SUDAN UNIVRESITY OF SCIENCE & TECHNOLOGY

COLLEGE OF GRADUATE STUDIES

Study of Genetic Variability, Quality Parameters, and Molecular Characterization in some Rice

(*Oryza sativa* L.) Genotypes

دراسة التباين الوراثي, صفات الجوده والتوصيف الجزيئي في بعض الطرز الوراثيه للأرز

A thesis Submitted in Partial Fulfillment of the Degree of (PhD) in Crop Science

By

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DEDICATION

I am lucky enough to have been given the supportive gift of amazing people in my life, without all of whom, this work would not have been completed. I dedicate the thesis to...

My Parents,

For their endless love, support and encouragement and they instilling in me from a young age the belief that I Can

My husband

OSMAN ALHOURY

For being more than the sky to me

Thank you for all of your love, support, and sacrifice,

You taught me that no mountains too high for me to climb.

My sister Dr. SARA & my brother Eng. MOHAMED

*For always supporting, helping, and
Standing by me.*

My family

and

My friends

I

ACKNWOLEDGMENT

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ABSTRACT

This experiment was conducted in two locations, Experimental farm of College of Agricultural Studies (Shambat), Sudan university of Science and Technology in the growing season of (2011 and 2013) and, the second location was the experimental farm University of Bakht Alruda (ED duiam) at the growing season 2012. In order to investigate genetic variability, quality parameters and molecular characterization in 18 rice genotypes. Data were recorded on growth traits yield traits. Results for the analysis of individual variation detected significant difference among the tested genotypes for most of the studied traits in all seasons. Combine analysis, showed significant differences for genotypes and interaction of genotype X season. The best yielding genotypes were Handao221 (4.03 t/ha) for the year 2011 and Nerica14 of 2012 (3.50 t/ha) and Yunlu33 -of season 2013 (2.43 t/ha), the best yielding genotype for combine analysis was Zhonghan3 (2.38 t/ha).

The seeds were taken to the laboratory for quality information which is percentage of a physic-chemical characteristics, minerals profile (Ca, P, Fe, Zn, Mn, Cu) and Physical prosperities (color, granule size, and taste) the results showed that Yulus genotypes were the best in quality while Nericas genotypes were the best content of protein .The three primers OPK16, OPL18 and OPG05 showed the average percentage of Polymorphic bands was 89.53%. Cluster analysis grouped the 18 genotypes into 2 distinct main clusters, and 5 sup cluster

مستخلص البحث

أجريت هذه التجربه في موقعين هما المزرعه التجريبيه لكلية الدراسات الزراعيه جامعة السودان للعلوم والتكنولوجيا للعام 2011 و2013 والمنطقه الثانيه هي المزرعه التجريبيه التابعه لجامعة بخت الرضا (الدويم) للعام 2012. وذلك بغرض الحصول علي معلومات عن التباين الوراثي ومعرفة صفات الجوده والتوصيف الجزيئي في 18 صنف من الأرز

استخدم تصميم القطاعات العشوائيه الكامله بعدد ثلاث مكررات و اخزت القياسات لعدد 14 صفه وهي صفات النمو وصفات الانتاجيه والنتيجه ان. تحليل التباين الفردي اظهر وجود فروقات معنويه لمعظم الصفات. واوضح تحليل التباين المشترك وجود فروقات معنويه للموسم, الطرز الوراثيه, التداخل بين الطرز الوراثيه والموسم..افضل الطرز الوراثيه انتاجيه هي   Handao221 (4.03) طن للهكتار للعام 2011 و الصنف Nerica14 (3.50) طن للهكتار للعام 2012 والصنف   Yunlu33 (2.43) طن للهكتار للعام 2013 والصنف   Zhonghan-3في النحليل المشترك (2.83)طن للهكتار

اخزت البزور المحصوده للمعمل لمعرفة معلومات الجوده وتمت دراسة النسبه المئويه للصفات الفيزوكيميائيه وهي (الرطوبه, البروتين, الالياف, الرماد, والنشويات). والمعادن الاتيه (Ca, P, Fe, Zn, Mn, Cu) والصفات الفيزيائيه (اللون , حجم الحبيبات والدرجة التزوق) الطرز الوراثيه yulus كانت الافضل في الجوده بينما الطرز الوراثيهNericas كانت الافضل في محتوي البروتين. البادئات الثلاثه OPK16, OPL18 وOPG05 اظهرت ان نسبة النطاقات متعددة الاشكال كان 89.53. تجمعت الاصناف في مجموعتين رئيسيتين و خمس مجاميع فرعيه

CHAPTER ONE

INTRODUCTION

Rice (*Oryza sativa* L.) is one of the world's most important cereal crop, (Gealy *et al*., 2003; Mohadesi *et al*., 2011; Rabbani *et al*., 2011) with about 154 million ha harvested in 2010 (FAOSTAT, 2010a). Population increases and climatic change have made it difficult to meet demand for rice (Nguyen, 2008; Fan, 2011; Teixeira *et al*., 2011; Laborte *et al*., 2012). However, yields in some areas have increased due to advances in plant breeding and crop management. A number of cultivars now offer increased yield potential (Moldenhauer *et al*., 2001). Raising the yield potential may be possible through higher yielding varieties and reducing the yield gap in farmer's fields (Laborte *et al*., 2012).

Exploring new regions for rice production could help to meet the world demand. Rice has been raised from latitudes 53ºN to 40ºS, though 75% of global rice production in 2004 was in tropical regions (Nguyen, 2008). Rice grown outside of the temperate region is grown in the Tropics of Cancer and Capricorn. However, temperate rice generally has greater yields (Nguyen, 1998). Most U.S. rice production is temperate rice (25ºN to 45ºN), or rice grown in latitudes north or south of 23º27' (Temperate Rice Research Consortium, 2011).

The world population is expected to reach 8 billion by 2030 and rice production must increase by 50 percent in order to meet the growing demand (Khush & Brar, 2002). Genetic variability for agronomic traits is the key component of breeding programmes for broadening the gene pool of both rice and other crops. However, the genetic variability for many traits is limited in cultivated germplasm .The demand for rice of superior quality is becoming a priority for rice breeding programs worldwide (Juliano, 1990)

The growing demand for this crop at the level of the Arab countries gives this crop a particular importance for investment, especially that Sudan has valleys in White Nile State which occupies to 35 thousand hectares flooded annually by waters of White Nile. Investment idea depend of building an earthen dams for tapping floods water and then exploit it in cultivation of (Upland Rice).

Recently in 2006, different lines from WARDA (West Africa Rice Development Association) and IRRI (International Rice Research Institute) are being evaluated for yield and earliness although, 82 aerobic rice varieties and lines were introduced in an attempt to save irrigation water and to reduce human diseases risks in the irrigated schemes. Also FAO is planning to rehabilitate the White Nile research farm to improve rice production.

Genotypes selection is one of the most important management decisions. This choice is generally based upon agronomic traits and variety yield potential. Selection of rice varieties with wide adaptability over diverse farming environments is important, prior to varietal recommendation in order to achieve a high rate of varietal adoption. Rice breeders are interested in developing high yielding cultivars with improved yield and other desirable agronomic characters. Successful cultivar needs to posses high and stable yield potential over a wide range of environmental conditions (Eberhart and Russell, 1969; Wricke and Weber, 1986; Becker and Leon, 1988, Fasoula and Fasoula, 2002). The basic cause for differences between genotypes in their yield stability is a wide occurrence of GEI. The change in rank and the relative differences over a range of locations is defined statistically as GEI (Genotype Environment Interaction), which is a differential genotypic expression across environments (Becker and Leon, 1988; Ceccarelli, 1989; Romagosa and Fox, 1993; Kang, 1998; Sharma, 1998; Janick, 1999). The presence of GEI in any genetic study simply leads to overestimation of genetical and statistical parameters (Sharma, 1998). However, the knowledge of GEI can help to reduce the cost of extensive genotype evaluation by eliminating unnecessary testing sites and by fine-tuning breeding programs.

Rice is the only cultivated cereal crop adapted to growing in both flooded and nonflooded conditions. Due to population growth of about 2.9% annually, there is a large share of an increase in rice consumption of about 2% and an increase in the demand for rice to an average of 4.9% per year (Anonymous, 1995). This implies that the over 2.7 billion people who rely on rice as their staple food today, will have multiplied to some 4.4 billion by the middle of the next century (Rothschild, 1995), therefore more rice has to be produced

It provides 27% of dietary energy and 20% of dietary protein in the developing world. Rice is cultivated in at least 114, mostly developing countries

and is the primary source of income and employment for more than 100 million households in Asia and Africa (FAO, 2004). Of the 840 million people suffering from chronic hunger, over 50% live in areas dependent on rice production (FAO, 2004). About 80% of the world's rice is produced on small farms, primarily to meet family needs, and poor rural farmers account for 80% of all rice producers (FAO, 2004). Less than 7% of the world's rice production is traded internationally (MacLean *et al*., 2002).

Most of the rice produced in the world is consumed as whole grain and the grain physical and chemical characteristics are therefore very important. There are different market classes of rice that are defined by a matrix of traits which include grain dimensions, grain chemistry, and grain appearance (Webb, 1991). Long Grain Rice has kernels which are 3 to 4 times longer than their width and relatively high amylose content (>20%) which causes the grains to remain separate after cooking. In the USA, certain long grain cultivars (e.g., Rexmont, Dixiebelle) with high amylose content (>24%) are recommended for canning purposes.

Cultivars grown in the world have variable cooking, sensory and processing qualities. Many chemists began to look into these cultivar differences in rice end-use in the twentieth century. The primary work on grain quality was conducted by Warth and Darabsett (1914) who studied the rice kernel response to dilute alkali. Some studies have already been conducted on the grain quality of O. *glaberrima* and NERICA genotypes. NERICA lines showed tremendous variability for cooking, sensorial and nutritional values. Results from the studies conducted by (Kishine *et al*. 2008) showed that NERICA genotypes with high amylose content (29%) inherited the gene from the *glaberrima* parents while the lower amylose content (22%) varieties received the gene from the sativa parents. Although rarely mentioned in Africa as a constraint, rice quality is considered the second most important problem after grain yield. Rice production in Africa is becoming more market-oriented where quality becomes a major issue, and quality is considered as an important character in the breeding program of Africa Rice Center. In some African countries, basic grain quality data are available in official documents (e.g. MINAGRA 1998).

The isolation procedure of starch from rice is different from that of corn, wheat, or potato, due to differences in protein properties. The majority of rice protein is alkali soluble; the alkaline steeping method is commonly used in separation of starch from rice (Resurreccion, Li, Okita, & Juliano, 1993).

Used molecular marker in the study for the tested genotypes, the molecular marker `technologies can assist conventional breeding efforts and are valuable tools for the analysis of genetic relatedness and identification and selection of desirable genotypes for crosses as well as for germplasm conservation in gene banks. Molecular markers, such as SSRs and RAPD have been widely used in rice germplasm evaluation. The use of molecular marker to interpret population structure provides much greater resolution than other types of markers because of high level of polymorphism at SSRs loci (Cho *et al*., 2000). Previous generations of molecular markers were unable to detect enough genetic polymorphism among closely related rice cultivars to make them efficient tools for interpreting population structure.

Objectives:

The specific objectives of the study are:

1-   To investigate genetic variability and characters association among different traits
2-   To estimate the heritability, correlation of grain yield and its components.
3-   To study genotypes x environment interactions
4-   To investigate rice quality parameters.
5-   To investigate Molecular characterization in Rice genotypes using Molecular markers (RAPD).

CHAPTER TWO

LITRITURE REVIEW

Rice (*Oryza sativa* L.) is the world leading cereal crop for human utilization, with cultivated area of almost 150 million ha and a total production of almost 600 million mega grams annually (Khush, 2005). Sub Saharan Africa produced about 21.6 million tons of rice in 2006 and accounted for 32% of rice import in the global international market to meet its demand (Africa Rice Center, 2008; FAO, 2005). This was the result of population growth (about 4% per annum) and the increased consumer preference in favor of rice in urban area (Africa Rice Center, 2008; Kijima *et al*., 2006; Atera *et al*., 2011). Rice yields have been increasing since the 1960's but since the 1990's growth in rice production has been slower than population growth (Mwaura, 2010).

Medium Grain Rice has kernels that are 2 to 2.9 times longer than their width and relatively low (16-18%) amylose content. Short Grain Rice has grain that is almost round with the kernels being 1.9 times longer than their width. (Kelly, 1985) reported that medium and short grains are used for products that are served cold. Glutinous Rice is also called Sweet or Waxy Rice and the kernels are completely opaque white. Aromatic Rice possesses a natural flavor that is similar to buttered popcorn in aroma. The most popular types of aromatic rice are Basmati from India and Pakistan and Jasmine from Thailand. The primary chemical components of the grain are starch, protein and lipids. According to Kelly (1985), these components determine how the rice whole grain, flour, or starch can be used. Milling yield of rice is considered to be the most important component of quality (Van Ruiten, 1985; Adair *et al*., 1973; Spadaro *et al*., 1980). In the USA, a one percent change in breakage can cause a $100,000 difference in profit for an average-sized rice mill (Hosney, 1998).

Grain yield in rice is an expression of different yield components under given environmental conditions. Therefore, yield stability is not function of the genotype alone, but on interaction of genotype with the particular environment. Varieties in a series of environments have stable average yield are known to have vast adaptability. However, varieties, which show high yielding genetic potential only in desirable conditions but poor yielding potential in un-desirable conditions known as varieties with finite adaptability (Lin and Bins, 1991).

Rice as an important source of food and cash income to both the urban and rural dwellers of the population is steadily on the increase. There are numerous and diverse factors that limit rice production which depends on the agroecologies. Basically, they can be classified as abiotic, which include physio-climatic conditions such as drought, flood, soil fertility, nutrient deficiencies and toxicities, erosion etc; and the biotic, which include weeds, diseases, insects and various vertebrate animal pests particularly birds and rodents. In general, yield losses due to insect pests are difficult to quantify due to field and environmental factors and the role of natural enemies of insect and pests, but not so common due to the availability and cost of machinery.

Rice cultivation ecology in Africa is highly diverse compared to the USA where irrigated rice is dominant. Cultivars in Africa also have a range of genetic variation. They comprise the two cultivated species - O. *sativa* L. and O. *glaberrima* Steud. - and their interspecific progenies called New Rice for Africa (NERICA), which have been developed by the Africa Rice Center and its partners. NERICA (New Rice for Africa) lines showed tremendous variability for cooking, sensorial and nutritional values. Results from the studies conducted by (Kishine *et al*. 2008) showed that NERICA varieties with high amylose content (29%) inherited the gene from the *glaberrima* parents while the lower amylose content (22%) varieties received the gene from the sativa parents. Watanabe *et al*. (2002) studied O.*glaberrima* lines, interspecific progenies and O. sativa lines and concluded that the progenies were superior to O. *glaberrima* parents based on the following traits: husking yield, milling yield, whiteness and translucency of milled rice. These selected references showed that germplasm from Africa needs to be further screened for different quality traits across different environments. Although rarely mentioned in Africa as a constraint, rice quality is considered the second most important problem after grain yield. Rice production in Africa is becoming more market-oriented where quality becomes a major issue, and quality is considered as an important character in the breeding program of Africa Rice Center. NERICA are high yielding rainfed rice varieties with early maturity and has shown high potential to revolutionize rice farming even in Africa's stress afflicted ecologies. Rice is particularly susceptible to water deficit at the reproductive stage (Pirdashti *et al*., 2004; Fukai and Lilley, 1994; Zeigler, 1994). However, NERICA varieties vary in their response to water deficit.

2.1 Rice production and Consumption:

Asia as a region produces around 90% of the world's rice. The top ten rice-producing countries in 2010, showing amount of paddy (unmilled) rice produced in metric tons areChina: 197,212,010; India: 120,620,000; Indonesia: 66,411,500 ;Bangladesh: 49,355,000; Vietnam: 39,988,900; Myanmar: 33,204,500; Thailand: 31,597,200; Philippines: 15,771,700; Brazil: 11,308,900; United States of America: 11,027,000 (www.irri.org). Asia as a region consumes around 90% of the world's rice. The top ten rice-consuming countries in 2007, showing the food supply of milled rice in metric tons are China: 102,640,324; India: 82,602,265; Indonesia: 28,146,034; Bangladesh: 25,196,763; Viet Nam: 14,255,523; Philippines: 11,470,307; Myanmar: 7,710,029; Japan: 7,214,929; Thailand: 6,904,528; Brazil: 6,318,838 (www.irri.org).

Average per person consumption of rice differs from country to country. The top ten consumers of rice on a per capita basis in 2007, showing average annual rice consumption (kilograms) per person are Brunei Darussalam: 245; Viet Nam: 166; Lao People's Democratic Republic: 163; Bangladesh: 160; Myanmar: 157; Cambodia: 152; Philippines: 129; Indonesia: 125; Thailand: 103; Madagascar: 102 (www.irri.org).

The top ten exporters of rice (milled) in 2009, showing the quantity exported in tons are Thailand: 6,902,450; Viet Nam: 3,411,040; Pakistan: 2,517,780; India: 2,131,270; United States of America: 1,705,590; Uruguay: 707,892; China: 622,161; Italy: 583,734; Egypt: 560,430 (www.irri.org).

The top ten importers of rice (milled) in 2009, showing the quantity imported in tons are Philippines: 1,752,450; Saudi Arabia: 1,258,730; Malaysia: 1,055,680; Côte d'Ivoire: 865,334; Iran (Islamic Republic of): 780,147; Iraq: 755,803; United Arab Emirates: 731,315; South Africa: 730,357; United States of America: 539,069; Cameroon: 463,406 (www.irri.org)

2.2 Genetic Variability and interrelationship among the different traits in Rice:

Genetic variability for agronomic traits is the key component of breeding programs for broadening the gene pool of rice and would require reliable estimates of heritability in order to plan an efficient breeding program (Akinwale

et al., 2011). Yield component breeding to increase grain yield would be most effective, if the components involved are highly heritable and genetically independent or positively correlated with grain yield. However, it is very difficult to judge whether observed variability is highly heritable or not. Moreover, knowledge of heritability is essential for selection based improvement as it indicates the extent of transmissibility of a character into future generations (Sabesan *et al*., 2009). The process of breeding is primarily conditioned by the magnitude and nature of interactions of genotypic and environmental variations in plant characters. It becomes necessary to partition the observed variability into its heritable and non-heritable components and to have an understanding of parameters such as genotypic coefficient of variation, heritability and genetic advance. The utilization of heritability and genetic advance of yield traits and inferences from significant genotypic correlation between yield and its components should permit selection of predictable rice genotypes for upland ecosystem.

Rice is highly polymorphic with wide geographical and genetic differentiation (Sarla *et al*., 2005). Rice landraces, maintained through traditional farming practices, possess high genetic diversity and specific traits such as disease resistance, environmental constraint, tolerance and nutritional quality which are often used in crop improvement (Camacho-Villa *et al*., 2005). Furthermore, landraces are adapted to local agro-environmental conditions which contribute to yield stability and hence, they continue playing an important role in traditional and subsistence farming (Camacho-Villa *et al*., 2005). However, extensive efforts to improve rice productivity have led to large-scale cultivation of high yielding genetically uniform varieties, the replacement of local cultivars and the concomitant decrease in rice genetic resources that created a widespread concern to promote conservation of traditional cultivars/landraces (Camacho-Villa *et al*., 2005; Barry *et al*., 2007).

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

unforeseen biotic or abiotic stress of one cultivar recommended for a wide range of environments (Annicchiarico, 2002). Ashraf *et al* (2001) reported that the adaptability of a variety over a diverse environment is usually tested by the degree of its interaction with different environments under which it is planted.

The study of the G X E interaction allows the classification of genotypes by their behaviors in two different situations, either stable or adapted to a particular environment in terms of their yield or in some other interesting agronomic feature. Generally, the term stability refers to the ability of the genotypes to be consistent, both with high or low yield levels in various environments. On the other hand, adaptability refers to the adjustment of an organism to its environment, e.g., a genotype that produces high yields in specific environmental conditions and poor yields in another environment (Balzarini *et al.,* 2005).

There are many statistical methods available to analyze the G X E interaction: for example, combined ANOVA, stability analysis and multivariate methods. Combined ANOVA is more often used to identify the existence of G X E interactions in multi-environmental experiments. However, the main limitation of this analysis is the assumption of homogeneity of variance among environments required to determine genotype differences. Although this analysis allows the determination of the components of variance arising from different factors (genotype, environment and the genotype x environment interaction), it does not allow to explore the response of the genotypes in the non-additive term: the genotype x season interaction (Zobel *et al.*, 1988; Gauch, 1992).

Association of plant characters, which is now statistically determined by correlation coefficients, has always been helpful as a basis for selection of desired entries. The Measurement of the genotypic correlations, not only between the traits under selection but between others as well, is a matter of considerable importance in selection practice, since they also permit the prediction of correlated responses. Phenotypic and genotypic correlation among characters give an indication of the use full characters which may be used as indicators in selection for other traits, Johnson., *et al* (1955) attributed the association among characters to linkage, while Adams (1967) reported that it was due to developmentally induced relationship among component that were only indirectly the consequence of gene action. Correlations among traits could

be utilized to enhance the rate of selection response in the primary traits (Moll and Stuber, 1974).

Abraham *et al* (1998) found that genotypic correlation coefficient were slightly higher than the association with days to 50% flowering, productive tillers/ plant, days to maturity and 1000 – grain weight. The positive genetic association of grain yield with flowering and maturity dates indicates limitation in development of early maturity types and high grain yield. Atif *et al* (2012) observed positive phenotypic and genotypic correlation coefficient between grain yield and number of filled grain/panicle, harvest index, panicle length, and number of grain/panicle. Sedghi (2011) observed positive significant association of grain yield with grain/panicle, days to maturity, number of productive tillers and days to flowering, Ullah *et al*. (2011) detected that grain yield was positive and significantly associated with panicle length, and grain/panicle. Hairmansis *et al* (2010) also recorded a positive and significant association of grain yield with filled grain/panicle, spikelets per panicle and spikelet fertility.

2.3 Rice in Sudan:

In the Sudan rice has been grown since 1905, but on a very limited acreage and information about methods of reproduction is lacking (Farah, 1981). Sudan produce an average of 3947 kg/ha (AOAD, 2008). Swamp and upland varieties were first tried as the Gezira research farm in 1951. Later extensive rice trials were carried out at Malakal and several varieties were selected at the Gezera Research Station although rice cultivation in the Sudan was known for something especially in south Sudan and White Nile area. Large scale production starts only in the years 1950 in the Upper Nile Province (Malakal) and in 1960 in Aweel. But for security reasons production was abandoned. Rice production was stated once again along the White Nile at Gassaba (A work *et al*, 1996).

Mister Assoumou Ndzaki the director of JICA organization in Sudan (2011) assured that Sudan has now reached an advanced stage in rice cultivation, which aims and including 5 states to produce Aerobic rice, and there is a desire by farmers to cultivate it in Sudan. He also stated that the Federal Ministry of Agriculture has been trying in five years to improve rice research in Rahad area village (44) Al hudiba proved success in rice cultivation, especially after the production of about 3 tons. Assoumou added that rice cultivation is a strategic partnership between the farmers and the Ministry of Agriculture, which

developed rice unit. In addition to increasing worker of agricultural, he indicated the obstacles facing rice cultivation, but he encourage farmer to exert efforts. Mr Roshi Hori the Japanese Ambassador indicated that the five states which adopt rice cultivation can make Sudan one of the global competitors of the rice production, the global production is about 19 billion tons, from which China consumes a big amounts, in addition to Saudi Arabia, Iraq and Emirates markets, in case of developing rice cultivation in Sudan it can be exported to Ethiopia and the State of South Sudan. There are efforts by Japanese government to give contribution to five states of (Gedaref, Gezira, Sennar, White Nile, River Nile, and Northern State) (www.akhirlahza.info, 2011).

2.4 Phenotypic (δp), Genotypic (δg) Variation, Heritability (h^2), Genotypic (GCV), Phenotypic (PCV) Coefficients of Variation and Genetic Advance (GA):

The development of high yielding cultivars with wide adaptability is the ultimate aim of plant breeders. Therefore, by exploiting the good adaptation and stability of yield and its component in rice genotype, it would be possible to develop/identify high yielding and well adapted varieties (Ogunbayo, 2011). Thus effective yield component breeding to increase grain yield could be achieved, if the component traits are highly heritable and positive correlated with grain yield (Sabesan *et al* 2009; Ullah *et al*. 2011). The knowledge of genetic variability present in a given crop species for the character under improvement is of paramount importance for the success of any plant breeding program, heritability and genetic advance (GA) are important selection parameters.

Success of breeders in changing the characteristics of a population depends on the degree of correspondence between phenotypic and genotypic values (Dabholkar, 1992 and Singh and Ceccarelli, 1995). In crop improvement, only the genetic component of variation is important since only this component is transmitted to the next generation. A quantitative measure, which provides information about the correspondence between genotypic and phenotypic variance is heritability (Dabholkar, 1992).

Heritability estimated along with (GA) is normally more helpful in predicting the grain under selection than heritability estimated alone. Therefore, the estimation of heritability for any traits requires the partitioning of the observed variation between genetic effects and environmental effects

(Cockerham, 1963). However when the phenotypic variability is large, traits with high heritability value are subject to large genetic grains per generation when selection I applied (Dudely and Moll, 1969; Hesse, 1975; Falconer, 1989; Nyqist, 1991).

2.5 Quality of rice genotypes:

The important factors in assessing the rice quality in amylases content is the determination of the water use pattern and maintenance of the quality of this crop (Pantuwan, 2001; Pantuwan *et al*., 2002; Yamauchi and Winn, 1996).

Rice quality studies showed that changing amount of amylases induced differences in rice grain quality (Juliano, 1982; Krishnasamy and Seshu, 1989; Olivem *et al*., 1957; Williams *et al*., 1958). These differences are very important in baking quality and consumers taste (Sanjiva *et al*., 1953; Virginia, 1958). All rice cultivars divided to Vaxi (0% amylases) and non-Vaxi (including little amylases 10 to 20, 20 to 25 and rich amylases 25 to 33%, respectively) groups (Juliano, 1970; Singh *et al*., 2000; Olivem *et al*., 1957). Meal amylases of rice are commercially more desirable than others due to swelling after baking; this kind also remains soft for a long time after baking and is found with less mucilage (Juliano, 1982).

Most of the rice produced in the world is consumed as whole grain and the grain physical and chemical characteristics are therefore very important. There are different market classes of rice that are defined by a matrix of traits which include grain dimensions, grain chemistry, and grain appearance (Webb, 1991). Long Grain Rice has kernels which are 3 to 4 times longer than their width and relatively high amylose content (>20%) which causes the grains to remain separate after cooking. In the USA, certain long grain cultivars (e.g.,Rexmont, Dixiebelle) with high amylose content (>24%) are recommended for canning purposes. Medium Grain Rice has kernels that are 2 to 2.9 times longer than their 436 Int. Res. J. Agric. Sci. Soil Sci. width and relatively low (16-18%) amylose content. Short Grain Rice has grain that is almost round with the kernels being 1.9 times longer than their width. (Kelly, 1985) reported that medium and short grains are used for products that are served cold.

Rice protein fractions are allergenic: glutelin, and globulin (Shibasaki *et al*., 1979). These are easily extracted from rice grain endosperm using low

concentrations of NaCl (Matsuda *et al*., 1988). In another study, rice grains pressurized at 100-400 MPa in distilled water released 0.2-2.5 mg per gram of proteins, which included globulins (Kato *et al*., 2000).

2.6 Molecular Characterization:

Molecular markers are a powerful complement to help define heterotic groups and to examine the relationships among inbred lines at the DNA level (Smith *et al*., 1997; Senior *et al*., 1998; Melchinger, 1999). And it's not influenced by environmental factors and are also fast, efficient and more sensitive than field testing to detect large numbers of distinct differences between genotypes at DNA level (Smith and Smith, 1992; Westmann and Kresovich, 1997 and Melchinger, 1999). Molecular markers have proven to be powerful tools in the assessment of genetic variation and in the elucidation of genetic relationship within and among species, follow the inheritance of important agronomic traits (Peleman and Van der Voort, 2003), and providing a more direct, reliable and efficient tool for germplasm characterization, conservation and management. Several types of molecular markers are available, including those based on restriction fragment length polymorphism (RFLP), random amplified polymorphic DNA (RAPD) (Welsh and Mc Clelland, 1990; Williams *et al*., 1990), amplified fragment length polymorphism (AFLP) (Vos *et al*., 1995), and simple-sequence repeats (SSRs) or micro satellite markers (Tautz, 1989).

Genetic diversity has been estimated on the basis of the morphological and physiological markers. Molecular markers offer additional advantages such as high polymorphism and independence from effects related to environmental conditions and the physiological stage of plant. Molecular characterization can be assessed again after several years of maintenance and new accessions can be related to existing collections which provides useful information for different breeding programmes (Bolaric *et al*., 2005). In addition, molecular markers provide information on possible genetic mechanisms for observed evolutionary patterns (Bautista *et al*., 2001). Molecular markers differ in efficiency, complexity and cost effectiveness (Yang *et al*., 1996; Pejic *et al*., 1998). PCR-based markers (RAPD, AFLP, SSR and SNP) are designed to amplify fragments that contain a micro satellite using primers complementary to unique sequences surrounding the repeat motif (Weber and May, 1989).

DNA markers have the potential to enhance the operation of a plant breeding program through a number of ways, ranging from finger printing of elite genetic stocks, assessment of genetic diversity, increasing the efficiency of selection for difficult traits. However, their greatest potential appears to be in accelerating the rate of gain from selection for desirable genotypes and in the manipulation of quantitative trait loci (QTLs) that condition complex economic traits. DNA markers also permit plant breeders to correctly map or place the various interacting genes that condition complex agronomic traits (Ejeta *et al*., 1999). Among the DNA markers, Random Amplified Polymorphic DNA Markers (RAPD) are commonly used because they are quick and simple to obtain, enabling genetic diversity analysis in several types of plant material, such as natural population, population in breeding programs and germpasm collection (Ferreira and Grattapaglia, 1996) RAPD markers provide an efficient assay for polymorphism which allows rapid identification and isolation of chromosome-specific DNA fragments. Genetic polymorphism detected with RAPD reveals one allele per locus, which corresponds to the amplification product In particular, RAPD is a useful predictive tool to identify areas of maximum diversity and may be used to estimate levels of genetic variability in natural population. Generally, it is concluded that genetic distance estimate is more efficient for the prediction of hybrid performance between closely related inbred lines than in crosses between distantly related inbred lines (Melchinger, 1999). Molecular markers are a powerful tool to delimit heterotic groups and to assign inbred lines into existing heterotic groups (Melchinger, 1999 and Menkir *et al*., 2004). Molecular markers can usually be identified from any plant tissue, even from young seedlings or kernels, while morphological markers frequently require the observation of whole mature plants. Selection can, therefore, occur earlier in the plant's cycle when using molecular markers than when using morphological markers (Ragot and Lee, 2007). Molecular markers are more powerful in assessing genetic diversity in comparison with the morphological data, pedigree data, heterosis data, and biochemical data, because these markers reveal differences at the level of DNA (Melchinger, 1999).

CHAPTER THREE
MATERIALS AND METHODS

3.1 Locations

A field experiments were conducted in Sudan in two locations. The first one was the college of Agricultural Studies, Sudan University of Science and Technology (Shambat) its located at longitude 32˚-35˚E, latitude 15˚-40˚N, and 280m above sea level. The climate of the locality is semi arid, with low relative humidity, the temperature varies between 45˚C maximum and 21˚C in summer (Adam, 2002). The experiment was conducted for two growing seasons in the period from July 2011 to January 2012, and July to November of 2013,The soil of the experimental site (shambat) is described as loam clay. Its characterized by a deep cracking moderately alkaline with low permeability low nitrogen content, ph of 7.5-8 and a high exchange able sodium percentage (ESP) (Abdelhafiz, 2001). The second one at Faculty of Agriculture and Natural Resources University of Bakht AL ruda, ED duim. (long. 32˚20′E), lat. 13˚ 39′ N and 380 msl. It has a dry saline cracking soil, pH of 8.3, during the growing season of 2012.

3.2 Plant Material:

The plant material used in this study includes 18 rice genotypes; 7 NERICA genotypes from West African Rice Development Association, Benin (WARDA) Named as (NERICA4, NERICA2, NERICA15, NERICA5, NERICA17, NERICA14 and NERICA12), 5YUNLU genotypes from China, named as (YUNLU22, YUNLU33, YUNLU30, YUNLU24 and YUNLU26), 3 genotypes from International Rice Research Institute (IRRI), Philippines, named as ((WAB12 (WAB 891SG12), WAB19(WAB-1-38-19-14-p2-HB) and WAB8 (WAB880-1-38-19-8)) and 3 other Chinese genotypes named as (HANDAO221, HANDAO502 and ZHONGHAN-3). The material was provided by the Laboratory of Agronomy Department, College of Agriculturai Studies, Sudan University of Science of Science and Technology, Sudan and from Agricultural Research Corporation (ARC), Wad-Madni, Sudan.

3. 3 Experimental Procedures:

3.3.1 Land preparation:

In Shambat location the land was deep ploughed, harrowed tow times and

leveled to prepare the experimental areas for the all seasons, then it divided to 54 plots for three replications, the plot size was 2×3 meters,

3.3.2 Sowing procedure:

Seeds were sown manually by in a hole, each hole was consisted of 3-4 seeds in depth of 3-4 cm, and then thinned to 2 plants per hole after two weeks from sowing the spacing between holes were 25cm.

3.3.3 Fertilization:

The phosphorous was applied in form of triple super phosphate (P_2O_5) as a basal dose in rate of 50kg/fed at the same day of sowing for both of the experiments, the Nitrogen in form of Urea (46% N) was applied in two equal split doses, in rate of 80kg/fed, the first one 40kg/fed after one month from sowing date, the second one after two months from sowing in the same rate.

3.3.4 Irrigation:

The land was irrigated tow times a week.

3.3.5 Weeding:

Weeding controlled manually every two weeks to avoiding the competition of weeds

3.4 Data collection and analysis

3.4.1 Parameters measured

Five plant were selected randomly for each plot and then took the average for following parameters

1- Plant height (cm): was measured for the main stem from the surface of the ground to the top of the panicle at maturity stage.
2- Number of leaves/plant: was counted for the five plants and the average was determined.
3- Number of Tillers/plant: counted for the tillers of five plants and the average were determined.

4- Stem diameter (cm): was determined at maturity on the stalk at 10cm above the ground level by the threat.

5- Leaf area (cm^2): three leaves of five plant in each plot was measured and calculate according to the following formula

Leaf area =Maximum Length ×Maximum Width × 0.75

6- Days to 50% flowering: Estimated as number of days from sowing to time when 50% of the plants/plot start to flower

7- Days to 50% maturity: Days from sowing to time when 50% of the panicles reached full maturity (panicles color turned to yellow).

8- Number of panicles/ m^2: Counted for one m^2/plot

9- Panicle length (cm): Average length of 10 panicles for five plants.

10- Number of grains/ panicle: The total number of filled and unfilled grains/panicle.

11- Number of filled grains/panicle: Filled grain from each panicle were counted and recorded as an average.

12- Percentage of unfilled grains/panicle:

$$\frac{\text{Number of unfilled grains/panicle}}{\text{Total number of Grain/Panicle}} X100$$

13- 100-grains weight (HGW) (g): Determined by weighing 100 grains samples taken at random from the bulk of grains from five plants harvested in each plot.

14- Grain yield (GY) (t/ha): Measured from the harvested area of one m^2 for each plot and converted to t/ha. Grain yield Ton/ha was determined as the following formula:

Grain yield Ton/ha =

$$\frac{\text{Grain weight/plot X 10000}}{\text{plot area}}$$

3.4.2 Statistical analysis:

The collected data for growth and yield was subjected to analysis of variances for a Randomized Complete Plock Design (RCBD) Individual analysis of variance was carried out for all studied characters in each season separately, Combined analysis of variance was done for all traits, by using MSTAT-C computer programme. The means were separated using the least significant difference (LSD) at 5% level of significance according to the formula:

$$L.S.D = \sqrt{\frac{2 \times \text{Error Mean square}}{r}} \times t$$

Where:

r= number of replications

t =level of significance for t-value at 0.05

3.4.3 Phenotypic (σ²ph) and genotypic (σ²g) variances:

The estimates of phenotypic (σ²ph) and genotypic (σ²g) variances were worked out according to the method suggested by Johnson *et al.* (1955) using mean square values from the individual and combined ANOVA tables as the following formula:

a. For the individual analysis of variance, they were estimated as follows:

$$\sigma^2 g = (M2 - M1) / r$$

$$\sigma^2 ph = \sigma^2 g + \sigma^2 e$$

Where:

r = number of replications.

σ²e = error or environmental variance.

M1, M2 = error and genotype mean squares.

b. For combined analysis of variance, they were estimated as follows

Genotypic variance $(\sigma^2g) = (M2-M1)/rS$

Phenotypic variance $(\sigma^2ph) = \sigma^2g + \sigma^2gS + \sigma^2e$

Where:

g = number of genotypes

S and r = number of seasons and replications, respectively.

σ^2e = error of environmental variance.

M1= expected mean squares of pooled error

M2= expected mean squares of genotypes x seasons interaction.

Phenotypic (PCV) and genotypic (GCV) coefficients of variation (individually and combined) were calculated based on the method advocated by Burton (1952) as the following formula:

Phenotypic coefficient of variation (PCV) = $\underline{\sqrt{\sigma^2Ph} \times 100}$

Grand mean

Genotypic coefficient of variation (GCV) = $\underline{\sqrt{\sigma^2g} \times 100\%}$

Grand mean

3.5 Quality of rice: the quality was determined on the laboratory of the food research center (Shambat) 2013.

3.5.1 Physico-chemical analysis:

Physico-chemical analyses were carried out according to methods described in AACC (2000). The moisture content at 105°C/12h, Crude protein was determined by the Kjeldhal's method (N × 5.95), as well as ash content at 550°C/5h. Crude fat in oxhlet apparatus (solvent in above reference).

Available carbohydrate was calculated by subtracting the sum of fat, protein, fiber and ash as a percentage from 100 as described by West *et al* (1988).

3.5.2 Mineral profile:

The mineral content included Ca, P, Zn, Mn and Cu the samples were extracted and determined by atomic absorption spectrophotometer (model: Instrument shimadzu – AA – 6800) according to method given in AOAC (2000)

3.5.3 Granules size:

The granules size of rice seeds were recorded using vernier calipers (model: E H B Stainless, Hardenend, Germany).

3.6 Molecular assessment of genetic diversity:

The experiment was conducted in the college of science, University of Khartoum

3.6.1 Plant material:

18 genotypes of rice were used in the investigation, Seeds of all genotypes were sown separately in pots and leaf samples pooled from all plants of each genotype then collected into label bags and used for genomic DNA isolation.

3.6.2 DNA Extraction Protocol (Sap Extarction Method):

Leaves tissues were Harvested (2 weeks old) in zip loc bags in a cooler with ice, then warmed the Extraction buffer at 65ºC water bath. 50 mM Tris, pH 8.0. 25 mM EDTA, 1 M NaCl, 1% CTAB, then added 5µl of Mercaptoethanol per 5ml warm extraction buffer, then placed the leaf tissues (1-5 leaves) in a 15ml centrifuge tube, added the extraction buffer (a total of 5ml) then mix in a blender, the buffer is mixed effectively with the pressed tissue sample. the sap extraction was Collected, after done with leaf samples of one genotype, the blender was cleaned with de-ionized tap water and wipe well with the paper towels.and then Placed the tubes containing extracts in a water bath set at 60ºC for 1 hr. the tubes was inverted gently to mix the extract for every 20mins during this incubation time.

The tubes were removed from the water bath and let it cool down for 5-10 mins (cool to at least 30ºC). Cooling can be hastened by placing the tubes in

room temp, and then the equal volume (5ml) of freshly prepared Chloroform/Isoamyl alcohol (24:1) was added. The tubes were inverted gently for several times and then let it set for at least 30 min. (or gently mix by inversion for 5-10 min.) and spin in a table top centrifuge at 6000 rpm for 10 min. (at room temp. or 4ºC). Then the upper supernatant was collected in a new 15ml tubes using P5000 pipette and 5ml tips (with wide-cut tip), and very gently added 2/3 volume (about 3ml) of cold isopropanol (2-propanol), and slowly tilt and invert the tubes so that DNA will precipitate, and Let it to set for at least 30 min. If DNA precipitation is big, no need to wait for 30 min. (OR Overnight is better) and spin for 10 min. at 4000 rpm (14,000 if micro), the supernatant was discarded carefully, don't let drain the DNA pellets,

The DNA was washed pellets with cold 70% ethyl alcohol (2-3ml) and spin for 1-2 min. at slow speed (2000 rpm). Supernatant was Discarded, the pellets was wash again with 70% ethyl alcohol, spin for 30 sec. at low speed and air dried the pellets briefly by inverting the tubes for 5 min. 1 ml of TE buffer (10 mM Tris + 1 mM EDTA, pH 8.0) was added and slowly stirred the DNA until it dissolve (incubation at 65ºC oven for 5 min. enhance dissolving) or (can be left overnight at 4ºC), and then added 5µl of RNase A (10mg/ml). Incubate at 37ºC water bath for 30-60 min. (or leave it overnight at room temp.) (OR @ 37ºC incubator for 1 hr). 1/10 volume (200µl) of 8M ammonium acetate & 2 volumes (2ml) of cold ethanol (95-100%) was added (you can mix the NH4.Acet+Ethol before use and put in the fridge). Mix by gentle inversion to precipitate the DNA, and let it set for at least 30 min. (OR overnight is better). Spin at 2000 rpm for 8-10 min.

The supernatant was discarded carefully and air-dried the pellets by inverting the tubes in a clean paper towel, and then 500µl was added (depending on the size of the pellet) of TE buffer (pH 7.5). Keep it in 4ºC overnight or at 65ºC for 5min. DNA was Transfered to the 1.5ml eppendorf tubes for long term storage, Quantified the DNA on spectrophotometer or fluorometer or using mass ladder, and finally the working stock was Prepared at a conc. of 10ng/ml of DNA in sterile H_2O.

3.6.3 RAPD analysis and primer selection:

Several primers were screened using a few DNA samples to select the appropriate primers suitable for study of rice genome. Eventually, ten primers

that produced strongly amplified polymorphic bands with these test templates were selected for RAPD-PCR analysis. The PCR reaction was conducted in 50 ml reaction volume 2 containing 1x PCR buffer, 1.5 mM MgCl , 0.2 mM of each dNTPs, 1 mM of forward and reverse primers, 1 U Taq DNA (promega) polymerase and 10 ng genomic DNA. Hot start and touchdown PCR temperature profile was used as follows: an initial denaturizing step at 94°C for 5 min, followed by 10 cycles of touchdown annealing temperature 60 to 50°C for 60 second in which the annealing temperature was decreased by 1°C every cycle. Another 30 cycles were starting then a final extension step at 72°C for 7 min was performed. The PCR product were mixed with 2.5 μl of 10 X loading dye (0.25% bromophenol blue, 0.25% xylene cyanol and 40% sucrose, w/v) and spun briefly in a microfuge before loading. The PCR products and 1 kp DNA ladder were electrophoresed 2% agarose gel at 100 volts followed by staining with ethidium bromide and photographed on polaroid 667 film under ultra-violet light.

3.6.4 Data Analysis:

For each primer, the number of polymorphic and monomorphic bands was determined. Bands clearly visible in at least one genotype were scored (1) for present, and (0) for absent and entered into a data matrix. Fragment size was estimated by interpolation from the migration distance of marker fragments. Percentage of polymorphism was calculated as the proportion of polymorphic bands over the total number of bands. The genetic dissimilarity (D) matrix among genotypes was estimated according to (Nei and Lei, 1979). The similarity coefficient was used to construct a dendrogram by the un-weighted pair group method with arithmetic averages (UPGMA) according to Rohlf (1993).

CHAPTER FOUR

RESULTS

4.1 Growth characters:

4.1.1 Plant height (cm):

Individual analysis of variance (ANOVA) indicated highly significant differences among tested genotypes in all seasons (2011-2012-2013), table (1, 2 and 3). Combine analysis showed highly significant different for season, genotypes, and season X genotypes, Table (4). Season 2011, Y26 and Y33 were the longest genotypes (80.70, 79.89 cm) respectively, followed by Y30, Y24, N12 and N15 (75.06, 74.85, 73.36, 71.83 cm) respectively, while N5 and Z3 were the shortest genotypes (52.43, 50.95 cm) respectively, Table (5). In season 2012, Z3 was the longest one (104.30 cm) followed by Y26, N15 (99.00 cm), while W19 and H221 were the shortest genotypes (73.67 and 71.00 cm) respectively, Table (5). Y26 and Y30 were the longest genotypes in season 2013 (80.97 and 78.13 cm) followed by Z3 (74.68 cm), N5 (74.56 cm), Y22 (71.99 cm), W19 (71.99 cm) and N15 (71.70 cm), while N12 was the shortest one (47.05 cm), Table (5). Over three seasons,Y26 was the longest plant (86.89 cm) followed by N15 (80.84 cm) while H502 and W19 were the shortest genotypes (64.32 – 63.36 cm) respectively, Table (5).

4.1.2 Number of leaves/plant:

Data for number of leaves/plant was not available data in season 2012. significant difference in season 2011 and non significant difference in season 2013 Table (1, 3). In combine analysis of variance recorded highly significant difference for season, genotypes, and season X genotypes, Appendix (1). In season 2011, H221 gave the highest number of leaves/plant (4.13), followed by N14 (3.73), while N17 and W19 gave the lowest number of leaves/plant (2.90 - 2.87) respectively, Table (6) In season 2013 the genotypes Y26 and N14 had the highest number of leaves (3.80- 3.73) respectively. The lowest number of leaves/plant were given by the genotypes H221 and Y30 (2.93), W12 and N5 (2.87) and Y22 (2.80), Table (6). Across season N14 (3.73) and Y26 (3.63) gave

the highest number of leaves, while H502 gave the lowest number of leaves (2.92), appendix (1).

Table (1): Mean Squares of growth traits of 18 rice genotypes evaluated at Shambat during the season 2011

Source	D.F	F. Value 2011						
		Plant height (cm)	Number of leaves /plant	Number of tillers/ plant	Stem diamet-er (cm)	Leaf Area (cm^2)	Days to 50% flowering	Days to 50% maturity
Repli-cation	2	7.0909	3.2639	1.7355	0.1903	12.2052	0.0350	1.8956
Genot-ypes	17	2.8065**	2.3337*	6.364**	1.531^{NS}	2.3997*	3.0037**	11.6207**
Error	34	-	_	_	_	_	_	_
Total	53	-	_	_	_	_	_	_
EMS	_	102.646	0.116	0.457	0.422	21.055	40.231	27.784
C.V%	_	15.82	10.36	7.15	17.71	20.48	8.34	4.82
SE±	_	2.3880	0.0803	0.1593	0.1531	1.0815	1.4950	1.2424

*=significance   **= high significant   ns =not significant

Table (2): Mean Squares of growth traits of 18 rice genotypes evaluated at Ed duaim during the season (2012)

Source	D.F	F. Value 2012			
		Plant height (cm)	Number of tillers/ plant	Days to 50% flowering	Days to 50% maturity
Replication	2	2.9687	2.7365	7.8938	2.4056
genotypes	17	3.1855**	3.0871**	10.3410**	3.6805**
Error	34	_	_	_	_
Total	53	_	_	_	_
EMS	_	81.144	1.976	5.865	25.989
C.V%	_	10.63	12.87	3.13	5.09
SE±	_	2.1232	0.3313	0.5708	1.2016

*=significance   **= high significant   ns =not significant

Table (3): Mean Squares of growth traits of 18 rice genotypes evaluated at Shambat during season (2013)

Source	D.F	F. Value 2013						
		Plant height (cm)	Number of leaves /plant	Number of tillers/ plant	Stem diameter (cm)	Leaf Area (cm^2)	Days to 50% flowering	Days to 50% maturity
Repli-cation	2	2.4276	5.4699	2.1799	0.4496	0.9199	3.7355	0.0531
Geno-types	17	3.8004**	1.3982ns	1.4240ns	1.4016ns	1.9363*	43.8959**	10.6982**
Error	34	–	–	–	–	–	–	–
Total	53	–	–	–	–	–	–	–
EMS	–	60.550	0.176	1.034	0.093	37.02	9.404	2.443
C.V%	–	11.66	13.16	12.69	14.89	22.72	3.92	1.32
SE±	–	1.8341	0.0988	0.5126	0.0720	1.4330	0.7228	0.3684

*=significance   **= high significant   ns =not significant

Table (4): Mean Squares of combine analysis foe growth traits of 18 rice genotypes evaluated at Shambat and Ed duaim during seasons (2011, 2012, and 2013)

Source	D.F	F. Value			
		Plant height (cm)	Number of tiller/ plant	Days to 50% flowering	Days to 50% maturity
Season	2	18.6105^{**}	47.1137^{**}	1.0464^{ns}	133.936^{**}
Error A	6	-	-	-	-
Genotype	17	4.2308^{**}	6.4116^{**}	11.120^{**}	15.974^{**}
season x genotype	34	2.6881^{**}	4.5965^{**}	1.7122^{*}	5.8027^{**}
Total	161	-	-	-	-
EMS	-	82.035	1.157	18.302	16.909
C.V %	-	12.62	11.36	5.58	3.76
SE ±	-	2.6208	0.2117	0.6877	0.7947

*=significance   **= high significant   ns =not significant

Table (5): Mean of plant height (cm) of the 18 rice genotypes evaluated at Shambat and Ed duaim in seasons (2011-2012-2013)

Genotypes	2011	2012	2013	Combine
WAB12	56.93 FG	80.67EFG	52.49H	63.36E
NERICA2	56.76 FG	86.33D	61.91F	68.34D
YUNLU26	80.70 A	99.00B	80.97A	86.89A
WAB19	63.95 CD	73.67H	71.98B	69.87D
ZHONGHAN3	50.95 H	104.33A	74.68B	76.66C
HANDAO221	67.56 C	71.00H	68.45C	69.00D
NERICA 15	71.83 B	99.00B	71.70B	80.84B
YUNLU22	61.76 DE	93.33C	74.16B	76.42C
HANDAO502	54.65 FGH	78.67FG	62.63EF	64.32E
YUNLU33	79.88 A	80.67EFG	65.07DE	75.21C
WAB8	63.70 CD	84.00DE	58.29G	68.66D
NERICA17	53.26 GH	86.67D	64.47EF	68.13D
NERICA5	52.43 H	79.67FG	74.56B	68.89D
NERICA14	57.06 FG	81.67EF	67.94CD	68.89D
YUNLU30	75.06 B	77.33G	78.13A	76.84C
YUNLU24	74.85 B	91.67C	62.29EF	76.27C
NERICA12	73.36 B	79.00FG	47.05I	66.47DE
NERICA4	57.89 EF	78.33FG	64.21EF	66.81DE
Mean	64.03	84.72	66.72	71.76
C.V%	15.82	10.63	11.66	12.62
L.S.D	3.962	3.523	3.043	3.457

Means with the same letter for each parameter are not significant at 5% level (LSD)

Table (6): **Mean of number of leaves/plant of the 18 rice genotypes evaluated at Shambat in seasons (2011-2013)**

Genotypes	2011	2013	Combine
WAB12	3.13EF	2.87FG	3.00IJK
NERICA2	3.20E	3.33BC	3.27EF
YUNLU26	3.47C	3.80A	3.63AB
WAB19	2.87G	3.33BC	3.10GHIJ
ZHONGHAN3	3.20E	3.40B	3.30DE
HANDAO221	4.13A	2.93FG	3.53BC
NERICA 15	3.37CD	3.00EF	3.18EFGH
YUNLU22	3.13EF	2.80G	2.96JK
HANDAO502	3.10EF	3.33BC	2.91K
YUNLU33	3.47C	3.40B	3.43CD
WAB8	3.07F	3.20CD	3.13FGHI
NERICA17	2.90G	3.13DE	3.01IJK
NERICA5	3.40CD	2.87FG	3.13FGHI
NERICA14	3.73B	3.73A	3.73A
YUNLU30	3.13EF	2.93FG	3.03HIJK
YUNLU24	3.13EF	3.13DE	3.13FGHI
NERICA12	3.40CD	3.00EF	3.20EFG
NERICA4	3.33D	3.13DE	3.23EFG
Mean	3.28	3.18	3.21
C.V%	10.36	13.16	12.93
L.S.D	0.1332	0.1641	0.159

Means with the same letter for each parameter are not significant at 5% level (LSD)

4.1.3 Number of tillers/plant:

Analysis of variance for individual seasons revealed highly significant difference among genotypes (1, 2, 3). In over season there was highly significant difference for season, genotype, and season X genotype, Table (4). In season 2011 the genotype N15 gave the highest number of tillers/plant (10.73) followed by N14 (10.67). Z3 gave the lowest number of tillers/plant (7.47), Table (7). In season 2012, H221 gave the highest number of tillers/plant (13.67) followed by W12 and Y26 (12.67). The lowest number of tillers/plant was given by N17 (9.33) followed by N14, Y30, N4, W19, N15 (9.00) Table (7). In season 2013 highest number of tillers/plant was given by the genotype Y22 (11.50) followed by H221 (10.40). N2 gave the lowest number of tillers/plant (5.13), Table (7). H221 gave the highest number of tillers/plant in combine analysis (11.49), while N4 gave the lowest number of tillers/plant (7.844), Table (7).

4.1.4. Stem diameter (cm):

Data for stem diameter was not available data in season 2012. Mean square revealed not significant among tested genotypes in seasons 2011 and 2013 table (1,3). While combine analysis showed highly significant different for season and not significant in genotypes and a significant different for season X genotype, Appendix (1). Y33 gave the highest diameter in separate analysis of 2011 (4.92 cm) then N12 (4.34 cm), while Y24, Y22, N2 and H502 gave the lowest diameter (3.32, 3.26, 3.09 and 3.08 cm) respectively, Table (8). In 2013, Y30 gave the highest measure of stem diameter (2.55 cm), while N12 and W8 gave the lowest measure (1.61 – 1.58 cm) respectively, Table (8). in combine analysis ,Y33 gave the highest measure of stem diameter (3.44 cm) , N2 and Y22 gave the lowest diameter (2.55, 2.54 cm) respectively, Table (8).

Table (7) Mean number of tillers/plant of the 18 rice genotypes evaluated at Shambat and Ed duaim during the seasons (2011-2012-2013)

Genotypes	2011	2012	2013	Combine
WAB12	9.50EF	12.67B	7.30GH	9.82DE
NERICA2	9.33FG	12.0C	5.13K	8.82HI
YUNLU26	7.63IJ	12.67B	9.70CD	10.0D
WAB19	10.13CD	9.33F	6.13J	8.53IJ
ZHONGHAN3	7.47J	10.67E	6.27J	8.24JK
HANDAO221	10.40BC	13.67A	10.40B	11.49A
NERICA 15	10.73A	9.00F	6.80I	8.85GHI
YUNLU22	9.13G	11.00DE	11.50A	10.54B
HANDAO502	9.67E	12.00C	8.23F	9.97D
YUNLU33	9.57EF	12.33BC	8.40F	10.10CD
WAB8	9.67E	11.00DE	7.67G	9.48EF
NERICA17	10.30C	9.33F	8.13F	9.26FG
NERICA5	9.97D	11.33D	10.06BC	10.46BC
NERICA14	10.66AB	9.33F	7.10HI	9.03GH
YUNLU30	7.83I	9.33F	9.50D	8.89GI
YUNLU24	10.20CD	10.67E	9.00E	9.96D
NERICA12	9.43EF	11.00DE	6.93HI	9.12KFGH
NERICA4	8.20H	9.33F	6.00J	7.84K
Mean	9.43	10.92	8.02	9.46
C.V%	7.31	12.87	12.69	11.36
L.S.D	0.2698	0.5498	0.3977	0.4106

Means with the same letter for each parameter are not significant at 5% level (LSD)

Table (8): Mean stem diameter (cm) of the 18 rice genotypes evaluated at Shambat during the seasons (2011-2013)

Genotypes	2011	2013	Combine
WAB12	3.77DE	2.00EFG	2.99BCD
NERICA2	3.08G	2.02DEFG	2.55H
YUNLU26	3.95CD	1.94G	3.12B
WAB19	3.38F	2.07CDEF	2.73EFGH
ZHONGHAN3	3.68E	1.97FG	2.99BCD
HANDAO221	4.10BC	1.80H	3.04BC
NERICA 15	3.80DE	2.30B	3.05BC
YUNLU22	3.26FG	1.82H	2.54H
HANDAO502	3.08G	1.80H	2.58GH
YUNLU33	4.92A	1.94G	3.44A
WAB8	3.66E	1.58I	2.62FGH
NERICA17	3.36F	2.16C	2.76EFG
NERICA5	3.40F	2.08CDE	2.74EFGH
NERICA14	3.69E	2.10CDE	2.90CDE
YUNLU30	3.38F	2.55A	2.80DEF
YUNLU24	3.32FG	2.08CDE	2.70EFGH
NERICA12	4.34B	1.60I	2.98BCD
NERICA4	3.85CDE	2.11CD	2.65FGH
Mean	3.66	1.99	2.83
C.V%	17.71	14.89	18.35
L.S.D	0.2541	0.1052	0.2003

Means with the same letter for each parameter are not significant at 5% level (LSD)

4.1.5 Leaf Area (cm^2):

Data for leaf area was missed in season 2012. The genotypes showed significant different in seasons 2011 and 2013 table (1, 3). While no significant difference was shown in combine analysis for season and season X genotypes, while there was highly significant in genotypes, Appendix (1).

In season 201, N12 and W12 gave the highest measuring in leaf area (30.20, 28.96 cm^2) followed by Z3 (26.10 cm^2). N14 and H502 gave the lowest measuring (16.0, 14.53 cm^2) respectively, Table (9). In season 2013, Z3 followed by W19 gave the highest leaf area (35.13, 34.95 cm^2), while H502, Y22 and W8 gave the lowest (19.96, 19.67 and 17.63 cm^2) respectively, Table (9). Z3 had the best measure in combine analysis (30.62 cm^2), followed by Y26 (29.96 cm^2) and W12 (29.46 cm^2), while H502 had the lowest (17.24 cm^2), Table (9).

4.1.6 Days to 50% flowering:

Mean square were highly significant among genotypes over all seasons (2011-2012-2013) table (1,2,3), On the other hand there was no significant difference in season, highly significant for genotypes and significant for season X genotype that's indicated by combine analysis, table (4). In season 201, N14 flowered in 67.00 days followed by W8 (67.33 days) and Y26 (69.33 days) which were the earliest genotypes, table (10). The latest genotypes were W19 (83.67 days), Y22 (84.33 days), N12 (85.67 days) and H221 (90.00 days), table (10). N14 was the earliest genotypes (65.33 days) in 2012, while Y30 followed by H221 were the latest genotypes (82.00, 81.33 days) respectively, table (10). In season 2013, W8 was the earliest genotype (66.67 days), while H221 and Y22 were the latest genotypes (90.0 and 83.33 days), table (10). Combine analysis of variance indicated that N14 was the earliest genotype (66.78 days), H221 and Y22 were the latest genotypes (87.11 and 82.67 days), table (10).

Table (9): Mean of leaf area (cm) of the 18 rice genotypes evaluated at Shambat during the seasons (2011-2013)

Genotypes	2011	2013	Combine
WAB12	28.96A	29.95BCD	29.46ABC
NERICA2	21.55 FGH	28.83CDE	25.19F
YUNLU26	24.96 BC	34.95A	29.96AB
WAB19	20.13 H	25.89GH	23.01GH
ZHONGHAN3	26.10 B	35.13A	30.62A
HANDAO221	22.17 EFG	23.69HI	22.91GHI
NERICA 15	25.12 BC	28.28DEF	26.70DEF
YUNLU22	22.56 DEF	19.67J	21.12HIJ
HANDAO502	14.52 J	19.96J	17.24K
YUNLU33	23.54 CDE	31.38B	27.47CDE
WAB8	24.06 CD	17.63J	20.85IJ
NERICA17	21.30 FGH	22.67I	21.99HIJ
NERICA5	16.32 I	25.74GH	21.02HIJ
NERICA14	16.01 IJ	25.52GH	20.76J
YUNLU30	22.70 DEF	27.13EFG	24.92FG
YUNLU24	22.56 DEF	27.89DEFG	25.23F
NERICA12	30.20 A	26.17FG	28.19BCD
NERICA4	20.51 GH	31.12BC	25.82EF
Mean	22.40	26.75	24.58
C.V%	20.48	22.74	21.91
L.S.D	1.795	2.380	2.068

Means with the same letter for each parameter are not significant at 5% level (LSD)

Table (10): Mean of Days to 50% flowering of the 18 rice genotypes evaluated at Shambat and Ed duaim during the seasons (2011-2012-2013)

Genotypes	2011	2012	2013	Combine
WAB12	75.67DE	77.67H	78.67DE	77.33E
NERICA2	76.33CD	76.33I	76.33F	76.33EF
YUNLU26	69.33GH	81.00BC	74.33HI	74.88FG
WAB19	83.67B	79.67DE	79.67CD	81.00C
ZHONGHAN3	73.33EF	79.67DE	75.00GH	76.00EF
HANDAO221	90.00A	81.33AB	90.00A	87.11A
NERICA 15	71.33FG	78.33FGH	74.67GH	74.77FG
YUNLU22	84.33B	80.33CD	83.33B	82.66B
HANDAO502	75.33DE	68.00L	75.00GH	72.77H
YUNLU33	73.67EF	78.33FGH	75.67FG	75.88EF
WAB8	67.33H	75.33J	66.67K	69.77I
NERICA17	78.67C	81.00BC	78.33E	79.33D
NERICA5	71.67FG	79.00EF	74.67GH	75.11F
NERICA14	67.00H	65.33M	68.00J	66.77J
YUNLU30	75.67DE	82.00A	79.67CD	79.11D
YUNLU24	75.67DE	78.00GH	73.33I	75.66F
NERICA12	85.67B	78.67FG	80.67C	81.66BC
NERICA4	73.67EF	73.33K	73.33I	73.44GH
Mean	76.01	77.40	76.52	76.64
C.V%	8.34	3.13	3.88	5.58
L.S.D	2.481	0.9472	1.161	1.633

Means with the same letter for each parameter are not significant at 5% level (LSD)

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4.1.7 Days to 50% maturity:

The number of days to reach maturity plays a significant role in the cropping system. Early maturing genotypes evacuate the land early for the next crop and escape from insects and pests attack and timely handled. Individual Mean square revealed highly significant difference among the evaluated genotypes for all seasons (2011- 2012- 2013), table (1, 2, 3) Combine analysis indicated highly significant difference in season, genotype, and season x genotype, table (4). In season 201, N12 were the earliest genotypes (89.33 days) table (11), while Y30 and H221were the latest genotypes to get mature (123.0 , 128.0 days) respectively, Table (11). In season 2012 the earliest genotype to reach maturity was N14 (84.00 days), while the latest genotypes were Y24 (104.40 days), N17 and H221 (104.30 days), Y30 (106.30 days) and W19 (106.70 days), Table (11). In season 2013, N14 showed the least number of days to get mature (111.00 days), while H221and W19 is the latest genotype to get mature (122.00 days).Table (11). Combine analysis indicated that H502 had the lowest number of days to mature (101.00 days), while H221 was the latest genotype (120.30 days), Table (11).

4.2 Yield characters:

4.2.1 Number of Panicle/m^2:

Mean square for genotypes were highly significant difference in season 2011, 2012, and 2013, Table (12, 13, 14). Combine analysis revealed highly significant for season and genotypes and significant for season X genotype, Table (15). Season 2011, Y22 gave the highest number of panicles/m^2 (591.70), followed by W19 (591.70, 586.70) respectively, while N2 gave the lowest number of panicle/m^2 (387.00), Table (16). In second season 2012, H221 gave the highest number of panicle/m^2 (205.00) followed by Y26 (173.30), while the lowest number of panicle/m^2 was given by N15 (123.30), Y22 (120.00) and N17 (118.30), Table (16). In season 2013, N17, H502 and Y26 gave the highest number of panicle/m^2 (449.70, 426.70 and 426.30) respectively, while N4 gave the lowest number of panicle/m^2 (209.30), Table (16).H502 and H221gave the highest number of panicle/m^2 in combine analysis (404.20 and 398.20) respectively, while N2 had the lowest number of panicle/m^2 (259.60) Table (16).

Table (11): Mean of Days to 50 % maturity of the rice genotypes evaluated at Shambat and Ed duaim during the seasons (2011-2012-2013)

Genotypes	2011	2012	2013	Combine
WAB12	116.33D	99.33FG	120.33C	111.22DE
NERICA2	98.66I	100.00EFG	116.33FGH	105.00G
YUNLU26	112.33E	102.67BC	120.00C	111.66CD
WAB19	120.33C	106.67A	122.00B	116.33B
ZHONGHAN3	109.66F	100.00EFG	120.00C	109.88EF
HANDAO221	128.0A	104.33B	122.33A	120.33A
NERICA 15	109.66F	101.33CDE	116.33FGH	109.11F
YUNLU22	101.66H	100.33DEFG	116.0FG	106.22G
HANDAO502	100.00HI	88.67H	114.33H	101.00I
YUNLU33	112.66E	98.67G	116.67FG	109.33F
WAB8	117.33D	101.67CDE	120.00C	113.00C
NERICA17	112.33E	104.33B	119.00D	111.88CD
NERICA5	95.00J	102.00CD	118.67E	105.22G
NERICA14	107.00G	84.00I	111.00I	101.77HI
YUNLU30	123.00B	106.33A	121.67B	117.55B
YUNLU24	116.66D	104.00B	115.67GH	112.11CD
NERICA12	89.33K	100.67DEF	118.33EF	102.77H
NERICA4	99.00I	98.67G	116.67G	104.77G
Mean	109.38	100.20	118.07	109.43
C.V%	4.82	5.09	1.32	3.76
L.S.D	2.062	1.994	0.61133	1.570

Means with the same letter for each parameter are not significant at 5% level (LSD)

4.2.2 Panicle length (cm):

Mean square among genotypes revealed highly significant difference in season 2011 Table (12), significant difference in season 2012 Table (13).and non significant difference in season 2013, Table (14). Combine analysis of variance showed highly significant difference in season and genotype, significant difference in season x genotype, Table (15). In season 2011, H221 had the longest panicle (17.58 cm) followed by Z3 (17.39 cm), while H502, Y33, and N5 (13.10, 13.03, and 12.68 cm) gave the shortest length of panicle, Table (17). In season 2012, Z3 gave the highest length of panicle (25.00 cm) followed by N2 (23.33 cm), while Y30 gave the shortest length of panicle (19.00 cm), Table (17). In season 2013, H221 had the longest panicle (22.02 cm), followed by Y26 (20.78 cm) and Z3 (20.67 cm) while H502 gave the shortest length of panicle (16.33 cm) Table (17). Over season Z3 had the longest panicle (21.02 cm). The second genotype in panicle length was H221 (20.09 cm) while H502 had the shortest length of panicle among the tested genotypes (17.03 cm), Table (17).

Table (12): Mean Squares for yield and yield component traits of 18 rice genotypes evaluated at Shambat, season (2011)

Source	D.F	F. Value 2011						
		Number of Panicles /plant	Panicle length (cm)	Number of grain/ panicle	Number of filled grain/ panicle	Percent-age of unfilled grain/ panicle	100-seed weight (gm)	Grain yield (t/ha)
Replication	2	1.3962	2.3905	0.9631	0.4371	0.7399	0.4016	0.3514
genotypes	17	2.6732^{**}	2.7124^{ns}	3.1770^{**}	3.7856^{**}	10.398^{**}	4.459^{**}	5.129^{**}
Error	34	-	–	-	-	-	–	–
Total	53	-	–	-	-	-	–	–
EMS	_	6132.898	2.489	94.942	64.899	57.251	0.079	0.462
C.V%	_	14.51	10.34	18.56	21.90	25.48	11.46	35.97
SE±	_	18.4585	0.3719	2.2966	1.8988	1.7834	0.066	0.1601

*=significance   **= high significant   ns =not significant

Table (13): Mean Squares for yield and yield component traits of 18 rice genotypes evaluated at Ed duaim, season (2012)

Source	D.F	F. Value 2012						
		Number of Panicles/ Plant	Panicle length (cm)	Number of grain/ panicle	Number of filled grain/ panicle	Percent-age of unfilled grain/ panicle	100-seed weight (gm)	Grain yield (t/ha)
Rep-lication	2	0.8428	3.4568	0.6476	9.0272	11.21	2.023	5.0411
genotypes	17	3.5651^{**}	1.894^{*}	2.3427^{*}	1.520^{ns}	1.689^{*}	4.4809^{**}	4.9375^{**}
Error	34	–	–	-	-	-	–	–
Total	53	–	–	-	-	-	–	–
EMS	_	377.369	3.520	615.06	682.42	180.4	0.039	0.418
C.V%	_	13.96	8.70	17.75	29.87	35.73	7.80	33.83
SE±	_	4.5788	0.442	5.8455	6.1573	3.166	0.046	0.1524

*=significance   **= high significant   ns =not significant

Table (14): Mean Squares for yield and yield component traits of 18 rice genotypes evaluated at Shambat, season (2013)

Source	D.F	F. Value 2012						
		Number of Panicles/ plant	Panicle length (cm)	Number of grain/ panicle	Number of filled grain/ panicle	Percentage of unfilled grain/ panicle	100-seed weight (gm)	Grain yield (t/ha)
Rep-lication	2	2.5875	0.8272	23.4829	22.2816	2.7420	0.3418	4.1191
genotypes	17	0.9564^{ns}	1.6019^{ns}	1.0249^{ns}	1.5499^{ns}	1.325^{ns}	1.878^{*}	4.916^{**}
Error	34	_	_	_	_	_	_	_
Total	53	_	_	_	_	_	_	_
EMS	_	7716.3	3.763	173.859	114.257	102.125	0.105	0.176
C.V%	_	25.22	10.10	24.34	29.34	29.29	15.67	29.27
SE±	_	25.339	0.4572	3.1079	2.5194	2.3819	0.0762	0.0990

*=significance   **= high significant   ns =not significant

Table (15): Mean Squares for yield and yield component traits of 18 rice genotypes evaluated for combine analysis

Source	D.F	F. Value						
		Number of Panicles/ plant	Panicle length (cm)	Number of grains/ panicle	Number of filled grain/ panicle	Percentage of unfilled grain/ panicle	100-seed weight (gm)	Grain yield t/ha
Season	2	205.484**	76.951**	83.6091**	12.5294**	1.1354^{ns}	61.5931**	3.8423*
Error A	6	-	-	-	-	-	-	-
Genotype	17	2.9532**	3.222**	2.5362**	1.2721^{ns}	3.6482**	4.6951**	4.399**
season x genotype	34	1.8112*	1.4174*	2.0945**	1.8992**	2.6395**	2.3869**	5.289**
Total	161	-	-	-	-	-	-	-
EMS	-	4740.377	3.228	290.132	296.866	115.627	0.076	0.354
C.V %	-	20.11	9.62	20.80	29.33	31.68	11.70	34.05
SE ±	-	13.9767	0.3623	5.4788	7.3731	3.8056	0.0320	0.1367

*=significance **= high significant ns =not significant

Table (16) Mean of number of panicles/m^2 for the rice genotypes evaluated in Shambat and Ed duaim in seasons (2011-2012-2013)

Genotypes	2011	2012	2013	Combine
WAB12	466.7 GH	126.67FGH	423.67AB	371.22BC
NERICA2	387.0J	128.33EFG	263.33I	259.55H
YUNLU26	495.0FG	173.33B	426.33A	364.88C
WAB19	586.7AB	133.33EF	306.67GH	353.33CDE
ZHONGHAN3	455.0H	126.67FGH	274.33HI	285.33GH
HANDAO221	537.7AB	205.00A	416.00ABC	398.22A
NERICA 15	510.0EF	123.33GHI	373.00DE	357.66CD
YUNLU22	591.7A	120.00HI	329.00FG	358.00CD
HANDAO502	567.7ABC	151.67C	426.67A	404.22A
YUNLU33	446.7HI	141.67D	308.33GH	298.88G
WAB8	514.0DEF	126.67FGH	313.00G	329.00EF
NERICA17	475.0GH	118.33I	449.67A	347.66CDE
NERICA5	541.0CD	150.00C	350.00EF	347.00CDE
NERICA14	513.3DEF	135.00DE	319.33FG	311.44FG
YUNLU30	420.3I	141.67D	383.67CDE	337.44DEF
YUNLU24	576.7AB	141.67D	390.67BCD	391.89AB
NERICA12	540.0CDE	131.67EF	306.67GH	348.33CDE
NERICA4	558.3BC	130.00EFG	209.33J	299.22G
Mean	510.15	139.16	348.31	342.42
C.V%	14.51	13.96	25.22	20.11
L.S.D	30.63	7.598	34.36	26.28

Means with the same letter for each parameter are not significant at 5% level (LSD)

Table (17): Mean of panicle length (cm) for the 18 rice genotypes evaluated at Shmbat and Ed duaim in seasons (2011-2012-2013)

Genotypes	2011	2012	2013	Combine
WAB12	14.45I	20.67F	19.74CD	18.28FGH
NERICA2	14.51 HI	23.33B	18.45FG	18.76DEF
YUNLU26	15.45 FG	21.67DE	20.78B	19.30CDE
WAB19	16.33 D	21.00EF	19.51DE	18.91DEF
ZHONGHAN3	17.38 AB	25.00A	20.67B	21.02A
HANDAO221	17.57 A	20.67F	22.02A	20.08B
NERICA 15	15.69 EFG	23.33B	20.38BC	19.80BC
YUNLU22	16.09 DE	20.33F	18.92EF	18.44FG
HANDAO502	13.10 JK	21.67DE	16.33J	17.03K
YUNLU33	13.03 JK	20.33F	19.89CD	17.75HIJ
WAB8	16.95 BC	23.00BC	18.37FGH	19.44BCD
NERICA17	13.42 J	20.33F	17.65HI	17.13JK
NERICA5	12.68 K	22.33CD	19.85CD	18.28FGH
NERICA14	16.52 CD	23.00BC	19.40DE	19.64BC
YUNLU30	14.76 HI	19.00G	18.23FGH	17.33IJK
YUNLU24	16.00 DEF	21.00EF	17.95GHI	18.23FGH
NERICA12	15.66 EFG	20.67F	17.32I	17.88GHI
NERICA4	15.09 GH	20.67F	20.12BCD	18.62EF
Mean	15.26	21.55	19.19	18.66
C.V%	10.34	8. 70	10.10	9.62
L.S.D	0.6170	0.7338	0.7587	0.6858

Means with the same letter for each parameter are not significant at 5% level (LSD)

4.2.3 Number of Grain/panicle:

Mean square for genotypes showed highly significant differences in seasons 2011 Table (12), significant different in season 2012, Table (13), and no significant different in season 2013, Table (14). Combine analysis recorded highly significant differences for season, genotype and season x genotype, Table (15). W8 and H221 had the highest number of grain/panicle (73.72, 71.07) in season 2011, H502 had the lowest number of grain/panicle (35.62) then W12 (38.06), Table (18). In season 2012, N15 gave the highest number of grain/panicle (184.00) while H502 gave the lowest number of grain/panicle (112.30), Table (18). In season 2013 the highest number of grain/panicle was given by H221 (67.77) followed by N5 (65.17). H502 gave the lowest number of grain/panicle (39.12), Table (18). In combine analysis N15 gave the highest number of grain/panicle (98.25), followed by N4 (92.89). H502 had the lowest number of grain/panicle (62.36), Table (18).

4.2.4 Number of filled grain/panicle:

The genotypes showed no significant differences in all seasons (2011-2012-2013), Table (12, 13, 14). While there were significant differences in season and no significant differences in both genotype and season x genotype in combine analysis, Table (15). In season 2011 the highest number of filled grain/panicle was given by W8 (55.25) and Y33 (53.69) followed by N17 (48.45) and H221 (46.97), while W19, W12 and H502 gave the lowest number of filled grain/panicle (32.94, 31.66 and 30.88) respectively, Table (19). N14 and W12 had the highest number of filled grain/panicle in season 2012 (117.00, 104.70) respectively, while W19 had the lowest of number of filled grain/panicle (47.00), Table (19). In 2013, H221 gave the highest number of filled grain/panicle (51.59) followed by N5 and Y30 (46.21 and 45.41) respectively. The lowest number of filled grain/panicle was given by W8 and H502 (23.38 and 23.34) respectively, Table (19). N14 had the best number of filled grain/panicle in combine analysis of variance (63.16) followed by N15 (59.81), W12 (58.28), N5 (56.74), Y33 (56.60), W8 (56.10), and H221 (56.08), while W19 and H502 had the lowest number of filled grain/panicle (38.28 and 45.19) respectively, Table (19).

Table (18): Mean of number of grain/panicle of the 18 rice genotypes evaluated at Shambat and Ed duaim in seasons (2011-2012-2013)

Genotypes	2011	2012	2013	Combine
WAB12	38.06 L	175.33AB	55.68EF	89.69BC
NERICA2	42.56 K	146.00C	55.16EF	81.24DEF
YUNLU26	57.61BCD	116.33GH	57.0CDE	77.00FG
WAB19	50.34FGH	127.66EF	51.11FG	76.04FGH
ZHONGHAN3	47.02HIJ	171.00B	51.54FG	89.85BC
HANDAO221	71.07 A	124.66EFG	67.77A	87.83BC
NERICA 15	53.93DEF	184.00A	56.82DE	98.25A
YUNLU22	43.69JK	141.33C	57.43CDE	80.8EF
HANDAO502	35.62L	112.33H	39.12I	62.35I
YUNLU33	60.81B	126.66EF	47.06GH	78.18FG
WAB8	73.72A	146.00C	44.84H	87.63BCD
NERICA17	54.39DE	119.00FGH	47.03GH	70.14H
NERICA5	55.34CD	138.00CD	65.17AB	86.17CDE
NERICA14	51.03EFG	130.00DE	47.76GH	76.2FGH
YUNLU30	55.53CD	120.33EFGH	59.96CDE	78.60F
YUNLU24	46.27IJK	122.00EFGH	47.39GH	71.88GH
NERICA12	58.81BC	147.33C	61.76BCD	89.29BC
NERICA4	49.19GHI	167.33B	62.13BC	92.88AB
Mean	52.49	139.7	54.15	80.89
C.V%	18.26	17.75	24.34	20.80
L.S.D	3.811	9.700	5.155	6.502

Means with the same letter for each parameter are not significant at 5% level (LSD)

Table (19): Mean of number of filled grain/panicle of the 18 rice genotypes evaluated at Shambat and Ed duaim in seasons (2011-2012-2013)

Genotypes	2011	2012	2013	Combine
WAB12	25.33G	121.3A	38.50DEFG	65.96AB
NERICA2	37.37CD	88.66EFGH	39.24CDEF	56.82DEF
YUNLU26	35.61DE	59.66KL	43.65BC	53.64F
WAB19	22.94GH	57.00L	34.83FGHI	47.05G
ZHONGHAN3	21.43H	91.00DEF	34.20GHI	57.40DEF
HANDAO221	40.30C	69.66JK	51.59A	64.10ABC
NERICA 15	40.00C	99.33CD	36.79EFGH	63.35ABCD
YUNLU22	33.86EF	95.33CDE	41.88BCD	60.30BCDE
HANDAO502	30.88F	81.33FGHI	23.34L	46.76G
YUNLU33	53.68A	86.66EFGH	29.45JK	58.97CDEF
WAB8	55.25A	89.66DEFG	23.38L	61.69BCD
NERICA17	38.45CD	71.66IJ	31.88IJK	52.64FG
NERICA5	33.33EF	80.66GHI	46.21B	60.73BCDE
NERICA14	43.66B	117.0A	28.81K	65.61AB
YUNLU30	35.50DE	69.66JK	39.59CDE	54.93EF
YUNLU24	32.87EF	78.66HIJ	33.46HIJK	52.79 FG
NERICA12	37.23CD	105.0BC	33.61HIJ	65.80 AB
NERICA4	44.53B	111.6AB	45.41B	68.75A
Mean	36.79	87.43	36.43	58.72
C.V%	21.90	29.87	29.34	29.33
L.S.D value	3.151	10.22	4.697	6.577

Means with the same letter for each parameter are not significant at 5% level (LSD)

4.2.5 Percentage of unfilled grain/panicle (%):

Mean square indicated highly significant differences among evaluated genotypes season 2011 Table (12). A significant difference in season 2012, Table (13), and no significant differences in season 2013 Table (14). in combine analysis there were no significant differences in season, and highly significant in both genotype and season x genotype, Table (15). W19 had the highest percentage of unfilled grin/panicle in season 2011 (53.93%), followed by Z3 (53.61 %). N4 (9.52%) exhibited the lowest percentage of unfilled grin/panicle, Table (20). W19 had the highest percentage of unfilled grin/panicle in season 2012 (54.33%), while N14 gave the lowest percentage of unfilled grin/panicle (10.00%), Table (20). In season 2013, W8 gave the highest percentage of unfilled grin/panicle (48.25%) followed by N12 (44.99%), while N4, Y26, and H221 gave the lowest percentage of unfilled grin/panicle (28.15, 24.80, and 24.40%) respectively, Table (20). W19 had the highest percentage of unfilled grin/panicle (48.68%) in combine followed by Z3 (44.03), while N4 (23.44%) and N14 (22.00%) gave the lowest percentage of unfilled grin/panicle, Table (20).

4.2.6 100-seed weight (gm):

Mean square due to genotypes revealed highly significant difference for 100-seed weight in season 2011 and 2012 Table (12, 13). and significant difference in season 2013 Table (14). In combine analysis there were highly significant difference in season, genotype and season X genotype, Table (15). N15 gave the highest weight of 100-seed in season 2011 (3.30 gm), then Z3 (3.00 gm) and Y24 (2.90 gm). Y30 (2.10 gm) and N14 (2.00 gm) gave the lowest weight of 100-seed, Table (21). Z3 gave the highest weight (2.83 gm) in season 2012, H221 gave the lowest weight of 100-seeds (1.96 gm), Table (21). In season 2013, Y33 (2.733 gm) and N5 (2.53 gm) were the best weight of 100-seed, W8 (1.70 gm), W19 (1.67 gm) and N15 (0.140 gm) were the lowest weight of 100-seed, Table (21). Across season, Y33 was the best genotype that gave (2.71 gm) followed by Z3 (2.63 gm), while the lowest weight of 100-seed were given by W19 (2.02 gm), Table (21).

Table (20): Mean Percentage of unfilled grain/panicle (%) for 18 rice genotypes evaluated at Shambat and Ed duaim in seasons (2011-2012-2013)

Genotypes	2011	2012	2013	Combine
WAB12	33.78EF	32.0FG	31.08HIJ	32.28EF
NERICA2	12.19IJK	41.66CD	31.34HIJ	28.39FG
YUNLU26	38.25CD	48.33B	24.80K	37.12CD
WAB19	53.93A	54.33A	37.78DEF	48.68A
ZHONGHAN3	53.61A	44.66BCD	33.82GHI	44.03B
HANDAO221	47.57B	44.33BCD	24.40K	38.76C
NERICA 15	25.86GH	46.66BC	36.03EFG	36.18CDE
YUNLU22	23.12H	32.33FG	30.91HIJ	27.90G
HANDAO502	13.54IJ	28.66G	42.54BC	28.24FG
YUNLU33	11.81JK	33.33FG	39.50CDE	28.21FG
WAB8	25.05GH	40.00DE	48.25A	37.75CD
NERICA17	27.27G	41.00DE	33.14GHI	33.80DE
NERICA5	40.09C	42.66CD	29.14J	37.30CD
NERICA14	14.90I	10.00H	41.09BCD	21.99H
YUNLU30	36.42DE	42.66CD	34.03FGH	37.70CD
YUNLU24	30.84F	36.00EF	30.07IJ	32.30EF
NERICA12	36.85D	28.66G	44.99AB	36.83CD
NERICA4	9.52K	29.33G	28.15JK	23.44H
Mean	29.69	37.58	34.50	33.93
C.V%	25.48	35.73	29.29	31.68
L.S.D	2.959	5.253	3.952	4.105

Means with the same letter for each parameter are not significant at 5% level (LSD)

Table (21): Mean of 100-seed weight for 18 rice genotypes evaluated at Shambat and Ed duaim in seasons (2011-2012-2013)

Genotypes	2011	2012	2013	Combine
WAB12	2.43EF	2.66E	2.03EFGH	2.37EFG
NERICA2	2.57D	2.63F	2.07DEFG	2.42DEF
YUNLU26	2.40EF	2.46H	2.07DEFG	2.31GH
WAB19	2.13I	2.26K	1.67J	2.02K
ZHONGHAN3	3.00B	2.83A	2.07DEFG	2.63AB
HANDAO221	2.37FG	1.96M	2.10CDEF	2.14IJ
NERICA 15	3.30A	2.50G	2.00FGH	2.60BC
YUNLU22	2.50DE	2.76C	2.13CDE	2.46DE
HANDAO502	2.40EF	2.33J	1.93H	2.22HI
YUNLU33	2.60CD	2.80B	2.73A	2.71A
WAB8	2.27GH	2.16L	1.70IJ	2.04JK
NERICA17	2.17HI	2.50G	1.97GH	2.21HI
NERICA5	2.20HI	2.80B	2.53B	2.51CD
NERICA14	2.00J	2.66E	2.17CD	2.27GH
YUNLU30	2.10IJ	2.36I	2.03EFGH	2.16I
YUNLU24	2.90B	2.73D	1.93H	2.52CD
NERICA12	2.70C	2.66E	1.80I	2.33FG
NERICA4	2.20HI	2.50G	2.20C	2.30GH
Mean	2.45	2.53	2.06	2.33
C.V%	11.46	7.80	15.67	11.70
L.S.D	0.1099	0.02766	0.1267	0.1052

Means with the same letter for each parameter are not significant at 5% level (LSD)

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4.2.7 Grain yield (t/ha):

The genotypes showed highly significant differences for grain yield in all seasons Table (12, 13, and 14). Combine analysis showed significante difference in season and highly significant difference for genotype and genotypes x seaon, Table (15). In season 2011, H221 gave the highest grain yield (4.03 t/ha), while the lowest yield was given by Y33 and N17 (1.10 t/ha), N2 and N4 (1.06 t/ha), Table (22). In season 2012, N14 was the first genotype (3.50 t/ha), while the lowest yield was showed by W19 (0.83 t/ha), Table (22). Y33 had the highest yield in season 2013 (2.43 t/ha), N12 gave the lowest yield (0.86 t/ha), Table (22). Over seasons, Z3, and H221 were gave the highest yield (2.38and 2.26 t/ha) respectively, while N17 and N2 were the lowest genotypes (1.14 t/ha) for both Table (22).

4.3 Correlation coefficient between different traits:

The correlation coefficient between different traits in each season was presented in tables (23, 24, 25). The correlation in combing between seasons 2011, 2012 and 2013 were presented in table (27) the correlation in combing between season 2011 and season 2013 were presented in appendix (2), that's because there were missing data in season 2012 like number of leaves, leaf area and stem diameter.

4.3.1 Correlations between grain yield (t/ha) and growth traits:

In season 2011 the result showed that there were weak positive correlations between grain yield and plant height (0.073), number of leaves/plant (0.109), stem diameter (0.091), leaf area (0.117), days to flowering (0.242), and days to maturity (0.468). A weakly negative correlation was observed between grain yield and number of tillers/plant (-0.045) Table (23). In season 2012 there were weakly positive correlations between grain yield and plant height (0.289), number of tillers/plant (0.147), negative correlations was observed with days to flowering (-0.412) and days to maturity (-0.464).Table (24). Season 2013 showed weakly positive correlations with grain yield and plant height (0.152), number of leaves/plant (0.105) and number of tillers/plant (0.233), negative correlations with days to flowering and days to maturity (-0.285) and (-0.328) respectively Table (25).

Table (22): Mean of grain yield (t/ha) for 18 rice genotypes evaluated at Shambat and Ed duaim in seasons (2011-2012-2013)

Genotypes	2011	2012	2013	Combine
WAB12	2.13E	2.00DE	1.03FG	1.73DEF
NERICA2	1.06J	1.33FG	1.03FG	1.14I
YUNLU26	2.40D	1.17GH	1.30DE	1.62FG
WAB19	3.70B	0.83I	1.03FG	1.85DE
ZHONGHAN3	3.06C	3.00B	1.10F	2.38A
HANDAO221	4.03A	1.83E	0.90GH	2.26AB
NERICA 15	1.40HI	1.23GH	1.03FG	1.22HI
YUNLU22	1.40HI	2.83B	1.16EF	1.80DEF
HANDAO502	1.70FG	2.16CD	2.00C	1.95CD
YUNLU33	1.10J	2.83B	2.43A	2.12BC
WAB8	1.76F	2.33C	0.90GH	1.66EFG
NERICA17	1.10J	1.00HI	1.33D	1.14I
NERICA5	1.66FG	1.50F	2.16B	1.77DEF
NERICA14	1.20IJ	3.50A	2.10BC	2.26AB
YUNLU30	1.90EF	1.00HI	2.06BC	1.65EFG
YUNLU24	1.83F	2.83B	2.10BC	2.25AB
NERICA12	1.46GH	2.00DE	0.86H	1.44GH
NERICA4	1.06J	1.00HI	1.26DE	1.11I
Mean	1.88	1.90	1.74	1.74
C.V%	35.97	33.83	29.27	34.05
L.S.D	0.2658	0.2529	0.1641	0.2271

Means with the same letter for each parameter are not significant at 5% level (LSD)

4.3.2 Correlations between grain yield (t/ha) and yield traits:

In season 2011 there were highly positive correlation between grain yield and percentage of unfilled grain/panicle (0.662). Weak positive correlations with number of panicles (0.129), panicle length (0.361), number of grain/panicles (0.125), 100-seed weight (0.027), and weak negative correlations with number of filled grain/panicle (-0.358).Table (23). In season 2012 there were positive correlations between grain yield and number of panicles/m^2 (0.0172), panicle length (0.317) number of grain/panicle (0.187), number of filled grain/panicle (0.488) and 100-seed weight (0.260), negative correlation with percentage of unfilled grain/panicle (-0.497) Table (24). In season 2013 there were positive correlations between grain yield and number of panicles (0.0002), number of grain/panicles (0.187), number of filled grain/panicle (0.109), percentage of unfilled grain/panicles (0.037), and 100-seed weight (0.431), and negative correlation with number of panicles/plant (-0.027) Table (25).

4.3.3 Correlations between grain yield (t/ha) and growth traits in combination:

Combination in season 2011-2012-2013 revealed that there was weakly positive correlation between grain yield and plant height (0.193), number of tillers/plant (0.209). Table (26), and negative correlations with days to flowering and days to maturity (-0.058, -0.103) respectively. In combination of season 2011 and season 2013 for the parameters that missed at season 2012 there were weakly positive correlation between grain yield and number of leaves (0.128), stem diameter (0.265) and leaf area (0.011). Appendix (2)

4.3.4 Correlations between grain yield (t/ha) and its component in combination:

Weakly positive correlation were observed in combining of seasons 2011-2012 and 2013 for number of panicles/m^2 (0.009), panicle length (0.133), number of grain/panicle (0.180), number of filled grain/panicle (0.233), percentage of unfilled grain/panicle (0.047) and 100-seed weight (0.280) Table (26).

4.3.5 Correlations among growth and yield component traits in individual analysis:

The results in season 2011 showed that, highly positive correlation between plant height and leaf area (0.557) , weak positive correlation with number of leaves/plant (0.276), stem diameter (0.369), days to maturity (0.228),

Table (23) Correlation coefficients among 14 traits of 18 rice genotypes season (2011)

traits	Plant height (cm)	Number of leaves/plant	Number of tillers/plant	Stem diameter (cm)	Leaf area (cm)^2	Days to 50% flowering	Days to 50% maturity	Number of panicles / m^2	Panicle length (cm)	Number of grain /panicle	Number of filled grain/ panicle	Percentage of unfilled grain/ panicle	100-seed weight (g)	Grain yield (t/ha)
Plant height (cm)	-													
Number of leaves/plant	0.276	-												
Number of tiller/plant	-0.023	0.0827	-											
Stem diameter (cm)	0.369	0.0755	0.0076	-										
Leaf area (cm)^2	0.557	0.2221	-0.0957	0.4053	-									
Days to 50% flowering	-0.095	-0.016	0.0709	-0.0445	-0.015	-								
Days to 50% maturity	0.228	0.1703	0.0244	0.0839	0.1046	-0.0089	-							
Number of panicles/m^2	0.164	-0.009	0.2728	-0.0379	0.0866	0.1578	-0.0078	-						
Panicle length(cm)	0.282	0.1522	0.0216	0.1423	0.3018	-0.0751	0.2034	0.1614	-					
Number of grain/panicle	0.266	0.3262	0.0352	0.3245	0.0942	-0.0674	0.3003	-0.1887	0.2396	-				
Number of filled grain/panicle	0.273	0.3476	0.0771	0.2250	0.0604	-0.2824	0.0644	-0.2271	0.0436	0.7097	-			
Percentage of unfilled grain/panicle	-0.059	-0.122	-0.0665	0.0703	0.0660	0.3048	0.2929	0.1090	0.2512	0.1678	-0.5599	-		
100-seed weight (g)	0.181	0.0377	-0.0007	0.0473	0.3533	-0.0401	-0.1362	0.1320	0.2404	-0.117	-0.0961	0.021	-	
Grain yield(t/ha)	0.073	0.1094	-0.0453	0.0916	0.1176	0.2428	0.4684	0.1295	0.3616	0.1255	-0.3586	0.663	0.028	-

Table (24) Correlation coefficients among 14 traits of 18 rice genotypes season (2012)

traits	Plant height (cm)	Number of tillers/ plant	Days to 50% flowering	Days to 50% maturity	Number of panicles/ m^2	Panicle length (cm)	Number of grain/ panicle	Number of filled grain /panicle	Percentage of unfilled grain/ panicle	100-seed weight	Grain yield (t/ha)
Plant height (cm)	-										
Number of tillers/ plant	-0.0019	-									
Days to 50% flowering	0.0502	0.1971	-								
Days to 50% maturity	-0.0849	0.0882	0.8033	-							
Number of panicles/m^2	-0.2035	0.3995	0.0243	0.0701	-						
Panicle length (cm)	0.6465	-0.0822	-0.3226	-0.2940	-0.1161	-					
Number of grain/panicle	0.2701	-0.1546	-0.0052	-0.0916	-0.3329	0.4468	-				
Number of filled grain/panicle	0.2646	-0.1545	-0.4004	-0.4676	-0.2564	0.4033	0.6482	-			
Percentage of unfilled grain/panicle	-0.1716	0.1377	0.5324	0.5732	0.1095	-0.2249	-0.0991	-0.8076	-		
100-seed weight (g)	0.2967	-0.0512	-0.0478	-0.1655	-0.3462	0.1725	0.2017	0.2259	-0.1717	-	
Grain yield(t/ha)	0.2893	0.1475	-0.4121	-0.4649	0.0172	0.3176	0.1878	0.4885	-0.4974	0.2600	-

Table (25) Correlation coefficients among 14 traits of 18 rice genotypes season (2013)

Traits	Plant height (cm)	Number of leaves/ plant	Numb-er of tiller/ plant	Stem diameter (cm)	Leaf area (cm)²	Days to 50% flower-ing	Days to 50% mature-ty	Number of panicles/ m²	Panicle length (cm)	Number of grain /panicle	Number of filled grain/ panicle	Percentage of unfilled grin/ panicle	100-seed weight (g)	Grain yield (t/ha)
Plant height (cm)	-													
Number of leaves/plant	0.1013	-												
Number of tillers/ plant	0.2666	-0.2557	-											
Stem diameter (cm)	0.4472	0.1449	-0.1252	-										
Leaf area(cm)²	0.2419	0.4888	-0.3306	0.5109	-									
Days to 50% flowering	-0.010	-0.4141	0.3047	-0.0311	-0.1692	-								
Days to 50% maturity	0.0931	-0.2042	0.2298	-0.0009	-0.0015	0.5703	-							
Number of panicle/ m²	0.0849	-0.0564	0.4267	0.2462	-0.0866	0.1384	0.1680	-						
Panicle length (cm)	0.3623	0.1489	0.0650	0.1730	0.4012	0.0404	0.3416	0.0973	-					
Number of grain/panicle	-0.043	0.0647	0.0233	-0.0244	0.2653	0.0909	0.2059	-0.2593	0.4045	-				
Number of filled grain/panicle	0.0097	0.0876	0.0878	0.0131	0.2451	0.1734	0.2416	-0.1666	0.4198	0.9367	-			
Percentage of unfilled grain/panicle	-0.065	-0.0754	-0.1515	-0.0733	-0.1537	-0.2173	-0.176	-0.1299	-0.294	-0.5026	-0.749	-		
100-seed weight(g)	0.1443	-0.0185	0.1789	0.2042	0.1059	0.0155	-0.136	-0.0541	0.1831	0.1677	0.1713	-0.1120	-	
Grain yield (t/ha)	0.1527	0.1053	0.2330	0.1122	0.0845	-0.2856	-0.328	-0.0278	0.0002	0.1872	0.1095	0.0377	0.4315	-

Table (26) Correlation coefficients among 14 traits of 18 rice genotypes, combine season (2011-2012-2013)

Traits	Plant height (cm)	Number of tillers/ plant	Days to 50% flower-ing	Days to 50% matu-rity	Number of panicles/ m²	Panicle length (cm)	Number of filled grain /panicle	Number of filled grain/ panicle	Percentage of unfilled grain/ panicle	100-seed weight (g)	Grain yield (t/ha)
Plant height (cm)	-										
Number of tillers/ plant	0.3305	-									
Days to 50% flowering	0.0251	0.1808	-								
Days to 50% maturity	-0.2719	-0.3579	0.1509	-							
Number of panicles/ m²	-0.4622	-0.1612	-0.0215	0.3490	-						
Panicle length	0.6123	0.1707	0.0014	-0.1869	-0.6632	-					
Number of grain /panicle	0.5858	0.4219	0.0775	-0.5113	-0.7429	0.6596	-				
Number of filled grain/panicle	0.5399	0.3551	-0.0546	-0.5361	-0.6289	0.5887	0.8821	-			
Percentage of unfilled grain/ panicle	0.0328	0.0542	0.2561	0.1562	-0.1907	0.1242	0.1067	-0.3155	-		
100-seed weight(g)	0.2969	0.3121	-0.0070	-0.4075	-0.0781	0.1110	0.3140	0.3047	-0.0576	-	
Grain yield (t/ha)	0.1930	0.2096	-0.0585	-0.1030	0.0091	0.1335	0.1802	0.2337	0.0472	0.2808	-

number of panicles (0.164), panicle length (0.282), number of grain/panicle (0.266), number of filled grain/panicle(0.273), and 100-seed weight (0.181), Negative correlations with number of tillers (-0.023), days to 50% flowering (-0.095), percentage of unfilled grain/panicle (-0.058). Table (23). Number of leaves/plant had weakly positive correlations with number of tillers/plant (0.0827), stem diameter (0.075), leaf area (0.221), days to maturity (0.170), panicle length (0.152), number of grain/panicle (0.326), number of filled grain/panicle (0.347) and 100-seed weight (0.037) and negative correlations between number of leaves and days to flowering (-0.0167), number of panicles (-0.008) and percentage of unfilled grain/panicle (-0.122). Table (23). Number of tillers/plant had weakly positive correlations with stem diameter (0.007), days to flowering (0.070), days to maturity (0.024), number of panicles (0.272), panicle length (0.021), number of grain/panicle (0.035), and number of filled grain/panicle (0.077)and there were negative correlations between number of tillers/plant and leaf area (-0.095), percentage of unfilled grain/panicle (-0.066), and 100-seed weight (-0.0007), Table (23). Stem diameter had weakly positive correlations with leaf area (0.405), days to maturity (0.083), panicle length (0.142), number of grain/panicle (0.324), number of filled grain /panicle (0.225), percentage of unfilled grain/panicle (0.070), and 100-seed weight (0.047) and negative correlations with days to flowering (-0.044), and number of panicle (-0.037). Table (23). Leaf area had weakly positive correlations with days to maturity (0.104), number of panicles (0.086), panicle length (0.301), number of grain/panicle (0.094), number of filled grain/panicle (0.060), percentage of unfilled grain /panicle (0.066), and 100-seed weight (0.353), and negative correlations were observed between leaf area and days to flowering (-0.015). Table (23). Days to 50% flowering had a weakly positive correlation with number of panicles (0.157), percentage of unfilled grain/panicle (0.304). There were a negative correlations between days to flowering and days to maturity (-0.008), panicle length (-0.075), number of grain/ panicle (-0.067), number of filled grain /panicle (-0.284), and 100-seed weight (-0.40). Table (23). Days to 50% maturity had weakly positive correlations with panicle length (0.203), number of grain/panicle (0.300), number of filled grain/panicle (0.064), percentage of unfilled grain/panicle (0.292), and negative correlations with number of panicle (-.0007) and 100-seed weight (-0.136). Table (23).

Number of panicles had weakly positive correlations with panicle length (0.161), percentage of unfilled grain/panicle (0.109), and 100-seed weight (0.132), it had a negative correlated with number of grain/panicle (-0.188), and number of filled grain/panicle (-0.227). Table (23). Panicle length had weakly positive correlations with number of grain/panicle (0.239), number of filled grain/panicle (0.043), percentage of unfilled grain/panicle (0.251), and 100-seed weight (0.240). Table (23). Number of grain/panicle highly positive correlations with number of filled grain/panicle (0.709), weakly positive correlations with percentage of unfilled grain/panicle (0.167), negative correlated with 100-seed weight (-0.116). Table (23). Number of filled grain/panicle had highly negative correlated with percentage of unfilled grain/panicle (-0.559), and negative correlated with 100-seed weight Table (23). Percentage of unfilled grain/panicle had weakly positive correlations with 100-seed weight (0.020) Table (23).

The results in season 2012 showed that there were highly positive correlations between plant height and panicle length (0.646), weakly positive correlations with days to flowering (0.0502), number of grain/panicle (0.270), Number of filled grain/panicle (0.204), and 100-seed weight (0.296), negative correlation between plant height and number of tillers/plant (-0.001), days to maturity (-0.0849), number of panicles (-0.203), and percentage of unfilled grain/panicle(-0.171). Table (24). Number of tillers had a weakly positive correlation with days to flowering (0.197), days to maturity (0.088), and number of panicles (0.399), percentage of unfilled grain/panicle (0.137), negative correlations with panicle length (-0.082), number of grain/panicle (-0.154), number of filled grain/panicle (-0.154), and 100-seed weight (-0.051). Table (24). There were highly positive correlations between days to flowering and days to maturity (0.803) and percentage of unfilled grain/panicle (0.532), negative correlation between days to flowering and number of panicles (0.024), panicle length(-0.322), number of grain/panicle (-0.005), number of filled grain/panicle(-0.400), and 100-seed weight (-0.047). Table (24). Highly positive correlations was indicated between days to maturity and percentage of unfilled grain/panicle (0.573), and there were a weakly positive correlation with days to maturity and number of panicles (0.070), negative correlations with panicle length (-0.294), number of grain/panicle (-0.091), number of filled grain/panicle (-0.467), and 100-seed weight (-0.464). Table (24).

Number of panicle had a weakly positive correlations with percentage of unfilled grain/panicle (0.109), and negative correlations with panicle length (-0.116), number of grain/panicle (-0.332), number of filled /panicle (-0.256), and 100-seed weight (-0.346). Table (24). Panicle length had weakly positive correlation with number of grain/panicle (0.446), number of filled grain/panicle (0.403), and 100-seed weight (0.172), negative correlations with percentage of unfilled grain/panicle (-0.224). Table (24). Number of grain/panicle had a highly positive correlation with number of filled grain/panicle (0.648), and 100seed weight (0.201), negative correlation with percentage of unfilled grain/panicle (-0.099) Table (24). Number of filled grain/panicle had a weakly positive correlation with 100-seed weight (0.225), negative correlation with percentage of unfilled grain/panicle (-0.807) Table (24). Percentage of unfilled grain/panicle had negative correlation with 100-seed weight (-0.171).

In season 2013 there were a weakly positive correlation between plant height and number of leaves (0.101), number of tillers (0.266), stem diameter (0.447), leaf area (0.242), days to maturity (0.093), number of panicle (0.084), panicle length (0.362), number of filled grain/panicle (0.009), and 100seed weight (0.144), negative correlations with days to flowering (-0.010), number of grain/panicle (-0.043), percentage of unfilled grain/panicle (-0.065). Table (25). Number of leaves had a weakly positive correlations with stem diameter (0.144), leaf area (0.488), panicle length (0.148), number of grain/panicle (0.064), number of filled grain/panicle (0.087), negative correlations between number of leaves and days to flowering (-0.414), days to maturity (-0.204), number of panicle (-0.056), percentage of unfilled grain/panicle (-0.075), and 100-seed weight (-0.018). Table (25). Number of tillers/plant had a positive correlation with day to flowering (0.304), days to maturity (0.229), number of panicle (0.426), panicle length (0.065), number of grain/panicle (0.023), and 100-seed weight (0.178), negative correlations with stem diameter (-0.125), leaf area (-0.330), percentage of unfilled grain/panicle (-0.151), and 100-seed weight (0.233) Table (25). Stem diameter had a highly positive correlation with leaf area (0.510), weak positive correlations with number of panicles (0.246), number of filled grain/panicle (0.013) and 100-seed weight (0.204), negative correlations with days to flowering (-0.031), number of grain/panicle (-0.024), percentage of unfilled grain/panicle (-0.073), Table (25). Leaf area had weakly positive correlation with panicle length (0.401), number of grain/panicle (0.265), number of filled grain/panicle (0.245), and 100-seed weight (0.105), negative

correlations between leaf area and days to flowering (-0.169), days to maturity (-0.001), number of panicles (-0.086), percentage of unfilled grain/panicle (-0.153) Table (25). Days to flowering had a positive correlations wit days to maturity (0.570), weakly positive correlation with number of panicles (0.138), panicle length (0.040), number of grain/panicle (.090), number of filled grain/panicle (0.173), 100-seed weight (0.015), negative correlation with percentage of unfilled grain/panicle (-0.217) Table (25). Days to maturity had weakly positive correlations number of panicles (0.168), panicle length (0.341), number of grain/panicle (0.205), number of filled grain/panicle (0.241), negative correlations with percentage of unfilled grain/panicle (-0.175), and 100-seed weight (-0.132), Table (25).

Number of panicle had weakly positive correlations with panicle length (0.097), and negative correlations with number of grain/panicle (-0.259), number of filled grain/panicle (-0.166), percentage of unfilled grain/panicle (-0.129), and 100-seed weight (-0.027). Table (25). Panicle length weakly positive correlations with number of grain/panicle (0.404), number of filled grain/panicle (0.419), and 100-seed weight (0.183), negative correlations with percentage of unfilled grain/panicle (-0.294) Table (25).There were weakly positive correlations between number of grain/panicle and number of filled grain/panicle (0.936), and 100-seed weight (0.167), negative correlations with percentage of unfilled grain/panicle (-0.502). Number of filled grain/panicle had weakly positive correlations with 100-seed weight (0.171), negative correlations with percentage of unfilled grain/panicle (-0.748) Table (25).percentage of unfilled grain/panicle had weakly positive correlations with 100-seed weight (-0.112) Table (25).

4.3.6 Correlation between traits in over seasons:

The correlations between characters in combing indicated that there were highly positive correlations between plant height and panicle length (0.612), number of grain/panicle (0.585), number of filled grain/panicle (0.539), weakly positive correlations between plant height and number of tillers/plant (0.330), days to flowering (0.025), percentage of unfilled grain/panicle (0.032), and 100-seed (0.246), negative correlations with days to maturity (-0.271), number of panicles (-0.462). Table (26).

The combining of number of leaves in season (2011-2013) had weakly positive correlations with stem diameter (0.144), leaf area (0.313), number of

panicles (0.054), panicle length (0.028), number of grain/panicles (0.155), number of filled grain/panicle (0.188), and 100-seed weight (0.060)and there were a negative correlations with number of tillers (-0.076) days to flowering (-0.194), and days to maturity (-0.007) and percentage of unfilled grain/panicle (-0.116). Appendix (2)

Number of tillers had weakly positive correlations with days to flowering (0.180), panicle length (0.170), number of grain/panicle(0.421), number of filled grain/panicle (0.355), percentage of unfilled grain/panicle(0.054) and 100-seed weight (0.312), negative correlations with days to maturity (-0.357), number of panicle (-0.116), Table (26). The leaf area in combining between seasons (2011-2013) had weakly positive correlations with days to maturity (0.203), panicle length (0.461), number of grain /panicle (0.205), number of filled grain/panicle (0.157), percentage of unfilled grain/panicle (0.028), and 100-seed weight (0.049), negative correlations were observed between leaf area and days to flowering (-0.066), and number of panicles (-0.223). Appendix (2). The stem diameter in combining between seasons (2011-2013) had highly positive correlations with number of panicles (0.601), and weakly positive correlations with number of grain/panicle (0.039), number of filled grain/panicle (0.080) and 100-seed weight (0.425), negative correlations were observed between stem diameter and leaf area (-0.049), days to flowering (-0.052), days to maturity (-0.358), panicle length (-0.522), percentage of unfilled grain/panicle(-0.131). Appendix (2). Days to flowering had weakly positive correlations with days to maturity (0.150), panicle length (0.002), number of grain/panicle (0.077), percentage of unfilled grain/panicle (0.256), and negative correlation with number of panicles (-0.021), number of filled grain/panicle (-0.054). Table (26). Days to maturity had weakly positive correlations with number of panicle (0.349) and percentage of unfilled grain/panicle (0.156), negative correlation with panicle length (-0.186) and 100-seed weight (-0.407) highly negative correlation with number of grain/panicle (-0.511) and number of filled grain/panicle(-0.536). Table (26).

Number of panicle had negative correlation with percentage of unfilled grain/panicle (-0.190), and 100-seed weight (-0.078) highly negative correlation with panicle length (-0.663), number of grain/panicle (-0.742), number of filled grain/panicle (-0.628). Table (26). Panicle length had highly positive correlations with number of grain/panicles (0.659), number of filled grain/panicle (0.588)

weakly positive correlation with percentage of unfilled grain/panicle (0.124) and 100-seed weight (0.111) Table (26). Number of grain/panicle had highly positive correlations with number of filled grain/panicle (0.882), weakly positive correlations with percentage of unfilled grain/panicle (0.106) and 100-seed weight (0.314) Table (26). Number of filled grain/panicle had weakly positive correlations with 100-seed weight and negative correlation with percentage of unfilled grain/panicle (-0.315) Table (26). Percentage of unfilled grain/panicle had negative correlation with 100-seed weight (-0.056) Table (26).

4.4 Genotypic (∂^2g) Phenotypic (∂^2 ph), variances and broad sense heritability h^2b (%):

The results of this study for the three seasons (2011, 2012 and 2013) estimates highest genotypic variances (∂^2g) 3420.56, 322.658 and 1895.627 for Number of Panicle/m^2 respectively. The lowest estimates of genotypic variance for three seasons 0.09, 0.04 and 0.03 were attended by 100-seed weight (gm) table (27). On the other hand, highest estimates of phenotypic variance (∂^2ph)(9553.454,700.027 and 9611.97), showed by Number of panicles/m^2 for the three seasons (2011, 2012 and 2013), respectively whereas, the lowest values 0.170, 0.084 and 0.135 obtained by 100- seed weight followed by 1.097, 0.966, and 0.406 for grain yield (Ton/ha) for the three seasons. In season 2011 and 2013the highest value of heritability (h^2) were revealed by days to 50% maturity (0.77and 0.76) respectively, the highest heritability in season 2012 estimated (h^2 = 0.75) for days to 50% flowering table (27). While the lowest value of heritability (h^2) in season 2011, were revealed by stem diameter (0.15) and (0.14) in season 2012 for number of filled grain/ panicle. In season 2013 the lowest value recorded by number of grain/panicle (0.018).

4.5 Genotypic (GCV) Phenotypic (PCV), coefficients of variation and genetic advance (GA):

Estimates of Genotypic Coefficient of Variation (GCV) in three seasons (2011, 2012 and 2013) regarded highest value 42.18, 55.44 and 51.43 by grain yield, On the other hand the lowest value 0.095 in season (2011) estimated for number of tillers / plant, in season 2012 and season 2013 panicle length (cm) had the lowest value (4.7, 2.3) respectively (Table, 28). On the other hand, (PCV) showed high values 44.40, 38.73 and 33.42 by grain yield (ton/ha) at the three season (2011, 2012 and 2013) table (28). While the lowest value in season 2011

(0.11) estimated for number of tillers/plant, in season 2012 and 2013 the lowest value was (7.00, 2.72) estimated for days to 50% maturity, highest value of genetic advance (GA) was recorded by number of panicle/m² (72.07, 25.12 and 39.83) respectively at the three seasons, while the lowest value of (GA) was estimated for number of tillers/m² (0.18, 1.5) in season 2011 and 2012 respectively. In season 2013 the lowest value was estimated for stem diameter (0.043) table (28).

Table (27): Genotypic variance, phenotypic variance and broad sense heritability for 14 traits of 18 rice genotypes

Traits	Genotypic variance			Phenotypic variance			Heritability ($h^2b\%$)		
	2011	2012	2013	2011	2012	2013	2011	2012	2013
Plant height(cm)	61.808	58.952	56.522	164.45	140.09	117.072	0.3758	0.421	0.4827
Number of leaves/plant	0.0516	-	0.0233	0.2176	-	0.1993	0.2373	-	0.1169
Number of tillers/plant	0.817	1.374	2.6756	1.274	3.350	3.7096	0.641	0.410	0.7212
Leaf area(cm²)	9.823	-	31.542	30.878	-	68.558	0.3181	-	0.4600
Stem diameter(cm)	0.0746	-	0.012	0.4966	-	1.105	0.1503	-	0.114
Days to 50% flowering	26.870	18.261	25.302	67.101	24.126	34.111	0.400	0.75	0.7417
Days to 50 % maturity	98.363	23.221	7.8986	126.14	49.210	10.3416	0.779	0.471	0.7637
Number of panicle/m²	3420.5	322.65	1895.6	9553.4	700.02	9611.97	0.358	0.460	0.1972
Panicle length(cm)	1.4206	1.049	0.755	3.9096	4.569	4.518	0.3633	0.229	0.1673
Number of grain/panicle	68.897	275.28	1.391	163.83	752.70	75.145	0.4205	0.365	0.0185
Number of filled grain/panicle	60.260	118.40	20.944	125.15	800.83	135.201	0.4814	0.147	0.1549
Percentage of unfilled grain/panicle %	179.35	41.47	11.073	236.60	221.90	113.198	0.758	0.186	0.0978
100Seed weight(gm)	0.0916	0.045	0.0303	0.170	0.084	0.1353	0.5388	0.535	0.2239
Grain yield(t/ha)	0.635	0.548	0.230	1.097	0.966	0.406	0.57	0.567	0.566

Table (28): Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and genetic Advance (GA) for 14 traits of 18 rice genotypes

Traits	GCV			PCV			GA		
	2011	**2011**	**2012**	**2013**	**2012**	**2013**	**2011**	**2012**	**2013**
Plant height(cm)	12.277	20.026	13.97	16.216	9.062	11.267	9.928	10.26	10.76
Number of leaves/plant	6.9147	14.193	-	14.016	-	4.7925	0.228	-	0.107
Number of tillers/plant	0.095	0.1193	16.75	24.030	10.72	20.408	0.188	1.546	2.861
Leaf area(cm^2)	13.989	24.80	-	30.942	-	20.988	3.641	-	7.847
Stem diameter (cm)	7.4452	19.202	-	18.917	-	4.474	0.218	-	0.043
Days to 50% flowering	6.8188	10.775	5.582	7.6326	5.52	6.5736	6.757	7.62	8.924
Days to 50 % maturity	0.9482	1.0738	7.00	2.7235	4.80	2.3802	18.04	6.819	5.059
Number of panicle/m^2	0.1083	4.2073	19.011	28.147	12.90	12.499	72.09	25.12	39.83
Panicle length (cm)	7.809	12.955	9.916	48.590	4.751	19.83	1.480	1.010	0.731
Number of grain/panicle	0.1581	0.2438	19.623	117.79	11.87	16.026	11.088	20.67	0.330
Number of filled grain/panicle	0.210	0.3040	32.362	31.913	12.44	12.560	11.09	8.619	3.710
Percentage of Unfilled Grain/panicle %	0.450	0.517	39.62	30.83.6	17.13	9.644	24.02	5.734	2.143
100Seed weight (gm)	12.318	16.781	18.20	17.829	8.36	8.437	0.457	0.319	0.169
Grain yield (t/ha)	42.18	55.44	51.43	44.40	38.73	33.42	1.248	1.148	0.743

4.6 Quality parameters:

4.6.1 Physico-chemical properties:

Analysis of Variance for Physico-chemical showed highly significant differences among tested genotypes in moisture, protein, fiber, fats, ash, and carbohydrate, Table (29). N15 gave the highest content of moisture and protein (9.15 and 8.32%) Y24 and H502 gave the lowest moisture and protein content (6.51 and 6.19%), Table (30). Y33 gave the best percentage of fiber content (5.48%), while N15 gave the lowest percentage of fiber content (2.43%) Table (30).Y30 had the best content of fats (2.35 mg), while W12 had the lowest content of fats (0.32 mg), N5 gave the highest percentage of ash content (1.14%). While H221 and Y22 gave the lowest ash content (0.50%), Table (30). W8 (89.20) had the best content of carbohydrate (89.20), while Y30 had the lowest content of carbohydrate (85.20%) table (30).

4.6.2 Minerals content:

There were high significant differences among rice genotypes for minerals content in the Rice genotypes Table (31). Y30 had the highest content of Ca (62.57 mg), P (444.30 mg), Fe (4.29 mg) and Zn (4.163 mg), While H221 had the lowest content of Ca (27.36 mg), W12 had the lowest content in P (93.67 mg), Z3 had the lowest content of Fe and Zn (0.80 and 0.70 mg). N15 had the heist content of Cu (1.82 mg), Y26 had the lowest content of Cu (0.19 mg) N15 had the highest content of Mn (5.82 mg), while H221 had the lowest content of Mn (0.51 mg). table (32).

4.6.3 Physical properties:

Genotypes displayed great variation in their colour. N 2, N5, N12, Y22, Y26, Y33, W12, W8 and Z3 their color was Beige. N 15 and Y30 their color is Brown. H221 and Yunlu24 their color is white. W 19 had a golden color. H502 is Beige to Brown, N17 was Greenish beige, N14 is Brown to beige, N4 is Brown, Gray, beige, table (33).

N17, N 5, N12, N4 Y22, Y33, Y30, Y24, W12, W19, Z3 and H502 gave the most desirable taste, while N2, N14 Y26, H221, W8 gave the normal taste. N15 is off taste table (33).

Table (29): Mean square for chemical characteristics of rice grains for 18 genotypes grown in seasons (2013)

Source	D.F	F. Value					
		Moisture (%)	Protein (%)	Fiber (%)	Fats (%)	Ash (%)	Carbo-Hydrate (%)
Rep-lication	2	1.352	0.796	1.27	0.1948	1.95	1.7691
genotypes	17	1005.250**	178.74**	841.57**	4165.59**	629.68**	121.27**
Error	34	–	–	–	–	–	–
Total	53	–	–	–	–	–	–
EMS	–	0.001	0.005	0.003	0.000	0.000	0.022
C.V%	–	0.41	1.04	1.21	2.26	1.86	0.17
SE±	–	0.0081	0.017	0.012	0.004	0.0032	0.0348

*significant   **=high Significant   ns=not significant different

Table (30): Mean of chemical characteristics of rice genotypes grains of 18 genotypes in seasons 2013

Genotypes	Moisture (%)	Protein (%)	Fiber (%)	Fats (%)	Ash (%)	Carbo-hydrate (%)
WAB12	8.500 J	6.497K	4.130 I	0.327 N	0.553 K	88.360 C
NERICA2	9.140 B	6.720 J	5.023 D	0.383 K	0.613 J	87.260HI
YUNLU26	8.463 K	6.823 I	3.770 M	0.400 J	0.647 I	88.390 D
WAB19	8.730 F	7.027 G	4.033 J	0.413 I	0.553 K	87.973 E
ZHONGHAN3	8.520 I	6.323 O	5.020 D	0.350 M	0.713 G	87.593 F
HANDAO221	8.767 E	7.240 E	4.553 E	0.363 L	0.503 M	87.340 G
NERICA 15	9.153 A	8.323 A	2.430 Q	1.557 D	0.760 F	86.930 K
YUNLU22	8.783 D	6.433 M	5.340 B	0.427 H	0.503 M	87.297GH
HANDAO502	8.650 G	6.197 P	3.807 L	1.573 C	1.087 B	87.337 G
YUNLU33	8.623 H	6.480KL	5.480 A	0.473 J	0.533 L	87.023J
WAB8	8.447 L	6.923 H	2.813 P	0.503 F	0.560 K	89.200 A
NERICA17	8.883 C	6.403 N	3.560 N	0.407 IJ	0.673 H	88.957 B
NERICA5	8.893 C	7.317 D	4.437 F	0.357LM	1.147 A	86.743 L
NERICA14	8.493 J	7.763B	3.317 O	1.810 B	0.713 G	86.730 L
YUNLU30	7.587 O	7.107 F	4.403 G	2.357 A	0.930 C	85.203M
YUNLU24	6.513 P	7.433 C	4.290 H	0.367L	0.703 G	87.207I
NERICA12	7.727 N	6.457LM	5.303 C	0.347 M	0.903 D	87.007 J
NERICA4	8.197 M	6.930 H	3.977 K	1.240 E	0.843 E	87.010 J
LSD	0.0123	0.0276	0.0214	0.0123	0.0123	0.0580

Means with the same letter for each parameter are not significant at 5% level (LSD)

Table (31): Mean square for minerals content of rice grains for 18 rice genotypes in grown in season (2013)

Source	D.F	F. Value					
		Ca	**P**	**Fe**	**Zn**	**Mn**	**Cu**
Rep-lication	2	0.88	0.779	1.085	0.894	1.0882	5.475
Genotypes	17	39441.4**	2842.73**	11.2824**	3299.99**	9289.5**	5344.4**
Error	34	_	_	_	_	_	_
Total	53	_	_	_	_	_	_
EMS	=	0.006	10.143	0.174	0.001	0.001	0.000
C.V%	_	0.16	1.57	20.22	1.41	1.60	1.85
SE±	_	0.0177	0.750	0.098	0.0071	0.0075	0.0028

*significant   **=high Significant   ns=not statistical deferent

Table (32): Mean values of minerals of grain rice for 18 genotypes

Genotypes	Ca	P	Fe	Zn	Mn	Cu
WAB12	40.160 P	93.667 P	1.313 H	1.297 M	0.927 K	0.257 M
NERICA2	45.287 K	118.667 M	2.117 E	1.563 K	0.737 P	0.307 L
YUNLU26	42.587 M	126.667 L	1.653 G	1.887 F	0.830 M	0.193 O
WAB19	50.637 F	108.667 N	1.227 H	1.640 J	0.633 Q	0.217 N
ZHONGHAN3	38.807 Q	105.000 O	0.807 I	0.720 N	0.813 N	0.353 J
HANDAO221	27.363 R	94.667 P	2.357 D	1.547 L	0.513 R	0.423 H
NERICA 15	60.037 B	347.667 B	3.147 B	3.937 B	5.827 A	1.827 A
YUNLU22	45.700 J	173.000 K	1.923 F	2.703 E	2.657 F	0.323 K
HANDAO502	55.617 D	292.333 D	2.293 D	2.950 D	3.690 D	1.217 C
YUNLU33	46.587 I	200.000 H	1.180 H	1.633 J	1.023 J	0.403 I
WAB8	40.683 N	229.000 F	2.017 EF	1.290 M	1.120 G	0.397 I
NERICA17	51.507 E	191.667 I	2.113 E	1.653 I	1.107 H	0.443 G
NERICA5	49.877 G	174.667 J	1.867 F	1.790 G	1.053 I	0.363 J
NERICA14	57.613 C	311.667 C	1.553 G	3.823 C	4.733 C	1.207 C
YUNLU30	62.570 A	449.333 A	4.297 A	4.163 A	5.207 B	1.687 B
YUNLU24	40.597 O	262.333 E	2.713 C	1.683 H	0.873 L	0.613 E
NERICA12	43.237 L	174.333 J	1.973 EF	1.543 L	0.753 O	0.513 F
NERICA4	47.940 H	203.000 G	2.610 C	2.697 E	3.073 E	0.843 D
LSD	0.0302	1.246	0.163	0.0123	0.0123	0.0123

Means with the same letter for each parameter are not significant at 5% level (LSD)

Table (33): Means of Physical characteristics of rice grain of 18 genotypes grown in (2013)

Genotypes	Color	Granule size (mm) *	Taste **
WAB12	Beige	6.0x2.0x2.0	5
NERICA2	Beige	7.0x2.0x1.8	4
YUNLU26	Beige	5.0x3.0x2.0	4
WAB19	Golden	7.0x3.0x1.0	5
ZHONGHAN3	Beige	7.0x2.0x1.9	5
HANDAO221	White	6.0x2.0x1.0	4
NERICA 15	Brown	7.0x2.0x1.5	2
YUNLU22	Beige	7.0x2.0x2.2	5
HANDAO502	Beige to Brown	5.0x2.0x1.6	5
YUNLU33	Beige	7.0x2.0x2.0	5
WAB8	Beige	7.0x2.0x2.0	4
NERICA17	Greenish Beige	7.0x2.0x1.5	5
NERICA5	Beige	7.0x2.0x2.0	5
NERICA14	Brown to beige	7.0x2.0x1.6	4
YUNLU30	Brown	5.0x2.5x2.0	5
YUNLU24	White	8.0x2.5x2.0	5
NERICA12	Beige	6.0x3.0x2.0	5
NERICA4	Brown, gray, beige	6.1x2.1x2.0	5

*Length x width x thickness

**5: Desirable, 4-3: Normal, 2-1: Off taste

4.7. Molecular characterization:

### 4.7.1: Genetic relationships among rice genotypes

Three primers were used to assess genetic diversity among 18 rice genotypes, Table (34). The selected primers and statistical analysis showed polymorphic bands among the genotypes with average of polymorphic bands per primer 20.6. The maximum percentage of polymorphic were produced by primers OPL18 and OPG05 (18 and 22 bands respectively) with (100%) polymorphism, while the minimum percentage were produced by primer OPK16 95.6% of 23 band.

Table (34): Polymorphism detected by the use of 3 random primers on 18 Rice genotypes

Name of primer code	Sequence of primer (5′- 3′)	Total No. of bands	No. of polymorphic bands	% of Polymorphic Bands
OPK16	GAGCGTCGAA	23	22	95.6
OPL18	ACCACCCACC	18	18	100
OPG05	CTGAGACGGA	22	22	100
Total	-	63	62	295.6
Average	-	21	20.6	89.53

Figure 1: **The PCR product of the amplified fragments of 18 rice genotypes**

The primer OPK16
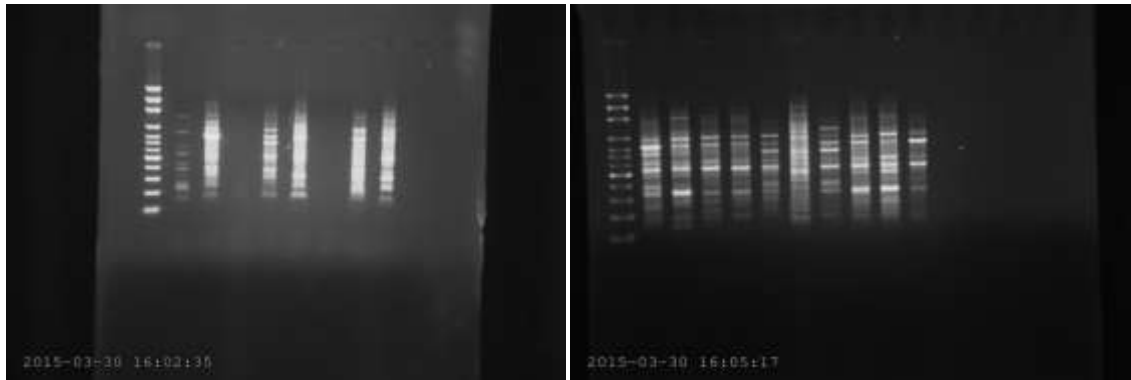
The primer OPL18
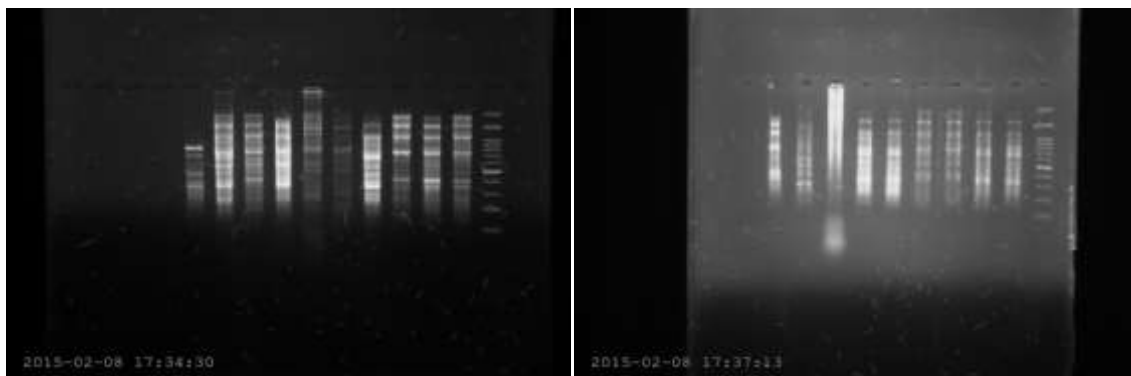
 The primer OPG05

4.7.2 Cluster analysis:

Cluster analysis was used to group the genotypes according to the constructed dendrogram. The dendrogram revealed that the genotypes that are derivatives of genetically similar type clustered more together.

The genetic similarity matrix of RAPD data for the 18 rice genotypes was constructed based on Nei and Li's (1979) coefficient of similarity and shown in Table (35). The genetic similarities of the 18 genotypes ranged from 0.00 to 0.67. However, the smallest genetic distance obtained was observed between the genotypes Z3 and Y24 Table (35). The 18 genotypes were separated into 2 distinct main clusters, and 5 sup cluster (Fig. 2), group 1 was the largest one including 15 genotypes in 4sub groups, the first sub group include the genotypes Y24 and N5. Second sub group include the genotypes W12, N2, Y26, H502, Y22, and W19. Third sub group include N14, N4, N12, Y30 and N17. The fourth sub group includes the high yielding genotypes N15 and H221. The second main group consists of 3 genotypes Z3, W8, and Y33. That's confirming the close genetic relationship for these genotypes,

The Yunlu's genotypes (24, 26, 22, 30, and 33) clustered in all groups, Nerica's genotypes (5, 2, 14, 4, 12, 17, and 15) clustered in the main group number one in different sub groups. WAB's genotypes (12, 19, and 8) were clustered in the two groups. H502 and H221 were presented in two separated sub groups at the first main group, Z3 presented at the second main group. In this study, the allelic diversity released by the 3 primers was sufficient enough to distinguish between the genotypes. The grouping of genotypes on polymorphism data corresponds well to their origin.

Table 35: Matrix of RAPD dissimilarity among 18 rice genotypes based on coefficient was used to construct a dendrogram by unweighted pair group method with arithmetic average (UPGMA) according to Rohlf (1993)
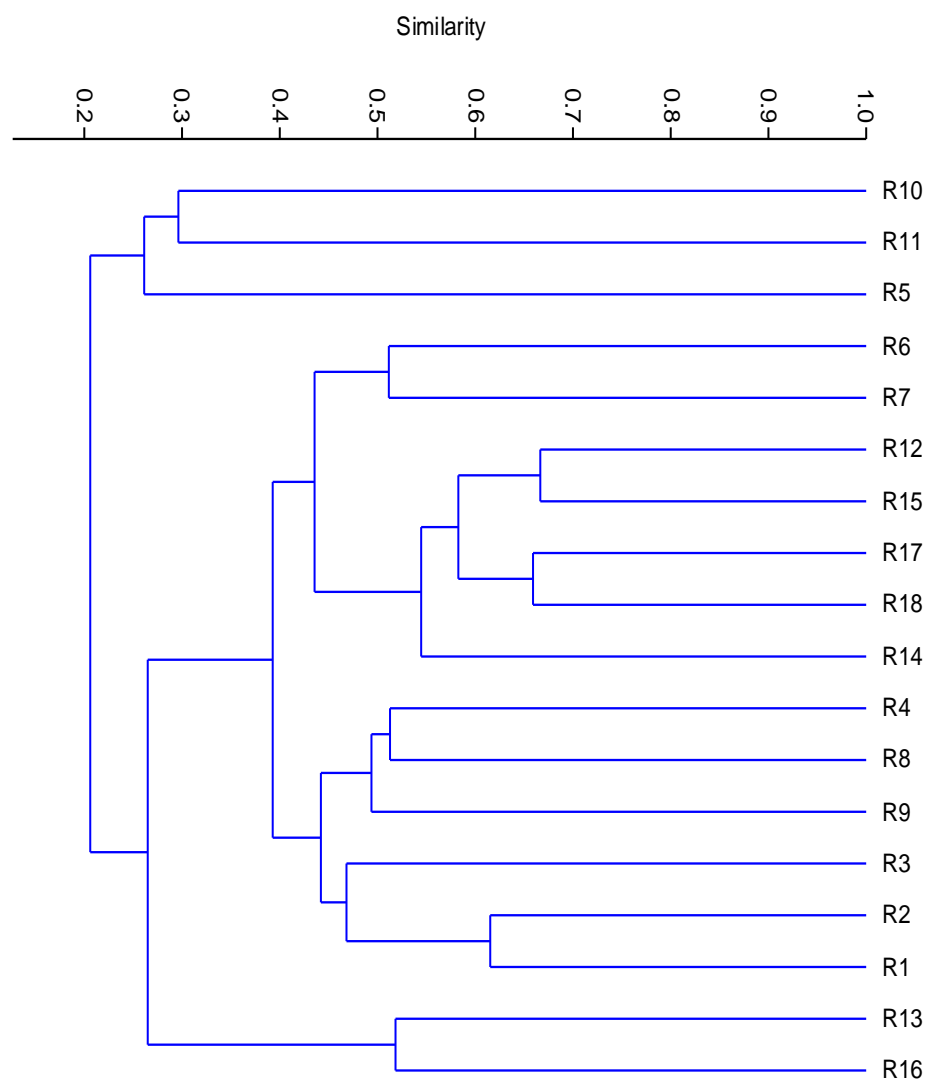
	R1	R2	R3	R4	R5	R6	R7	R8	R9	R10	R11	R12	R13	R14	R15	R16	R17	R18
R1	1.00																	
R2	0.62	1.00																
R3	0.41	0.53	1.00															
R4	0.43	0.50	0.49	1.00														
R5	0.15	0.14	0.17	0.13	1.00													
R6	0.41	0.41	0.24	0.34	0.17	1.00												
R7	0.47	0.43	0.41	0.46	0.17	0.51	1.00											
R8	0.44	0.41	0.46	0.51	0.14	0.45	0.41	1.00										
R9	0.39	0.49	0.37	0.49	0.19	0.43	0.46	0.50	1.00									
R10	0.24	0.23	0.32	0.39	0.25	0.17	0.23	0.33	0.32	1.00								
R11	0.20	0.21	0.22	0.24	0.27	0.19	0.24	0.31	0.29	0.30	1.00							
R12	0.31	0.43	0.28	0.36	0.26	0.40	0.34	0.40	0.48	0.25	0.39	1.00						
R13	0.38	0.29	0.18	0.26	0.00	0.26	0.38	0.20	0.22	0.06	0.08	0.25	1.00					
R14	0.40	0.44	0.33	0.34	0.15	0.48	0.44	0.39	0.43	0.18	0.22	0.49	0.46	1.00				
R15	0.34	0.45	0.32	0.36	0.19	0.43	0.42	0.43	0.42	0.14	0.30	**0.67**	0.32	0.57	1.00			
R16	0.28	0.23	0.22	0.21	**0.00**	0.16	0.26	0.13	0.20	0.06	0.15	0.20	0.52	0.40	0.30	1.00		
R17	0.39	0.46	0.26	0.33	0.26	0.47	0.46	0.32	0.45	0.19	0.29	0.58	0.31	0.56	0.56	0.23	1.00	
R18	0.41	0.50	0.31	0.40	0.20	0.48	0.44	0.42	0.43	0.22	0.29	0.59	0.30	0.56	0.60	0.26	0.66	1.00

R1:W12- R2:N2- R3:Y26- R4:W19- R5:Z3- R6:H221- R7:N15- R8:Y22- R9:H502-
R10:Y33- R11:W8- R12:N17- R13:N5- R14:N14- R15;Y30- R16:Y24- R17:N12- R18:N4

Matrix= Minimum similarity= 0.00 (R16;R5) - Maximum similarity= 67% (R15; R12)

PRIMERS= OPK16; OPL18; OPG5

Figure (2) Dendrogram constructed for 18 rice genotypes based on genetic distances using 3 RAPD Primers

R1:W12- R2:N2- R3:Y26- R4:W19- R5:Z3- R6:H221- R7:N15- R8:Y22- R9:H502-
R10:Y33- R11:W8- 12:N17- R13:N5- R14:N14- R15;Y30- R16:Y24- R17:N12- R18:N4

CHAPTER FIVE

DISSCUSSION

5.1 Growth characters

5.1.1 Plant height (cm)

Plant height in rice is a complex character and it's the end product of several genetically controlled factors (Cheema *et al* 1987). It showed highly significant in individual and combine analysis of variation, the highest mean of plant height was observed in season 2012 then 2013 and 2011. This may due to the fact that Ed duiem environment was more favorable than Shambat, it had the lowest total of temperature for the growing seasons, appendix (3). Hussain *et al.* (2005) reported that water and soil condition, planting and sowing method affect plant height in rice.

5.1.2 Number of leaves/plant:

By increasing the number of leaves, the photothynsis operation will be increased which is helpful for plant physiologically. Season 2011 indicated high number of leaves more than season 2013. The genotypes N14, Y26 and H221 gave the highest number of leaves/plant among the tested genotypes.. Reduction in leaf growth leads to less photosynthesis hence retarded overall plant growth as the resources required for growth processes become limited in supply (Mwai, 2002). That may explain why season 2013 had the lowest stem diameter more than season 2011. All these factors, finally, resulted in better assimilation activities .These results were corresponding with the results of Hossain *et al.* (1999)

5.1.3 Number of tillers/plant

High significant differences were shown by number of tiller in all season for individual and combine analysis. This observation is in agreement with the result supported by Zahid *et al.* (2005), who studied twelve genotypes of coarse rice to check their yield performance in Kallar tract and reported highly significant variation for different traits including the number of productive tillers plant[-1]. Number of tillers is important for yield component in rice. The mean

number of tillers in season 2012 was higher than season 2011 and season 2013, season 2012 was the highest average of rain fall (Appendix 3). That might explain why the number of tiller was reducing in season 2013, according to (Nahvi *et al*, 2004), the number of tillers per square meter is reduced by the increasing of irrigation intervals.

Genotype H221 had the largest number of tillers and highest number of panicles in season 2012, and highest grain yield. These results agreed with Chaturvedi (2005) who found that number of tillers per unit area is the most important component of yield. Sabeti and Jafar zadeh (2006); and Hamidulsalam and Altaf hossain (2002) stated that by increasing the density, the number of fertile tillers per hill is decreased because the competition between plants was increased and therefore low number of fertile tillers per hill. Balasubramaniyan and Palaniappan (1991) attributed higher tiller numbers per plant to greater space available for individual plant to put forth more tillers.

5.1.4 Stem diameter (cm):

High stem diameter will ease the translation of the nutrition from roots to shoot. Highly significant stem diameter was reported in season 2011- 2013. Season 2011 had the largest mean of stem diameter than season 2013. Stem diameter may affect the grain yield, as the genotype Y33 had the highest stem diameter and high grain yield This different in stem diameter detected among the evaluated genotypes indicate the existence of wide range of variability in the tested material. This variation can be attributed to genetic as well as environmental factors. These finding are in agreement with those obtained by Badda (1995), Silva *et al* (2003) Adam (2004) in maize.

5.1.5 Leaf area (cm) ^{2}:

Large leaf area results in a large amount of photothynsis operation which affected plant positively. Bharali *et al*. (1994) found higher direct effect of leaf area on grain yield. The mean of leaf area in season 2013 was higher than season 2011this might be due to the higher temperature in season 2011 than season 2013 (Appendix, 2). Similar result was achieved by Li *et al*. (1994) who reported the effect of temperature and photosynthesis efficiency of leaf area. The leaf area is different from genotype to another and is affected by the temperature, photoperiod and other traits like plant height and plant population density.

Individual and combine analysis showed that N12, Z3, Y26 and W12 had the highest leaf area among the tested genotypes. This result was in agreement with Safaee *et al.* (2007) who found that leaf area index and leaf area duration reduction resulted in a shortage in assimilation which increased competition within the plant hence is a reduction in the number of fertile tillers and then number of grains. A study by Mhaskar *et al.* (2007) in crossing between japonica and indica japonica, indicated that generally the increase in flag leaf area of Japonica /indica japonica was higher than japonica/japonica. This was mainly due to hybrid vigor resulted from the crosses between japonica and indica japonica (there are genetic diversity among them), while no significant difference between japonica/ indica japonica and indica japonica/indica japonica.

5.1.6 Days to 50 % flowering:

The average days to flowering were higher at ED duaim in season 2012 than season 2013 and season 2011 at Shambat. H221 was the latest genotype to flowering in all seasons in individual and combine analysis and it was the highest yielding genotype in season 2011 and combine analysis. Days to flowering affected the yield according to Zaman *et al*. (2005) who investigated genetic variability of characters contributing to genetic diversity in 15 rice genotypes. They found that days to 50% flowering made the largest contribution to yield than other traits. Sikuku *et al*. (2010) reported that the genotype N2 was the least affected by water deficit because it took the least number of days to attain 50% flowering in the plants watered after every 2, 4 and 6 days. In this research H221 took the least number of days to flowering more than N2.

5.1.7 Days to 50 % maturity:

Days to maturity plays a significant role in the cropping system. Early maturing genotypes evacuate the land early for the next crop and escape from insects and pests attack and timely handled. Highly significant different was observed in all season and combine analysis for Days to maturity, this was in fine with Karim *et al*. (2007) who studied 41 rice genotypes for variability and genetic parameter analysis and found highly significant mean sum of square due to genotypes for days to maturity, he reported that variation for days to maturity was attributed by genetic constituent rather than environment. Short duration lines were a good source for breeder to use as parents. Season 2013 had the highest number of days to get mature followed by season 2011 and season 2012.

The genotype N12 was the latest genotype to get mature in season 2012 and it was the highest yielding one, which explained the relation between yield and latest maturing. When the plant flower latterly it will mature latterly too and hence avoid the harm environment resulting in high yielding. This result was matching with Kawakata and Yajima (1995) and Yoshida (1978) findings a determining role for temperature and day duration on panicle emergence and their impacts on physiological, growth and maturity processes and finally, on the highest grain yield.

5.2 Yield characters

5.2.1 Number of panicles/m^2

Number of panicles/m^2 indicated highly significant difference in all tested seasons in combine analysis except for the genotype X season. Season 2011 had the highest average of number of panicle/m^2 followed by season 2013 and season 2012, and it had the highest average number of tillers. That's mean number of tillers was affect directly by number of panicle/m^2. This result is matching with Nuruzzaman *et al*. (1997) who reported that the number of panicles in a yield component largely depends on the number of productive tillers. De Datta (1981) mentioned that Panicle number is influenced by the number of tillers that develop during the vegetative stage. Drought stress causes the reduction in the number of heads per square meter because in drought stress in the period of vegetative growth the assimilation is reduced. Therefore, these assimilate were used by the stem and it cause plant to produce fewer fertile heads per square meter. Kawakata and Yajima (1995) and Yoshida (1978) suggested a determining role for temperature and day duration on panicle emergence and their impacts on physiological, growth and maturity processes and finally, on the highest grain yield. This finding disagreed with this study because the high temperature did not affect the number of panicles. Disregarding temperature, the difference between the genotypes was due to genetic differences because panicle growth is a part of the overall crop growth process.

Genotype H221 had the highest number of tiller/plant and it had the highest number of panicles/m^2, N17 had the lowest number of tillers and lowest number of panicles in season 2012. This finding was in agreement with those obtained by Mohadesi, *et al* (2010) as increasing the number of plant in square meter, the number of heads in square meter is increased, and there was a positive

correlation between grain yield and the number of head per square meter. This result disagreed with the result by Khalid *et al*. (2012) who studied sixteen genotypes x location in ED duaim and Kosti and reported that N17 gave the highest number of Panicles/m^2 (461.6, 447.5). The study disagreed with Sabeti and Zeng and Shannon (2000); Hamidusalam and Altaf hossain (2002) who suggested that by increasing the density, the number of tillers and the number of fertile tillers in hill are reduced but the number of heads per square meter and the grain yield were increased. The result also disagreed with Baloch *et al* (2002); Hamidulsalam and Altaf hossain (2002) who revealed that by reduction of density, the number of heads per hill is increased because the low density has more influence on each of plants and each plant has more space around it and receives more light and has better assimilation activity. Therefore, plants having less density grow better and have more heads.

5.2.2 Panicle length (cm):

Panicle length indicated highly significant difference in individual analysis of season 2011, and season and genotype in combine analysis, this contrasted Tahir *et al*. (2002) who studied genetic variability for different characters in ten rice genotypes. He found that these traits were under the genetic control and could be used in the selection of the desirable traits. Sikuku *et al*. (2010) indicated that there was no significant difference (P≤0.05) in panicle length among the varieties. Season 2012 had the highest panicle length than season 2013 and season 2011. The genotype Z3 had the highest length of panicle in season 2011-2012-2013 and it gave the highest grain yield in combine analysis. This result was in contrast with the result of Khalid *et al*. (2012).

5.2.3 Number of grains/panicle:

Highly significant difference in combine analysis among all genotypes for season, genotype, season X genotypes were noticed. Tahir *et al*. (2002) reported highly significant variation for the grains panicle^{-1} for different genotypes. Other factors as soil fertility, plant nutrients and weather condition might also be responsible for higher grain numbers. Season 2012 had the best number of grain/panicle than season2013 and season 2011; this might be attributed to the temberature at ED duaim location appendix (3). Grain/panicle affected on grain yield according to Akram *et al*. (1994) who stated that greater number of grainspanicle^{-1} is one of the major criteria which contributed to higher grain

yield. The genotype H502 had the lowest number of grain/ panicle in season 2011-2012-2013, and combine analysis too, and it had the lowest panicle length. N15 and N4 had the largest number of grain/panicle but not the largest grain yield which agreed with Khalid *et al*. (2012) who showed that increasing the number of spikelets/panicle does not always result in higher grain yield. H221 had the highest number of grain /panicle and highest panicle length at Shambat in seasons 2011-2013 which agreed with the result of Shahram *et al*. (2012) who noted that grains number in panicle is affected by factors such as panicle growth conditions and the formation of its component including primary and secondary branches and florets before emergence and also panicle fertility rate and photosynthetic products supply during the maturity period.

5.2.4 Number of filled grain/panicle:

In individual analysis of variance there were highly significant differences in season 2011. Although high significant difference in combine analysis was found on season and genotypes X season. Butler *et al*. (2002) and Shah and Bhurer (2005) founded a significant difference between cultivars in terms of the number of filled grains. Season 2012 at ED duaim showed the highest average number of filled grain/panicle more than the seasons 2011 and 2013 at Shambat. That could be attributed to the environmental reasons. Yoshida (1981) attributed the contribution of climatic conditions to the number of filled grains during meiosis division time, the heading stage and maturity period. H502 in season 2013 showed the lowest number of filled grain/panicle and had the lowest number of grain /panicle in the same season. The genotype H221and N5 had the highest number of filled grain/panicle and highest number of grain/panicle at the same season. Temperature in season 2012 Ed duaim during flowering period may affected directly empty panicles phenomenon that reduced grain yield for most genotypes. Rice is grown mainly in tropical and sub tropical zones, and a high temperature at flowering can induce floret sterility and can limit grain yield (Matsui *et al*., 1997).

5.2.5 Percentage of unfilled grin/panicle:

Individual analysis showed highly significant difference in season 2011, significant difference in season 2012 and not significant difference in season 2013 and in combine analysis. Season 2012 recorded the highest percentage of unfilled grain/panicle more than 2013 and 2011, the genotype W19 gave the

highest percentage of unfilled grain/panicle in season 2011 and 2012, W8 and N12 had the highest percentage of unfilled grain/panicle in season 2013. N4 gave the lowest percentage of unfilled grain/panicle in season 2011 and 2013. N14 gave the lowest percentage of unfilled grain/panicle in season 2012. The result agreed with a result by Atif *et al.* (2012) who showed that N14 had the lowest percent of unfilled grain/ panicle of (0.000). It is important to reduce spikelet sterility or increase spikelet fertility (Luzikihupi, 1998).

5.2.6 100-seed weight:

Grain weight is determined by the supply of assimilates during the ripening period and the capacity of the developing grain to accumulate the translocated assimilates (Ntanos and Koutroubas, 2002). In addition, grain weight is variable proportion of spikelet's sterility regulation by moisture, therefore the reason which may be behind grain yield loss with moisture and decrease in the number of filled grain/ panicle and 100 -seed weight. Heavy 1000-grain weight is an important trait, which should be considered in selection for high yield (Prasad *et al.*, 2001; Sürek and Beser, 2003). Highly significant difference was notice in individual analysis among tested genotypes in season 2011 and 2012, significant in season 2013 Combine analysis showed highly significant in season, genotype, genotype X season. Hashemi *et al.* (1995) showed that there was a significant on the 1000 grain weight. Tahir *et al.* (2002) reported highly significant variation among different traits and observe that these traits were under the control of genotypic difference among the genotypes.

Season 2012 had the highest 100-seed weight followed by season 2011 and season 2013. Season 2013 had the most desirable environment and rain fall (Appendix 3). This contrasted Rahim *et al* (2012) who found that water limitation in the period of growth and germination decreased seed weight and amount of amylase in rice. The genotype Z3 had the highest weight of 100 -seed in season 2011 and 2012, and it had the highest leaf Area in season 2011. W8 had the lowest 100-seed weight in season 2013 and it had the lowest leaf area in the same season this was in agreement with Bharali *et al.* (1994) who reported the influence of 1000-grain weight by flag leaf area. Other factors like adoptability, temperature, soil fertility, season and time might also be responsible for thousand grain weight. This might be due to the difference

between cultivars in terms of the panicle emergence time, grain size, grain filling duration and the sensitivity level to high environmental temperatures

5.2.7 Grain yield (t/ha):

Grain yield is the result of many traits that's affected directly or in-directly on yield. Planting methods and growing environment are therefore among factors influencing yield of the crop. Proper spacing is said to ensure good water management (Mazid, *et al.*, 2003) and photosynthetic activities and assimilate partitioning (Kundu, *et al.*, 1993), thereby resulting in good yield in well spaced rice fields. Planting date affected grain yield due to the suitable growth season duration, coincidence of the phonological stages- especially the heading and grain filling stages with day length and temperature when favorable will positively influence on dynamic formation of the yield components and ultimately the generation of active sinks in addition to the higher dry matter accumulation capacity. Grain yield in early planting date declined due to panicle shedding, low dry matter production and the plant height. (Noorbakhshian, 2003, Pirdashti*et al.*, 2003 and Gines *et al.*, 1987). There was a significant difference among genotypes in terms of grain yield. Individual analysis of variance showed highly significant difference among tested genotypes on yield in all seasons. Combine analysis showed highly significant except for season. Same result is achieved by Zahid *et al.* (2005), who studied twelve genotypes of coars rise to check their yield and yield performance in Kallar tract and reported highly significant variation in the grains yield which might be due to the environment (Mahpattra, 1993) or the correlation of grain yield/plant with various yield contributing characteristic like fertility of soil, flag leaf area, grain/panicle and gain weight and correlation these traits.

Season 2012 indicated the highest yield (1.90t/ha) followed by season 2011 (1.88 t/ha) then season 2013 (1.74t/ha). This may be attributed to the temperature according to Kawkata and Yajima (1995). Yoshida (1978) suggested a determining role for temperature and day duration on panicle emergence and their impact on physiological, growth and maturity process and finally on the highest grain yield. Parasad *et al.* (2001) and Hassan *et al.* (2003) studied the effect of environment, temperature and genotypes and found significant heritability for yield contributing traits. In spite of desirable temperature and

rainfall in 2013 appendix (3) it had the lowest grain yield this finding was in contrast with Kato *et al.* (2004).

H221, N14 and Y33 had the highest grain yield on season 2011-2012-and 2013, respectively. Z3 had the highest yield on combine analysis. The study agreed with Atif *et al* (2012) who suggested that all the genotypes gave high grain yield which ranged from 2.17 to 4.03 t ha-1 under irrigated conditions, simple and combined analysis of variance indicated that genotypes differed significantly in grain yield. NERICA 4, NERICA 14, NERICA 15, YUNLU 33 and WAB-1-38-19-14-P2-HB were higher yielding genotypes giving 3.78, 4.03, 3.24, 3.55 and 3.51 t ha-1 respectively. Similar finding was obtained by Atif *et al* (2012). NERICA 14 and YUNLU 33 were classified as high yielding and stable genotypes across environments (locations and years) because of their high grain yield and best performance of traits

5.3 Correlations coefficients among yield and yield contributing traits:

Simple correlation coefficients among yield and yield contributing traits for 18 rice genotypes were calculated for the three seasons (Table 23, 24, 25, and 26). Complete knowledge on interrelationship of plant character like grain yield with other characters is of paramount importance to the breeder for making improvement in complex quantitative character like grain yield for which direct selection is not much effective. Hence, association analysis was undertaken to determine the direction of selection and number of characters to be considered in improving grain yield.

Correlation coefficient less than -1 were observed in this study, similar result was obtained by many workers (Abdel-Mula *etal*, 1993; Fadlalla, 1994; Gasim, 1994 and Ahmed, 1995. Such results are expected to occur, as explained by Pandy and Gritton (1975), when genotypes correlation has a high error variance than line or family variance.

This study revealed that plant height had a positive correlation with grain yield, in all tested seasons in individual and combine analysis this results were agreed with many workers like Prasad *et al.* (2001) who studied genetic variability, coefficient of selection and correlation for various yield and yield contributing parameters and found significant correlation between grain yield and plant height. Rasheed *et al*. (2002) and Girish *et al*. (2006) reported positive

association of plant height with grain yield. The significant positive correlation between grain yield per plant with the plant height agreed with Xu (1986); Pandy and Gritton (1974) found the same result and Sharma and Kumar (1987) in maize The result is disagreed with Zahid *et al.* (2005) who studied 14 genotypes of basmati rice and he reported that reported that plant height has negative correlation with yield. Khan *et al*. (1991), also reported negative correlation between plant height and tillers per plant.

Number of tiller/plant had a positive correlation with grain yield in seasons 2012, 2013 and combine analysis, this result in agreement with the result by Khalid *et al* (2012) who reported that Grain yield was positively and significantly (P≤ 0.01) correlated with number of tillers/plant, Luzikihupi (1998) stated that number of tillers plant^{-1}, is the most important traits that directly contributed to the grain yieldha^{-1}. In season 2011 number of tillers/plant had a negative correlation with grain yield, this result is agree with Zahid *et al*. (2006) who found that there were a negative correlation between number of tillers per plant and grain yield and he mentioned this might be due to increased frequency of barren tillers.

Days to flowering had a positive correlation with days to maturity at seasons 2012, 2013 and combine analysis that's similar with the result by Mehetre *et al*. (1996) who reported that Days to maturity were positively and significantly correlated with days to 50% flowering.

Number of panicles/m^2 had appositive correlation with grain yield in seasons 2011, 2012 and combine and that's similar with Mirza *et al*. (1992); Amal and Eatemad (2012) who stated that a positive correlation among panicle/plant and grain yield /plant.

Panicle length had a positive correlation with grain yield, it may due to the reason that if the panicle is long it will bring a lot of grains witch increase the yield, the result is agree with Mirza *et al*. (1992) who reported positive correlation among panicle length and grain yield /plant. Sharma and Sharma (2007) found highly significant positive correlation of grain yield per plant with panicle length in forty four extra early and early maturing rice genotypes. Khalid *et al* (2012) reported that Grain yield was positively and significantly (P≤ 0.01) correlated with panicle length (cm) in both seasons (2008-2009), Prasad *et al*., 2001; Iftekharuddaula *et al*., 2002; Sürek and Beser, 2003) found that the panicle

length had positive direct effect on grain yieldha[-1] (0.247). Amal and Eatemad (2012) who find highly significant and positive between panicle length and grain yield.

Panicle length had appositive correlation with number of grain/panicle this similarly to the result by Mirza *et al*. (1992) who studied 25 early maturing genotypes for interrelationship and found that number of Grain panicles is positively correlated with panicle length.

Number of grains/panicle exhibited the positive correlation with grain yield in seasons 2012, 2013, and combine over seasons. Sharma and Sharma (2007) found highly significant positive correlation of grain yield per plant with grains per panicle, in forty four extra early and early maturing rice genotypes. Lidanski *et al* (1987) reported that there were Positive correlations between number of grains per cob and grain yield per plant in maize. Bhatti *et al*. (2005) reported that number of grains per panicle has a positive genotypic and phenotypic correlation with grain yield. Similarly Mirza *et al*, (1992), reported positive correlation among number of grain and yield plant[-1].

Number of filled grain/panicle had a positive correlation with grain yield in season 2013 and combine analysis this in agreement with many research workers reported similar findings Luzikihupi, 1998 who reported that filled grains/panicle has a high significant correlation with grain yield, Khalid *et al* (2012) reported grain yield was positively and significantly (P≤ 0.01) correlated with number of filled grains/panicle. Prasad *et al*., 2001; Iftekharuddaula *et al*., 2002; Sürek and Beser, 2003) reported Positive correlation of number of filled grainspanicle-1 with grain yield/ha. Luzikihupi (1998) showed that number of filled grains/ panicle were the most important traits that directly contributed to the grain yield/ha. Number of filled grain/panicle had a negative correlation with percentage of unfilled grain/panicle at all seasons and combine analysis this result in agreement with Mehetre *et al*. (1996) who reported negative relationship between number of filled grains/panicle and number of unfilled grains/panicle.

100-seed weight had a positive correlation with grain yield at all seasons and combine analysis this result is agree with the result by Mirza *et al*. (1992) and Bhatti *et al*. (2005) who reported that 1000-grain weight has positive genotypic and phenotypic correlation with grain yield, Süerk (2003) and Kato *et*

al. (2008) stated grain yield was positively and significantly (P≤ 0.01) correlated with 1000 grain weights. Prasad *et al*., 2001; Iftekharuddaula *et al*., 2002; Sürek and Beser, 2003) indicated that the significant positive correlation between 1000 grain weight and grain yieldha-1 resulted mainly from the direct effect of 1000 grain weight.

These results suggest that the selection for these components would be effective in the improvement of grain yield. This close association could be attributed to the effect of genes rather than effect of environmental factors, the selection of the characters may improve the grain yield. This association may be due to linkage (Yassin, 1973) or to developmentally induced relationships between these components that are only indirectly the consequence of gene action (Adams, 1967). Negative correlation could be attributed to the competition between these characters for assimilates during their development (Adams, 1967). Similar results were obtained by Gandi *et al* (1963) and Ahmed (1995).

5.4 Heritability (h^2):

Heritability was over 50% in characters, such as, number of tillers/plant in season 2011 and 2013, days to 50% flowering in season 2012 and 2013, days to 50% maturity in season 2011 and 2013 and percentage of unfilled grain/panicle in season 2011, So, these estimates are helpful in making selection on the basis of phenotypic performance. Some additive portion of genetic variance is fixable in nature; so the selection of these traits is expected to be effective. For effective selection, genetic advance was computed because high heritability does not necessarily mean an increased genetic response to signify the selective advantage accruing in an additive character Johnson *et al* (1955).

Low heritability estimate were exhibited by number of leaves/plant in season 2011 and 2013, stem diameter in season 2011 and 2013, number of panicle/m^2 in season 2013. panicle length in season 2012 and 2013, number of grain/panicle in season 2013, number of filled grains/panicle in season 2012 and 2013, percentage of unfilled grain/panicle in season 2012 and 2013, 100-seed weight in season 2013, This result could be due to the variation of environmental component involved in these trait. The moderate heritability estimate for grain yield was attributed to the fact that yield is a complex trait and is controlled by many genes. Since high heritability does not always indicate high genetic gain.

Heritability with genetic advance considered together should be used in predicting the ultimate effect for selecting superior varieties (Ali *et al*., 2002). High heritability and genetic advance were recorded for the days to 50 % maturity in season 2011, number of grain/ panicle in season 2012, percentage of unfilled grain /panicle in season 2011. These results suggested that these traits were primarily under genetic control and selection for these traits can be achieved through their phenotypic performance. High heritability estimates with low genetic advance observed for number of tillers/plant in season 2011 and grain yield in season 2013 indicated non additive type of gene action and that genotype $\times$ environment interaction played a significant role in the expression of the traits.High heritability and high genetic advance for plant height have been shown by Rao and Patil (1996). Zahid *et al*. (2005) studied 14 genotypes of basmati rice and observe high heritability coupled with high genetic advance for plant height and 1000-grain weight. Bello *et al*. (2007) revealed that the low heritability estimates of grain yield are due to the direct and indirect multiplicative effects of yield components on grain yield.

5.5 Phenotypic (PCV) and Genotypic (GCV) Coefficient of Variation:

Phenotypic variability estimated for eighteen genotypes can be attributed to phenotypic as well as genotypic variability. Similar conclusions were detected by others in different cereal crops under different environments (Khalafalla, 1993 and Abuelgusim, 1989). Most of the characters, estimates for phenotypic variance were greater than their respective genotypic ones, this result indicates that large proportion of phenotypic variance was due to environmental effects. In general, the morphological characters had low genotypic variance than their respective phenotypic ones indicating that most differences among genotypes were mainly environmental factors.

Genotypic coefficient of variation measures the variability of any trait. The extent of the environmental influence on any trait is indicated by the magnitude of the differences between the genotypic and phenotypic coefficients of variation. Large differences reflect high environmental influence, while small differences reveal high genetic influence.

Grain yield showed a relatively high GCV in season 2011and season 2012 (55.44, 51.43) Table (28). Number of grain/panicle had the highest PCV in season 2013 (117.793), Table (28). Generally the GCV was near to PCV for

some traits, indicating a highly significant effect of genotypic on phenotypic expression with very little effect of environment. Similar findings were also reported in sorghum by (Haussmann *et al*. 2002) for stay-green and yield per plant and (Rao and Patil, 1996) for head length panicle exertion and plant height characters. On the other hand, large difference between GCV and PCV was observed for the characters like plant height, number of leaves/plant, leaf area, stem diameter, panicle length, percentage of unfilled grains/panicle, 100- seed weight and yield. This indicated the rule of environmental influence on these characters.

High GCV and PCV was observed for grain yield at the three seasons, the high GCV for this traits indicated further selection could improve the genotypes, this result was in agreement with Sharma and Sharma (2007) who observed high GCV for grain yield per plant in forty four extra early and early maturing rice genotypes. Das *et al.* (2007) found very high PCV and GCV for grain yield among 20 promising lowland rice genotypes. Jaiswal *et al*. (2007) observed highest genotypic coefficient of variation for grain yield in twenty-five indigenous aromatic rice genotypes. Nayak and Reddy (2005) reported that the grain yield had maximum GCV and PCV values. Johnson *et al.* (1955) reported that effectiveness of selection depends not only on heritability but also on genetic advance. In the present investigation, high heritability associated with high genetic advance was found in the characters like days to maturity, this indicated that this character were mostly governed by additive gene action. Nair and Rosamma (2007) observed high heritability associated with high genetic advance for the characters like days to flowering, plant height, grain per panicle and grain yield in fifty rice genotypes of different eco-geographical origin. Das *et al*. (2007) reported high heritability associated with high genetic advance for the character grain yield per plant. Jaiswal *et al*. (2007) observed high heritability (broad sense) coupled with high genetic advance for the characters like grain yield per plant, number of panicle bearing tillers and number of grains per panicle in twenty-five indigenous aromatic rice genotypes.

5.6 Quality:

N15 was indicated the highest percentage of Moisture and protein of (9.153, 8.323 %) respectively Table (29). Followed by Nerica 5 that gave the highest percentage of Ash (1.147 %) table (29), Yulu (33, 30) gave the highest

percentage of Fibers and Fats (5.480, 2.357%) respectively, Table (29). This result is agreed with the result by Dingkuhn *et al* (1998) that the Nerica's genotypes contains 2% more protein than other rice genotypes. Pathiraje *et al* 2010 indicated that all rice types contained approximately the same quantity of crude protein, crude fiber, crude fat and ash. The rice varieties with red pericarp contained significantly (p<0.05) higher crude fiber content than did the rice with white pericarp. The results further showed that the crude protein content in parboiled rice was relatively higher as compared to their unparboiled counterparts. Neria (4, 2, 5) were content (8.2, 9.1, 8.9) percentage of protein respectively, Hossain *et al.* (2009) found that Fertilizer had showed significant influence on protein percentage in brown rice. The highest protein (7.78%) was found by recommended chemical fertilizer dose and the lowest (6.80%) was found by control. Pandey *et al*. (1999) and Hemalatha *et al*. (2004) reported that all the sources of organic manures improve the soil fertility, yield and quality of rice.

5.7 Molecular markers and genetic diversity:

Large amount of genetic diversity (89.53%) among genotypes was revealed by selected primers. The estimated diversity in this study was higher than in some previous rice studies, such as reported by Melo *et al*. (2001)in maze, who obtained 61.46% of polymorphic bands working with hybrids and Lanza *et al*. (1997), who obtained 80.6% of polymorphism between inbred lines using RAPD markers. The amount of genetic diversity observed in molecular studies depends on the number types of primers used and amount of diversity among the genotypes used in the investigation. In this study, genetic diversity might be due to highly divergent genotypes examined. More appropriately, the chosen primers were able to recognize the genetic differences among genotypes. On the other hand, the knowledge of genetic similarity and genetic dissimilarity is meaningful for practical breeding. However, molecular markers are important tools to avoid from the replication of genetic material in the evaluation of genotypes.

The extent of genetic variation in 18 rice genotypes was characterized based on dissimilarity matrix by UPGMA dendrogram which divided the genotypes in to tow major clusters and five sup cluster. The Yunlu's genotypes (24, 26, 22, 30, and 33) clustered in all groups, YUNLU 22 and 26 clustered together at the group one in sup group number two they are very similar in morphological and agronomic traits and they were differed from other YUNLU's genotypes. Brondani *et al.* (2006) reported six clusters constructed from analysis of 192 rice accessions. Ram *et al.* (2007) reported that the cluster dendrogram revealed 5 clusters from 35 rice accessions.

Nerica's genotypes (5, 2, 14, 4, 12, 17, and 15) clustered in the main group number one in different sub groups This results agreed with results obtained by Semagn *et al.* (2006), who studied genetic relationship among 18 NERICA varieties, he found distinct separation of NERICAs 1 to 7 from NERICA,s 8 to 18 in both cluster. WAB's genotypes (12, 19, and 8) were clustered in the two groups. H502 and H221 were presented in two separated sub groups at the first main group, Z3 presented at the second main group.

The high yielding genotypes N15 and H221 were clustered together in group one at sup group number four.

Lanza *et al.* (1997) described that RAPD markers are useful to establish consistent heterotic groups between corn lines. Boppenmeier *et al.*, (1992) and Melchinger (1993), described that molecular DNA markers have been used to analyze the genetic relationships among maize inbred lines and to examine the relationship between DNA marker-based genetic distance and single-cross grain yields in maize genotypes.

Generally, the information of RAPD markers for diversity analysis can be used for better understanding of the genetic relationships among the inbred lines, more effective utilization of the inbred lines in the breeding programs for the development of varieties, and formation of heterotic populations used to derive promising inbred lines.

CHAPTER SIX

Summary and Conclusions

- 1-Highly significant differences were observed in seasons for most of the traits among tested genotypes indicating real genetic variation.
- 2- Zhonghan-3 was the highest yielding genotype in average of the three seasons (2.38t/ha), followed by HANDO221 (2.25t/ha).
- 3-Yunlu's genotypes showed highest quality characteristic more than Nerica's and WAB genotypes. Yunlu 30 identified as the best genotype.
- 4-the present study indicated that among yield components grain yield had the highest genotypic and phenotypic coefficient of variation, number of panicle/m^2 and percentage of unfilled grain/panicle was higher heritability and genetic advance, although these traits correlated positively with grain yield, and they could be used as selection criteria in breeding program in the future
- Results revealed that RAPD was a useful tool in the assessment of genetic diversity among rice genotypes.

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APPENDEX

Appendix (1) Mean square for 18 rice genotype evaluated at Shambat during seasons 2011-2013

Source	D.F	F. Value		
		Leaf Area (cm^2)	Stem diameter (cm)	Number of leaves/ plant
Season	1	3.5173^{ns}	785.84^{**}	0.1706^{ns}
Error A	4	-	-	-
Genotype	17	2.8762^{**}	1.2343^{ns}	1.8461^{*}
season x genotype	17	1.3328^{ns}	1.7385^{*}	1.7083^{*}
Total	107	-	-	-
EMS	-	29.008	0.272	0.173
C.V %	-	21.91	18.35	12.93
SE ±	-	1.6414	0.0398	0.1173

*=significant   **= high significant   ns =not significant

Appendix (2) Correlation coefficients among 14 traits of 18 rice genotypes, combine season (2011-2013)

traits	Plant height	Number of leaves	Number of tiller	Stem diameter	Leaf area	Days to 50% flowering	Days to 50% maturity	Number of panicle	Panicle length	Number of grain/panicle	Number of grain /panicle	Percentage of unfilled grin/panicle	100-seed weight
Number of leaves	0.1752												
Number of tillers	0.0748	-0.0763											
Stem diameter	0.1171	0.1445	0.3298										
Leaf area	0.4157	0.3138	-0.3422	-0.0495									
Days to 50% flowering	-0.0598	-0.1942	0.1509	-0.0522	-0.0664								
Days to 50% maturity	0.2161	-0.0070	-0.1354	-0.3584	0.2034	0.1114							
Number of /panicle	0.0143	0.0549	0.5278	0.6011	-0.2234	0.0803	-0.3069						
Panicle length	0.3016	0.0283	-0.2610	-0.5229	0.4611	0.0073	0.4650	-0.4194					
Number of grain/panicle	0.1024	0.1550	-0.0005	0.0399	0.2056	0.0146	0.2205	-0.2038	0.2814				
Number of filled grain/panicle	0.1287	0.1889	0.0821	0.0807	0.1576	-0.0536	0.0836	-0.1264	0.1801	0.8573			
Percentage og unfilled grain/panicle	-0.0400	-0.1167	0.1686	-0.1319	0.0281	0.1298	0.2485	-0.1212	0.1360	-0.1499	-0.6141		
100-seed weight	0.0961	0.0604	0.2756	0.4259	0.0490	-0.0327	-0.3151	0.3477	-0.1838	0.0101	0.0503	-0.1101	
Grain yield	0.0671	0.1284	0.1848	0.2650	0.0111	0.0652	0.1454	0.2248	-0.0325	0.1225	-0.1244	0.3971	0.2644

Appendix (3): Mean minimum and maximum for rain fall temperature (°C) and relative humidity (%) at Shambat and Ed duaim during seasons (2011-2012 and 2013)

Weather and climate seasons	Total rain fall			Mean temperature °C						Relative humidity %		
	2011	2012	2013	2011		2012		2013		2011	2012	2013
Element month				max	Min	Max	min	Max	min			
June	0.1	56.4	0.0	41.8	26.2	39.4	26.5	41.5	26.7	23	43	27
July	23.4	169.9	14.4	39.8	26.7	34.3	23.6	40.4	25.9	33	68	33
August	9.3	127.7	69.0	38.2	26.5	32.1	23.4	35.4	25.8	44	65	57
September	TR	25.9	3.2	39.3	26.1	36.3	24.4	38.8	26.4	35	55	41
October	2.2	3.2	0.2	39.9	25.1	38.4	25.1	38.4	24.5	29	47	27
November	0.0	0.0	0.0	32.7	16.7	35.8	22.2	35.3	19.6	25	34	27
December	0.0	0.0	0.6	31.8	17.2	32.3	18.6	31.6	15.9	33	37	32
Total	35	383.1	78.4	224.2	165	249	164	261.4	285	31.7	49.8	31

Max: Maximum

Min: Minimum