57	31.46	36.21	75.51	56.32
PH	630.54	64.13	117.48	3.34	8.90	12.05	54.59	13.55
PWT	1.17	0.07	0.61	0.23	8.37	24.78	11.41	5.82
1000GW	56.29	5.76	10.16	0.67	9.94	13.19	56.75	15.42
NG/P	220.23	9.10	147.38	3.77	3.16	12.72	6.18	1.62
PB/P	2.08	0.17	0.71	0.23	3.92	7.98	24.08	3.96
Y/P	191.44	20.53	27.16	0.82	24.96	28.71	75.59	44.70
Y/ha	13.25	1.41	1.96	0.23	26.68	31.45	72.00	59.77

50% F = 50% flowering, DM = Days to maturity, PL= Panicle length, T/P = Tillers per plant, PH = Plant height, WG/P = Weight of grain per plant, PWT= Panicle weight, 1000GW = 1000 grain weight, NGP = Number of grains per panicle, PB/P = Primary branches per panicle, Y/P = Yield per plant, Y/ha = Yield per ha.

4.8 Path analysis for combined sites

Path coefficient analysis results for yield and some yield components using genotypic correlations obtained when all data from three sites were pooled are shown in (Table 22) and (Appendix 4) The relationship between number of primary branches per panicle with yield ($r = 0.326^{**}$) was mainly caused by indirect effect (0.245) via number of tillers per plant. As for the relationship between number of tillers with yield ($r = 0.730^{**}$) it was largely due to direct effect of tillers per plant (0.655) and to the lesser extent the indirect effect via panicle length. The relation

between 1000 grains weight with yield ($r = 0.4277^{**}$) was mainly due to the indirect effect via number of number of tillers per plant (0.3571) and to a lesser extent through panicle length (0.156). Px_7 was 0.634 being higher than any of the direct and indirect effects.

Table 22: Path matrix for combined sites for six yield component variables

	P L	NPB/P	NG/P	PWT	T/P	1000TGW
P L	0.2596	0.0793	0.0177	-0.0441	0.1597	0.1567
NPB/P	0.0058	0.019	-0.0006	-0.0007	0.0071	0.0015
NG/P	0.0119	-0.0059	0.175	0.0583	-0.0155	0.0501
PWT	-0.002	-0.0005	0.004	0.012	-0.0028	-0.0019
T/P	0.4033	0.2457	-0.0579	-0.1511	0.6557	0.3571
1000WT.	-0.0819	-0.0109	-0.0389	0.0216	-0.0739	-0.1358
Total r	0.596^{**}	0.3266[*]	0.0992	-0.1041	0.7303^{**}	0.4277^{**}

Direct (along the diagonal) and indirect effect of yield components

* = $p \leq 0.05$ and ** = $p \leq 0.01$

PL = Panicle length, NPB/P = Number of primary branches per panicle, NG/P = Number of grains per panicle, PWT = Panicle weight, TP = Tillers per plant, 1000TGW = 1000 grains weight

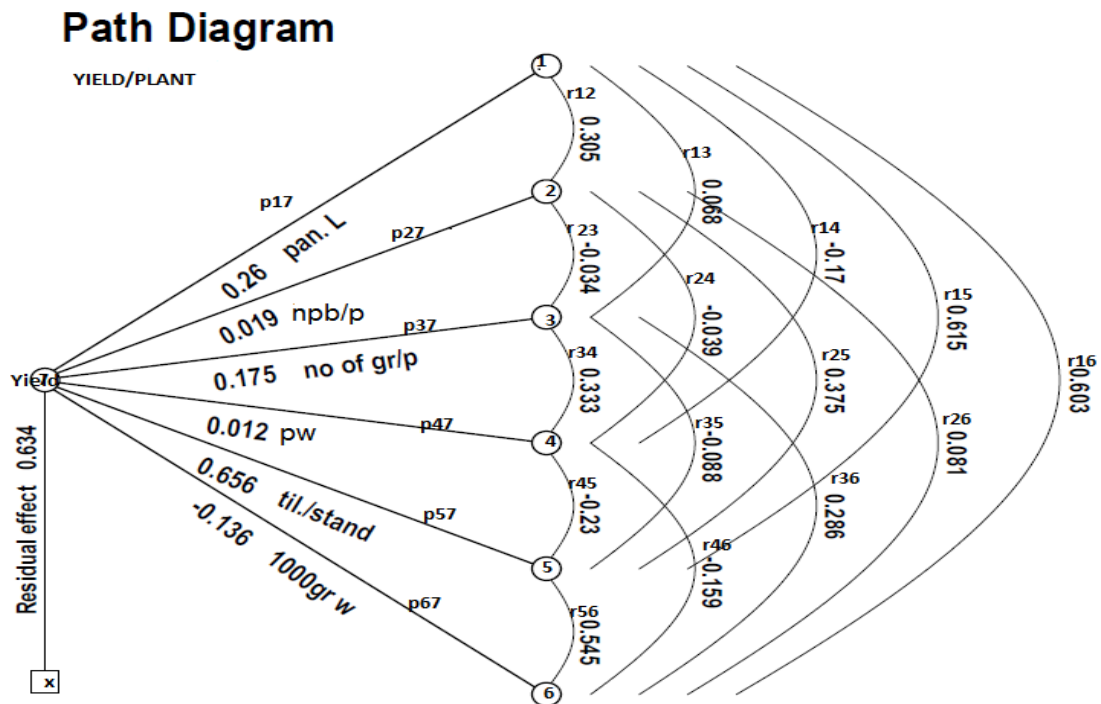


Figure 1: Path diagram

4.9 Stability parameters for grains yield components

4.9.1 Regression analysis

4.9.2 Days to 50% flowering

Results on regression analysis on days to 50% flowering as shown in (Table 23) indicated that tested genotypes responded significantly with change of environments on days to 50% flowering except for IR07M101. Genotype IR 05N359 responded close to average while six out of fourteen tested genotypes responded above the average and the rest responded below average. The b values ranged from -0.59 for IRR1 123 to 2.70 for IR 09N505 and differed significantly from unit value ranging from -1.591 for IRR1 123 to 1.701 for IR09N505. The variances of deviation (S^2d) ranged from -2.22 for IR 02A149 to 7.04 for IR 09N505. There was great variation

for coefficients of determination (R^2) among genotypes tested for this variable, ranging from 0.06 for IR 06A107 to 0.99 for SARO5.

Table 23: Stability parameters for days to 50% flowering for each genotype across locations

Genotypes		Mean	S.E. \bar{x}	b-value	SE _b	b-1	S ² d	R ²
IR 09L325	A	81.11	0.94	0.434*	1.329	-0.566**	-2.20	0.92
IR 09N505	B	88.88	1.69	2.701**	2.389	1.701**	7.04	0.81
IRRI 146	C	83.33	0.97	1.355**	1.371	0.355*	-2.10	0.98
IR 05N359	D	87.88	0.73	0.944**	1.032	-0.056	0.14	0.68
IR 02A149	E	81.55	0.41	0.028	0.565	-0.972**	-2.22	0.06
IR 08M110	F	84.77	1.73	1.872**	2.446	0.872**	0.02	0.89
IR 07M101	G	85.55	0.76	1.163**	1.074	0.163*	-2.10	0.97
IR 06A107	H	87.44	0.81	0.305*	1.145	-0.695**	6.13	0.06
IR 07A166	I	96.11	1.11	0.510**	1.569	-0.490*	1.15	0.30
IR 07A167	J	97.55	1.02	0.649**	1.442	-0.351*	-2.00	0.89
IR 09A136	K	82.44	0.70	0.221*	0.989	-0.779**	2.16	0.06
IR 03A550	L	87.88	1.19	1.754**	1.682	0.754**	3.84	0.74
IRRI 123	M	81.33	0.57	-0.591**	0.805	-1.591**	1.89	0.32
(SARO5)	N	87.55	1.38	2.655**	1.951	1.655**	-2.17	0.99
Overall mean		86.67	1.00	1.866	1.413	1.590	0.19	0.61

* $p \leq 0.05$ and ** $p \leq 0.01$

4.9.3 Days to maturity

Most of genotypes tested responded significantly with change of environments for this character, their regression coefficients ranged from $b = 0.00$ for IR 09L325 to $b = 2.60$ for IR 07A167 (Table 24). Genotypes IRRI 146, IR 06A107, IR 07A166, IR 07A167, IR 03A550, IR 03A550 and SARO5 had above average responses to the environments and the rest of genotypes had below average response. Most of genotypes deviated significantly from unit value; b-1 ranged from -1.00 for IR

09L325 to 1.603 for IR 07A167 .The S^2d varied ranging from -2.60 for IR 02A149 to 20.90 for IRR1 123. The variation was high for coefficient of determination ranging from $R^2 = 0.00$ for IR 09L325 to $R^2 = 0.98$ for IR 02A149.

Table 24: Stability parameters for days to maturity for each genotype across locations

Genotypes	Code	Mean	SE \bar{x}	b-value	SE b	b-1	S^2d	R^2
IR 09L325	A	100.11	1.26	0.004	1.781	-1.000**	3.20	0.00
IR 09N505	B	109.11	1.62	0.879**	2.284	-0.121*	12.90	0.58
IRRI 146	C	105.22	1.37	1.124**	1.931	0.124*	-0.90	0.95
IR 05N359	D	108.55	1.38	0.692**	1.932	-0.308*	-0.30	0.85
IR 02A149	E	103.66	1.01	0.382*	1.428	-0.620**	-2.60	0.98
IR 08M110	F	105.11	1.17	0.772**	1.654	-0.229*	-1.60	0.94
IR 07M101	G	104.33	0.72	0.493*	1.018	-0.507**	-0.90	0.80
IR 06A107	H	108.33	1.97	1.579**	2.785	0.579**	2.30	0.93
IR 07A166	I	110.88	2.82	2.217**	3.987	1.217**	7.30	0.93
IR 07A167	J	113.55	2.89	2.603**	4.086	1.603**	4.20	0.96
IR 09A136	K	102.66	0.55	0.206*	0.777	-0.794**	-1.20	0.45
IR 03A550	L	106.77	1.52	1.173**	2.149	0.173*	-1.10	0.96
IRRI 123	M	103.66	1.22	0.593**	1.725	-0.407*	20.90	0.29
(SARO5)	N	108.00	1.52	1.284**	2.149	0.284*	6.20	0.84
Overall mean		106.43	1.50	1.047	2.120	-0.000	1.21	0.74

* $p \leq 0.05$ and ** $p \leq 0.01$

4.9.4 Panicle length

Results showed that there was significant response to change of environments among tested genotypes for panicle length (Table 25) , Genotypes IR 05N359, IR 07A167, IR 09A136, IR 03A550 and SARO 5 had regression coefficients close to unit value hence had average response, b- values ranged from 0.32 for IRR1 123 to 1.48 for IR06A107. The genotypes varied for S^2d value ranging from -0.46 for IR

08M110 to 1.86 IRRI 146. High coefficients of determination (R^2) (0.99) were recorded for IR 09L325, IR 03A550 (0.99) while the lowest was (0.35) for IRRI 123.

Table 25: Stability parameters for panicle length for each genotype across locations

Genotypes	Code	Mean	SE \bar{x}	b-value	SE b	b-1	S ² d	R ²
IR 09L325	A	23.50	0.72	1.174**	1.018	0.174*	-0.45	0.99
IR 09N505	B	22.90	0.58	0.521**	0.820	-0.479*	0.63	0.67
IRRI 146	C	22.26	0.69	0.976**	0.975	-0.024	1.86	0.77
IR 05N359	D	24.97	0.67	1.039**	0.947	0.039	0.33	0.91
IR 02A149	E	22.48	0.79	1.235**	1.117	0.235*	0.88	0.90
IR 08M110	F	24.55	0.55	0.704**	0.777	-0.296*	-0.46	1.00
IR 07M101	G	23.91	0.83	1.354**	1.173	0.354*	-0.27	0.98
IR 06A107	H	23.28	0.89	1.480**	1.258	0.480**	-0.20	0.98
IR 07A166	I	24.82	0.63	0.985**	0.890	-0.015	0.15	0.92
IR 07A167	J	25.23	0.72	1.148**	1.018	0.148*	-0.19	0.97
IR 09A136	K	23.50	0.71	1.095**	1.003	0.095	-0.02	0.95
IR 03A550	L	22.40	0.65	1.037**	0.919	0.037	-0.46	0.99
IRRI 123	M	24.13	0.92	0.328*	1.300	-0.672**	1.15	0.35
(SARO5)	N	23.38	0.65	0.922**	0.919	-0.078	-0.25	0.97
Overall mean		23.66	0.71	1.022	1.009	-0.000	0.06	0.88

* $p \leq 0.05$ and ** $p \leq 0.01$

4.9.5 Plant height

The tested genotypes responded differently with change of environments for this character, their b-values ranged from 0.577 for IR 06A107 to 1.448 for IR 07M101 (Table 26). Genotype IR 09A136 had average response for this character with b value of 1.00, IR 09L325 had value close to average response (0.979). IRRI 146, IR 02A149, IR 07M101, IR 03A550 and SARO5 had above average responses while the rest of genotypes had below average responses. There was high variation for S²d

among the tested genotypes across environments ranging from -8.02 for IR 09L325 to 14.07 for IRR1 123. All genotypes had high coefficients of determination R^2 ranging from 0.99 to 0.83.

Table 26: Stability parameters for plant height for each genotype across locations

Genotypes	Code	Mean	SE \bar{x}	b-value	SE b	b-1	S ² d	R ²
IR 09L325	A	92.66	3.02	0.979**	4.284	-0.021	-8.02	0.99
IR 09N505	B	81.68	2.16	0.714**	3.045	-0.286*	-7.46	0.99
IRRI 146	C	84.92	4.78	1.420**	6.758	0.420*	-7.84	0.99
IR 05N359	D	97.21	2.91	0.968**	4.114	-0.032	0.01	0.95
IR 02A149	E	83.18	3.57	1.253**	5.047	0.253*	-5.40	0.99
IR 08M110	F	81.85	2.84	0.944**	4.015	-0.056	-7.89	0.99
IR 07M101	G	97.12	4.05	1.448**	5.726	0.448*	-7.57	0.99
IR 06A107	H	93.00	1.93	0.577**	2.729	-0.423*	-7.76	0.99
IR 07A166	I	93.24	2.18	0.647**	3.082	-0.353*	-4.09	0.99
IR 07A167	J	95.71	1.87	0.624**	2.644	-0.376*	-7.91	0.94
IR 09A136	K	88.97	3.23	1.009**	4.567	0.009	-7.98	0.99
IR 03A550	L	88.18	3.97	1.274**	3.930	0.274*	-7.32	0.99
IRRI 123	M	88.60	2.78	0.793**	3.930	-0.207*	14.07	0.83
(SARO5)	N	92.85	3.94	1.349**	5.571	0.340*	-5.91	0.99
Overall mean		89.94	3.08	0.999	4.245	0.000	-61.01	0.97

* $p \leq 0.05$ and ** $p \leq 0.01$

4.9.6 Panicle weight

There was difference in response across environments for panicle weight (Table 27), b-values ranging from (-1.01) for IR 03A550 to (3.80) for IRR1 146. Genotype IR 09N505 had b value of 1.01 which means had average response over all environments, IRR1 146, IR 07M101, IR 07A166, IR 09A136 responded above average while the rest of genotypes responded below average. The variance of deviation (S²d) ranged from (-0.11) for IR 09L325, IR 05N359, and SARO5 to (0.01) for IR 09N505 and IR 07A167. There was high variation for R^2 among the tested

genotypes ranging from ($R^2 = 0.00$) for IRRI 123 to $R^2 = 0.99$ for IRRI 146 and IR 05N359.

Table 27: Stability parameters for panicle weight for each genotype across locations

Genotypes	Code	Mean	\bar{x} SE	b-value	SE _b	b-1	S ² d	R ²
IR 09L325	A	3.16	0.09	0.705**	0.012	-0.295*	-0.11	0.00
IR 09N505	B	2.91	0.16	1.010**	0.226	0.010	0.01	0.50
IRRI 146	C	3.43	0.31	3.809**	0.438	2.800**	-0.10	0.99
IR 05N359	D	3.06	0.27	3.513*	0.381	2.510**	-0.11	0.99
IR 02A149	E	2.92	0.31	0.719**	0.438	-0.281*	-0.02	0.41
IR 08M110	F	4.48	0.10	0.262*	0.141	-0.738**	-0.09	0.28
IR 07M101	G	3.44	0.13	1.459**	0.183	0.459*	-0.10	0.95
IR 06A107	H	2.97	0.26	0.677**	0.367	-0.33*	-0.09	0.73
IR 07A166	I	2.73	0.18	1.275**	0.254	0.275*	-0.08	0.87
IR 07A167	J	2.71	0.24	-0.596**	0.339	-1.596**	0.01	0.25
IR 09A136	K	2.92	0.18	2.015**	0.254	1.010**	-0.05	0.89
IR 03A550	L	3.43	0.28	-1.010**	0.395	-2.010**	-0.05	0.67
IRRI 123	M	2.58	0.17	-0.062	0.240	-1.060**	-0.03	0.00
(SARO5)	N	3.44	0.11	0.223*	0.155	-0.777**	-0.11	0.47
Overall mean		3.15	0.19	0.806	0.273	-0.001	-0.06	0.64

* $p \leq 0.05$ and ** $p \leq 0.01$

4.9.7 1000 grains weight

Genotypes responded significantly for this variable across locations (Table 28) except for IRRI 123 and SARO 5 had values of 1.06. Regression coefficients ranged from 0.08 for IR 08M110 to 1.58 for IR 07A166, while IR 09L325, IR 05N359, IR 02A149, IR 07A166 and IR 09A136 responded above average. Variances of deviation (S²d) from regression ranged from -0.59 for IR 05N359 to 7.66 for IR 02A149. The coefficients of determination ranged from 0.62 for IR 08M110 to 0.98 for IR 09A136.

Table 28: Stability parameters for 1000 grains weight for each genotype across locations

Genotypes	Code	Mean	SE \bar{x}	b-value	SE _b	b-1	S ² d	R ²
IR 09L325	A	24.08	1.09	1.175**	1.541	0.175*	1.09	0.92
IR 09N505	B	22.05	0.62	0.502**	0.876	-0.498*	1.26	0.66
IRRI 146	C	21.86	0.76	0.732**	1.074	-0.268	2.80	0.71
IR 05N359	D	23.86	0.98	1.175**	1.385	0.175	-0.59	0.99
IR 02A149	E	25.02	1.48	1.494**	2.092	0.494*	7.66	0.81
IR 08M110	F	25.46	0.87	0.089	1.230	-0.911**	6.04	0.62
IR 07M101	G	24.50	0.70	0.673**	0.989	-0.327*	1.41	0.78
IR 06A107	H	23.43	0.79	0.928**	1.117	-0.072	0.11	0.95
IR 07A166	I	24.04	1.57	1.585**	2.219	0.585**	12.51	0.75
IR 07A167	J	24.98	1.14	0.785**	1.611	-0.215*	-0.36	0.97
IR 09A136	K	23.80	1.05	1.217**	1.484	0.217*	-0.27	0.98
IR 03A550	L	24.82	0.77	0.772**	1.088	-0.228*	2.27	0.73
IRRI 123	M	24.66	0.90	1.065**	1.272	0.065	-0.08	0.97
(SARO5)	N	25.67	0.99	1.063**	1.399	0.063	4.14	0.79
Overall mean		24.15	0.97	0.946	1.384	0.05	1.83	0.83

* $p \leq 0.05$ and ** $p \leq 0.01$

4.9.8 Number of grains per panicle

Tested genotypes except IR05N359 and IR07M101 responded significantly across environments for this yield component character (Table 29), b-values ranged from -0.92 for IR 07A167 to 3.45 for IR 08M110. Genotype IR 07M101 had value close to 1 (0.969), IR 09L325, IRRI 146 IR 08M110, IR09A136 and SARO5 responded above average while the rest responded below average. The S²d ranged from -29.82 for IR 07M101 to 84.97 for IR 09L325. The coefficients of determination ranged from high for IR 07M101 (0.97) to the lowest (0.00) for IRRI 123.

Table 29: Stability parameters for number of grains/panicle for each genotype across locations

Genotypes	Code	Mean	SE \bar{x}	b-value	SE b	b-1	S ² d	R ²
IR 09L325	A	108.79	4.04	3.293**	5.656	2.293**	84.97	0.63
IR 09N505	B	82.33	2.83	0.272	3.99	-0.728**	-25.48	0.22
IRRI 146	C	94.67	3.01	1.261**	4.256	0.261	0.95	0.48
IR 05N359	D	92.11	2.03	0.914**	2.87	-0.096	-24.81	0.73
IR 02A149	E	91.00	4.61	-0.405**	6.518	-1.405**	48.19	0.03
IR 08M110	F	108.22	3.40	3.457**	4.807	2.453**	-18.74	0.95
IR 07M101	G	104.89	2.25	0.969**	3.181	-0.041	-29.82	0.97
IR 06A107	H	90.33	2.95	0.818**	4.171	-0.192	8.19	0.24
IR 07A166	I	89.22	4.39	-0.170*	6.207	-1.170**	21.20	0.01
IR 07A167	J	91.44	2.80	-0.920**	3.959	-1.920**	-27.68	0.85
IR 09A136	K	97.77	2.70	1.976**	3.817	0.976**	-11.29	0.79
IR 03A550	L	96.22	5.22	0.854**	7.381	-0.156	35.36	0.17
IRRI 123	M	86.55	0.80	0.036	1.131	-0.973**	-26.73	0.00
(SARO5)	N	102.22	2.21	1.643**	3.124	0.647**	-9.91	0.70
Overall mean		95.41	3.08	0.999	4.362	-0.00	1.74	0.48

* $P \leq 0.05$ and ** $p \leq 0.01$

4.9.9 Number of primary branches /panicle

Genotypes tested responded significantly with changing environments for number of primary branches per panicle (Table 30), except for IR09L325, IR 07M101 and IRRI 123 which had b values of 1.0. Regression coefficients varied from -0.44 for IR 02A149 to 2.69 for IR07A166. Genotypes IR09N505, IRRI 146, IR 07A166, IR 07A167 and SARO5 responded above average while the rest of genotypes responded below average. The S²d also varied among tested genotypes ranging from 0.00 for IR08M110 -0.04 for SARO 5. The coefficient of determination ranged from 0.95 for IRM08M110 to 0.00 for IRR 123. Variation were also observed for coefficient of determination R², ranging from 0.05 for (IR 05N359) to 0.99 for IRRI 146.

Table 30: Stability parameters for number of primary branches /panicle for each genotype across locations

Genotypes	Code	Mean	SE \bar{x}	b-value	SE b	b-1	S ² d	R ²
IR 09L325	A	10.67	0.28	1.077**	0.395	0.077	-0.13	0.92
IR 09N505	B	10.67	0.23	1.884**	0.325	0.884**	-0.11	0.94
IRRI 146	C	10.44	0.17	1.705**	0.239	0.705**	-0.14	0.99
IR 05N359	D	10.67	0.23	-0.269*	0.325	-1.266**	0.05	0.05
IR 02A149	E	10.11	0.20	-0.449*	0.282	-1.449**	-0.11	0.48
IR 08M110	F	10.78	0.22	0.897**	0.311	-0.103	0.00	0.48
IR 07M101	G	10.67	0.16	1.077**	0.226	0.077	-0.13	0.92
IR 06A107	H	10.78	0.22	0.628**	0.311	-0.372*	-0.14	0.94
IR 07A166	I	11.67	0.40	2.692**	0.565	1.692**	0.12	0.82
IR 07A167	J	11.33	0.23	1.884**	0.325	0.884**	-0.11	0.94
IR 09A136	K	10.44	0.17	-0.180	0.239	-1.180**	-0.08	0.07
IR 03A550	L	10.22	0.14	0.448**	0.497	-0.552**	-0.11	0.48
IRRI 123	M	9.67	0.16	1.077**	0.226	0.077	-0.13	0.92
(SARO5)	N	9.88	0.26	1.525**	0.367	0.522**	-0.04	0.79
Overall mean		10.57	0.21	0.999	0.330	-0.000	-0.05	0.69

* $p \leq 0.05$ and ** $p \leq 0.01$

4.9.10 Number of tillers/plant

Results (Table 31) showed that, there were differences in response across the environments for number of tillers per plant, Genotypes IR07M101 and IR 06A107 had regression coefficients of 1.05 and 1.08 respectively which mean that these genotype had average responses over environments. IR 09N505 IR 08M110 IR 07A166 and IR07A167 responded above average while the rest of genotypes responded below average. Regression coefficient ranged from 0.597 for SARO 5 to 1.511 for IR09N505. S²d ranged from -0.59 for IR07M101, IR07A166 and IR 07A167 to -0.06 (IR07M101). Coefficients of determination ranged from 1.00 for IR 07A166, IR07A167 and SARO5 to 0.99 for the rest of genotypes except for IR 07M101 which had R² of 0.95.

Table 31: Stability parameters for number of tillers per plant for each genotype across locations

Genotypes	Code	Mean	SE \bar{x}	b-value	SE b	b-1	S ² d	R ²
IR 09L325	A	9.22	0.89	0.783**	1.258	-0.217*	-0.58	0.99
IR 09N505	B	11.64	1.95	1.511**	2.757	0.511**	-0.48	0.99
IRRI 146	C	10.54	1.32	1.164**	1.866	0.164*	-0.37	0.99
IR 05N359	D	9.55	0.91	0.789**	1.038	-0.211*	-0.44	0.99
IR 07M101	E	9.98	1.18	1.057**	1.668	0.057	-0.59	0.99
IR 08M110	F	10.71	1.38	1.227**	1.591	0.227*	-0.34	0.99
IR 07M101	G	9.08	0.77	0.637**	1.088	-0.363*	-0.06	0.95
IR 06A107	H	9.56	1.23	1.089**	1.739	0.089	-0.55	0.99
IR 07A166	I	10.82	1.47	1.284**	2.078	0.284*	-0.59	1.00
IR 07A167	J	11.18	1.33	1.148**	1.880	0.148	-0.59	1.00
IR 09A136	K	9.26	0.99	0.881**	1.399	-0.119	-0.58	0.99
IR 03A550	L	9.02	0.94	0.843**	1.329	-0.157	-0.58	0.99
IRRI 123	M	10.00	1.10	0.990**	1.555	-0.010	-0.50	0.99
(SARO5)	N	9.14	0.69	0.597**	0.972	-0.403*	-0.50	1.00
Overall mean		9.14	1.15	1.000	1.587	-0.00	-0.48	0.98

* $p \leq 0.05$ and ** $p \leq 0.01$

4.9.11 Yield per hectare

Most of genotypes tested responded differently with changing environments for yield per hectare (Table 32), except for IR 07M101 and IRRI 123 which had b values 1.078 and 1.024 respectively. Genotypes IRRI 146, IR 05N359, IR 07A167, IR 09A136 and IR 03A550 responded above average while the rest responded below average, b-values ranged from (0.23) IR 09L325 to (1.78) IR 03A550. Low values of S²d were observed for most genotypes ranging from -0.01 for IRRI 146, IR 08M110 and IR 08M110 to 0.32 for IR 09L325. The coefficient of determination was lowest (0.34) for IR09L325 to above 0.90 for rest of the genotypes.

Table 32: Stability parameters for yield (tons per hectare) for each genotype across

Genotypes	Code	Mean	SE \bar{x}	b-value	SE b	b-1	S ² d	R ²
IR 09L325	A	4.72	0.19	0.234*	0.268	-0.766**	0.32	0.34
IR 09N505	B	4.63	0.24	0.639**	0.339	-0.370*	0.00	0.98
IRRI 146	C	4.66	0.50	1.359**	0.570	0.359*	-0.01	0.99
IR 05N359	D	3.61	0.48	1.297**	0.678	0.297*	0.01	0.99
IR 02A149	E	3.25	0.36	0.944**	0.509	-0.056	0.09	0.96
IR 08M110	F	5.72	0.34	0.932**	0.480	-0.068	-0.01	0.99
IR 07M101	G	5.28	0.40	1.078**	0.565	0.078	0.01	0.99
IR 06A107	H	4.82	0.27	0.738**	0.381	-0.262*	0.00	0.98
IR 07A166	I	4.72	0.21	0.579**	0.296	-0.421*	-0.00	0.97
IR 07A167	J	5.10	0.54	1.465**	0.763	0.465*	0.00	0.99
IR 09A136	K	3.91	0.54	1.434**	0.763	0.434*	0.00	0.99
IR 03A550	L	3.44	0.68	1.780**	0.961	0.780**	0.26	0.97
IRRI 123	M	4.45	0.38	1.024**	0.537	0.024	-0.01	0.99
(SARO5)	N	3.97	0.18	0.496**	0.254	-0.504**	0.00	0.97
Overall mean		4.44	0.37	0.999	0.526	-0.000	0.04	0.93

* $p \leq 0.05$ and ** $p \leq 0.01$

4.9.12 Relationships among stability parameters

4.9.13 Days to 50% flowering

The relationship between regression coefficients and means for days to 50% flowering (Fig.2) indicated that, Genotypes D (IR05N359) had b-value close to 1 and above average, while genotype J (IR07A167) had low b value with highest mean. The relation between S²d and mean indicate that genotype F (IR08M110) had zero S²d values with below average mean (Fig.3). The relation between S²d and b values (Fig 4) showed that D (IR05N359) had low S²d and responded close to unit value, H (IR06A107) had responded below average with high S²d, and genotype B (IR09N505) responded above average with high S²d value. There was variation for coefficient of determination which ranged from R² = 0.06 for E (IR02A149), H (IR06A107) and K (IR09A136) to 0.99 for N (SARO).

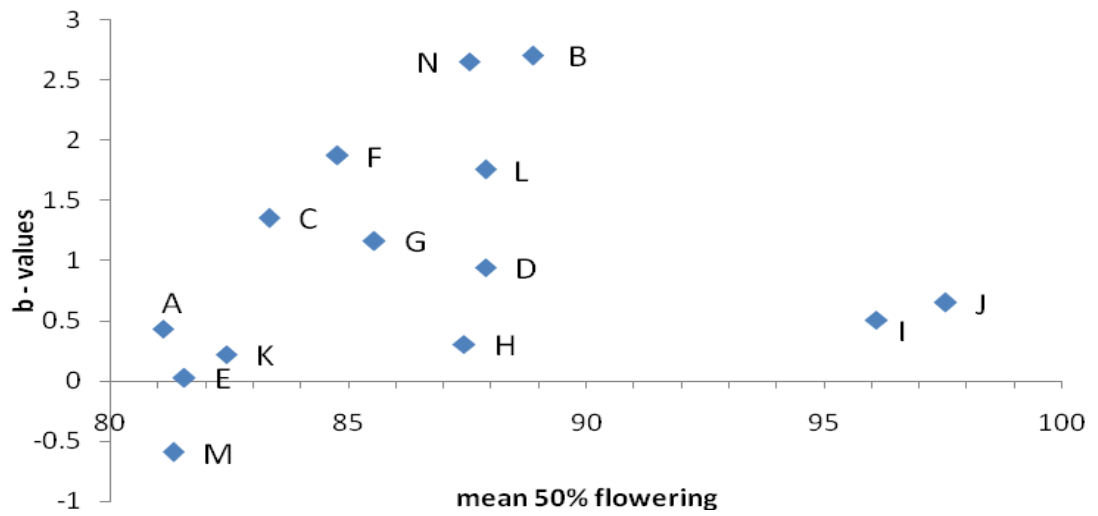


Figure 2: Mean 50% flowering vs. b - values

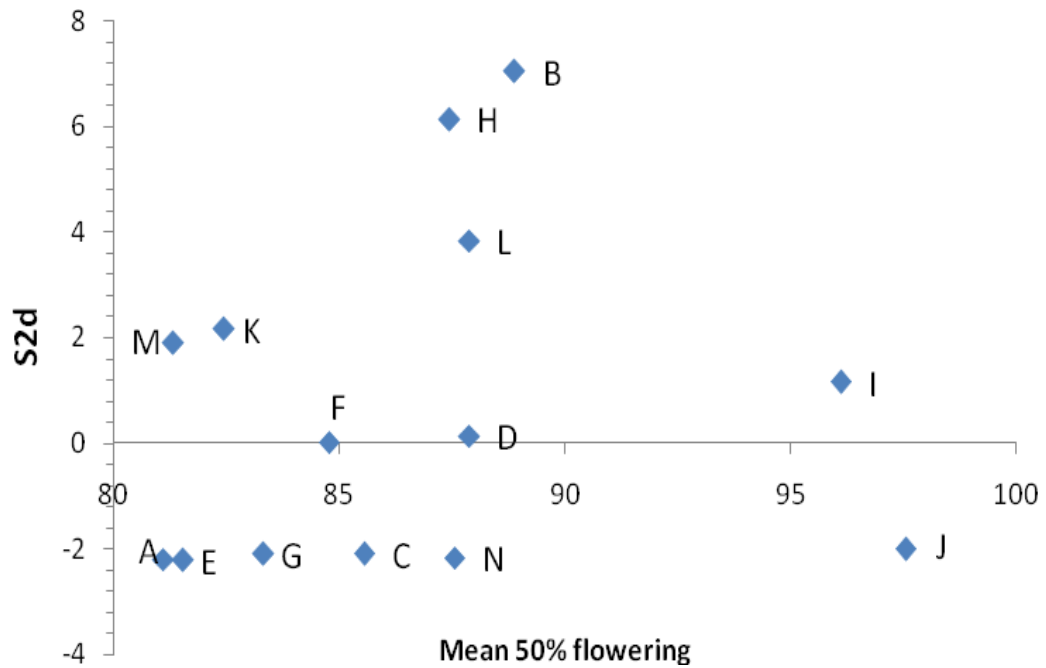


Figure 3: Mean 50% flowering vs. S²d

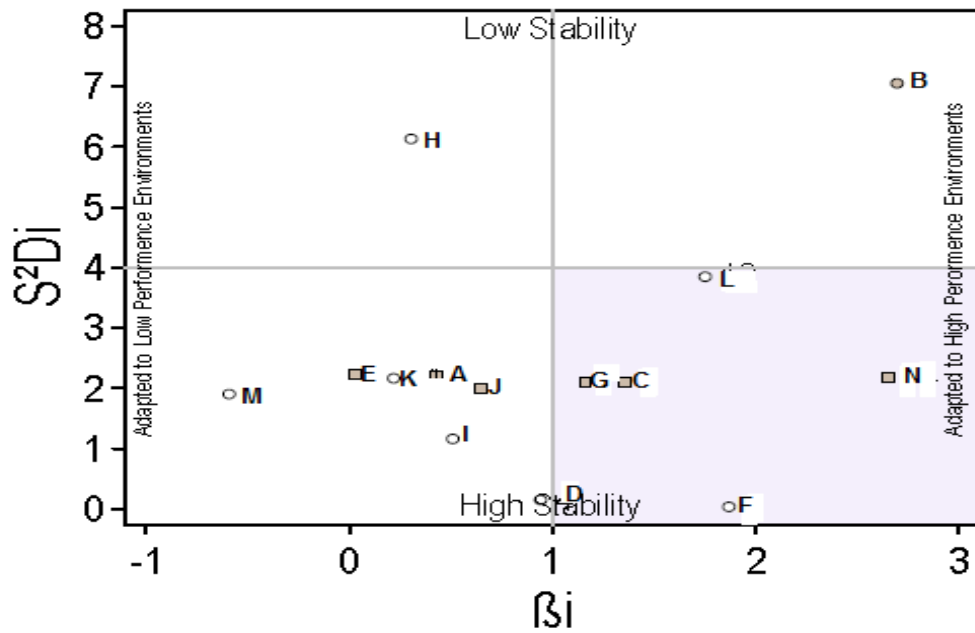


Figure 4: S^2d vs. $b =$ values for 50% flowering

4.9.14 Days to maturity

Scatter diagram presented in (Fig.5) shows the relation between b-values with mean days to maturity. Genotypes A (IR09L325), E (IR02A 149), K (IR09A136) had below average means (less days to maturity), with b values of above unit value. Genotype J (IR07A167) had above average mean and b-value above one while genotype A (IR03L325) had least mean with b value of zero. Relation between S^2d and b- values (Fig.7) indicated that Genotype A (IR09L325) had b-value of 0.00 with low S^2d , B (IR09N505) had b-value close to unit with high S^2d value, and M (IRRI123) had below average b value but had highest S^2d value. On the other hand, genotypes I (IR07A166) and J (IR07A167) had above average b-values. Coefficients of determination R^2 ranged from 0.00 for A (IR03L325) to 0.96 for L (IR03A550).

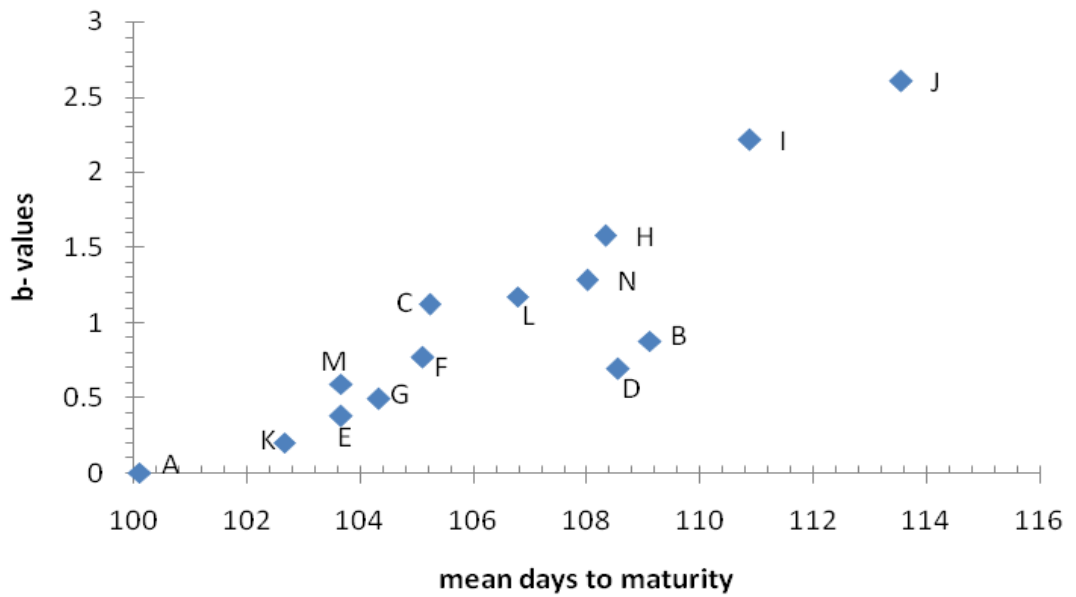


Figure 5: b- values vs. mean days to 50% flowering

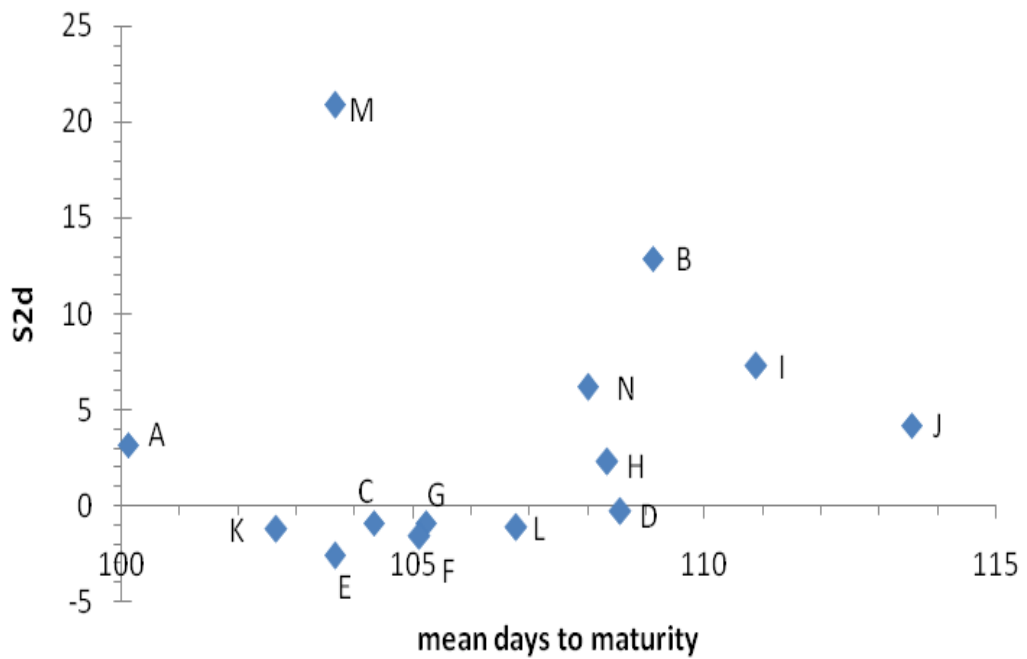


Figure 6: S²d vs mean days to maturity

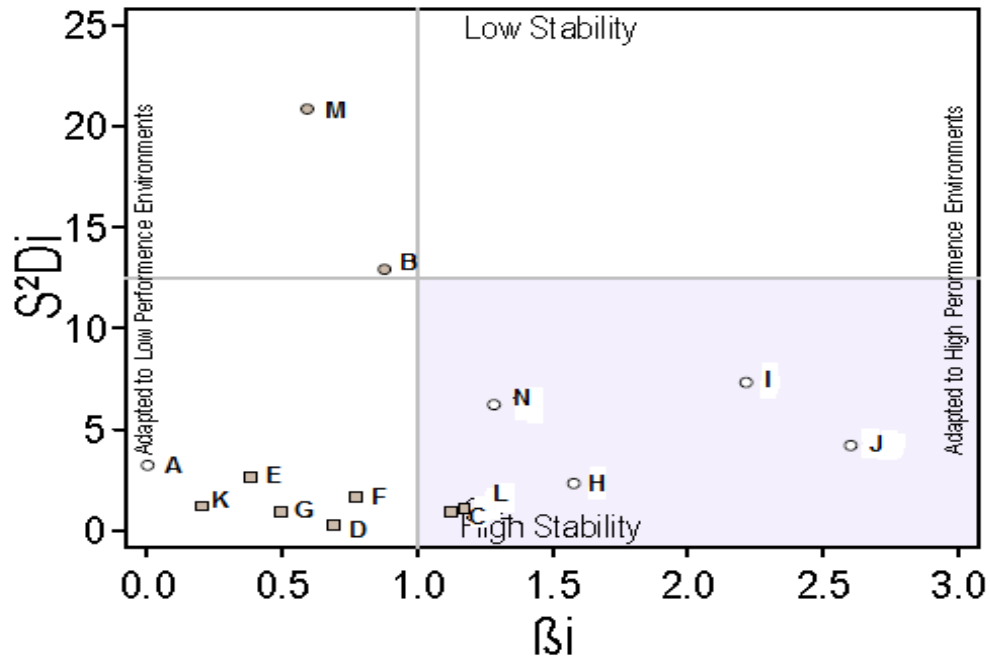


Figure 7: S^2d vs. b values

4.9.15 Plant height

The relation between mean plant height and regression coefficient (Fig. 8) indicated that genotypes F (IR08M110) and K (IR09A136) had below average means, b -value close to unit value. On the other hand A (IR09L325) and D (IR05N359) had b -value close to unit but had above average mean, B (IR09N505) had low b value and below average mean, G (IR07M101) had high b -value with above average mean. The relation between S^2d and b values (Fig. 10) indicated that Genotype A (IR09L325) had unit b -value with S^2d close to zero while M (IRRI123) had highest S^2d with b -value close to 1. The rest of genotypes had b -values of below unit value. Genotypes showed high coefficients of determination ranging from 0.83 to 0.99.

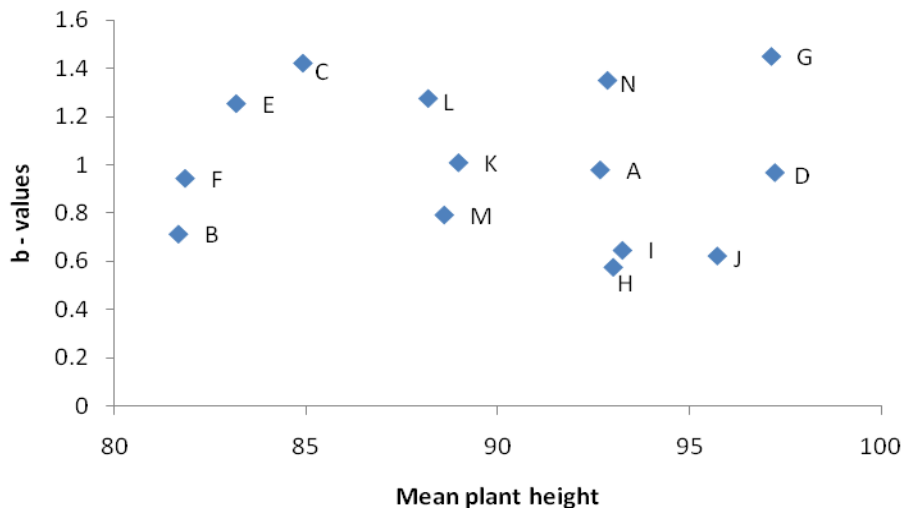


Figure 8: Scatter diagram b values vs. mean plant height

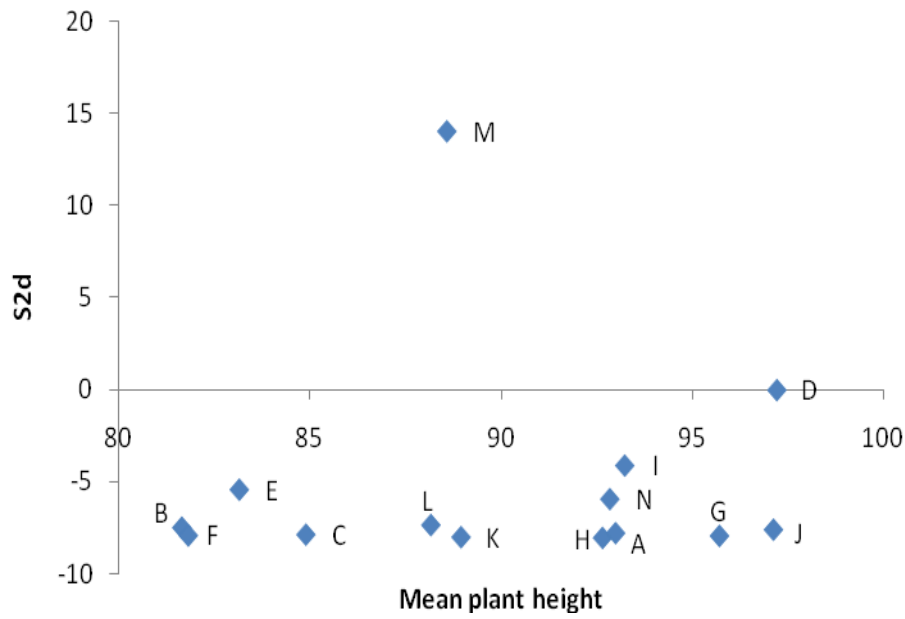


Figure 9: Scatter diagram b S²d vs. mean plant height

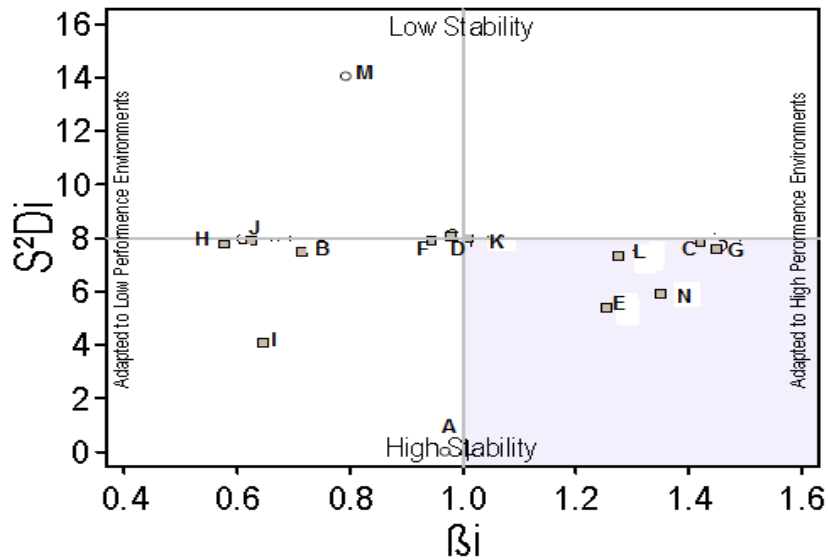


Figure 10: Scatter diagram of S^2d vs. b-values

4.9.16 Panicle length

Scatter diagrams shown in (Fig. 11) indicated the relationship between the mean performance and b-value for panicle length. Genotypes I(IR07A166),J(IR07A167) and K (IR09A136),had high means but low average response while Genotype M (IRRI123) had high mean and average response ,genotype N(SARO 5) had highest mean but had below average response , C (IRRI146) had low mean but above average response while L (IR03A 550), and N (SARO 5) had below average response.

The graph of S^2d vs. mean panicle length (Fig.12) indicated that genotypes I (IR06A166), J (IR07A167) and K (IR09A136), had above average means with low S^2d . Figure 13 shows S^2d vs. b values. Genotypes D (IR05N359), L (IR03A550), N (IRRI 123) and I (IR07A166) had b values close to unit and also had low S^2d values, while Genotype C (IRRI 146) had b value close to one but had high S^2d . Genotypes

A (IR09L325), K (IR09A136), J (IR06A167), G (IR07M101) and H (IR06A107) had low S^2d value but had relatively high b-values.

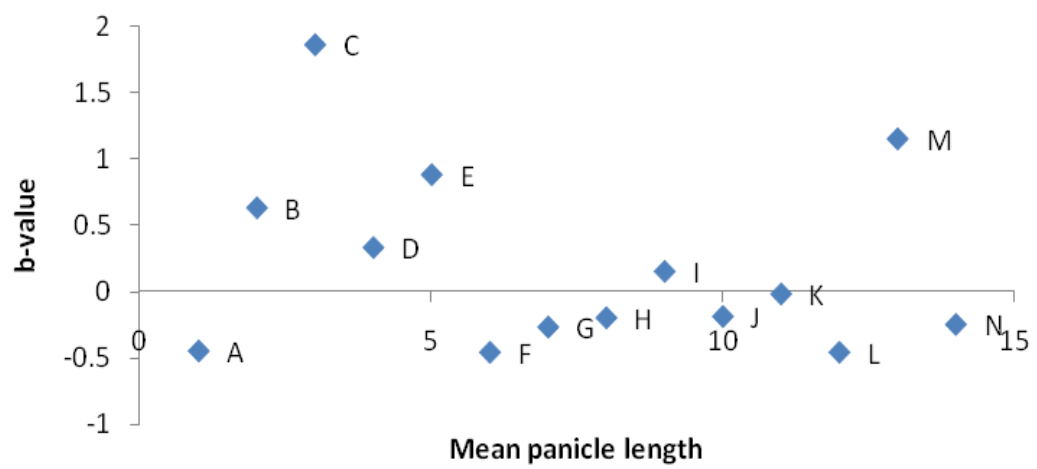


Figure 11: Scatter diagram b-value vs. mean panicle length

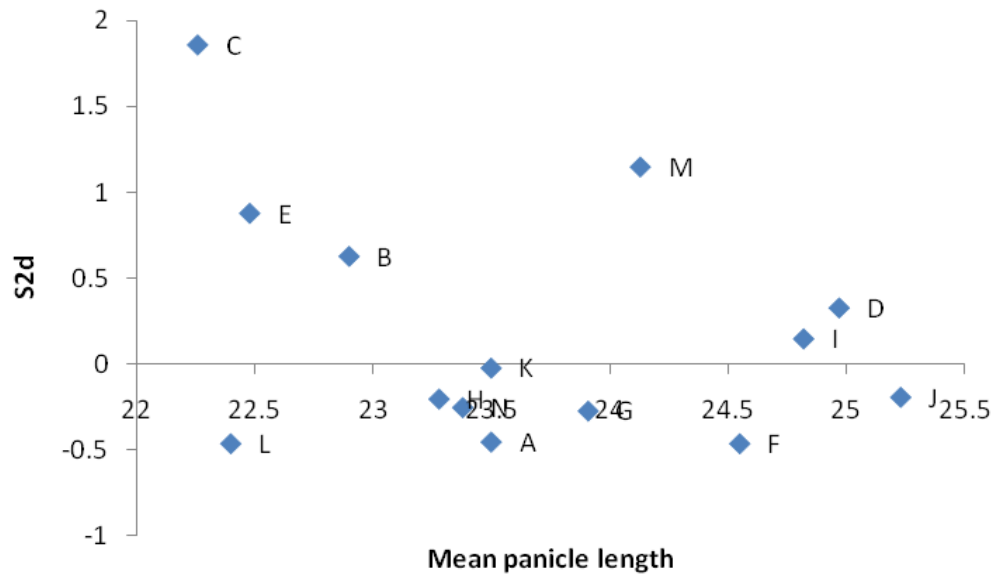


Figure 12: S²d vs. mean panicle length

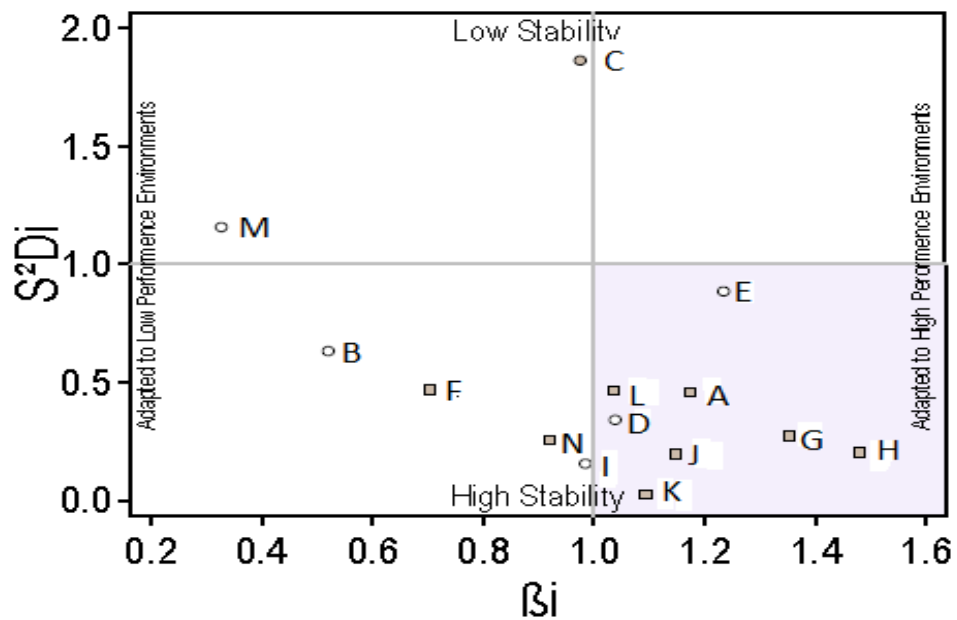


Figure 13: S²d vs. b-value for panicle length

4.9.17 Number of primary branches per panicle

Scatter diagram shown in (Fig. 14) indicated the relationship between mean and b-values for number of primary branches per panicle. Genotype A (IR09L325) and G (IR07101) had above average mean and responded on average, M (IRRI123) had b-value close to one but with mean performance below average. B (IR09N505), C (IRRI146) J(IR07A167) I (IR07A166) had high mean performance as well as b-values above average.

The relation between S^2d and mean presented in (Fig. 15) indicated that genotype F (IR08M110) had average mean and $S^2d = 0$ while I (IR07A166) had above average mean as well as high S^2d . Coefficients of determination (R^2) ranged from $R = 0.99$ for C(IRRI 146) to 0.07 for K(IR09A136).

Figure 16 indicated that genotypes D (IR05N 359) and N (SARO 5) had low S^2d ; genotype G (IR07M101) had b- value close to one but had high S^2d while genotype A (IR09L325) had average response as well as low S^2d .

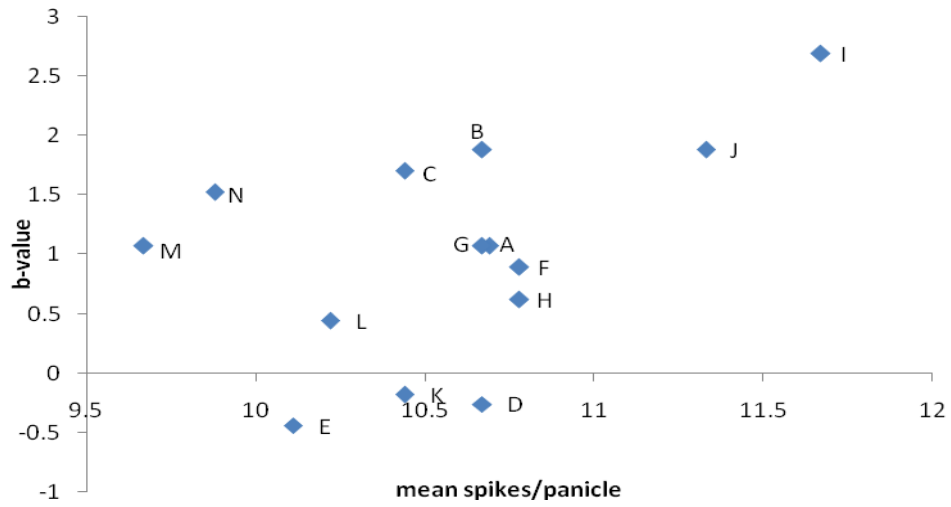


Figure 14: Scatter diagram b-value vs. mean number of primary branches/ panicle

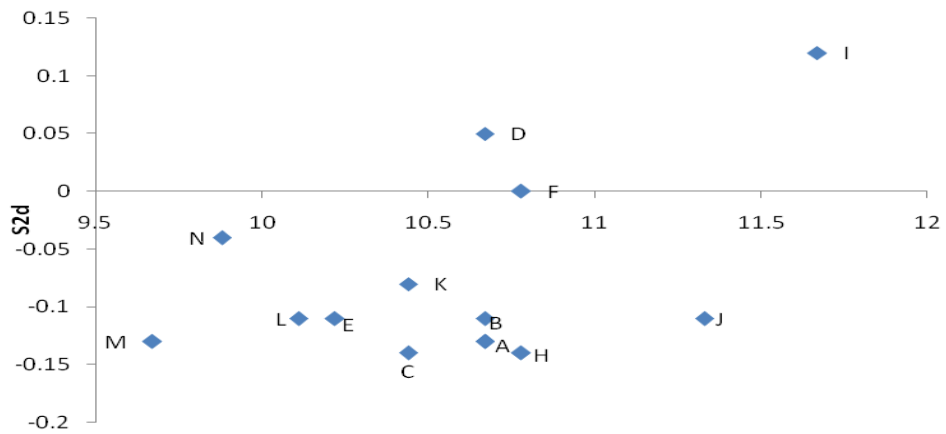


Figure 15: S²d vs. Mean number of primary branches/ panicle

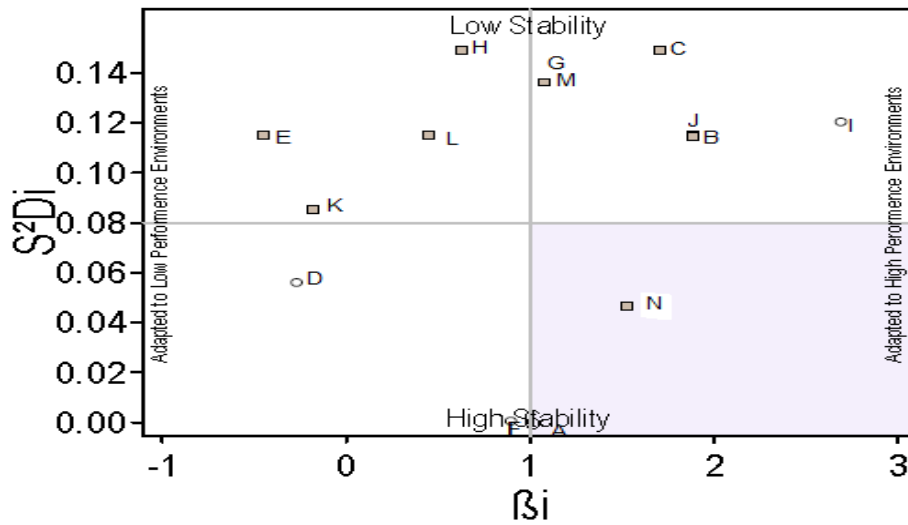


Figure 16: Scatter diagram S²d vs. b-value primary branches /panicle

4.9.18 Number of grains per panicle

The relationship between b-values and means for number of grains per panicle is shown in (Fig. 17). Genotype H (IR06A107) had b-value close to one and performed above average mean while M (IRRI123) had b-value of zero and below average mean. Genotypes F (IR08M110) and A (IR09L325) had high b-values with high mean performance. The relation between S²d and mean (Fig. 18) indicated that genotype C(IRRI146) had S²d value of 0 with average mean while A(IR09L325) had high S²d value and above average mean. For grains per panicle (Fig.19) genotypes D (IR05N359), G (IR07M101), H (IR06A107) and L (IR03A550) had b-value close to 1 with low S²d.

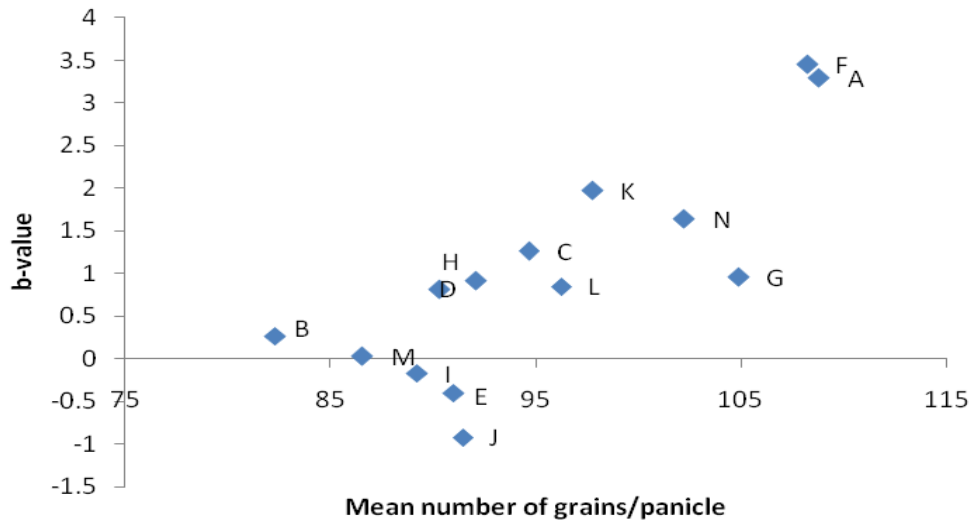


Figure 17: b-value vs. mean number of grain /panicle

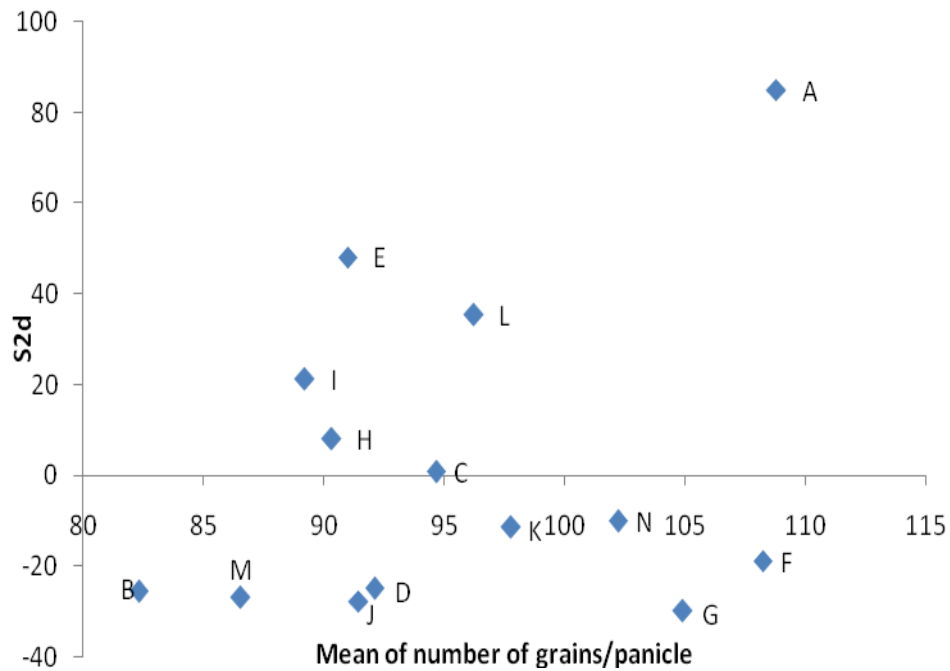


Figure 18: S^2d vs. grain/panicle

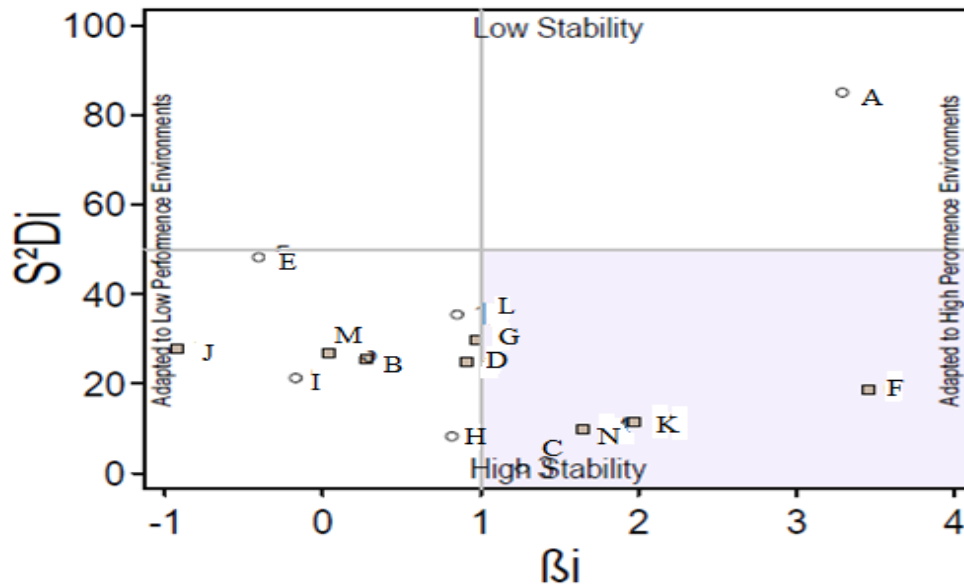


Figure 19: Scatter diagram of S^2d vs. b-value for number grains/ panicle

4.9.19 Panicle weight

Scatter diagrams showing relationships between b-values and mean performance of panicle weight as shown in (Fig. 20) showed that genotypes I(IR06A166), B(IR09N505) and G(IR07M101) had b-values close to one and had below average mean while D(IR05N359) and C(IRRI 146) responded above average but with means below average. Genotypes E (IR02A149), H (IR06A107), M (IRRI123) and N (SARO 5) had low response with low mean performance while Genotype F (IR08M110) had low response but high mean. The relation between S^2d and mean as shown in (Fig. 21) indicated that J (IR06A 167) and B (IR09N505) had below average mean with low S^2d . (Fig.19) (IR08M110) had S^2d below zero with high mean. The S^2d vs. b-value (Fig.22) indicated that B(IR09N505) and E(IR02A149) had average response with low S^2d , while genotypes A(IR09L325), F (IR08M110), H(IR06A107) and N(SARO 5) had low response with high S^2d value, and genotypes

J(IR06A167), M(IRRI123) and L(IR03A550) had low S^2d with low b-values. Genotypes D (IR05N359) and C (IRRI146) responded above average but had high S^2d .

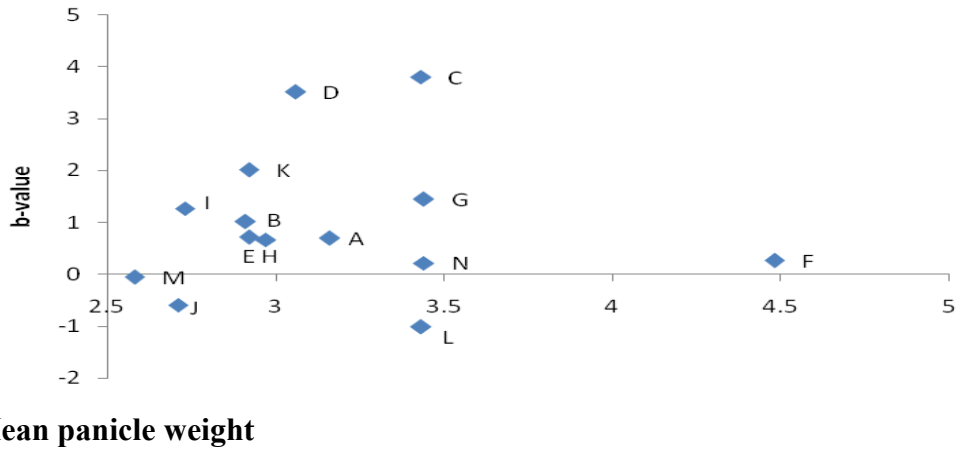


Figure 20: b-value vs. panicle weigh

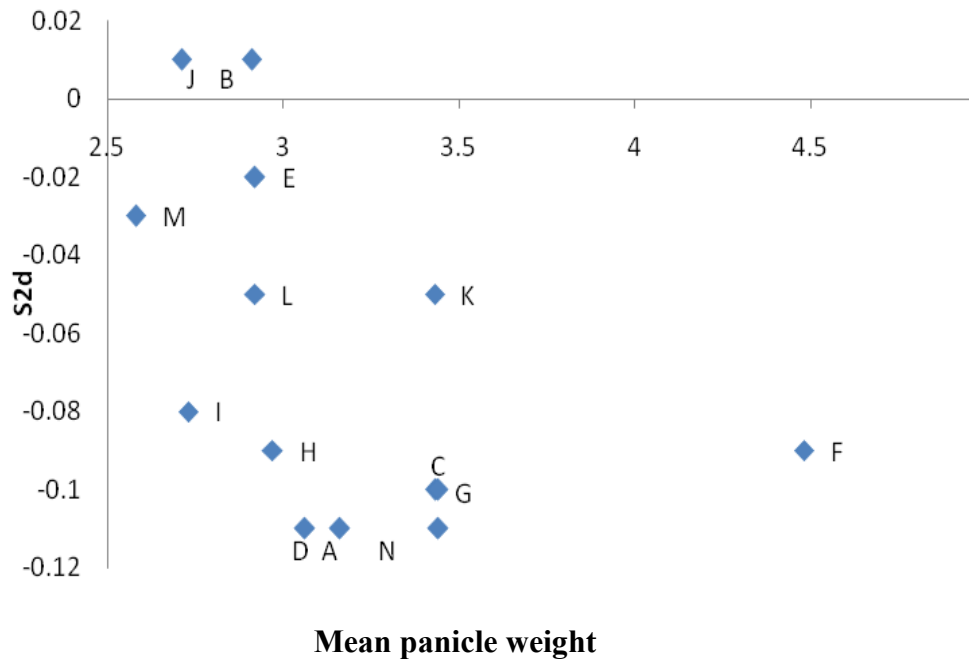


Figure 21: S^2d vs. mean panicle weight

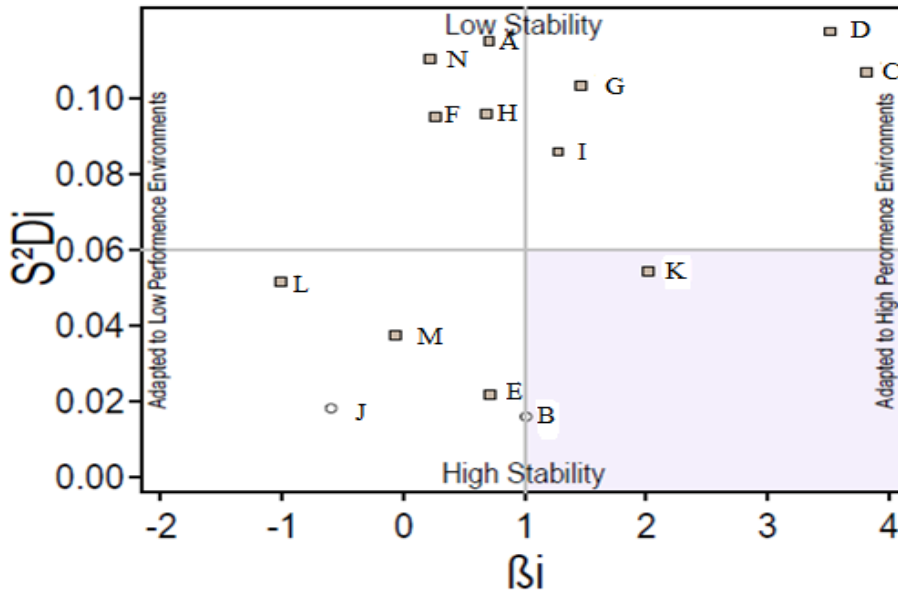


Figure 22: Scatter diagram S^2d vs. b - value for mean panicle weight

4.9.20 Mean number of tillers/plant

The relationship between regression coefficients and mean number of tillers per stand as shown in (Fig. 23) indicates that genotypes H (IR06A107), E (IR02A149) and M (IRRI 123) responded close to average with average mean performance while Genotype B (IR09N505) responded above average with high mean performance. Scatter diagram of S^2d against mean tillers per stand (Fig.24) shows that Genotype G (IR07101) had low S^2d with low mean while B (IR09N505) had high mean and high S^2d on the negative side. C (IRRI 146), F (IR08M110), I (IR07A166) and J (IR07A167) had above average mean with negative S^2d . The relation between S^2d and b -value (Fig 25) indicated that genotype G (IR07101) had low S^2d with low b -value while B (IR09N505) had relatively high S^2d and b -value.

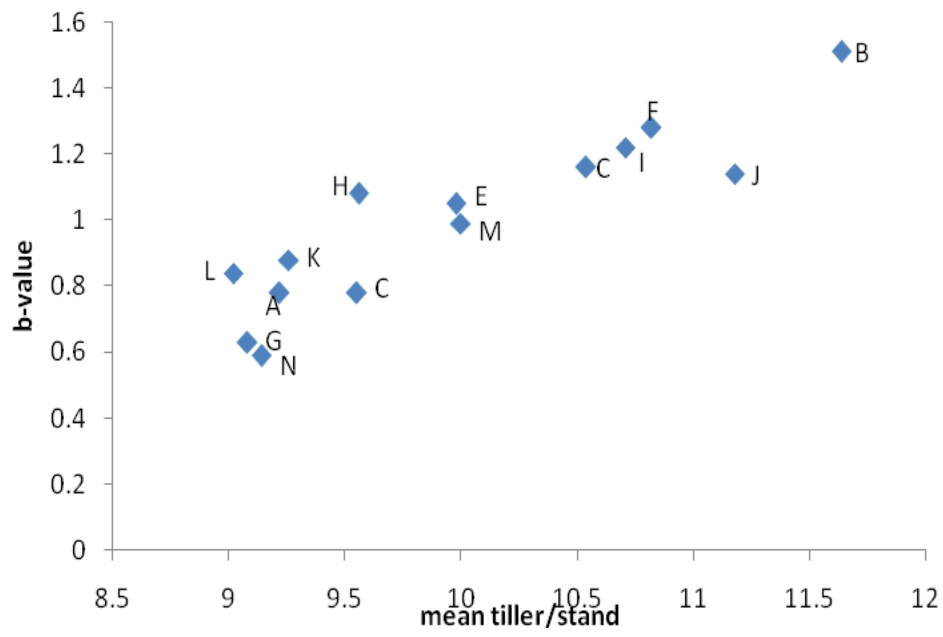


Figure 23: b-values vs. mean tillers/plant

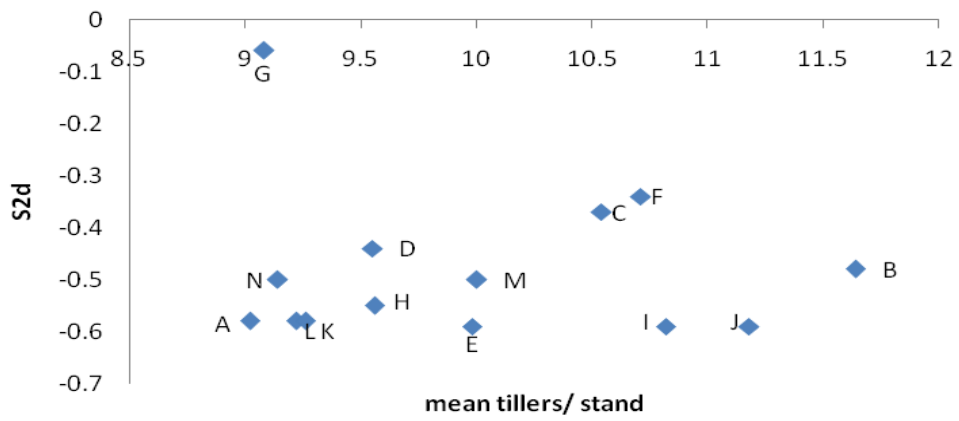


Figure 24: Scatter diagram of S²d vs. mean tillers/plant

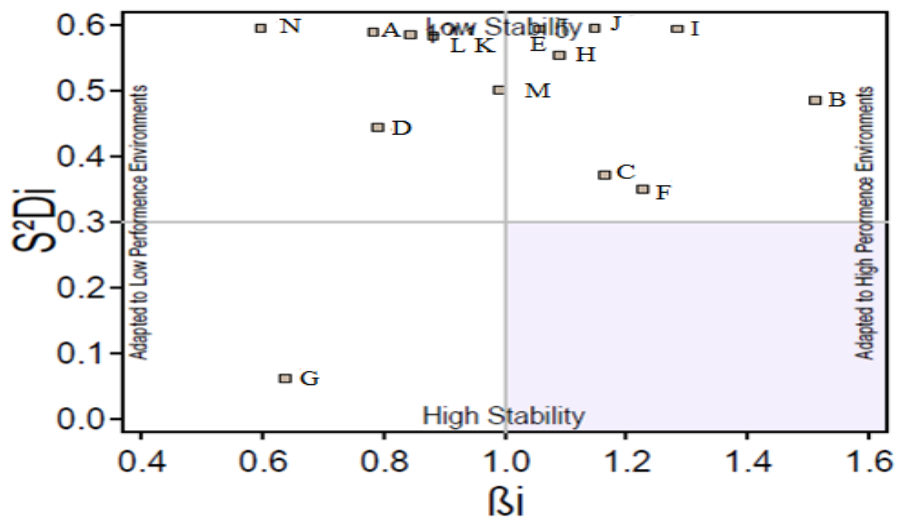


Figure 25: Scatter diagram S^2d vs. b-value for tillers/plant

4.9.21 Weight of 1000 grains

The scatter diagram of b-value against mean 1000 grain weight (Fig. 26) indicated genotype N(SARO 5) and M(IRRI123) had regression coefficients close to unity and mean performance above average. The relationship between S^2d and mean 1000 grain weight (Fig. 27) indicates that genotypes H(IR06A107) and M(IRRI 123) had b-values close to unity and had mean performance above average. The relationships between S^2d and b-value as shown in (Fig. 28) shows that genotypes B(IR09N505), J(IR06A167) and H(IR06A107) had low S^2d and low b-values. On the other hand K(IR09A136) had low S^2d but high b-value, while genotypes I(IR06A166) and E(IR02A 149) had high S^2d and high b-values.

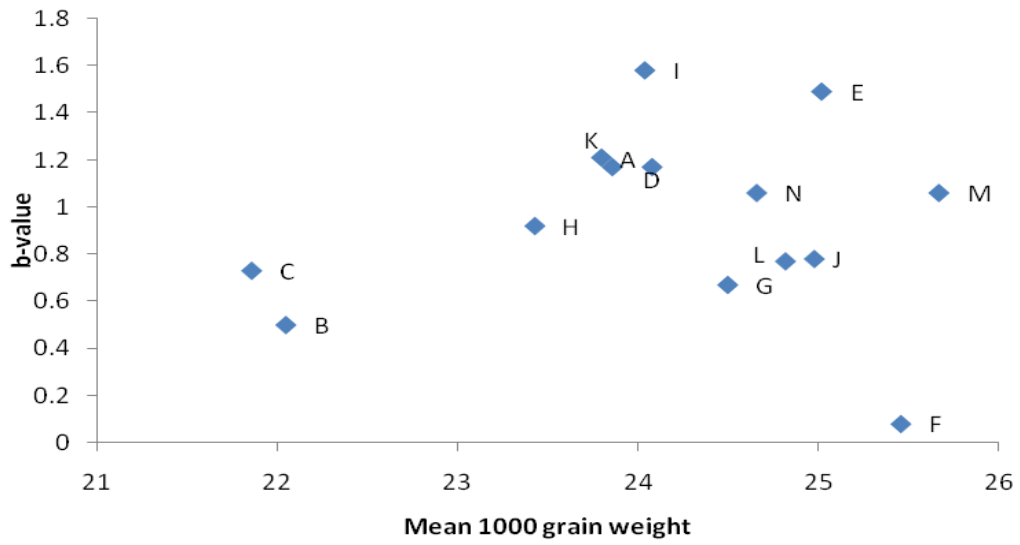


Figure 26: Scatter diagram of b-value vs. mean1000grains weight

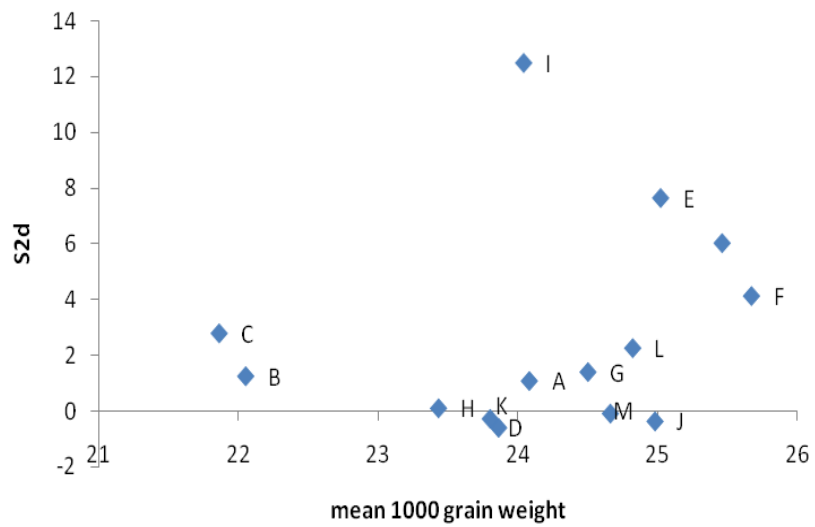


Figure 27: Scatter diagram of S²d vs. mean1000grains weight

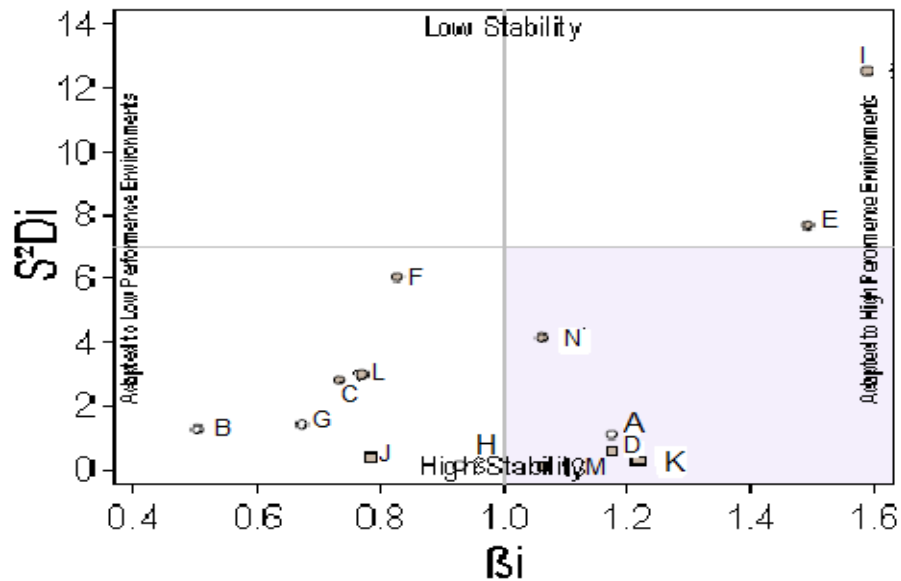


Figure 28: Scatter diagram S^2d vs. b -value for 1000 grain weight

4.9.22 Yield/ha

The relationship between regression coefficient and mean performance for yield in tons per hectare (Fig. 29) indicated that M(IRRI 123) and G (IR07M101) had regression coefficients close to unity and also had means of above average. The relation between S^2d and mean as shown in (Fig. 30) indicated genotypes N(SARO 5), I(IR06A 166), B(IR09N505), H(IR06A107) had S^2d of zero and low b -value. While J(IR06A167) and K(IR09A136) had S^2d of zero and b -value above average. The relation between S^2d and regression coefficient (Fig 31) showed that N(SARO 5), I(IR06A166), B(IR09N505), and H(IR06A107) had low S^2d values and low b -values. Genotypes D(IR05N359), J(IR06A 166) and K(IR 09A136) had low S^2d but high b -values. A(IR09L325) had high S^2d but low b -value and L(IR03A550) had high S^2d with high b -value.

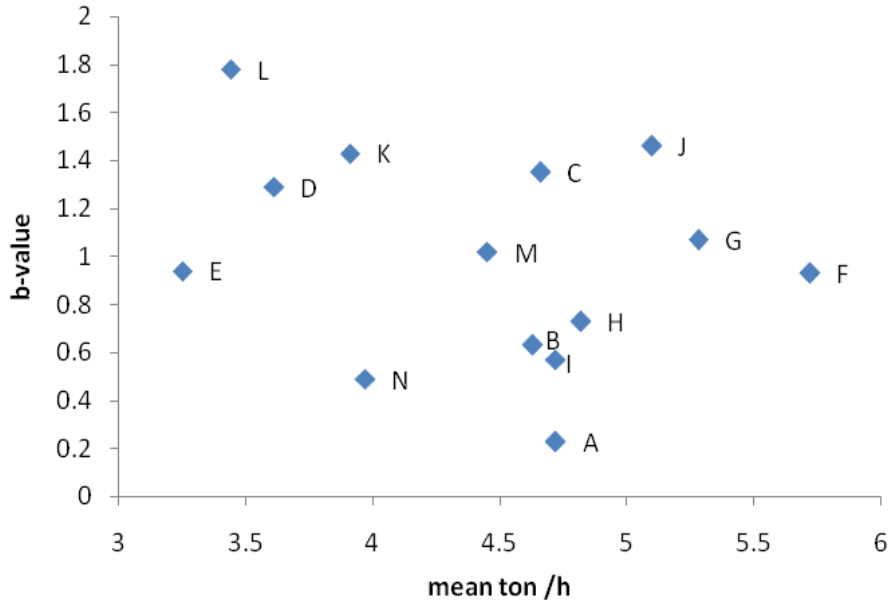


Figure 29: Scatter diagram b values vs. mean ton/ha

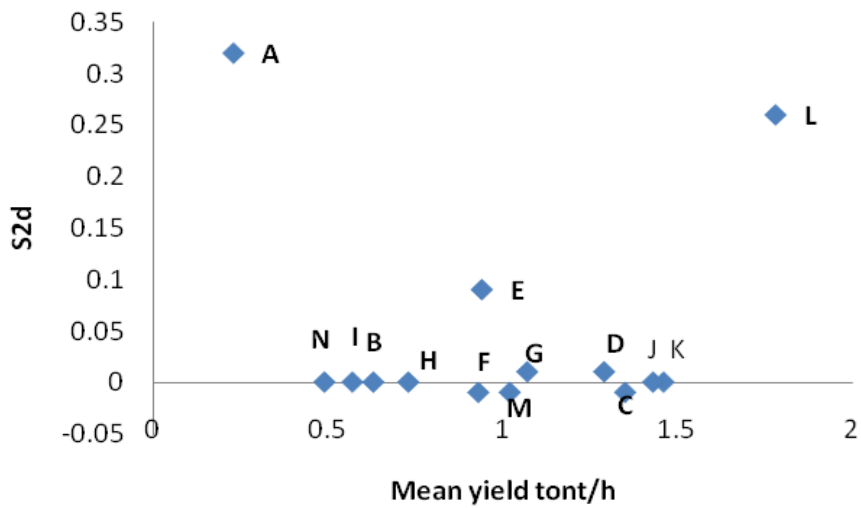


Figure 30: Scatter diagram of S2d – value vs. mean ton /ha

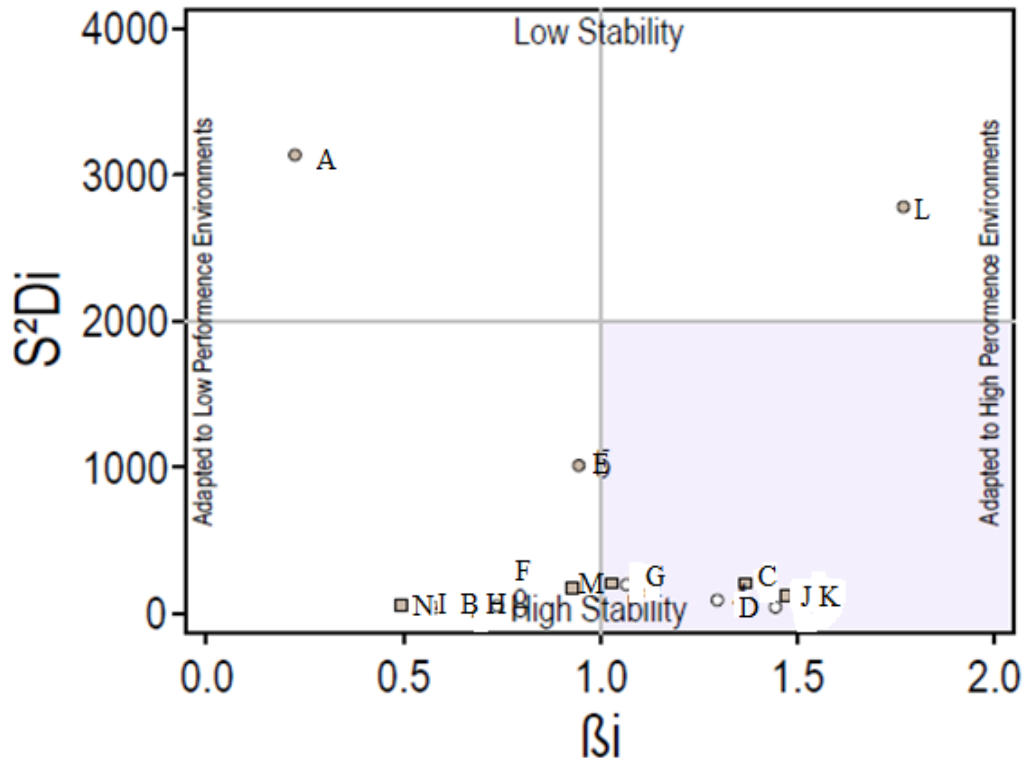


Figure 31: Scatter diagram of s^2d - value vs. mean ton/ha

CHAPTER FIVE

5.0 DISCUSSION

5.1 Genotypic and Environmental Variation

In the present investigation results revealed variation among genotypes for all studied traits at Mwera site, while at Kibokwa most characters showed significant differences except for days to maturity, number of tillers per plant and number of primary branches per panicle and at Cheju site there was variation between genotypes among the studied variables except for panicle length, tillers/plant, 1000 grain weight, number grains/panicle and number of primary branches per panicle. This present study indicated that there was variation among genotypes for the studied characters across all three locations which implying that there is potential genetic variability among genotypes. According to Yoshida (1981) variation among genotypes is important for genetic selection and crop improvement.

The magnitude of variation between genotypes was reflected by the differences in mean performance between genotypes for the studied traits. High genetic variability for different quantitative traits in rice was also reported earlier by Khan *et al.* (2009), Umadevi *et al.* (2009) and Ullah *et al.* (2011).

The location mean performance indicated that Mwera was the best site for almost all the studied variables followed by Kibokwa and Cheju, the possible reason of this performance is water availability; water was readily available at Mwera compared to other two sites where there was water shortage during rice growth period. Difference

on performance of genotypes for yield components across and within location revealed that there were genetic differences between genotypes. The rank changes in performance for different studied variables indicated the degree of variability in performance of genotypes across locations, existence of genotype and environment interaction necessitate more genotypes evaluations at different locations before release.

Results showed that genotypes IR07A 167 and IR08M110 were comparatively high yielding genotypes in combined comparison; also had reasonable good yield performance at individual sites. The variation of yield performance in rice across environments was reported earlier by Patel *et al.* (2012). Also location differences show that it is possible to identify specific sites for rice production in Zanzibar.

The study showed that all studied genotypes were early maturity ranging from 102 days to 119 days. International Rice Research Institute (1992) categorized varieties that take 105 to 120 as early maturing; and 136 – 160 as late matures varieties. IR09L325 matured earlier at all sites and IR07A167 was latest at all three sites, the studied genotypes were varied across locations due to genotype environment interaction. Early maturing genotypes for rice are important as these can evacuate land quite early for the next crop and also escape unpredictable weather caused by world climatic change. Farmers prefer early maturity genotypes to ensure successful growth and early production of the crop.

Panicle length showed an influence on grain yield, genotype IR07A167 that had highest mean panicle length was the highest yielding genotype, this might be due to the association between panicle length and grain yield of rice genotypes as reported earlier by Ullah *et al.* (2011).

5.2 Components of Variance

The estimates of variance components indicated that phenotypic variances of the studied variables were slightly higher compared to genotypic variances; this implies that the characters were slightly influenced by environmental factors than genetic potential of genotypes. The findings were inconformity with Akinwale *et al.* (2011), Singh and Chakraborty (1996) and Devi *et al.* (2006) who found similar results in rice genotypes.

Genotypic and phenotypic coefficients of variability measure the variability of studied characters and the extent of environmental influence on the expression of the character. This is indicated by the magnitude of the differences between the genotypic and phenotypic coefficients of variation where large differences reflect environmental influence if the phenotypic coefficient of variation is higher. Johnson *et al.* (1955) classified GCV and PCV as low (0-10%), (moderate 10-20%) and high (greater than 20%)

This study revealed that PCV was slightly higher than GCV for all studied characters indicating the presence of environmental influence to some degree in the phenotypic

expression of these characters. The results were in agreement with Akinwale *et al.* (2011) who reported similar results on rice.

Day to 50% flowering, days to maturity, panicle length had low moderate genotypic and phenotypic coefficients of variation, this might due to the presence of both positive and negative alleles in the population, moderate genotypic and phenotypic coefficients of variation for days to 50% flowering, plant height and panicle length were reported earlier by Iftekharuddeula *et al.* (2011).

The small difference between GCV and PCV for days to 50% flowering, days to maturity, plant height and yield per plant, indicated that there was relatively less influence of environment on these characters; the findings were in agreements with Yadav (2000) who found small difference between GCV and PCV on days to maturity and plant height in rice genotypes. The higher differences between genotypic and phenotypic coefficients of variation were observed for panicle weight and yield per plant indicating high influence of the environment for the traits.

5.3 Estimates of Heritability in Broad Sense

The broad sense heritability is the relative magnitude of genotypic and phenotypic variances for the traits and it is used as a predictive role in selection procedures (Allard, 1960). According to Robinson (1949) heritability estimates are classified as low (0 - 30%), moderate (30 – 60%) and high (> 60%). From this study the high broad sense heritability accompanied by high genetic advance was found in number of tillers per plant, plant height, grain yield/ plant suggesting that these traits are

primarily under genetic control and results were in agreement with Akhtar *et al.* (2011), Jayasudha and Sharma (2011) who found similar results when evaluating rice genotypes. High heritability and genetic advance for these characters suggests that selection for these characters can be executed from early generation of crop improvement. Vange and Ojo (1997) reported that high heritability values indicate the predominance of additive gene action in the expression of traits and can be used to select an individual plant. High heritability accompanied with high genetic advance was observed for number of tillers per plant and yield per plant indicating that direct selection based on their phenotypic expression can be executed at early stages of crop improvement.

Number of grains per panicle, days to 50% flowering, panicle weight and panicle length, 1000 weight, number of primary branches per panicle had low to medium broad sense heritability coupled with low genetic advance indicating that these traits were highly influenced by environment or this could be due to different in genetic makeup of studied genotypes. Direct selection for these traits will be ineffective; this implies that selection based on phenotypic expression of this trait should be done at late generations of crop improvement; the results were in contrary with Akinwale *et al.* (2011) who found high broad sense heritability for these traits. This could be due to different populations and or environments as heritability is a characteristic of population and environment.

5.4 Interrelationships among Yield Components

Results of genotypic and phenotypic correlation over all three sites revealed significant genotypic correlations among yield components elucidating true association as they were less affected by environmental influences. The correlations that were consistently significant at all locations and in addition to the combined analysis were days to 50% flowering with days to maturity, number of primary branches per panicle with days to 50% flowering, and grain yield per plant with yield per ha. Thus, these variable relationships are less affected by environmental changes and could be more reliable in selection during breeding activities.

Grain yield per hectare had significant positive genotypic correlations with panicle length, number of tillers per plant, plant height and number of primary branches per panicle; this implies that selection for these traits could be used for direct selection of grain yield. With respect to panicle length the findings were in conformity with Ogunbayo *et al.* (2014) who found grain yield had high significant correlation with panicle length and for plant height the results were in agreement with Abarshahr *et al.* (2011) and Badru *et al.* (2011) who found positive significant correlation between yield and plant height. Ishiyaku and Singh (2003) reported that the vegetative phase of plants have been found useful in allowing for the development of optimum canopy for high yielding. Contrary with the findings of Jayasudha and Sharma, (2010) who reported that there were no correlations between yield and plant height, the possible reason for negative relationship between plant heights with yield of rice might be due to fact that tall plants accumulate more photosynthetic products in vegetative part and less in reproductive parts i.e. seed formation. For number of tillers, findings were

in agreement with Akinwale *et al.* (2011) who found strong positive correlations between yield and number of tillers per plant and these results suggest that selection of genotypes having these traits could be effective for yield increase of the rice genotypes.

Days to 50% flowering, had significant positive genotypic and phenotypic correlation with days to maturity the findings were in agreement with Babu *et al.* (2006), and Selvaraj *et al.* (2011) who found positive significant association between days to 50% with days to maturity, implying that genotypes late in reaching 50% flowering will be late maturing. Results suggest that the variables are influenced by similar environmental and physiological phenomena.

Significant positive genotypic and phenotypic correlations between panicle lengths with number of primary branches per panicle implies that high yield could be realized by improving rice genotypes with long panicles because panicle length and number of primary branches per panicle had significant positive correlation with yield. Number of tillers per plant had positive significant genotypic and phenotypic correlation with primary branches per panicle per plant suggesting that more tillers would result in more primary branches ultimately more yield of the genotypes as these yield components showed correlation with each other but also had correlations with yield. This implies that improving these traits would result in increased yield of rice.

5.5 Path analysis

Path coefficient analysis for some yield components characters using grain yield as a dependent variable and other characters as independent variables revealed that the relationship of panicle length with yield was significant and positive ($r = 0.5966^{**}$) which is largely due to the positive indirect effect (0.4033) through number of tillers per plant and to lesser extent, the direct effect (0.2596). It indicates that panicle length interacts well with tillers per plant in the relationship with yield. Similarly, if other variables are held constant panicle length would have an independent contribution on yield. Thus panicle length can be used as a reliable criterion for selection aimed at improving yield of these rice genotypes. The findings were in agreement with Seyoum *et al.* (2012) who found direct effect of panicle length on yield of rice genotypes.

The correlation between number of primary branches per panicle with grain yield was significant and positive ($r = 0.3266^{*}$) which is largely due to indirect effect (0.2457) through number of tillers per plant. Thus number of primary branches per panicle interacted well with tillers per plant in the relationship with yield.

The correlation between number of tillers per plant grain yield was significant and positive ($r = 0.7303^{**}$) which largely due to the direct effect (0.6557) and to a lesser extent, indirect effect through panicle length (0.1597). Thus, tillering is an important yield component for yield improvement in these genotypes. The findings are in agreement with Sadeghi, (2011) who found direct relation between grain yields with number of tillers per plant.

The correlation between 1000 grain weight with yield was significant and positive ($r = 0.4277^{**}$) and this was largely due to the indirect effect through number of tillers per plant (0.3571) and to a lesser extent, indirect effect through panicle length (0.1567), signifying the importance of tillering and panicle length in influencing yield of rice. The negative direct effect of 1000 grain weight on yield (-0.1358) was counterbalanced to a considerable extent by indirect effect via number of tillers per plant and panicle length and making the total correlation between yield and 1000 grain weight to be positive and significant (0.4277^{**}). This also points to the importance of compensatory mechanisms in a system of variable interrelations as pointed out by Dewey and Lu (1959).

The study reveals the importance of panicle length, tillers per plant, 1000 grain weight and number of primary branches per panicle in their influence on grain yield. Tillers per plant interacted well with panicle length, 1000 grain weight and primary branches with tillers per plant in influencing yield of rice.

However, this study revealed high residual effect (0.634), which indicated that there were other variables not included in the present study which determine rice yield and need to be included in future studies.

5.6 Stability Analysis

Results of stability parameters showed that genotypes were responsive to environmental change. According to Eberhart and Russell (1966) a stable genotype is the one which has b-value equal to one and S^2d of zero and high mean performance.

With respect to grain yield this study revealed significant coefficient of regression implying that genotypes were responsive to changing environments. Genotypes IR07A101 responded on average and had above average mean yield coupled with 0.0 (S^2d); therefore results suggest that this genotype is stable and could be recommended for production and improvement of other varieties. These results are inconformity with those of El-Degwy (2009) who found stable genotypes in rice yield but contrary with those of Biswar *et al.* (2012) who reported that none of rice genotypes was stable for yield. On other hand, genotype IR08M110 had highest mean yield but responded close to unit but with S^2d on negative side indicating that the genotype is only suitable to low performing environments, while genotype IR02A149 responded close to average with S^2d around zero but had mean performance below average. The results suggest that intercrossing these genotypes IR 08M110, IR 07M101, IR 07A167, IR 02A149, IRRI 123, IR 02A149, SARO 5, IR 07A166, IR 09N505, IR 06A107, IR 05N359, IRRI 146, IR 09A136 can result to segregates that are stable and high yielding for these environments.

Genotypes IR07M101 and IR07A167 had high mean performance with zero S^2d values but responded above average which imply that genotypes are adapted to high yielding environments e.g. high fertilizer rates but have poor yield in unfavourable environments hence they can be recommended only for high yielding environments.

With respect to 1000 grains weight results indicated that genotype IR06A107 had below average mean but had average response and had S^2d close to zero implying that although IR06A107 had low mean it was stable for this character. On the other

hand, genotypes IR02A149 had high mean but responded above average with high S^2d indicating that this genotype can be adapted to high performance environments while IR08M110 had high mean but responded far below average with high S^2d . The later shows that this genotype is adapted to low performance environments. Therefore these findings suggest that intercrossing genotypes IRR1 123, IR 07A167, IR 02A149 IR06A10, IR08M110, IR06A SARO 5, IR 05N359, IR09L325, would result to genotypes with high 1000 grain weight adapted well in all studied locations.

Results of stability parameters for panicle weight indicated that genotype IR09N505 had regression coefficient ($b = 1$) with 0.0 S^2d , implying that the genotype was stable for this character over all tested environments. On the other hand, IR08M110 had highest mean performance but had below average response to the environments. These findings suggest that crossing IR09N505, IR08M11, IR 08 M 110, IR 07A166, IR 09N505, IR 06A107 IR 07A167, IR 09N505 would result to segregates with stable panicle weight.

Stability parameters for number of tillers per plant indicated that genotypes responded differently with change of environments. Genotypes IR07M101 and IRR1123 had above average mean and responded close to average but had S^2d on negative side implying that they are not stable and can perform well in high performance environments e.g. high fertilizer rates and adequate water supply. Almost all genotypes had low negative S^2d which implies that they are unstable for this character. Results suggest that intercrossing IR 09N505, IR 07A167, IR 08M110,

IR 07A166, IRRI 146 IR 06A107, IR 02A149, IRRI 123, IR07M101 can result to segregates with stable more number of tillers per plant.

Stability parameters for number of primary branches per panicle indicated that almost all genotypes were responsive to environments. Genotype IR08M110 had above average mean, responded on average and deviation from regression of 0.00, suggesting that this genotype is stable for this character over all tested environments. On the other hand, genotypes IR09L325 and IR07M101 had above average mean, responded close to average but had negative S^2d which implies that they are not stable genotypes for this character. Genotype IR07A166 showed above average mean, responded above average and S^2d close to zero. The above average response implies that this genotype can be adapted to high performance environments. The findings suggest that intercrossing genotypes IR08M110, IR09L325, IR07M101 IR07A166 would give segregates that are stable with more number of primary branches per panicle resulting to more rice yield as number of branches per panicle had positive significant correlation with rice yield.

With respect to days to 50% flowering, results indicated that genotypes tested had average response. This indicated that genotypes were responsive on days to 50% flowering; genotype IR05N359 responded on average and had S^2d close to zero implying that the genotype is stable for this character. On the other hand, genotype, IR08M110 responded above average, with S^2d of 0.0 and below average mean which implies that this genotype can be adopted for high performing environments while genotype IR09L325 showed least days to 50% flowering therefore results suggest

that intercrossing IR09L325, IR05N359, IR09A136, IR02A149, IRR1123, IR07M101, IR08M110, and IR07A166 would result to segregates with stable and earliness in flowering.

For plant height results indicated that genotypes responded significantly, implying that genotypes showed different reactions to changing environments. Genotypes IR09L325, IR08M110 and IR09A136 responded close to average but had negative S^2d values implying that genotypes are not stable. On the other hand, IR05N359 had close to unit b value with S^2d of 0.0 indicating that the genotype is stable over all tested environments. Intercrossing IR08M110, IR09N505, IRR1146, IR09A136, IR09L325, can result to short statured desirable plants for Zanzibar (75cm-100cm) with stable genes and high yield potential as genotype IR08M110 had high mean grain yield. Appendix 4 indicates genotypes with characteristics of good mean performance and stability for the different variables.

CHAPTER SIX

6.0 CONCLUSION AND RECOMMENDATIONS

6.1 Conclusions

Results obtained from this study show the overall performance of 13 introduced rice genotypes. High variation among genotypes is evidence that these genotypes have potential germplasm that can be used for selection of best rice lines for improvement and production. The rank changes in performance for different studied characters indicate the degree of variability in relative performance of genotypes across tested locations. This confirms the existence of $G \times E$ interaction which indicates the importance of more evaluation of these genotypes before recommendation to farmers.

Phenotypic coefficient of variability was slightly higher than genotypic coefficient of variability indicating there was influence of environment on expression of traits. The estimate of broad sense heritability varied among studied characters, high to medium heritability were observed for yield per plant, number of tillers per plant, panicle length, thousand grain weight, grain weight per panicle and days to maturity which implies selection can be done based on phenotypic expression of these characters. High heritability and high genetic advance for number of tillers per plant is evidence of additive gene action for this character. Correlation analysis revealed that yield had positive phenotypic and genotypic correlation with plant height, thousand grains weight, panicle length, number of tillers per plant, number of primary branches per panicle, and grain yield per plant, therefore these traits should be considered during improvement and selection from these genotypes.

Path analysis revealed the importance of panicle length, tillers per plant, 1000 grain weight and primary branches per panicle in influencing yield. Tillers per plant interacted favourably with panicle length, 1000 grain weight and primary branches in influencing grain yield of rice in these genotypes.

Stability analysis revealed that there was variation for studied variables implying that genotypes responded differently with changing environments. With respect to grain yield genotype IR07M101 showed stability over all tested environments, genotype IR08M110 although had highest mean yield was suitable only in low performing environments. Intercrossing genotypes IR08M110, IR07M101, IR07A167, IR 02A149, IRR1123, IR 02A149, SARO5, IR07A166, IR09N505, IR06A107, IR 05N359, IRR1146, IR 09A136 can result to segregates that are stable and high yielding.

6.2 Recommendations

1. Genotypes IR08M110, IR07M101 and IR07A167 had higher yields compared to check (SARO 5) thus can be used for production and improvement programs.
2. Selection can be relied upon phenotypic expression of yield per plant, number of tillers per plant and panicle length, as these traits had high to medium broad sense heritability coupled with high genetic advance indicating additive gene effect.
3. Improving yield should be done by selecting genotypes based on number on number of tillers per plant, panicle length, 1000 grain weight and number of primary branches per panicle.
4. Genotype IR07M101 can be recommended as a stable genotype for yield across studied environments. While IR07A167 can be recommended for high yielding environments.

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APPENDICES

Appendix 1: Weather condition of the experimental sites

Location	Month	Rainfall 2012	Temperature (°C) 2012	
		(mm)	min	max
Mwera	February	36.0	23.1	31.4
	March	49.9	25.2	33.4
	April	245.7	23.9	30.3
	May	135.1	23.4	30.0
	June	50.8	21.7	28.8
	July	16.5	20.7	29.9
Kibokwa	February	32.0	22.2	32.2
	March	42.4	24.1	33.1
	April	241.5	23.0	30.1
	May	132.8	23.1	29.9
	June	48.2	21	27.2
	July	35.8	20.7	29.5
Cheju	February	34.0	23.2	31.2
	March	47.0	23.1	32.3
	April	228.4	22.5	29.8
	May	128.4	23.2	29.5
	June	42.5	23.3	27.4
	July	37.7	21.0	28.1

Source: Tanzania Meteorological Agency – Zanzibar Station (Kizimbani)

Appendix 2: Information on soil characteristics of three rice irrigation schemes of Unguja Island

Cheju site- Soils originated from Miocene clay and limestone. It is classified as Gypsic Vertisol in FAO classification. 0-30 cm, Black (2.5y 2/0) humic sandy clay loam, strong and coarse angular and sub angular blocky, massive, moist firm to very firm, sticky and plastic when wet. Mwera site - Classified as Eutric Gleysol, 0-30cm black (10YR 2/1) sandy clay loam to sand clay moderate medium sub angular blocky, moist friable, slightly sticky and plastic when wet, high organic matter. Kibokwa site, 0-30cm- dark brown soil (7.5YR 3/2) humic clay loam, massive moist friable, wet sticky and plastic.

Exchangeable ions mill equivalent/100g

Site	Depth	Na	K	Mg	CEC	% Base saturation
CHEJU	0-30cm	0.129	0.065	8.8	25.4	44.00
MWERA	0-30cm	0.15	0.03	1.60	24.8	27.01
KIBOKWA	0-30cm	0.28	0.05	5.20	22.5	37,4

Source – Zanzibar Agricultural Research Institute, Kizimbani soil laboratory.

Appendix 3: Genotypes with desirable means and stability parameters for the studied variables.

Variable	Mean	b- value	S ² d	Genotypes
Days to 50% flowering	Early			IR09L325,IR09A136, IRO2A149, IRRI123
		$b \approx 1$		IR07M 101, IR05N359
			$S^2 d \approx 0.0$	IR08M110, IR05N359, IR07A166
Days to maturity	Early			IR09L325,IR09A136, IR02A149,IRRI123
		$b \approx 1$		IRRI 146, IR03A550
			$S^2 d \approx 0.0$	IR09A136, IRRI146, IR07M101, IR03A550, IR05N359, IR06A107
Plant height	Short			IR09N505, IR08M110, IR02A149, IRRI 146
		$b \approx 1$		IR0M110, IR09A136, IR09L325, IRRI146

			$S^2 d \approx 0.0$	IR05N359
Panicle length	Long			SARO 5, IRRI 123, IR 03A550, IR 09A136, IR 07A167, IR 07A166
		$b \approx 1$		IRRI 123, IR 02A149
			$S^2 d \approx 0.0$	IR 09A136, IR 07A166, IR 05N359, IR 07A167
Primary branches per panicle	Many			IR 07A166, IR 07A167
		$b \approx 1$		IRRI 123, IR 07M101, IR 09L325
			$S^2 d \approx 0.0$	IR 08M110,
Grains per panicle	Many			IR 08M110, IR 09L325, IR 07M101, SARO 5,
		$b \approx 1$		IR 06A107, IR 05N359, IRRI 146, IR 03A550, IR 07M101
			$S^2 d \approx 0.0$	IRRI 146, IR 06A107
Panicle weight	High			IR 08M110
		$b \approx 1$		IR 07A166, IR 09N505, IR 06A107
			$S^2 d \approx 0.0$	IR 07A167, IR 09N505
Tillers per plant	Many			IR 09N505, IR 07A167, IR 08M110, IR 07A166, IRRI 146,
		$b \approx 1$		IR 06A107, IR 02A149,

				IRRI 123,
			$S^2 d \approx 0.0$	IR 07M101
1000 grain weight	High			IRRI 123, IR 08M110, IR 07A167, IR 02A149
		$b \approx 1$		SARO 5, IRRI 123, IR 05N359, IR 09L325
			$S^2 d \approx 0.0$	IR 06A107, IR 09A136, IR 05N359, IRRI 123, IR 07A167.
Yield (ton/ha)	High			IR 08M110, IR 07M101, IR 07A167
		$b \approx 1$		IR07M101,IR 02A149, IRRI 123 , IR 08M110, IR 02A149.
			$S^2 d \approx 0.0$	SARO5, IR 07A166, IR 06A107, IRRI 123 ,IR 05N359, IRRI 146 , IR 07A167,IR09A136, IR07M101, IR 06A107, IR 08M110.

Appendix 4: Path coefficient analysis of some yield components characters of studied rice genotypes

Effect of panicle length	r_{17}	0.5966 **
Direct effect	p_{17}	0.2596
Indirect effect via primary branches per panicle	$r_{12}P_{27}$	0.0058
Indirect effect via number of grains per panicle	$r_{23}P_{37}$	0.0119
Indirect effect via panicle weight	$r_{34}P_{47}$	-0.0020
Indirect effect via tillers per plant	$r_{45}P_{57}$	0.4033
Indirect effect via 1000grains weight	$r_{56}P_{67}$	-0.0819
Total r		0.596**
Effect of number of primary branches per panicle	r_{27}	0.3266*
Direct effect	p_{27}	0.0190
Indirect effect via panicle length	$r_{12}P_{17}$	0.0793
Indirect effect via number of grains per panicle	$r_{23}P_{37}$	-0.0059
Indirect effect via panicle weight	$r_{34}P_{47}$	-0.0005
Indirect effect via tillers per plant	$r_{45}P_{57}$	0.2457
Indirect effect via 1000 grains weight	$r_{56}P_{67}$	-0.0109
Total r		0.3266*
Effect of number of grains per panicle	r_{37}	0.0992
Direct effect	p_{37}	0.1750
Indirect effect via panicle length	$r_{13}P_{17}$	0.0177
Indirect effect via primary branches per panicle	$r_{23}P_{27}$	-0.0006
Indirect effect via panicle weight	$r_{34}P_{47}$	0.0040
Indirect effect via tillers per plant	$r_{45}P_{57}$	-0.0579
Indirect effect via 1000grains weight	$r_{56}P_{67}$	-0.0389
Total r		0.0992

Effect of panicle weight	r_{47}	-0.1041
Direct effect	p_{47}	0.0120
Indirect effect via panicle length	$r_{12}P_{17}$	-0.0441
Indirect effect via primary branches per panicle	$r_{23}P_{27}$	-0.0007
Indirect effect via number of grains per panicle		0.0583
Indirect effect via tillers per plant	$r_{45}P_{57}$	-0.1511
Indirect effect via 1000grains weight	$r_{56}P_{67}$	0.0216
Total r		-0.1041
Effect of tillers per plant	r_{57}	0.7303**
Direct effect	p_{57}	0.6557
Indirect effect via panicle length	$r_{12}P_{17}$	0.1597
Indirect effect via primary branches per panicle	$r_{23}P_{27}$	0.0071
Indirect effect via number of grains per panicle	$r_{34}P_{37}$	-0.0155
Indirect effect via panicle weight	$r_{45}P_{47}$	-0.0028
Indirect effect via 1000 grains weight	$r_{56}P_{67}$	-0.0739
Total r		0.7303**
Effect of 1000 grains weight	r_{67}	0.4277**
Direct effect	p_{67}	-0.1358
Indirect effect via panicle length	$r_{12}P_{17}$	0.1567
Indirect effect via primary branches per panicle	$r_{23}P_{27}$	0.0015
Indirect effect via number of grains per panicle	$r_{34}P_{37}$	0.0501
Indirect effect via panicle weight	$r_{45}P_{47}$	-0.0019
Indirect effect via tillers per stand	$r_{56}P_{57}$	0.3571
Total r		0.4277**
Residual, P_{x7}		0.634