# GENETIC VARIABILITY AND CHARACTER ASSOCIATIONS INUPLAND RICE (*Oryza sativa* L.) GENOTYPES EVALUATED AT GOJEB AND GURAFERDA, SOUTHWESTERN ETHIOPIA

**M.Sc. THESIS**

**By**

**AWEL BESHIR HUSEN**

**OCTOBER, 2018**

**JIMMA UNIVERSITY**

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**AWEL BESHIR HUSEN**

**A Thesis**

***Submitted to the School of Post Graduate Studies, Jimma University College of Agriculture and Veterinary Medicine, in Partial Fulfillment for the Requirements for the Degree of Master of Science in Agriculture (Plant Breeding)***

**Major Advisor: Prof. Sentayehu Alamerew**

**Co-advisor: Wosene Gebreselassie (Assoc. Professor)**

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**JIMMA UNIVERSITY**

## Jimma University College of Agriculture and Veterinary Medicine

## Thesis Submission Request Form (F-08)

Name of student: **Awel Beshir Husen** ID No: **RM 1348/09**

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I have completed my thesis research work as per the approved proposal and it has been evaluated and accepted by my advisers. Hence, I hereby kindly request the Department to allow me to present the findings of my work and submit the thesis.

Awel Beshir _____
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# DEDICATION

I dedicatedthis thesis manuscript to my father Beshir Husen Saydo and my mother Shkuriya Zeyne Abdo; who did a lot for my educational endeavor.

## STATEMENT OF THE AUTHOR

I declare that this thesis is my work and that all sources of materials used for this thesis have been acknowledged. This thesis has been submitted to the Jimma University College of Agriculture and Veterinary Medicinein partial fulfillment of the requirements forM.Sc. degree in plant breeding. The thesis is deposited at the Jimma University College of Agriculture and Veterinary Medicine Library to be made available to borrowers under the rules of the Library. I solemnly declare that this thesis is not submitted to any other institution anywhere for the award of academic degree, diploma or certificate.

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# BIOGRAPHICAL SKETCH

The author, Awel Beshir Husen, was born on November 16, 1992 at Enemore and Ener, Gurage Zone of Southern Nations, Nationalities and Peoples Regional State, Ethiopia. He attended his Elementary and Junior Secondary School education at Weshe Awasir Elementary and Junior Secondary School from 1999 to 2006 and his Senior Secondary and Preparatory School education at Gunchire Preparatory and Senior Secondary School from 2007 to 2010. After the completion of his Senior Secondary and Preparatory School education, he joined Wolaita Sodo University and graduated withB.Sc. degree in Plant Sciences in 2013.

Soon after his graduation, he served at Addis Ababa City Administration, Yeka Sub-city, Woreda 8 from 2013 to 2014 as urban agriculture officer. Then, he was employed by Southern Agricultural Research Institute, Bonga Agricultural Research Center as a junior cereal crops breeder in 2014. After serving for two years at this research center, he joined Jimma University College of Agriculture and Veterinary Medicine for M.Sc. degree study in plant breeding in 2016.

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# LIST OF ACRONYMS AND ABBREVIATIONS

| | |
|---|---|
| AATF | African Agricultural Technology Foundation |
| ANOVA | Analysis of Variance |
| CSA | Central Statistical Agency of Ethiopia |
| EIAR | Ethiopian Institute of Agricultural Research |
| FAO | Food and Agricultural Organization |
| FNRRTC | Fogera National Rice Research and Training Center |
| FRG | Farmers Research Group |
| GCV | Genotypic Coefficient of Variation |
| IGC | International Grains Council |
| IRRI | International Rice Research Institute |
| MoA | Ministry of Agriculture |
| NVT | National Variety Trial |
| PCA | Principal Component Analysis |
| PCV | Phenotypic Coefficient of Variation |
| PVT | Preliminary Variety Trial |
| SAS | Statistical Analysis System |
| SNNPR | Southern Nations Nationalities and People's Region |
| WARDA | West Africa Rice Development Association |

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**Genetic Variability and Character Associations in Upland Rice (*Oryza sativa* L.) Genotypes Evaluated at Gojeb and Guraferda, Southwestern Ethiopia**

## ABSTRACT

*Rice is an important cereal crop grown in different parts of Ethiopia.Despite information on genetic variability is a pre-requisite for further improvement of any crop, studies on genetic variability and association of charactersamong the rice genotypes in southwestern Ethiopia is very limited. Therefore, this research was conducted to estimate the extent of genetic variation and association among yield and yield related characters in upland rice genotypes. A total of 36 upland rice genotypes were evaluated for 18 characters using simple lattice design at two locations (Gojeb and Guraferda) during the 2017 main cropping season. The combined analysis of variance over the two locations revealed that the genotypes showed highly significant($P \leq 0.01$) differences for all the characters studied, except for days to 50% heading, panicle weight, thousand seed weight, lodging incidences anddisease (leaf blast and brown spot). Similarly genotype × location interactions revealed highly significant ($P \leq 0.01$) differences for panicle shattering and grain yield and significant ($P \leq 0.05$) differences for days to 85% maturity, plant height, number of fertile tillers per plant, number of unfilled spikelets per panicle and biomass yield.Higher phenotypic coefficient of variation (PCV) and moderate genotypic coefficient of variation (GCV) were observed for panicle shattering.Moderate to high broad sense heritability was observed for days to 85% maturity, panicle length, number of total tillers per plant, number of fertile tillers per plant, number of filled spikelets per panicle, number of unfilled spikelets per panicle, biomass yield, harvest Index, number of panicles per meter square and plant height. Among the studied characters number of total tillers per plant, number of fertile tillers per plant, number of panicles per meter square, biomass yield and harvest Index had moderate values of genetic advances as percent of mean. Grain yield showed positive and highly significant correlations with days to 85% maturity, panicle length, number of fertile tillers per plant, number of panicles per meter square, biomass yield and harvest index at both genotypic and phenotypic levels. Phenotypically, number of panicles per meter square and genotypically, harvest index exerted the maximum positive direct effect on grain yield. The squared distance ($D^2$) analysis grouped the 36 genotypes in to four clusters. This makes the genotypes become moderately divergent. The Chi-square ($x^2$) test showed that all inter-cluster squared distances was highly significant. The principal component analysis revealed that four principal components have accounted for 70.54% of the total variation. The present study revealed that number of panicles per meter square and harvest index can be considered for selection. However, there was no sufficient genetic variation for the characters studied in the rice genotypes therefore,it is better to widen the genetic base of the rice genotypes by hybridization and introduction of more rice germplasms from International Rice Research Institute and African Rice Center for a successful breeding program in Southwestern Ethiopia. In addition, in order to give confirmative results, further studies in more locations and years, supported with molecular breeding approach should be conducted on rice genetic variability and character association.*

**Key words**: Upland rice, Variability, Heritability, Genetic advance, Character association.

# 1. INTRODUCTION

Rice belongs to the genus *Oryza* within the grass family *Gramineae* (*Poaceae*). There are about 25 species of *Oryza*. Of these only two species are cultivated, namely *Oryza sativa* and *Oryza glaberrima*. *Oryza sativa* isoriginated in southern and southwestern tropical Asia (Fuller, 2011). The other species of cultivated rice, *Oryza glaberrima,* is indigenous to Inner delta of Niger River and some areas around Guinean coast of Africa are considered to be center of diversity ofAfrican rice(Wopereis *et al*., 2013). The two cultivated species of riceare diploids with a chromosome number of 2n = 2x = 24 and they are normally a self-pollinated crop but up to 3% natural out crossing may be occurred depending on the type of cultivar and the environment they have grown (Poehlman *et al*.,1995).

Rice(*Oryza sativa* L.) has been domesticated, cultivated and consumed by many people worldwide for more than 10,000 years longer than any other crop (Onyango *et al*., 2014). It is the most important food crop and energy source for about half of the world's population (Manjappa *et al*., 2014). More than 3.5 billion people in the world depend on rice for more than 20% of their daily calories (IRRI, 2012). It has also been used as animal feed, production of alcoholic beverages such as wine, rice bran oil, fuel and manufacture of insulation materials (Chakravarthi and Naravaneni, 2006). Rice grain contains 75 to 80% starch, 12% water and 7% protein (Hossain *et al*., 2015;Oko *et al*., 2012). Minerals like calcium, magnesium and phosphorus are present along with some traces of iron, copper and zinc. In addition, rice is a good source of niacin, thiamine and riboflavin (Oko *et al*., 2012).

Globally, rice is grown in more than 117 countries across all habitable continents covering a total area of about 163 million hectares with a global production of about 740 million metric tons (FAOSTAT, 2014). Asia is the leader in rice production accounting for about 90% of the world's production. Over 75% of the world supply is consumed by people in Asian countries and thus, rice is of immense importance to food security of Asia (IGC, 2014).The world largest volume of rice production is concentrated in China, India, Indonesia, Vietnam, Thailand, Bangladesh, Burma, Philippines, Brazil and Japan. The share of the above top ten rice producing countries account for about 32.9, 24.4, 11.0, 7.0, 6.0, 5.4, 5.3 2.9 and 1.8 % of the world production, respectively(FAO, 2013).

Rice is also an important staple food crop in many African countries. It is largely cultivated in West Africa(Smith, 2001). It has been the most rapidly growing food source across the continent. However, the local production is largely insufficient to meet the consumption needs. Annual rice production in Sub-Saharan Africa (SSA) is estimated to be 14.5 million metric tons. Most of this rice is produced by smallholder farmers. In contrast, Africa‘s rice consumption is about 21 million metric tons creating a deficit of about 6.5 million metric tons per year valued at US$ 1.7 billion that is imported annually. Overall, imported rice accounts for roughly 31 percent of Sub-Saharan Africa local rice consumption (AATF, 2013).

Cultivation of rice in Ethiopia is a recent phenomenon it was started first at Fogera and Gambella Plains in the early 1970’s (Tamirat*et al*., 2017) and grown under widely varying conditions of altitude and climate. It is important cereal crop cultivated in different parts of the country next to teff, maize, wheat and sorghum (MoA, 2010). Currently, rice is considered as a strategic food security crop and used as a food crop, income source, employment opportunity and animal feed has been well recognized in Ethiopia (Teshome and Dawit, 2011). Considering the importance and potential of the crop, it has been recognized by the Government as “the new millennium crop of Ethiopia” to attain food security. The potential area for rice production in Ethiopia is estimated to be about 30 million hectares(5 million hectares highly suitable and about 25 million hectares suitable) (MoA, 2010). According to CSA (2017) the average rice productivity in Ethiopia is about 2.8 t $ha^{-1}$, which is much lower than that of the world’s average(4.4 t $ha^{-1}$) (FAO, 2016). This lowproductivity of rice in Ethiopia is attributed to a number of factors such as shortage of improved varieties, lack of recommended crop management practices, lack of pre- and post-harvest management technologies and lack of awareness on its utilization (Tesfaye *et al*., 2005).

Among the major rice growing regions of Ethiopia, Southern Nations, Nationalities and Peoples Region (SNNPR) is one of the largest producers of upland rice. In the region, rice is mainly cultivated in Kaffa (Gimbo), Bench Maji (Guraferda, Menit Goldia and Menit Shasha) and Sheka (Yeki) Zones (EIAR/FRG II, 2012; Mebratu*et al*., 2015). Out of the total rice produced in the country in 2016/17, 7,408.6 tons were produced in SNNPRwith average annual productivity of 2.0 t $ha^{-1}$ (CSA, 2017). Rice yield gap survey done at Guraferda and Gojeb districts of Bench Maji and Kaffa Zones, respectively revealed that the major rice

production and productivity constraints in the order of importance were shortage of improved varieties, diseases, weeds, insect pests, drought and poor management practice (BARC, 2015).

To initiate appropriate breeding procedure in crop improvement programme and developing genotypes with high productivity, information on the extent and pattern of genetic variability and associations among yield and yield related characters becomes a pre-requisite (Kumar *et al.*, 2013; Tiwari *et al.*, 2011). Previous research work on genetic variability and associated characters within rice genotype has been widely reported by different researchers. For instance, Mulugeta *et al*. (2016) reported the presence of wide genetic variation among 22 upland rice genotypes in their genetic variability study at Pawe, Northwestern Ethiopia. Mulugeta *et al*. (2012) reported the presence of genetic variation among 14 rice genotypes in their genetic variability study at Southwestern Ethiopia.Tefera *et al*. (2017) reported high phenotypic and genotypic coefficients of variation for plant height, number of unfilled grain per panicle, biomass yield and grain yield in their genetic variability study in lowland rice genotypes at Fogera and Pawe, Ethiopia. According to Mulugeta *et al*. (2016) grain yield exhibited positive and significant phenotypic and genotypic correlations with days to maturity, plant height, fertile tillers per plant, unfilled grains per panicle and biomass yield.

Despite information on the extent and pattern of genetic variability andassociation among charactersbecomes a pre-requisite for further improvement of any crop, studies on genetic variability and association of characters among the rice genotypes in southwestern Ethiopia is very limited and the information is not sufficiently available. Hence, the present study was under taken with the following objectives:

**General Objective**

- To determine the extent of genetic variability and character associations in upland rice genotypes evaluated at Gojeb and Guraferda.

**Specific Objectives**

- To estimate the extent of phenotypic and genotypic variancesand coefficients of variation, heritability and genetic advancein upland rice genotypes.
- To determine the correlations among characters and thereby compare the direct and indirect effects of the yield related characters on yield.

# 2. LITERATURE REVIEW

## 2.1. Taxonomy, Origin and Distribution of Rice

Rice is a plant belonging to the kingdom *plantae*, division *magnoliophyta*, class *liliopsida*, order *poales*, family *gramineae (poaceae)*, genus *Oryza.* The genus *Oryza* consists of 25 species, of which 23 are wild species and two,*O. sativa* and *O. glaberrima* are cultivated (Brar and Khush, 2003). O. *sativa, O. glaberrima* and 14 wild species are diploids with 2n = 24 chromosomes and the other eight wild species are tetraploids with 4n = 48 chromosomes (Vaughan *et al.,* 2005). The species *O. sativa* is made up of three subspecies namely: *Indica, Japonica* and *Javanica*. The species of the genus *Oryza* are broadly classified into four complexes *viz*. Sativa, Officinalis, Ridley and Meyeriana. Of these, Sativa and Officinalis complexes are the best studied. The Sativa complex comprises the cultivated species *O. sativa* and *O. glaberrima* and their wild ancestors' *viz.,* perennial rhizomatous *O.longistaminata, O.barthii* (formerly *O. breviligulata*) *andO. rufipogon, O. nivara* and *O. sativa f. spontanea* The species of Sativa complex constitute the primary gene pool of rice while the species belonging to Officinalis complex constitute the secondary gene pool. The species belonging to Meyeriana and Ridleyi complexesconstitute the tertiary gene pool (Khush, 1997).

The centers of origin and diversity of *O. sativa* and *O. glaberrima* have been traced using archaeological evidences, geographical distribution and genetic diversity. River valleys of Yangtze and Mekonin China are the primary centers of origin of *O. sativa.* On the other hand, Niger River delta in Africa is the centre of origin of *O. glaberrima* (Huang *et al.,* 2012). The foothills of the Himalayas, northern parts of Myanmar and Yunnan Province of China are some of the centres of diversity for Asian rice species. The centre of diversity of *O. glaberrima* is believed to be the Inner delta of River Niger and some areas around Guinean coast. *O. sativa* is believed to have evolved from *O. nivara* while *O. barthii* is believed to be the progenitor of *O. glaberrima* (Barry *et al.,* 2007).

*Oryza sativa* is the most widely grown worldwide, including in Asian, European Union, North and South American, Middle Eastern and African countries. *Oryza glaberrima,* however, is grown solely in West African countries (Huang *et al.,* 2012). Asian rice was domesticated

about 8,200–13,500 years ago in the Pearl River valley region of China and later spread from East Asia to Southeast and South Asia. The crop was then introduced to Europe through Western Asia route and to the Americas during European colonization (Huang *et al.*, 2012).African rice was domesticated in inland delta of upper Niger river, which is today Mali about 3500 years ago and extended to Senegal. However, this rice species did not spread further from its original region because the Asian species was introduced through east Africa by the Portuguese during the 16th century and spread to the west (Vaughan *et al.*, 2005).

### 2.2. Nutritional and Economic Benefits of Rice

Rice is one of the most important food crops among three major food crops in the world and forms the main diet of about more than half of the world's population. It occupies a unique position in many nations because for its importance in traditional diets and the main source of income of many peoples in the world. It is essential for its nutrition, food security and economy of many peoples (Smith and Dilday, 2003). Therefore, improving the productivity of rice would contribute to hunger eradication, poverty alleviation, national food security and economic development (FAO, 2004). Rice is the main source of energy and is an important source of protein providing substantial amounts of the recommended nutrient intake of zinc and niacin. However, rice is very low in calcium, iron, thiamine and riboflavin and nearly devoid of beta-carotene (Gopalan *et al*., 2007).

Tran (2004) stated that 1 billion of the world populace are engaged directly or indirectly with rice production. Rice farming serves as a source of employment, which tends to improve food security. It provides 54% of energy for rural lives and feeds more than 95% of rural families (Norman & Kebe, 2006). Rice is becoming an increasingly accepted food in Africa because it is easy to store and cook (Africa Rice, 2011). Rice farming is the prime activity, energy source and income for about 100 million households in Africa (Sanint *et al.*, 1998). The development of rice sector could be an engine for economic growth across the continent, which would contribute to eliminating extreme poverty and food insecurity, and raise the social wellbeing of millions of poor people. Rice production will create employment along the value chain and in related sectors, and lead to improve nutritional and health status of the rural

agricultural poor. It will allow families to better finance education, giving the next generation more opportunities to break the remaining shackles of underdevelopment (Africa Rice, 2011).

### 2.3. Rice Production Status and Development in Ethiopia

Rice production in Ethiopia has started a few decades ago and now the country is proved to have the potential to grow different rice types for rainfed lowland, upland and irrigated ecosystems (Teshome and Dawit, 2011). It grows from sea level to as high as 3000 meters and it needs a hot and humid climate. It is best suited to regions that have high humidity, prolonged sunshine and an assured supply of water. According to Shahi (1994), in Ethiopia rainfed upland rice could be grown in the altitudinal range of 1000 to 2000 meter above sea level. It is cultivated in Amhara, Tigray, Oromia, SNNPR, Gambella and Benshangule Regions of Ethiopia (MoA, 2010). Rice has become a commodity of strategic significance in Ethiopia for domestic consumption as well as export market for economic development (Hegde and Hedge, 2013). Even though rice is not a traditional staple food in Ethiopia, it is considered a high potential emergency and food security crop (Tereke, 2006).

The trend of rice production in the country is increasing at high rate in terms of area coverage, number of sub-districts and number of farmers (Mekonnen, 2017). The total cultivated area at the national level has increased from 45,454.18 in 2015/16 to 48,418.09 hectares in 2016 / 17. The cultivated area has increased in 2016 /17 as compared to 2015/ 16 by about 6.52%. Accordingly, rice production has increased from a total of 1,268,064.47 quintals in 2015/16 to 1,360,007.26 quintals in 2016/17 and productivity in quintal per hectare has increased from 27.90 in 2015/16 to 28.09 in 2016/17. The number of participant farmers increased from 134,363 2015/16 to 150,041 in 2016/17 cropping season (CSA, 2017).However, rice remains as a minor crop in Ethiopia both in area coverage and production compared to a large area and favorable agro-climatic conditions.

### 2.4. Rice Breeding Strategies in Ethiopia

In Ethiopia, the importance of rice as a food security crop, source of income and employment opportunity due to its relative high productivity as compared to other cereals is recognized by farmers as well as private investors who frequently request for improved varieties for different

agro-ecologies. This, therefore, calls for the need to establish a strong research and development system to bring about productive, sustainable, stable and profitable rice farming system in the country (Tamirat*et al*., 2017). Improved variety is one of the major inputs required for increasing production and productivity of crops. However, a given improved variety has limited life span with its potential because of the dynamic nature of the environment. On the other hand, the producers as well as the consumers' demand for improved variety is also changing from time to time, thereby requiring redesigning of the breeding objectives accordingly. These situations make variety development a continuous and dynamic activity (FRG II, 2011).

The rice breeding system in Ethiopia has focused mainly on the introduction of improved varieties from a range of different sources, including the International Rice Research Institute (IRRI), the Africa Rice Center (the ex-WARDA), Guinea and Madagascar. Federal and regional research centers are concentrating on the evaluation and release of new varieties for local producers (IRRI, 2006). Varieties are developed by advancing promising materials from nursery stage to variety trial following different breeding stages either at regional and/or national level. Varieties can also be developed through introducing commercial varieties that are released and found under production in other countries and conducting adaptation trial at different target locations. To alleviate problem of shortage of improved varieties, 20 improved rice varieties have been developed and officially released in the country. Of which, seven are upland New Rice for Africa (NERICA) rice varieties including NERICA-4 and NERICA-3 released for rain-fed upland ecosystem and NERICA-1, NERICA-2, NERICA-6, NERICA-14 and NERICA-15 released for upland irrigated ecosystem. Out of the remaining 13 released varieties, four varieties are irrigated, two varieties are lowland rain-fed, and seven varieties are upland rain-fed types (Sewagegne, 2011). However, there is stilla shortage of improved varieties in the country. Therefore, to overcome this and thereby increase rice productivity, it is important to be developed different rice varieties, which have high productivity and resistance to biotic and abiotic stresses.

## 2.5. Variability, Heritability and Genetic Advance

### 2.5.1. Variability

Variability is defined as the presence of differences among individuals with in a population. Variation results due to difference either in genetic constitution of the individual of a plant population or environment; where the plant population are growing(Tiwari *et al.,* 2011). Phenotypic variability is the total variability which is observable. Phenotypic value of variation of an individual is made up of genotypic and environmental deviation. In attempting to develop improved varieties, the plant breeder often bases his/her observation on the measurement of the phenotype. The phenotypic variability in a given environment can be measured easily, but it reflects non genetic as well as genetic influence on the phenotypic expression (Bello *et al.,* 2009). Variation of phenotypic value is, therefore determined by variance attributable to genotypic values and environmental deviation (Falconer, 1990; Singh and Ceccarelli, 1996;Welsh, 1990).

According to Welsh (1990), environment is the sum total of all factors to which the organism is exposed. The various environmentalfactors are called biotic or abiotic depending up on their biological and /or non-biological nature (Singh, 1993;Welsh, 1990). Thus, environmental deviations such as differences in fertility level of the soil, moisture content of the soil and seasonal fluctuations contribute to the component of variation. It is very difficult to determine the presence, amount or types of genetic variability if phenotypic expressions are strongly influenced by the environment (Welsh, 1990). Although some environmental variation can be reduced by proper experimentation, its total elimination is impossible because it includes, by definition the non-genetic variance and much of these are beyond experimental control (Gomez and Gomez, 1984).

Genetic variation is defined as the genetic differences among individuals within a population(Falconer and Mackay, 1996;Sharma, 2006). It is a raw material in plant breeding for developing high yielding genotypes and maintaining the productivity of genotypes by incorporating genes for disease and insect resistance as well as tolerance to abiotic stress as drought, cold and salinity (Allard, 1964). The quantum of genetic variation available for

exploitation and the extent to which the desirable characters are heritable is the core of plant breeding because proper management of diversity can produce permanent gain in the performance of plant and can buffer against seasonal fluctuations. Selection is also effective when there is a significant amount of genetic variability among the individual's with-in breeding materials (Tiwari *et al.,* 2011). Genetic parameters such as genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV) are useful in detecting the amount of variability present in the germplasm (Idris *et al*., 2012).

Genetic variability studies for agronomic characters are the key component of breeding programme for broadening the gene pool of rice (Dutta *et al*., 2013). A large number of studies have been conducted to determine phenotypic and genotypic variability for yield and yield related characters of rice. Limbani *et al.* (2017) reported high phenotypic coefficient variation (PCV) and genotypic coefficient of variation (GCV) values for number of fertile tillers per plot (44.07 and 42.75%), number of unfilled grains per panicle (57.89 and 57.25%), harvest index (53.57 and 52.58%), grain yield per plot (49.20 and 47.14%), number of infertile tillers per plot (97.39 and97.08%) and number of filled grains per panicle (41.21 and 40.36%).Tefera *et al*. (2017) reported highphenotypic coefficient variation (PCV) and genotypic coefficient of variation (GCV) values for plant height (31.74 and 28.41%), number of unfilled grains per panicle (52.41and 32.32%), grain yield (33.65 and 24.80%) and biomass yield (33.67 and 28.85%). Tuwar *et al.* (2013) reported high phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) values for plant height, number of tillers per plant, number of fertile tillers per plant and grain yield per plant.

Veludandi *et al.* (2017) and Mulugeta *et al*. (2016) also reported high phenotypic coefficient variation (PCV) and genotypic coefficient of variation (GCV) values for biological yield.According to Ogunbayo *et al*. (2014) moderate phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) values were observed for panicle shattering (17.51 and 16.28%). Tefera *et al*. (2017) reported low genotypic coefficient of variation (GCV) values for days to 85% maturity (7.00%) and number of filled grains per panicle (8.54%). Mulugeta *et al.* (2016)also reported low phenotypic coefficient variation (PCV) values for days to85% maturity (2.75%), plant height (8.61%) and panicle length (8.87%).

### 2.5.2. Heritability

Heritability defined as a component which provides information regarding the amount of transmissible genetic variation out of the total variation and determines the response to selection (Ghosh and Sharma, 2012). The degree to which the genes of an individual influence the phenotype variation is described by the heritability of a given character. It is important to know that heritability estimate is specific to a given population and environment (Bhadru *et al.,* 2012). The most important function of heritability in the study of quantitative characters is its role to predict and indicate the reliability of the phenotypic value as a guide to breeding value (Falconer and Mackay, 1996). Characters are less influenced by environment usually have a high heritability. This may influence the choice of the breeder to decide which selection procedure to use and which selection method would be most useful to improve the character to predict the gain from selection and to determine the relative importance of genetic effects (Bhadru *et al.,* 2012). Heritability estimation in a given population depends on the partitioning of observed variation into component that reflects unobserved genetic and environmental factors (Wray and Visscher, 2008).

Heritability can be either broad sense or narrow sense. Broad sense heritability is the relative magnitude of genotypic and phenotypic variance (VG/ VP) for the characters including additive, dominant and epistasis (multi-genetic interaction), where individuals are directly affected by their parents phenotype. It is used as a predictive role in selection procedures (Allard, 1960). This gives an idea of the total variation ascribable to genotypic effects, which are exploitable portion of variation (Falconer, 1989). Narrow senseheritability is the ratio of additive and phenotypic variance (VA/ VP) and it expresses the extent to which phenotypes are determined by the genes transmitted by the parents (Falconer, 1989).

A large number of studies have been conducted for yield and yield related characters on rice to estimate heritability. According to Konate *et al*. (2016) biomass yield (68.77%), plant height (81.94%) and yield per plant (62.23%)had the highest heritability estimates in 20 inbred lines of rice in research station of African rice center in Benin.Osundare *et al*. (2017) also reported high heritability estimates for days tomaturity (63.25%) and grain yield

(99.99%) and moderate heritability estimates for plant height (48.90%) and number of tillers (53.40%).Mulugeta *et al*. (2012) andOgunbayo *et al*. (2014)reported high heritability estimates for days to maturity, plant height, panicle lengthand panicle shattering. Tefera *et al*. (2017) reported high heritability estimates for plant height (80.10%), panicle length (65.50%) and biomass yield (73.41%) and moderate heritability estimates for days tomaturity (43.56%), number of filled grains per panicle (36.25%), number of unfilled grains per panicle (38.03%) and grain yield (54.35%), while low heritability estimates for number of fertile tillers per plant (18.24%) and harvest index (25.97%). Mulugeta *et al*. (2016)reported moderate heritability estimates for panicle length (35.95%), plant height (44.72%), number of fertile tillers per plant (30.92%) and biomass yield (33.53%), while low heritability estimates for number of unfilled grains per panicle (27.15%) and grain yield (29.53%).

### 2.5.3. Genetic advance

Genetic advance expected from selection refers to the improvement of characters in genotypic value for the new population compared with the base population under one cycle of selection at given selection intensity (Singh, 2001). It denotes the improvement in the genotypic value of the new population over the original population (Ghosh and Sharma, 2012). The estimate of the heritability alone is not very much useful on predicting resultant effect for selecting the best individual because it includes the effect of both additive genes as well as non-additive genes (Bisne*et al*., 2009). Estimates of heritability and genetic advance will help in knowing the nature of gene action affecting the concerned character and also indicates the scope of genetic improvement for these characters through selection. High heritability coupled with high genetic advance exhibited by the characters controlled by additive genes, (Panse *et al.*, 1957; Singh *et al*., 2013) and can be improved through simple or progeny selection methods. Thus, selection for the characters having high heritability associated with high genetic advance leads to accumulate more additive genes. It can enhance the opportunities for further improvements of their performance. High heritability coupled with better genetic advance also confirms the scope of selection in developing new genotypes with desirable characteristics (Ajmal *et al.,* 2009). Therefore, heritability in conjunction with genetic advance would give a more reliable index of better selection value (Akinwale *et al*., 2011).

Shaikh*et al*. (2017) reported high heritability coupled with high genetic advance as percent of mean for plant height (67.07 and 21.48%), number of fertile tillers per plant (86.43 and 29.16%), thousand seed weight (88.54 and 27.94%) and grain yield (98.24 and 48.20%) and also high heritability coupled with moderate genetic advance as percent of mean for number of filled grains per panicle (69.83 and 18.31%). Whilemoderate heritability coupled with low genetic advance as percent of meanwere reported for days to maturity (48.15 and 4.14%) and panicle length (45.68 and 8.50%). Konate *et al*. (2016) reported high heritability coupled with moderate genetic advance as percent of mean for biomass yield (68.77 and 10.94%) and yield per plant (62.23 and 13.00%) and high heritability coupled with low genetic advance as percent of meanfor plant height (81.94 and 5.93%). Mulugeta *et al*. (2012) reported high heritability coupled with moderate genetic advance as percent of mean for plant height (92.17 and 16.55%) and thousand seed weight (83.17 and 10.09%) and high heritability coupled with low genetic advance as percent of mean for days to maturity (82.45 and 4.98%) and panicle length (79.25 and 5.72%). Ogunbayo *et al*. (2014) reported high heritability coupled with moderate genetic advance as percent of mean for plant height (90.65 and 14.85%) and high heritability coupled with low genetic advance as percent of mean for number of tillers (66.22 and 9.52%), days to maturity (86.86 and 5.14%) and panicle length (72.21 and 8.90%).

### 2.6. CorrelationCoefficient

Correlation coefficient measures the relationship between two variables (Dabholkar, 1992). It simply measures mutual association without regard to causation (Dewey and Lu, 1959). While selecting the suitable plant type, correlation studies would provide reliable information in nature, extent and the direction of the selection, especially when the breeder needs to combine high yield potentials with desirable agronomic characters and grain quality characters. Phenotypic and genotypic correlation studies among yield and yield component characters give a better insight on the relationship between them (Jayasudha and Deepak, 2010). Phenotypic correlations involve both genetic and environmental effects (Hallaure and Miranda, 1988). Genotypic correlation is the association of breeding values (additive genetic variance) of the two characters (Falconer, 1989) and it plays a key role in the development and execution of suitable breeding programs (Immanuel*et al.*, 2011). Correlation due to genetic causes are mainly pleiotropic effect of genes and linkage (a phenomenon of genes

inherited together) between genes affecting different characters. Pleiotropy is the property of genes, which affect two or more characters; as a result, it causes simultaneous variations in the two characters when the genes are segregating (Singh, 1993; Falconer and Mackay, 1996). Grain yield, which is the major economic character in rice, depends on several component characters, which are mutually related. Consequently, selection for yield may not be satisfying without taking into consideration yield component characters. Thus, positives correlated between yield and yield components are requires for effective yield component breeding increasing grain yield in rice (Ogunbayo *et al*., 2014).

Association of grain yield with component characters has been extensively studied at both phenotypic and genotypic levels. According to Harsha *et al*. (2017),Idris *et al*. (2012), Khare *et al.* (2014), Mulugeta *et al*. (2016), Ogunbayo *et al*. (2014) and Sadeghi (2011) grain yield showed significant and positive association with days to 85% maturity, plant height, panicle length, number of filled grains per panicle, number of fertile tillers per plant, number of panicles per meter square, biomass yield and harvest index at both phenotypic and genotypic levels. Mulugeta *et al*. (2016) also reported significant association of grain yield with days to 50% heading and number of unfilled grains per panicle at genotypic level only. Venkata *et al.* (2014) reported significant and positive genotypic and phenotypic associations between days to 50% heading and days to 85% maturity. They also reported significant and positive genotypic correlation of biomass yield with days to 50% heading and days to 85% maturityand significant and positive correlation of days to 85% maturity with plant height, number of fertile tillers per plant, biomass yield and thousand seedweight.

### 2.7. Path Coefficient

The estimates of correlation coefficients provide only the relationship between yield and yield associated traits, but do not indicate the relative importance of direct and indirect influence of each of yield related characters on grain yield (Dewey and Lu, 1959). Therefore, in order to find out the interrelationship between grain yield and other yield attributes, direct and indirect effects are worked out using path coefficient analysis. This is because of yield being acomplex character, has been observed to be associated with a number of componentcharacters.Forfullunderstandingofthecomplexrelationshipsbetweengrainyieldandot

her characters,thecomputationofdirectandindirecteffectsofthesecharacterson grainyieldisessential. Aycicek and Yildirim (2006) recommended that study of direct and indirect effects of yield components to increase the yield provides the basis for its successful breeding program and hence, the problem of yield decrease can be more effectively tackled on the basis of performance of yield components and selection for closely related characters. To improve grain yield via selection of its components path coefficient analysis is a useful tool for understanding grain yield formation and provides valuable additional information about the characters (Garcia *et al*., 2003). Theadvantageofpathcoefficientanalysisisthat,it permitsthepartitioningofthecorrelationcoefficientintoitscomponents, onecomponent beingthepathcoefficientorstandardizedpartialregressioncoefficientthatmeasuresthedirecteffecto fapredictor variableuponitsresponsevariable, thesecondcomponentbeingtheindirecteffect(s)ofapredictor variables(DeweyandLu,1959;SharmaandAhmed,1978).

Khare *et al*. (2014) reported number of fertile spikelets per panicle, days to maturity, number of fertile tillers per plant and plant height exhibited positive direct effect on grain yield.Chandrashekhar *et al.* (2017) reported positive direct effect on grain yield per plant was exhibited by days to flowering, number of fertile tillers per plant, number of filled spikelets per panicle and harvest index. Harsha *et al*. (2017) also reported number of fertile tillers per plant and panicle length showed positive direct effect on grain yield per plant at phenotypic level and days to maturity, number of effective tillers per plant and panicle length showed positive direct effect on grain yield per plant at genotypic level.

### 2.8. Multivariate Analysis

#### 2.8.1. Cluster analysis

Clusteranalysis is a multivariate method, which aims to classify a sample of subjects based on a set of measured variables into a number of deferent groups such that similar subjects are placed in the same group (Chahal *et al.,* 2002). Its objective is to sort genotypes into groups, or clusters, so the degree of association will be strong between members of the same cluster and weak between members of different clusters. The cluster analysis will be performed using

a measure of similarity levels and Euclidean distance (Everitt, 1993;Eisen *et al.*, 1998). There are broadly two types of clustering methods, distance-based methods and model based methods. Distance-based methods, in which a pair wise distance matrix is used as input for clustering analysis. The result can be visualized as a tree or dendrogram in which cluster may be identified. Model based methods, in which observations from each cluster are assumed to be random draws from some parametric model and inference about parameters corresponding to each cluster and cluster membership of each individual are performed jointly using maximum-likelihood or Bayesian methods (Johnson and Wichern, 1992).

Another important aspect in cluster analysis is determining the optimal number of cluster or number of acceptable cluster. In essence, this involves deciding where to ‘’cut’’ a dendrogram to find the true or natural groups. An acceptable cluster is defined as a group of two or more genotypes with a within-cluster genetic distance less than the overall mean genetic distance and between cluster distances greater than their within cluster distance of the two cluster involved (Mohammadi and Prasanna, 2003). The resulting cluster of individuals should then exhibit high internal (within cluster) homogeneity and high external (between clusters) heterogeneity. Thus, if the classification is successful, individuals within a cluster shall be closer when plotted geometrically and difference clusters shall be farther apart (Hair *et al.*, 1995). Maji *et al*. (2012) clustered 123 rice populations into seven distinct groupings by using Ward's method. A large number of genotypes was placed in cluster 5 (65 genotypes) followed by cluster 1 (20), cluster 4 (14) and cluster 3 (9), cluster 2 (8) and cluster 6 (7).Ahmed *et al.* (2014) grouped 48 rice genotypes in to five clusters following Ward’s method.

### 2.8.2. Genetic divergenceanalysis

The pattern and level of genetic diversity in a given crop gene pool can be measured in terms of genetic distances. Genetic distances are measures of the average genetic divergence between cultivars or populations (Souza and Sorrells, 1991). Moll *et al*. (1965) defined genetic divergence of two varieties as a function of their ancestry, geographic separation and adaptation to differing environments. It can be also defined as the extent of gene differences between cultivars as measured by allele frequencies at a sample of loci (Nei, 1987). ). It results from the many genetic differences between individuals and may be manifested in

differences in DNA sequence, in biochemical characteristics (e.g. in protein structure or isoenzyme properties), in physiological properties (e.g. abiotic stress resistance or growth rate) or in morphological characters. Genetic similarity is the converse of genetic distances, as it is refers to the extent of gene similarities among cultivars (Smith, 1984). The $D^2$ technique based on multivariate analysis developed by Mahalanobis (1928) is the most potent technique for quantifying the degree of genetic diversity among the genotypes, which in turn is much helpful in selecting parents for hybridization (Arunachalam, 1981; Kwon *et al*., 2002). Several workers studied genetic divergence previously.Rajesh *et al.* (2010) studied genetic divergence in 29 genotypes of rice and found that the mode of distribution of genotypes from different geographic regions into various clusters was at random indicating that the geographic diversity and genetic diversity were not related. The characters days to 50% flowering, grain yield and plant height contributed maximum towards genetic divergence.

### 2.8.3. Principal component analysis

Principal component analysis is a multivariate techniques used for examining relationships among several quantitative variables (Crossa *et al.*, 1995). The main idea of PCA is to reduce the dimensions of a data set with large numbers of variables while conserving the variance of the original data. The PCA generates three important products, the eigenvalues, eigenvectors and scores, the dominant modes representing the most important characteristics from the original data. Generation of a scatter plot from two or more PCs in space reveals sets of similar individuals (Warburton and Crossa, 2002) and relationships between two or more variables (Mohammadi and Prasanna, 2003). Furthermore, it is possible to derive detailed information from the plot of observations over the first two principal components. The resulting diagram can give the researcher an idea about the correctness and inference of cluster analysis results (Bensmail *et al.*, 1997). This will allow visualization of the differences among the individuals and identify possible groups. The first step in PCA is to calculate Eigen values, which define the amount of total variation that is displayed on the PC axes. The first PC summarizes most of the variability present in the original data relative to all remaining PCs. The second PC explains most of the variability not summarized by the first PC and uncorrelated with the first and so on (Jollife, 1986). Maji *et al*. (2012) reported that principal

component analysis resulted in the first two components with Eigen value greater than 1 accounting for 78% of the total variation.

# 3. MATERIALS AND METHODS

## 3.1. Description of the Experimental Sites

The experiment was conducted during the main cropping season of 2017 in two locations (Gojeb and Guraferda), Southwestern Ethiopia. Gojeb experimental site is located in Kaffa zone of Southern Nations, Nationalities and Peoples Regional State (SNNPR), which is located 439 km away from Addis Ababato the Southwest direction. Geographical location of Gojeb experimental site is situated at 07º 15 '0" N latitude and 036º 0' 0" E longitude with an altitude of 1235 m.a.s.l. Its average annual rainfall is 1710 mm with minimum and maximum temperatures of 16.7$^0$C and 24$^0$C, respectively. The soil type of the experimental site at Gojeb is volcanic origin, and is classified as the Andosol orders with clay loam texture. Guraferda experimental site is also located in Bench Maji Zone of Southern Nations, Nationalities and Peoples Regional State (SNNPR), which is located 590 km away from Addis Ababato the Southwest direction. Guraferda experimental site is situated at 06° 50' 368" N latitude and 035° 17' 16" E longitude with an altitude of 1138 m.a.s.l. The annual average temperatures range from 25 to 39°C. The area receives maximum rainfall from June to September and the amount ranges between 1200 to 1332 mm per annum. The soil type of Guraferda is in the Acrisol orders with sandy clay loam texture (Asfaha *et al.*, 2015and Mebratu *et al.*, 2015).

## 3.2. Experimental Materials

In this experiment, 33 upland rice genotypes (Table 1), obtained from two different sets of variety trials conducted by rice breeding section of Fogera National Rice Research and Training Center (FNRRTC)and three released varieties (NERICA-12, NERICA-4 and Adet), a total of 36genotypes, were used.

Table 1: Description of the experimental materials

| No | Genotypes | Status | Seed source | Origin |
|---|---|---|---|---|
| 1 | ART15 8-10-36-4-1-1-B-B-1 | 2016/17 PVT | FNRRTC | Africa Rice Center |
| 2 | ART15 10-17-46-2-2-2-B-B-2 | 2016/17 PVT | FNRRTC | Africa Rice Center |
| 3 | ART16 9-16-21-1-B-2-B-B-1 | 2016/17 PVT | FNRRTC | Africa Rice Center |
| 4 | ART16 9-29-10-2-B-1-B-B-1 | 2016/17 PVT | FNRRTC | Africa Rice Center |
| 5 | ART16-4-1-21-2-B-2-B-1-1 | 2016/17 PVT | FNRRTC | Africa Rice Center |
| 6 | ART16-4-13-1-2-1-1-B-1-1 | 2016/17 PVT | FNRRTC | Africa Rice Center |
| 7 | ART16-5-10-2-3-B-1-B-1-2 | 2016/17 PVT | FNRRTC | Africa Rice Center |
| 8 | ART16-9-1-9-2-1-1-B-1-1 | 2016/17 PVT | FNRRTC | Africa Rice Center |
| 9 | ART16-9-4-18-4-2-1-B-1-1 | 2016/17 PVT | FNRRTC | Africa Rice Center |
| 10 | ART16-9-4-18-4-2-1-B-1-2 | 2016/17 PVT | FNRRTC | Africa Rice Center |
| 11 | ART16-9-6-18-1-1-2-B-1-1 | 2016/17 PVT | FNRRTC | Africa Rice Center |
| 12 | ART16-9-9-25-2-1-1-B-2-1 | 2016/17 PVT | FNRRTC | Africa Rice Center |
| 13 | ART16-9-9-25-2-1-1-B-2-2 | 2016/17 PVT | FNRRTC | Africa Rice Center |
| 14 | ART16-9-29-16-1-1-1-B-1-1 | 2016/17 PVT | FNRRTC | Africa Rice Center |
| 15 | ART16 15-10-1-1-B-1-B-B-1 | 2016/17 PVT | FNRRTC | Africa Rice Center |
| 16 | ART16 15-10-1-1-B-1-B-B-2 | 2016/17 PVT | FNRRTC | Africa Rice Center |
| 17 | ART16-13-11-1-2-B-2-B-2-1 | 2016/17 PVT | FNRRTC | Africa Rice Center |
| 18 | ART16-16-1-14-3-1-1-B-1-2 | 2016/17 PVT | FNRRTC | Africa Rice Center |
| 19 | ART16-16-11-25-1-B-1-B-1-2 | 2016/17 PVT | FNRRTC | Africa Rice Center |
| 20 | ART16-17-7-18-1-B-1-B-1-1 | 2016/17 PVT | FNRRTC | Africa Rice Center |
| 21 | ART16-21-5-12-3-1-1-B-2-1 | 2016/17 PVT | FNRRTC | Africa Rice Center |
| 22 | ART16-9-29-12-1-1-2-B-1-1 | 2016/17 NVT | FNRRTC | Africa Rice Center |
| 23 | ART16-9-14-16-2-2-1-B-1-2 | 2016/17 NVT | FNRRTC | Africa Rice Center |
| 24 | ART16-9-33-2-1-1-1-B-1-2 | 2016/17 NVT | FNRRTC | Africa Rice Center |
| 25 | ART16-9-122-33-2-1-1-B-1-1 | 2016/17 NVT | FNRRTC | Africa Rice Center |
| 26 | ART15-19-5-4-1-1-1-B-1-1 | 2016/17 NVT | FNRRTC | Africa Rice Center |
| 27 | ART16-5-9-22-2-1-1-B-1-2 | 2016/17 NVT | FNRRTC | Africa Rice Center |
| 28 | ART16-21-4-7-2-2-2-B-2-2 | 2016/17 NVT | FNRRTC | Africa Rice Center |
| 29 | ART16-9-16-21-1-2-1-B-1-1 | 2016/17 NVT | FNRRTC | Africa Rice Center |
| 30 | ART15-13-2-2-2-1-1-B-1-2 | 2016/17 NVT | FNRRTC | Africa Rice Center |
| 31 | ART15-16-45-1-B-1-1-B-1-2 | 2016/17 NVT | FNRRTC | Africa Rice Center |
| 32 | ART16-5-10-2-3-B-1-B-1-1 | 2016/17 NVT | FNRRTC | Africa Rice Center |
| 33 | ART16-4-1-21-2-B-2-B-1-2 | 2016/17 NVT | FNRRTC | Africa Rice Center |
| 34 | NERICA-12 | Released variety | FNRRTC | Africa Rice Center |
| 35 | NERICA-4 | Released variety | FNRRTC | Africa Rice Center |
| 36 | Adet | Released variety | FNRRTC | Africa Rice Center |

PVT = Preliminary Variety Trial and NVT = National Variety Trial, FNRRTC = Fogera National Rice Research and Training Center.

Figure 1: Picture indicating overview of the field experiment

### 3.3. Experimental Design

The field experiment was laid out in 6x6 simple lattice design. The gross plot size of the experiment was $7m^2$ (4 m length and 1.75 m wide) each and there were seven rows at 0.25 m interval.Because of the effects of varietal and fertilizer competitionone outer most rows in either side of each plot is discarded as a border rows. The net (harvestable) plot size of the experiment was $5m^2$ (4 m length and 1.25 m wide) each There were a 0.35, 0.6 and 1m distance between plots, incomplete blocks and replications, respectively. Fertilizer was applied at a rate of 100kg DAP and 100kg urea per ha as per national recommendation.All DAP was applied during planting while urea was applied in three splits, with one third at planting, one third at tillering and the remaining one third at panicle initiation. The seeds were drilled in rows with seed rate of 60kg/ha. Hand weeding was used for weed control and all other agronomic practices were done uniformly.

### 3.4. Data Collected

Based on the standard evaluation system for rice developed by International Rice Research Institute (IRRI, 2013) and Biodiversity International (2007) the following eighteen yield and yield related characters were recorded from the central five rows of each plot.

**Data collected on plant basis**

**Plant height:** The height of five randomly taken plants were measured at harvest maturity from the ground level to the tip of the tallest panicle in centimeter and expressed as an average of five plants in each plot.

**Panicle length:** The panicle offive randomly taken plants weremeasured at harvest maturity from the node where the first panicle branch starts to the tip of the panicle in centimeter and averaged

**Number of total tillers per plant:** The number of total tillers per plant were counted from five randomly taken plants at booting stage and averaged.

**Number of fertile tillers per plant:** The number of fertile tillers per plantwere counted from five randomly taken plants at harvest maturity and averaged.

**Number of filled spikelets per Panicle:** The numbers of filled spikelets per panicle werecounted from five main panicles of five randomly taken plants at harvest maturity and averaged.

**Number of unfilled spikelets per panicle:**The number of unfilled spikelets per paniclewere counted from five main panicles of five randomly taken plants at harvest maturity and averaged.

**Panicle weight:** Five main panicles from five randomly taken plants were harvested and weighed in gram at harvesting.

**Disease severity:** Based on IRRI (2013) leaf blast and brown spot infections from three randomly taken plants from the inner central rows of each plot were visually scored on 0-9 scale at heading stage where, 0 was no disease observed and 9 was >75% leaf area affected. The disease severity was calculated using the formula suggested byShrestha and Mishra (1994).

$$DS = \frac{\text{Sum of all numerical rating}}{\text{Total numberof plants rated x maximum score of scale}} x100$$

**Data collected on plot basis**

**Days to 50% heading:** The number of days from the date of emergency up to the date when the tips of the panicle first emerged from the main shoots on 50% of the plants in a plot.

**Days to 85% maturity:** The number of days from the date of emergency to the date when 85% of grains on panicle are matured.

**Number of panicles per meter square:** Number of panicles was counted by random draw of $0.25m^2$ quadrant (0.5 m x 0.5 m)in the center of each plot.

**Biomass yield:** At harvest maturity, total above ground (shoot plus grain) biomass was harvested from an area of $0.25m^2$ (0.5 m x 0.5 m) and oven dried at $70^0C$ for 72 hours and weighed in gram and then converted into the entire plot.

**Harvest index:** It is the ratio of grain yield per plot in gram to biomass yield per plot expressed in percent at harvest maturity.

**Thousand seed weight:** The weight of 1000 seeds in gram from bulked seeds, which was collected from the five central rows of each plot were measured and adjusted at 14% seed moisture basis.

**Panicle shattering:** Based on Biodiversity International (2007) panicle shattering was visually scored on 1-9 scale as the extent to which seeds have shattered from the panicle at harvest maturitywhere,1 = <1% (very low), 3 = ~3% (low), 5 = ~15% (moderate), 7 = ~35% (high) and 9 =>50% (very high).

**Lodging Incidence:**Lodging incidence was scored visually as a percentage of plants that were lodged at maturity. It was assessed on a 1–9 point scale where 1 was totally upright (no lodging) and 9 was totally lodged (lodging score: 1 = no lodging, 3 = 0–10% lodging, 5 = 11–25% lodging, 7 = 26–50% lodging, 9 = >50% lodging) (TTSM, 2003).

**Grain Yield:** Taken by weighing grain yield in gram obtained from five central rows in each plot and converted into kilogram per hectare at 14% moisture content.

### 3.5. Statistical Analysis

#### 3.5.1. Analysis of variance (ANOVA)

Prior to executing individual location statistical analysis, data were checked for the normality assumption and all data met the normality assumption except, scored data's *viz*. leaf blast, brown spot, lodging incidence and panicle shattering. Arc sin and square root transformation methods were used as per the standard procedure set by Gomez and Gomez (1984) in order to normalize the distributionof scored data's. According to Gomez and Gomez (1984), percentage data lying within the range of 0 to 100%, the arc sin transformation should be used and also percentage data lying within the range of either 0 to 30% or 70 to 100%, the square root transformation should be used. By considering this rule, arc sin transformation method was usedfor leaf blast and brown spot because the percentage data ranged from 0 to 50% and square root transformation method was used for lodging incidence and panicle shatteringbecause the percentage data ranged from 0 to 30% (Appendix Table 6).Then the transformed data was used for further analysis. The analysis of variance for individual location was carried out according to the following model.

$$P_{ijk} = \mu + g_i + bk_{(j)} + r_j + e_{ijk}$$

Where: Pijk = phenotypic value of ith genotype under jth replication and kth incomplete block within replication j; $\mu$ = grand mean; gi= the effect of ith genotype; bk (j) = the effect of incomplete block k within replication j; rj = the effect of replication j; and eijk = the residual or effect of random error.

Table 2: Skeleton for analysis of variance for individual location in simple lattice design

| **Sources of variation** | **Degree of freedom (df)** | **Sum of square (SS)** | **Mean Square (MS=SS/df)** | **Computed *F*** |
|---|---|---|---|---|
| Replication | (R-1) | SSR | MSR | $MS_R/MS_E$ |
| Treatments | | | | |
| -(unadj.) | ($K^2$-1) | SSG | MSG | $MS_G/MS_E$ |
| -(adj.) | ($K^2$-1) | SSG | MSG | $MS_G/MS_E$ |
| Blocks with in reps (adj.) | R (K-1) | SSB | MSB | $MS_B/MS_E$ |
| Error | | | | |
| -Intra block | (K-1) (RK-K-1) | SSE | MSE | |
| -RCBD | (R-1) ($K^2$-1) | SSE | MSE | |
| Total | ($RK^2$-1 | TSS | | |

R = number of replication, G = number of genotypes, k = block sizes, $SS_R$ and $MS_R$ are sums of squares and mean of replication, respectively; $SS_G$ and $MS_G$ are sums and mean squares of genotypes, respectively; $SS_b$ and $MS_b$ are sums and mean squares of blocks within replication respectively, SSe and MSe are sum and mean squares of intra-block and RCBD error, respectively and $SS_t$ is sum of squares of the total.

In order to examine the interaction between location and genotype and todetermine the necessity of a separate technology recommendation for each location computing combined analysis over location is important.To compute a combined statistical analysis across locations, test of homogeneity of error variances of each character for the two locations were performed by using F- max test method of Hartley (1950), which is based on the ratio of the largest mean square of error to the smallest mean square of error. The F-max test showed all characters met the homogeneity assumption. Then all the characters were subjected to pooled analysis of variance over locations using the SAS (v 9.3) general linear model (GLM) procedures (SAS, 2014). Mean separation among treatment means were done by using LSD (least significant difference) at 5% probability level.The combined analysis of variance over locations was carried out according to the following model.

$$Pijks = \mu + gi + bk(j)(s) + rj(s) + ls + (gl)is + eijks$$

Where: Pijks= phenotypic value of ith genotype under jth replication at sth location and kth incomplete block within replication j and location s; μ = grand mean; gi = the effect of ith genotype; bk(j)(s) = the effect of incomplete blocks within replication j and location s; rj(s) = the effect of replication j within location s; ls = the effect of location

s; (gl)is = the interaction effects between genotype and location; and eijks = the residual or effect of random error.

Table 3:Skeleton for combined analysis of variance over locations in simple lattice design

| **Sources of variation** | **Degree of freedom** | **Mean Square (MS)** | **Expected Mean Square(EMS)** |
|---|---|---|---|
| Location(L) | L-1 | MSL | $\sigma^2e+ R\sigma^2gl + G\sigma^2l$ |
| Replication | R-1 | MSR | $\sigma^2e + G\sigma^2r$ |
| Blocks within replication | R(K-1) | MSB | $\sigma^2e + R\sigma^2gl+ R\sigma^2g$ |
| Genotypes(G) | G-1 | MSG | $\sigma^2e + R\sigma^2gl + RL\sigma^2g$ |
| GXL interaction | (G-1)(L-1) | MSGXL | $\sigma^2e+ R\sigma^2gl$ |
| Error | LG(R-1)-(RK) | MSE | $\sigma^2e$ |

$\sigma^2g$ = genotypic variance, $\sigma^2e$= environmental variance, $\sigma^2l$ = location variance, $\sigma^2r$ = replication variance, and $\sigma^2gl$ = genotype x location interaction variance, G = number of genotypes, R = number of replications, K = number of blocks, MSG = mean square of genotype, MSGXL = mean square of genotype by location and MSE = mean square of error.

### 3.5.2. Analysis of genetic parameters

#### 3.5.2.1. Estimation of variance components and coefficient of variations

Estimates of variance components were computed using the formula suggested by Burton and De Vane (1953) as follows:

Genotype variance ($\sigma^2g$) = $(MSG - MSGXL)/RL$

Where: MSG = mean square of genotype, MSGXL = mean square of genotype by location, R = number of replications, L = number of locations.

Phenotypic variance ($\sigma^2p$) = $\sigma^2g + \sigma^2gl\ /L + \sigma^2e\ /LR = MSG\ /RL$

Where: $\sigma^2g$ = genotypic variance, $\sigma^2gl$ = genotype x location interaction variance, L = number of locations, $\sigma^2e$ = environmental variance, R = number of replications, MSG = mean square of genotype,

Genotype x location interaction variance ($\sigma^2gl$) =$(MSGXL - MSE)/R$

Where: MSGXL = mean square of genotype by location and MSE = mean square of error, R = number of replications.

Environmental variance ($\sigma^2 e$) =mean square of error(MSE)

Then by using the methods suggested by Singh and Chaudhury (1985) phenotypic and genotypic coefficient of variations were computed as follows:

$$\text{Phenotypic coefficients of variation (PCV)} = \frac{\sqrt{\sigma^2 p}}{\bar{x}} x100$$

$$\text{Genotypic coefficients of variation (GCV)} = \frac{\sqrt{\sigma^2 g}}{\bar{x}} x100$$

Where: $\sigma^2 p$ = phenotypic variance; $\sigma^2 g$ = genotypic variance and $\bar{x}$ = grand mean of the character under study.

According to Sivasubramanian and Menon, (1973) PCV and GCV values were classified as high (>20%), moderate (10-20%) and low (<10%).

### 3.5.2.2.Estimation of broad sense heritability ($h^2 b$)

Broad sense heritability ($h^2 b$) for all characters was estimated as the following method given by Johnson *et al*. (1955) andclassified as low (<30%), moderate (30-60%) and high (>60%).

$$h^2 b = \frac{\sigma^2 g}{\sigma^2 p} x100$$

Where: $h^2 b$ = broad sense heritability, $\sigma^2 g$ = genotypic variance and$\sigma^2 p$ = phenotypic variance.

### 3.5.2.3. Estimation of expected genetic advance under selection (GA)

The expected genetic advance for each character at 5% selection intensity (k) was computed using the methodology illustrated by Allard (1999) as follows:

$$GA = k * \sigma ph * h^2 b$$

Where: GA = genetic advance, $h^2 b$ = broad sense heritability, σph = phenotypic variance and k = the selection differential at 5% selection intensity (k = 2.063).

### 3.5.2.4. Estimation of genetic advance as percent of mean (GAM)

The genetic advance as percent of mean was computed with the following method suggested by Johnson *et al*. (1955) and classified as low (<10%), moderate (10-20%) and high (>20%).

$$\text{GAM} = \frac{\text{GA}}{\bar{\text{X}}} \text{ x } 100$$

Where: GAM = genetic advance as percent of mean, GA = genetic advance under selection and $\bar{X}$= grand mean of the characters.

### 3.5.3. Correlation and path coefficient analysis

### 3.5.3.1. Phenotypic and genotypic correlation coefficient analysis

The phenotypic and genotypic correlation coefficients were computed by the method described by Singh and Chaudhury (1985). In order to estimate phenotypic and genotypic correlation coefficients, first covariance estimates between all pairs of characters were calculated as follows:

Genotypic covariance $\left(\text{COV } g_{xy}\right)=\frac{\text{MSPg}-\text{MSPe}}{r}$

Phenotypic covariance$\left(\text{COV } p_{xy}\right) = \text{cov } g_{xy} + \frac{\sigma e_{xy}}{r}$

Where: MSPe = mean sum of cross product for error, MSPg = mean sum of cross products for genotypes, COV $e_{xy}$ = environmental covariance between characters x and y and r = number of replications.

Phenotypic correlation coefficients ($rp_{xy}$) = $\text{pcov}(x,y)/\sqrt{(\sigma^2 px * \sigma^2 py)}$,

Genotypic correlation coefficients ($rg_{xy}$)= $\text{gcov}(x,y)/\sqrt{(\sigma^2 gx * \sigma^2 g\,y)}$

Where: pcovx.y and gcovx.y are phenotypic and genotypic covariance between variables x and y, respectively; $\sigma^2$px and $\sigma^2$gx are phenotypic and genotypic variances for variable x; and $\sigma^2$py and $\sigma^2$gy are phenotypic and genotypic variances for the variable y, respectively.

The significance of association among characters was tested by calculating t-value and compared with the tabulated value of‘t’ at n-2 degree of freedom at 5% and 1% probability levels,where n = number of genotypes.

### 3.5.3.2. Phenotypic and genotypic path coefficient analysis

The direct and indirect effect of yield related characters on yield and among themselves were computed using the following method suggested by Dewey and Lu (1959).

$$rij = Pij + \Sigma rikpkj$$

Where: rij = mutual association between the independent character (i) and dependent character (j) as measured by the correlation coefficient.

Pij = component of direct effects of the independent character (i) on the dependent character (j) as measured by the path coefficient and,

Σrikpkj = summation of components of indirect effect of a given independent character (i) on the given dependent character (j) via all other independent characters (k).

Whereas the contribution of the remaining unknown characters measured as residual effect estimated by the formula as follows:

Residual effect= $\sqrt{1 - R^2}$ , Where: $R^2 = \Sigma pij\ rij$

Where: $R^2$ is the residual factor, Pij is the direct effect of yield by $i^{th}$ character, and rij is the correlation of yield with the $i^{th}$ character.

### 3.5.4. Multivariate analysis

### 3.5.4.1. Cluster analysis

Clustering was performed using the proc cluster procedure of SAS version 9.3 (SAS, 2014) by employing the method of average linkage clustering strategy of the observation. The number of cluster was determined by following the approach suggested by Copper and Milligan (1988) by looking into three statistics namely Pseudo F, Pseudo $t^2$ and cubic clustering criteria. The points where local peaks of the CCC and pseudo F-statistic join with

small values of the pseudo-$t^2$ statistic followed by a larger pseudo-$t^2$ for the next cluster combination was used to determine the number of clusters. The dendrogram was constructed by using Minitab 14 software package based on the average linkage and Mahalanobis(1936) used as a measure of dissimilarity (the distance) technique.

### 3.5.4.2. Genetic divergence analysis

Genetic divergence between clusters was determined using the generalized Mahalanobis $D^2$ statistics (Mahalanobis, 1936) using the equation. In matrix notation, the distance between any two groups was estimated from the following relationship.

$$D^2ij = ((Xi - Xj)\, S-1\, (Xi - Xj)$$

Where: $D^2_{ij}$ = the squared distance between any two genotypes i and j

$X_i$ and $X_j$ = the vectors of the values for $i^{th}$ and $j^{th}$ genotypes, respectively.

$S^{-1}$ = the inverse of the pooled covariance matrix with in groups.

The $D^2$ values obtained for pairs of clusters were considered as the calculated values of Chi-square ($X^2$) and tested against tabulated $X^2$ values at n-1 degree of freedom at 1% and 5% probability levels, where n = number of characters considered (Singh and Chaudhury, 1985).

### 3.5.4.3. Principal component analysis (PCA)

Principal component analysis was computed using correlation matrix of SAS version 9.3 (SAS, 2014) in order to examine the relationships among the quantitative characters that are correlated among each other by converting into uncorrelated characters called principal components. Below is the general formula to compute scores on the first component extracted (created) in a principal component analysis:

$$PC1 = b11(X1) + b12 + \cdots b1p\ (Xp)$$

Where: $PC_1$ = the subject's score on principal component 1 (the first component extracted);

$b_{1p}$ = the regression coefficient (or weight) for observed variable p, as used in creating principal component1

Xp = the subject's score on observed variable p.

# 4. RESULTS AND DISCUSSION

## 4.1. Analysis of Variance (ANOVA)

The analysis of variance for individual location for different characters at Gojeb and Guraferda are presented in Appendix Table 2 and 3, respectively. Analysis of variance at Gojeb revealed that the genotypes differed significantly for days to 85% maturity, plant height, panicle length, number of fertile tillers per plant, number of unfilled spikelets per panicle, harvest index and panicle shattering. Similarly, at Guraferda the genotypes showed significant difference for days to 85% maturity, plant height, panicle length, number of fertile tillers per plant, biomass yield and panicle shattering. The combined analyses of variance (ANOVA) for different characters are presented in Table 4. The mean squares due to location showed that there was highly significant difference ($p<0.01$) for days to 85% maturity, plant height, number of total tillers per plant, number of fertile tillers per plant, number of unfilled spikelets per panicle, panicle weight, biomass yield, thousand seed weight and grain yield (kg $ha^{-1}$)and significant location difference ($P<0.05$) for brown spot. Ogunbayo *et al*. (2014) observed significant location effect for days to maturity, number of panicles per meter square, plant height and grain yield.

The combined analysis of variance revealed significant differences among genotypes for all the characters studied, except for days to 50% heading, panicle weight, thousand seed weight, lodging incidence and reaction to disease (leaf blast and brown spot), indicating large amount of variability was present among the material for effective selection.Tefera *et al*. (2017) reported significant differences among genotypes for biomass yield, days to maturity, filled grains per panicle, fertile tillers per plant, grain yield, harvest index, plant height, panicle length and number of unfilled grains per panicle.Mulugeta *et al*. (2012) reported significant differences among genotypes for days to maturity, plant height, panicle length and grain yield per hectare in upland rice genotypes in Southwest Ethiopia. Mulugeta *et al*. (2016) reported significant difference among genotypes for days to maturity, panicle length, plant height, grain yield, filled grains per panicle, biomass yield, unfilled grains per panicle and fertile tillers per plant. Ogunbayo *et al*. (2014) also reported significant difference among genotypes for days to maturity, number of panicles per meter square, plant height and grain yield.

The mean squares due to genotype × location interactions were highly significant ($p<0.01$) for panicle shattering and grain yield (kg $ha^{-1}$) and significant ($P<0.05$) for days to 85% maturity, plant height, number of fertile tillers per plant, number of unfilled spikelets per panicle and biomass yield(Table 4). This significant difference of genotype × location interactions indicates differential response of genotypes to the two locations for these characters. Therefore, location specific breeding strategy might be adopted for each location for these characters. Ogunbayo *et al.* (2014) founds significantgenotype x location interaction effects for days to maturity, plant height and grain yield. Tefera *et al.* (2017) also reportedsignificantgenotype x location interaction effects for biomass yield, days to maturity, number of fertile tillers per plant, plant height, panicle length and grain yield.

Table 4: Mean squares of combined analysis of variance for 18 charactersof 36 upland rice genotypesevaluated in 2017 main cropping season across two locations

| **Characters** | **MSL(1)** | **MSG(35)** | **MSGxL(35)** | **MSE(60)** | **CV** |
|---|---|---|---|---|---|
| DH | $15.34^{ns}$ | $9.55^{ns}$ | $7.01^{ns}$ | 6.10 | 3.04 |
| DM | 108.51** | 22.61** | 13.91* | 8.29 | 2.46 |
| PH | 190.44** | 79.67** | 19.72* | 11.75 | 4.11 |
| PL | $0.75^{ns}$ | 2.98** | $1.51^{ns}$ | 1.08 | 4.82 |
| TTPP | 26.52** | 6.14** | $2.67^{ns}$ | 2.61 | 13.21 |
| FTPP | 18.20** | 6.11** | 3.67* | 2.09 | 14.97 |
| FSPP | $123.58^{ns}$ | 324.73** | $165.40^{ns}$ | 155.29 | 12.73 |
| USPP | 27.04** | 5.74** | 3.96* | 2.33 | 13.78 |
| PW | 15.80** | $2.56^{ns}$ | $1.82^{ns}$ | 1.76 | 8.78 |
| $Pan/m^2$ | $30.25^{ns}$ | 120.29** | $47.55^{ns}$ | 44.95 | 14.36 |
| BY | 4033402.78** | 1128445.63** | 686545.63* | 413372.20 | 15.68 |
| HI | $0.0001^{ns}$ | 0.0067** | $0.0036^{ns}$ | 0.0027 | 14.64 |
| TSW | 55.95** | $10.48^{ns}$ | $7.06^{ns}$ | 6.68 | 9.06 |
| +LB | $11.61^{ns}$ | $26.55^{ns}$ | $25.02^{ns}$ | 16.78 | 19.13 |
| +BS | 72.35* | $24.90^{ns}$ | $21.97^{ns}$ | 16.27 | 15.08 |
| $LI | $0.001^{ns}$ | $0.50^{ns}$ | $0.42^{ns}$ | 0.32 | 20.10 |
| $PSht | $0.92^{ns}$ | 2.47** | 2.12** | 0.29 | 22.71 |
| GY | 1898539.52** | 288979.76** | 226956.50** | 111151.56 | 12.68 |

The numbers in the brackets indicates degree of freedom, + = mean squares are based on arc sin, $ = mean squares are based on square root transformation * = significant at ($P\leq0.05$), ** = significant at ($P\leq 0.01$), MSL = mean squares of locations, MSG = mean squares of genotypes, MSGxL = mean square of genotype x location interaction, MSE = mean squares of error, CV = coefficient of variation. DH = days to heading, DM = days to maturity, PH = plant height, PL = panicle length, TTPP = number of total tillers per plant, FTPP = number of fertile tillers per plant, FSPP = number of filled spikelets per panicle, USPP = number of unfilled spikelets per panicle, PW = panicle weight, $Pan/m^2$ = number of panicles per meter square, BY = biomass yield, HI = harvest index, TSW = thousand seed weight, LB = leaf blast, BS = brown spot, LI = lodging,PSht = panicle shattering, GY = grain yield (kg $ha^{-1}$).

### 4.2. Range and Mean of Different Characters

Estimated range, mean and standard deviation of 12 characters are presented in Table 5. The mean performance of the 36 upland rice genotypes for 18 characters is shown in Appendix Table 5 and 6. The mean values for grain yield ranged from 1979.5 to 3562.7 kg $ha^{-1}$ and 17 (51.5%) of genotypes gave higher yield than the best checks (NERICA-4). The highest grain yield (3562.7 kg $ha^{-1}$) was obtained from the genotype ART15-13-2-2-2-1-1-B-1-2 followed by genotype ART16-21-4-7-2-2-2-B-2-2 (3236.2 kg $ha^{-1}$) and genotype ART15 8-10-36-4-1-1-B-B-1 (3147.2 kg $ha^{-1}$). While the lowest was harvested in genotype ART16-5-10-2-3-B-1-B-1-2 (1979.5 kg $ha^{-1}$) followed by ART16-13-11-1-2-B-2-B-2-1 (2048.4 kg $ha^{-1}$) (Appendix Table 6). Wide variability displayed by grain yield might be due towide genetic variation among the tested materials as well as influence of genotype x location interaction. Xing and Zhang (2010) reported that rice varieties display tremendous levels of variation in yield owing to diversity of genetic and non-genetic factors. Mulugeta *et al.* (2016)reported significant variation in grain yield among rice genotypes grown under rainfed upland condition in Northwest Ethiopia. Mulugeta *et al.* (2012) also observed significant variation in grain yield among upland rice genotypes in Southwest Ethiopia.

Days to 85% maturity ranged from 113 to 126 days. Among the tested 36 genotypes, 47.2% exhibited days to maturity lower than the grand mean indicating that those genotypes were earlier maturing as compared to the others. The earliest days to 85% maturity was recorded in the genotype NERICA-4 (113 days)and the maximum were recorded in the genotype ART16-21-4-7-2-2-2-B-2-2 (126 days) (Appendix Table 5), indicating thereby this genotype is late maturing genotype.The wide variation among genotypes for days to maturity offers opportunity for the development of upland rice varieties for different agro ecologies of Ethiopia receiving diverse distribution of rainfall.Hence, early maturing rain fed rice varieties could be developed for short season rainy areas such as for most of Somalia region and late maturing varieties could be evolved for Southwestern Ethiopia with long rainy season. Variation in days to maturity in different genotypes have been reported byDemewez*et al.* (2014), Mishu *et al.* (2016), Mulugeta*et al.* (2016)and Osundare *et al.* (2017)in upland rice genotypes. In general, genotypes that displayed long time to mature gave greater grain yield $ha^{-1}$ than genotypes that took short period of time to mature (Appendix Table 5 and 6). This

difference could be attributed to effective translocation and utilization of photosynthetic assimilates in late maturing genotypes for long time grain filling period. Demewez*et al.* (2014) also observed the highest grain yield in late maturing upland rice genotypes.

Plant height ranged from 75.15 to 93.85cm. Maximum plant height was recorded in genotype ART16-16-1-14-3-1-1-B-1-2 (93.85 cm) followed by ART16-16-11-25-1-B-1-B-1-2 (93.45 cm), ART16-5-10-2-3-B-1-B-1-2 (91cm) and ART16-5-10-2-3-B-1-B-1-1 (89.5cm). The minimum plant height was recorded in genotype ART16-9-1-9-2-1-1-B-1-1 (75.75cm), ART16-13-11-1-2-B-2-B-2-1 (75.5cm) and NERICA-4 (76.35cm). According to IRRI upland rice plant height is classified as semi-dwarf (less than 90 cm), intermediate (90-125 cm) and tall (more than 125 cm). Based on this classification, in the present study 91.67% of the tested genotypes grouped under the semi-dwarf class whereas the remaining 8.33% genotypes fall within the intermediate statured class. Generally, genotypes that recorded 78.75 to 86.15cm plant height measurement gave the highest grain yield $ha^{-1}$ (Appendix Table 5 and 6). Taller genotypes produced low grain yield because they were susceptible to lodging. Results from this study indicated the importance of selection of semi dwarf plants in order to increase grain yield. Mulugeta *et al*. (2012) reported plant height as an important character for selection of high yielding rice plants and recommended that selection of semi-dwarf genotypes is important in order to increase rice grain yield in Southwest Ethiopia.

Panicle length also differed significantly in different genotypes ranging from 19.6 to 23.15cm. Maximum panicle length (23.15cm) was recorded in genotype ART15 8-10-36-4-1-1-B-B-1 followed by genotype ART16-16-1-14-3-1-1-B-1-2 (23cm) and ART16-9-4-18-4-2-1-B-1-2 (23cm). The genotype ART16-4-1-21-2-B-2-B-1-1 displayed the shortest panicle length with 19.6cm measurements. It was observed that genotypes showing high plant height had also long panicles and vice versa (Appendix Table 5), this might be due to strong positive association between plant height and panicle length. Variation in panicle length in different genotypes have been reported by Osundare *et al.* (2017) and Mulugeta *et al*. (2016).

The mean values of number of total tillers per plant ranged from 10.3 to 15.8. The highest number of total tillers per plant was recorded by genotype ART16-16-11-25-1-B-1-B-1-2 (15.8) followed by genotype ART15-19-5-4-1-1-1-B-1-1 (15.4), ART16-9-4-18-4-2-1-B-1-2

(14.6) and ART16-9-1-9-2-1-1-B-1-1 (14.55). Lower number of total tillers per plant was obtained from genotype ART16-16-1-14-3-1-1-B-1-2 (10.3) followed by genotype ART16-9-33-2-1-1-1-B-1-2 (10.35), ART16-5-9-22-2-1-1-B-1-2 (10.4) and ART16 15-10-1-1-B-1-B-B-2 (10.45) (Appendix Table 5). The mean values of number of fertile tillers per plant ranged from 7.75 to 13.9. Higher number of fertile tillers per plant was recorded by genotype ART16-9-4-18-4-2-1-B-1-2 (13.9) followed by genotype ART15-13-2-2-2-1-1-B-1-2 (13.85), ART15 8-10-36-4-1-1-B-B-1 (11.4) and ART16-9-29-12-1-1-2-B-1-1 (11.25). Lower number of fertile tillers per plant was recorded by genotype ART15-16-45-1-B-1-1-B-1-2 (7.75) followed by genotype ART16-5-10-2-3-B-1-B-1-2 (8.1) and ART16-5-9-22-2-1-1-B-1-2 (8.15). In this study the genotypes, which produced higher number of fertile tillers per plant showed higher grain yield $ha^{-1}$ (Appendix Table 5 and 6). Dutta *et al*. (2002) reported genotype with high number of fertile tillers gave high grain yield.

Like other characters, number of filled spikelets per panicle and number of unfilled spikelets per paniclealso differed significantly in the studied rice genotypes. Number of filled spikelets per panicle ranged from 71.25 to 112.05. A maximum number of filled spikelets per panicle was recorded by genotype ART16 15-10-1-1-B-1-B-B-2 (112.05) followed by genotype ART16-9-6-18-1-1-2-B-1-1 (111.5) and ART15 10-17-46-2-2-2-B-B-2 (110.5). A minimum number of filled spikelets per panicle was recorded from genotype ART16-13-11-1-2-B-2-B-2-1 (71.25) followed by genotype ART16-9-1-9-2-1-1-B-1-1 (77) and ART16-9-9-25-2-1-1-B-2-1 (83.8). Number of unfilled spikelets per panicle ranged from 8.5 to 13.15. A maximum unfilled spikelets per panicle was recorded from genotype NERICA-12 (13.15) followed by genotype ART16-16-11-25-1-B-1-B-1-2 (12.35) and ART16-9-33-2-1-1-1-B-1-2 (12.3). A minimum unfilled spikelets per panicle was obtained from genotype ART16-21-4-7-2-2-2-B-2-2 (8.5) followed by genotype NERICA-4 (8.6) and Adet (8.7). The mean values for number of panicles per meter square ranged from 37.75 to 65.5. The highest number of panicles per meter square were recorded from the genotype ART16-9-4-18-4-2-1-B-1-2 (65.5) followed byART16-9-9-25-2-1-1-B-2-1 (59). The lowest number of panicles per meter square were recorded from genotypeART16-4-1-21-2-B-2-B-1-2 (37.75).

The mean values of biomass yield ranged from 2720 to 5600. The highest biomass yield were harvested in genotype ART16-21-4-7-2-2-2-B-2-2 (5600) followed by ART16-5-9-22-2-1-1-

B-1-2 (5000) and ART15 10-17-46-2-2-2-B-B-2 (4935), while the lowest biomass yield was harvested from genotype ART15-16-45-1-B-1-1-B-1-2 (2720) followed by ART16-9-1-9-2-1-1-B-1-1 (3170) andNERICA-4 (3175). The mean values of harvest index ranged from 28 to 45%. Highest harvest index measurement was recorded in genotype ART15-13-2-2-2-1-1-B-1-2 (45%) followed by ART15 10-17-46-2-2-2-B-B-2 (43%), ART15 8-10-36-4-1-1-B-B-1 (42%) and NERICA-12 (42%). The lowest measurement was obtained in genotype ART16-9-33-2-1-1-1-B-1-2 (28%) followed by ART15-16-45-1-B-1-1-B-1-2 (30%). Variability in harvest index among the tested genotypes indicates, their efficiency ability in partitioning assimilate into grain yield. Relatively, genotypes that exhibited the highest harvest index measurement also gave the highest grain yield per hectare (Appendix Table 6). Yoshida *et al.* (1981) reported that the high yielding potential of a genotype is usually associated with increased grain-to-straw ratio or harvest index of genotypes in rice.

Panicle shattering ranged from 0.75-15%.The highest panicle shattering percentage was recorded in genotype ART16-9-29-16-1-1-1-B-1-1 (15%), ART16-5-10-2-3-B-1-B-1-2 (15%) and ART16-9-1-9-2-1-1-B-1-1 (15%), while the lowest measurement was exhibited in genotype ART16-9-6-18-1-1-2-B-1-1 (0.75%). According to Biodiversity International (2007) panicle shattering is classified as very low (<1%), low (~3%), moderate (~15%), high (~35%) and very high (>50%). Based on this classification, about 52.8% of the tested genotypes group under the moderately shattered class, 44.4% genotypes fall within low shattering class and the remaining 2.8% grouped in very low shattering percentage (Appendix Table 6).

### 4.3. Estimates of Genetic Parameters

#### 4.3.1. Estimates of variance components and coefficient of variations

Estimates of phenotypic variance ($\sigma^2p$), genotypic variance ($\sigma^2g$), phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) values for 12 characterswere presented in Table 5. The Phenotypic coefficient of variation (PCV) values ranged from 2.03% for days to 85% maturity to 32.95% for panicle shattering (Table 5). According to Siva Subramanian and Menon(1973), PCV and GCV values greater than 20% are regarded as high, whereas values less than 10% are considered low and values between 10% and 20% to be

medium. Based on this delineation, panicle shattering had high PCV value. Ogunbayo *et al*. (2014) reported high phenotypic coefficient of variation (PCV) value for panicle shattering, indicates wide variation in shattering percentage among the tested genotypes. On the other hand, number of total tillers per plant, number of fertile tillers per plant, number of unfilled spikelets per panicle, number of panicles per meter square, biomass yield, harvest index and grain yield (kg $ha^{-1}$) had medium phenotypic coefficient of variation (PCV). It indicates considerable amount of phenotypic variation is presented among the tested genotypes for these characters.Mulugeta*et al.* (2016)and Shaikh *et al.* (2017) reported medium PCV estimates for number of fertile tillers per plant. Hasan *et al.* (2013) reported medium PCV estimates for grain yield $ha^{-1}$. While days to 85% maturity, plant height, panicle length and number of filled spikelets per panicle had low PCV values, indicates there is low phenotypic variation among the tested genotypes for these characters.Low PCV values for days to 85% maturity, plant height and panicle length has beenreported byImmanuel *et al.* (2011), Mulugeta*et al.* (2012) and Ogunbayo *et al*. (2014).

The genotypic coefficient of variation (GCV) values ranged from 1.26 for days to maturity to 11.07% for panicle shattering (Table 5). A medium GCV value was observed for panicle shattering.Ogunbayo *et al*. (2014) reported medium genotypic coefficient of variation (GCV) value for panicle shattering. Whereas low GCV values were observed for days to 85% maturity, plant height, panicle length,number of total tillers per plant, number of fertile tillers per plant, number of filled spikelets per panicle, number of unfilled spikelets per panicle, number of panicles per meter square, biomass yield, harvest index and grain yield (kg $ha^{-1}$).Theselow values indicate there was no sufficient genetic variation among the tested genotypes for these characters. Therefore, selection based on these characters may not be effective for further improvement of the crop and it is better to create genetic variability either by hybridization or introduction of more rice germplasms. Similar results have been reported by Konate*et al*. (2016) for plant height, biomass yield and grain yield. Demewez*et al.* (2014) also reported low GCV values for days to maturity, plant height, panicle length, number of filled spikelets per panicle and harvest index, Hassan *et al.* (2013) andOgunbayo *et al*. (2014)reported low GCV values for days to 85% maturity and plant height. Ogunbayo *et al*.

(2014) reported low GCV estimates for number of panicles per meter square and panicle length.

Table 5: Estimates of range, mean, variance components and coefficient of variations, broad sense heritability, genetic advance and genetic advance as percent of mean for 12 characters of 36 upland rice genotypes combined over the two locations

| Characters | Range | Mean ±SD | $\sigma^2p$ | $\sigma^2g$ | $\sigma^2gl$ | PCV (%) | GCV (%) | $h^2b$(%) | GA (k=5%) | GAM (%) |
|---|---|---|---|---|---|---|---|---|---|---|
| DM | 113-126 | 117.24±2.88 | 5.65 | 2.18 | 2.81 | 2.03 | 1.26 | 38.58 | 1.89 | 1.61 |
| PH | 75.15-93.85 | 83.50±3.43 | 19.92 | 14.99 | 3.98 | 5.35 | 4.64 | 75.25 | 6.92 | 8.30 |
| PL | 19.6-23.15 | 21.53±1.04 | 0.74 | 0.37 | 0.22 | 4.00 | 2.83 | 50.00 | 0.89 | 4.13 |
| TTPP | 10.3-15.8 | 12.23±1.61 | 1.54 | 0.87 | 0.03 | 10.15 | 7.63 | 56.50 | 1.45 | 11.86 |
| FTPP | 7.75-13.90 | 9.67±1.45 | 1.53 | 0.61 | 0.79 | 12.79 | 8.08 | 39.87 | 1.02 | 10.55 |
| FSPP | 71.25-112.05 | 97.93±12.46 | 81.18 | 39.83 | 5.06 | 9.20 | 6.44 | 49.06 | 9.12 | 9.31 |
| USPP | 8.5-13.15 | 11.08±1.53 | 1.43 | 0.44 | 0.82 | 10.79 | 5.99 | 30.77 | 0.76 | 6.89 |
| Pan/$m^2$ | 37.75-65.5 | 46.68±6.7 | 30.07 | 18.19 | 1.30 | 11.75 | 9.14 | 60.49 | 6.84 | 14.65 |
| BY | 2720-5600 | 4100.97±642.94 | 282111.41 | 110475 | 136586.72 | 12.95 | 8.10 | 39.16 | 429.09 | 10.46 |
| HI | 0.28-0.45 | 0.35±0.05 | 0.002 | 0.001 | 0.0005 | 12.78 | 9.04 | 50.00 | 0.05 | 14.29 |
| $PSht | 1(0.75)-3.94(15) | 2.39±0.54 | 0.62 | 0.07 | 0.91 | 32.95 | 11.07 | 11.29 | 0.18 | 7.53 |
| GY | 1979.5-3562.7 | 2629.89±333.39 | 72244.94 | 15505.82 | 57902.47 | 10.22 | 4.73 | 21.46 | 119.00 | 4.53 |

$ = values based on square root transformation and values in the bracket are de-transformed values, SD = standard deviation, $\sigma^2p$ = phenotypic variation,$\sigma^2g$ = genotypic variation,$\sigma^2gl$ = interaction variation,PCV = phenotypic coefficient of variation,GCV = genotypic coefficient of variation,$h^2b$= broad sense heritability,GA = genetic advance,GAM = genetic advance as percent of mean, DM = days to maturity, PH = plant height, PL = panicle length, TTPP = number of total tillers per plant, FTPP = number of fertile tillers per plant, FSPP = number of filled spikelets per panicle, USPP = number of unfilled spikelets per panicle, Pan/$m^2$ = number of panicles per meter square, BY = biomass yield, HI = harvest index, PSht = panicle shattering, GY = grain yield (kg $ha^{-1}$).

### 4.3.2. Estimates of broad sense heritability ($h^2b$)

The estimates of broad sense heritability for 12 characters are presented in Table 5. According to Johnson *et al*. (1955) heritability estimates was classified as low (<30%), medium (30-60%) and high (>60%). Based on this delineation, high heritability estimates were recorded for plant height (75.25%) and number of panicles per meter square (60.49%). This indicates the predominance of genetic factors in the inheritance of these characters. High heritability estimates in plant height has been reported by Ajmera *et al*. (2017),Konate*et al*. (2016) and Mulugeta*et al.* (2012). Ogunbayo *et al*. (2014) also reported high heritability estimates for plant height and number of panicles per meter square. Days to 85% maturity, panicle length, number of total tillers per plant, number of fertile tillers per plant, number of filled spikelets per panicle, number of unfilled spikelets per panicle, biomass yield and harvest index had medium heritability. This also indicates the possibility of improving these characters by selection. Similar results have been reported by Demewez *et al*. (2014) for number of filled spikelets per panicle and Tefera *et al*. (2017) for days to 85% maturity, number of filled spikelets per panicle and number of unfilled spikelets per panicle. Shaikh *et al*. (2017) also reported medium heritability estimates for panicle length.

Low heritability estimate was recorded from panicle shattering (11.29%) and grain yield (21.46%) indicates the predominance of non-genetic variance effects in the inheritance of these characters. The low heritability estimate for grain yield could be attributed to the fact that yield is a complex character and controlled by many genes (Osman *et al*., 2012) which indicates greater role of environment on the expression of this character and therefore, direct selection for this character may be ineffective due to the masking effect of the environment. Therefore, selection might be effective after creating variability either by hybridization or introduction of more germplasms. Similar result has been reported by Mulugeta*et al*. (2016).

### 4.3.3. Estimates of genetic advance as percent of mean (GAM)

Genetic advance as percent of mean had ranged from 1.61% for days to 85% maturity to 14.65% for number of panicles per meter square (Table 5). Among all the characters studied moderate values of genetic advance as percent of mean (10 to 20%) were recorded for

characters *viz*. number of total tillers per plant, number of fertile tillers per plant, number of panicles per meter square, biomass yield and harvest index. Mulugeta*et al*. (2016) reported moderategenetic advance as percent of mean estimates for number of fertile tillers per plant and biomass yield. Sumanth*et al*. (2017) reported moderategenetic advance as percent of mean estimates for harvest index. While, low genetic advance as percent of mean (below 10%) were recorded for days to 85% maturity, plant height, panicle length, number of filled spikelets per panicle, number of unfilled spikelets per panicle, panicle shattering and grain yield (kg $ha^{-1}$). Mulugeta*et al*. (2016) reported lowgenetic advance as percent of mean estimates fordays to 85% maturity, plant height, panicle length and filled spikelet per panicle.

High estimate of heritability associated with moderate genetic advance as percent of mean value was observed for number of panicles per meter square and suggesting greater role of additive gene action for inheritance of this character and selection will be effective, while low heritability coupled with low genetic advance as percentage of mean estimates were recorded for panicle shattering and grain yield (kg $ha^{-1}$) which explain the dominance of non-additive gene action and genotype x environment interaction played significant role in the expression of these characters. Therefore, direct selection on these characters will be ineffective.

### 4.4. Correlation Coefficient Analysis

#### 4.4.1. Phenotypic and genotypic correlation of grain yield with other characters

Phenotypic and genotypic correlation estimates between various characters are presented in Table 6. Grain yield had positive and significant associations with days to 85% maturity, panicle length, number of fertile tillers per plant, number of panicles per meter square, biomass yield and harvest index at both phenotypic and genotypic levels. In addition grain yield had significant and positive correlation with number of filled spikelets per panicle at phenotypic level only. This signified that for these characters which were positively and significantly associated, the improvement for one character will simultaneously improve the other. Thereforegrain yield of rice can be improved by selecting genotypes having higher performances for these positively and significantly associated characters.

Chandrashekhar*et al*. (2017) reported that significant and positive correlation of grain yield with fertile tillers per plant, filled spikelets per panicle and harvest index at genotypic and phenotypic levels. Ogunbayo *et al.* (2014) reported that significant and positive correlation of grain yield with panicle length and number of panicles per meter square. Khare*et al*. (2014) reported that days to maturity, panicle length and filled spikelets per panicle showed positive and significant association with grain yield at both genotypic and phenotypic levels. Mulugeta*et al.* (2016) reported that significant and positive correlation of grain yield with days to maturity, fertile tillers per plant and biomass yield at both genotypic and phenotypic levels.

On the other hand grain yield showed negative and significant associations with number of unfilled spikelets per panicleand panicle shattering at both phenotypic and genotypic levels. This indicated improvement in these characters and yield seems to be practically difficult as they are controlled by different genes. Therefore, improvement of these negatively and significantly correlated characters will decrease in grain yield (kg $ha^{-1}$). Negative correlation of grain yield with number of unfilled spikelets per panicle had reported by Mustafa and Elsheikh (2007) and Oladosu *et al*. (2018). However, plant height and number of total tillers per plant showednon-significant associations with grain yield at both phenotypic and genotypic levels.Similarly number of filled spikelets per panicleshowed positive and non-significant association with grain yield at genotypic level only.

### 4.4.2. Phenotypic and genotypic correlation among other characters

Days to 85% maturity was positively and significantly correlated with panicle length (rp = 0.261*, rg = 0.388*) and biomass yield (rp = 0.289**, rg = 0.361*) at both phenotypic and genotypic levels. However, it displayed negative and significant association with panicle shattering (rp = -330**, rg = -0.354*) at both phenotypic and genotypic levels, indicates the improvement of this character, which was negatively correlated, will antagonistically affect the other (Table 6). Chandrashekhar*et al*. (2017) and Mulugeta *et al*. (2016) reported that significant and positive correlation of days to maturity with biomass yield at both genotypic and phenotypic levels. Ogunbayo *et al*. (2014) also reported that positive correlation of days to 85% maturity with panicle length and negative correlation with panicle shattering.

Plant height had significant and positive correlation with panicle length (rp = 0.377**, rg = 0.369*) and number of unfilled spikelets per panicle (rp = 0.265*, rg = 0.360*) at both phenotypic and genotypic levels. Mulugeta *et al*. (2016) reported a similar result for plant height association with panicle length and number of unfilled spikelets per panicle. Similarly, plant height had significantly and positively correlated with number of filled spikelets per panicle (rp = 0.252*) at phenotypic level only. Chandrashekhar*et al*. (2017) reported that non-significant and positive correlation of plant height with number of filled spikelets per panicle at phenotypic level. While, plant height displayed negative and significant correlation with harvest index (rp = -0.235*) at phenotypic level only. Panicle length was positively and significantly correlated with number of total tillers per plant (rp = 0.246**, rg = 0.399*), number of fertile tillers per plant (rp = 0.372*, rg = 0.464*), number of panicles per meter square (rp = 0.242*, rg = 0.384*) at both phenotypic and genotypic levels. Although, it was positively and significantly correlated with harvest index (rg = 0.393*) at genotypic level only. It had non-significant correlation with the remaining characters (Table 6).

Number of total tillers per plant displayed positive and highly significant association with number of fertile tillers per plant (rp = 0.708**, rg = 0.720**) at both phenotypic and genotypic levels. However, it displayed negatively and significantly correlated with number of filled spikelets per panicle (rp = -0.331**) at phenotypic level and number of unfilled spikelets per panicle (rg = -0.327**) at genotypic level only. It had non-significant correlation with the rest of the characters. Number of fertile tiller per plant had highly significant and positively correlated with number of panicles per meter square (rp = 0.513**, rg = 0.697**) and harvest index (rp = 0.360**, rg = 0.553**) at both phenotypic and genotypic levels. However, it displayed negatively and significantly correlated with number of unfilled spikelets per panicle (rp = -340**, rg = -0.505**) and panicle shattering (rp = -325**, rg = -0.351*) at both phenotypic and genotypic levels(Table 6). It had non-significant correlation with the rest of the characters. Chandrashekhar*et al*. (2017) reported that positive correlation of number of fertile tillers per plant with harvest index at phenotypic and genotypic levels.

Number of filled spikelets per panicle showed significant and positive association with biomass yield (rp = 0.293**) at phenotypic level only. While, it displayed negatively and

significantly correlated with panicle shattering (rp = -0.257*) at phenotypic level only. Number of unfilled spikelets per panicle was significant and positive association with panicle shattering (rp = 0.341**, rg = 0.418**) at both phenotypic and genotypic levels. However, it displayed negatively and significantly correlated with number of panicles per meter square (rp = -0.320**, rg = -0.587**) at both phenotypic and genotypic levels. It had also significant and negative association with harvest index (rg = -0.356*) at genotypic level only. It had non-significant correlation with the remaining characters(Table 6).

Number of panicles per meter square had significant and positive association with biomass yield (rp = 0.341**, rg = 0.386*) and harvest index (rp = 0.263*, rg = 0.428**) at both phenotypic and genotypic levels. However, it displayed negatively and significantly correlated with panicle shattering (rp = -0354**, rg = -0.469**) at both phenotypic and genotypic levels. Biomass yield revealed significant and negative correlation with panicle shattering (rp = -0.314**, rg = -0.358*) at both phenotypic and genotypic levels. Harvest index had significant and negative association with panicle shattering (rp = -0.375**, rg = -0.492**) at both phenotypic and genotypic levels (Table 6).

Table 6: Phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficients of 12 yield and yield related characters of 36 upland rice genotypes combined over the two locations

| | **DM** | **PH** | **PL** | **TTPP** | **FTPP** | **FSPP** | **USPP** | **Pan/m$^2$** | **BY** | **HI** | **PSht** | **GY** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **DM** | **1** | 0.055 | 0.261* | 0.049 | 0.117 | 0.144 | -0.149 | 0.227 | 0.289** | 0.048 | -0.330** | 0.454** |
| **PH** | 0.07 | **1** | 0.377** | -0.005 | -0.085 | 0.252* | 0.265* | -0.129 | 0.125 | -0.235* | 0.035 | -0.024 |
| **PL** | 0.388* | 0.369* | **1** | 0.246* | 0.372** | 0.069 | -0.101 | 0.242* | 0.19 | 0.2 | -0.192 | 0.309** |
| **TTPP** | 0.057 | 0.008 | 0.399* | **1** | 0.708** | -0.331** | -0.194 | 0.184 | -0.023 | 0.16 | -0.045 | 0.071 |
| **FTPP** | 0.134 | -0.167 | 0.464** | 0.720** | **1** | -0.051 | -0.340** | 0.513** | 0.184 | 0.360** | -0.325** | 0.406** |
| **FSPP** | 0.164 | 0.233 | 0.046 | -0.273 | -0.027 | **1** | 0.114 | 0.018 | 0.293** | 0.037 | -0.257* | 0.288** |
| **USPP** | -0.196 | 0.360* | -0.138 | -0.327* | -0.505** | 0.07 | **1** | -0.320** | -0.163 | -0.114 | 0.341** | -0.334** |
| **Pan/m$^2$** | 0.32 | -0.158 | 0.384* | 0.267 | 0.697** | 0.035 | -0.587** | **1** | 0.341** | 0.263* | -0.354** | 0.526** |
| **BY** | 0.361* | 0.103 | 0.213 | 0.043 | 0.239 | 0.315 | -0.134 | 0.386* | **1** | 0.103 | -0.314** | 0.428** |
| **HI** | 0.041 | -0.218 | 0.393* | 0.188 | 0.553** | 0.16 | -0.356* | 0.428** | 0.217 | **1** | -0.375** | 0.438** |
| **PSht** | -0.354* | 0.015 | -0.241 | -0.054 | -0.351* | -0.314 | 0.418** | -0.469** | -0.358* | -0.492** | **1** | -0.637** |
| **GY** | 0.487** | -0.043 | 0.480** | 0.159 | 0.533** | 0.31 | -0.577** | 0.636** | 0.487** | 0.627** | -0.722** | **1** |

* = significant at P≤0.05, ** = significant at P≤0.01, DM = days to maturity, PH = plant height, PL = panicle length, TTPP = number of total tillers per plant, FTPP = number of fertile tillers per plant, FSPP = number of filled spikelets per panicle, USPP = number of unfilled spikelets per panicle, Pan/m$^2$= number of panicles per meter square, BY = biomass yield, HI = harvest index, PSht = panicle shattering, GY = grain yield (kg ha$^{-1}$).

### 4.5. Path coefficient analysis

#### 4.5.1. Phenotypic path coefficient analysis

In this study, characters that showed significant correlation with grain yield (kg $ha^{-1}$) were advanced to path coefficient analysis at both phenotypic and genotypic levels. The phenotypic path coefficient analysis between yield and yield related characters are presented in Table 7. The phenotypic path coefficient analysis revealed that number of panicles per meter square (0.223) had the maximum positive direct effect on grain yield followed by days to 85% maturity (0.218) and harvest index (0.213). The phenotypic correlations were also positive and significant for these characters. This indicated true relationship between those characters and yield importance in determining this complex character and should be given prior attention in practicing selection aimed at the improvement of grain yield of rice, because of major influences of those characters on grain yield.Hasan *et al*. (2013) reported number of panicle per meter square had maximum positive direct effect on grain yield. On the other hand, number of unfilled spikelets per panicle and panicle shattering had negative direct effect on grain yield with negative phenotypic correlation.In such situations, direct selection for genotypes that are highest number of unfilled spikelets per panicle and panicle shattering might be ineffective for grain yield improvement in upland rice genotypes, and yield of rice might increase with the reduction of these characters.

Panicle length (0.012), number of fertile tillers per plant (0.019), number of filled spikelets per panicle (0.003), number of unfilled spikelets per panicle (0.030), biomass yield (0.035) and panicle shattering (0.100) exhibited positive phenotypic indirect effect on grain yield passing through number of panicles per meter square. The phenotypic path coefficient analysis also revealed that panicle length (0.013), number of fertile tillers per plant (0.004), number of filled spikelets per panicle (0.022), number of unfilled spikelets per panicle (0.014), biomass yield (0.030) and panicle shattering (0.093) had positive indirect effect on grain yield through days to maturity. Similarly, panicle length (0.010), number of fertile tillers per plant (0.013), number of filled spikelets per panicle (0.006), number of unfilled spikelets per panicle (0.011), biomass yield (0.011) and panicle shattering (0.106) had positive indirect effect on grain yield through harvest index.Therefore, along with number of panicles per

meter square, days to 85% maturity and harvest index, indirect selection of genotypes with large number of fertile tillers, high number of filled spikelets per panicle and biomass yield might be considered simultaneously during in the process of selection for grain yield improvement program in upland rice genotypes. The phenotypic path coefficient analysis exhibited the residual value of 0.606 indicated that the characters in the path analysis expressed the variability on grain yield by 39.4%, the remaining 60.6% was the contribution of other factors, such as the characters not studied and also the environment.

Table 7: Path coefficients at phenotypic level of direct (bolded along diagonal) and indirect effects of the characters of 36 upland rice genotypes

| | **DM** | **PL** | **FTPP** | **FSPP** | **USPP** | **Pan/m$^2$** | **BY** | **HI** | **PSht** | **rp** |
|---|---|---|---|---|---|---|---|---|---|---|
| **DM** | **0.218** | 0.013 | 0.004 | 0.022 | 0.014 | 0.051 | 0.030 | 0.010 | 0.093 | 0.454** |
| **PL** | 0.057 | **0.048** | 0.014 | 0.010 | 0.009 | 0.054 | 0.020 | 0.043 | 0.054 | 0.309** |
| **FTPP** | 0.025 | 0.018 | **0.037** | -0.008 | 0.031 | 0.114 | 0.019 | 0.077 | 0.092 | 0.406** |
| **FSPP** | 0.031 | 0.003 | -0.002 | **0.152** | -0.010 | 0.004 | 0.030 | 0.008 | 0.073 | 0.289** |
| **USPP** | -0.033 | -0.005 | -0.013 | 0.017 | **-0.092** | -0.071 | -0.017 | -0.024 | -0.096 | -0.334** |
| **Pan/m$^2$** | 0.049 | 0.012 | 0.019 | 0.003 | 0.030 | **0.223** | 0.035 | 0.056 | 0.100 | 0.526** |
| **BY** | 0.063 | 0.009 | 0.007 | 0.044 | 0.015 | 0.076 | **0.102** | 0.022 | 0.089 | 0.428** |
| **HI** | 0.010 | 0.010 | 0.013 | 0.006 | 0.011 | 0.059 | 0.011 | **0.213** | 0.106 | 0.438** |
| **PSht** | -0.072 | -0.009 | -0.012 | -0.039 | -0.031 | -0.079 | -0.032 | -0.080 | **-0.283** | -0.637** |

Residual effect = 0.606, * = significant at P≤0.05, ** = significant at P≤0.01, DM = days to 85% maturity, PL = panicle length, FTPP = number of fertile tillers per plant, FSPP = number of filled spikelets per panicle, USPP = number of unfilled spikelets per panicle, Pan/m$^2$ = number of panicles per meter square, BY = biomass yield, HI = harvest index, PSht = panicle shattering, rp = phenotypic correlation with grain yield (kg ha$^{-1}$).

### 4.5.2. Genotypic path coefficient analysis

The genotypic path coefficient analysis revealed that harvest index (0.280) had the highest positive direct effect on grain yield, followed by days to 85% maturity (0.186) and biomass yield (0.167). The genotypic correlation of these characters with grain yield were positive and significant, signified that there is true association between these characters and grain yield. Thus, these characters could be major selection criteria for breeding activity. On the other hand, number of unfilled spikelets per panicle and panicle shattering had negative direct effect on grain yield with negative genotypic correlation.In such situations, direct selection of

genotypes with highest number of unfilled spikelets per panicle and high shattering characteristics might be ineffective for grain yield improvement in upland rice genotypes.

Panicle length (0.056), number of unfilled spikelets per panicle (0.088), number of panicles per meter square (0.034), biomass yield (0.036) and panicle shattering (0.146) exhibited positive genotypic indirect effect on grain yield passing through harvest index. The genotypic path coefficient analysis also revealed that panicle length (0.056), number of unfilled spikelets per panicle (0.048), number of panicles per meter square (0.025) and panicle shattering (0.105) had positive indirect effect on grain yield through days to 85% maturity. Similarly, panicle length (0.03), number of unfilled spikelets per panicle (0.033), number of panicles per meter square (0.031) and panicle shattering (0.106) had positive indirect effect on grain yield through biomass yield. The genotypic path coefficient analysis exhibited the residual value of 0.443 indicated that the characters in the path analysis expressed the variability on grain yield by 55.7%, the remaining 44.3% was the contribution of other factors, such as the characters not studied and also the environment.

Table 8: Path coefficients at genotypic level of direct (bolded along diagonal) and indirect effects of the characters of 36 upland rice genotypes

| | **DM** | **PL** | **FTPP** | **USPP** | **Pan/m$^2$** | **BY** | **HI** | **PSht** | **rg** |
|---|---|---|---|---|---|---|---|---|---|
| **DM** | **0.186** | 0.056 | -0.005 | 0.048 | 0.025 | 0.060 | 0.011 | 0.105 | 0.488** |
| **PL** | 0.072 | **0.143** | -0.017 | 0.034 | 0.030 | 0.036 | 0.110 | 0.071 | 0.480** |
| **FTPP** | 0.025 | 0.066 | **-0.037** | 0.125 | 0.055 | 0.040 | 0.155 | 0.104 | 0.533** |
| **USPP** | -0.037 | -0.020 | 0.019 | **-0.247** | -0.047 | -0.022 | -0.100 | -0.124 | -0.577** |
| **Pan/m$^2$** | 0.060 | 0.055 | -0.026 | 0.145 | **0.079** | 0.065 | 0.120 | 0.139 | 0.636** |
| **BY** | 0.067 | 0.030 | -0.009 | 0.033 | 0.031 | **0.167** | 0.061 | 0.106 | 0.487** |
| **HI** | 0.008 | 0.056 | -0.021 | 0.088 | 0.034 | 0.036 | **0.280** | 0.146 | 0.627** |
| **PSht** | -0.066 | -0.034 | 0.013 | -0.103 | -0.037 | -0.060 | -0.138 | **-0.296** | -0.722** |

Residual effect = 0.443, * = significant at P≤0.05, ** = significant at P≤0.01, DM = days to maturity, PL = panicle length, FTPP = number of fertile tillers per plant, FSPP, USPP = number of unfilled spikelets per panicle, Pan/m$^2$ = number of panicles per meter square, BY = biomass yield, HI = harvest index, PSht = panicle shattering, rg = genotypic correlation with grain yield (kg ha$^{-1}$).

### 4.6. Multivariate Analysis

#### 4.6.1. Cluster analysis

The genotypes were partitioned into four distinct groups based on their similarities in characteristics (Table 9 and Appendix Fig. 1), this makes the genotypes to be moderately divergent. Cluster I contained the highest number of genotypes 17 (47%), followed by clusters II that contained 15 (42%) genotypes. It also comprising two checks (NERICA-12 and Adet). These genotypes may be regarded as having the overall characteristics of these checks. In contrast, cluster III and IV had the smallest number of genotypes, consisted of 3 (8%) and 1 (3%), respectively. This cluster analysis showed that the rice genotypes were originated from different sources. Genotypes falling in a particular cluster indicate their close relationship among themselves as compared to the other clusters. Therefore, it could be expected that genotypes within a cluster are less genetically different with each other, but are diverse from the genotypes belonging to other clusters. Hossain *et al*. (2015) grouped thirty three drought tolerant rice (*Oryza sativa* L.) genotypes into seven clusters. The cluster I and II were comprised of the maximum number of genotypes (8) in each followed by cluster V containing 5 genotypes. Khare *et al*. (2014) clustered sixty upland rice accessions into seven groups. The cluster III contained highest 14 accessions, followed by clusters I comprised 11.

Table 9: Distribution of the 36 upland rice genotypes in different clusters

| Clusters | Number of genotypes | Proportion (%) | Name of Genotypes |
|---|---|---|---|
| Cluster I | 17 | 47 | ART16-9-4-18-4-2-1-B-1-2, ART16-9-9-25-2-1-1-B-2-1. ART16-9-14-16-2-2-1-B-1-2, ART16-9-16-21-1-2-1-B-1-1, ART16-16-11-25-1-B-1-B-1-2, ART16-5-10-2-3-B-1-B-1-1, ART16-4-1-21-2-B-2-B-1-1, ART16 15-10-1-1-B-1-B-B-1, ART15 10-17-46-2-2-2-B-B-2, ART15 8-10-36-4-1-1-B-B-1, ART16-9-4-18-4-2-1-B-1-1, ART16-9-33-2-1-1-1-B-1-2, ART16 15-10-1-1-B-1-B-B-2, ART16-16-1-14-3-1-1-B-1-2, ART16-9-6-18-1-1-2-B-1-1, ART16-5-9-22-2-1-1-B-1-2, ART15-13-2-2-2-1-1-B-1-2 |
| Cluster II | 15 | 42 | ART16-17-7-18-1-B-1-B-1-1, NERICA-12, ART16 9-29-10-2-B-1-B-B-1, ART15-19-5-4-1-1-1-B-1-1, ART16-9-29-12-1-1-2-B-1-1, ART16-5-10-2-3-B-1-B-1-2, ART16-13-11-1-2-B-2-B-2-1, ART16-4-1-21-2-B-2-B-1-2, ART16-9-9-25-2-1-1-B-2-2, ART16-9-29-16-1-1-1-B-1-1, ART16 9-16-21-1-B-2-B-B-1, ART16-21-5-12-3-1-1-B-2-1, ART16-4-13-1-2-1-1-B-1-1, Adet, ART16-9-122-33-2-1-1-B-1-1 |
| Cluster III | 3 | 8 | ART16-9-1-9-2-1-1-B-1-1, NERICA-4, ART15-16-45-1-B-1-1-B-1-2 |
| Cluster IV | 1 | 3 | ART16-21-4-7-2-2-2-B-2-2 |

### 4.6.2. Comparison of genotype performance among clusters

Mean value of the 12 characters for each cluster group is presented in Table 10. Cluster I was characterized by the highest cluster mean estimate for plant height, number of filled spikelets per panicle, number of unfilled spikelets per panicle and harvest index. However, it produced the lowest cluster mean estimate for number of total tillers per plant. Cluster II was characterized by having higher cluster mean values for harvest index and panicle shattering. However, it produced the lowest cluster mean estimate for days to 85% maturity and number of panicles per meter square. Cluster III was characterized by having the lowest cluster mean value for plant height, panicle length, number of fertile tillers per plant, number of filled spikelets per panicle, biomass yield, harvest index and grain yield (kg $ha^{-1}$). Cluster IV produced the highest cluster mean values for days to 85% maturity, panicle length, number of

total tillers per plant, number of fertile tillers per plant, number of panicles per meter square, biomass yield and grain yield (kg $ha^{-1}$). However, it produced the lowest cluster mean values for number of unfilled spikelets per panicle and panicle shattering.Therefore, these typical characteristics in each clusters may be used for the variety development program through selection or/and hybridization.

Table 10: Clusters mean values for 12 characters of 36 upland rice genotypes

| **Characters** | **Cluster I** | **Cluster II** | **Cluster III** | **Cluster IV** |
|---|---|---|---|---|
| DM | 117.82 | 116.26* | 116.37 | 125.80** |
| PH | 84.86** | 83.44 | 77.93* | 78.90 |
| PL | 21.88 | 21.23 | 21.17* | 22.00** |
| TTPP | 12.11* | 12.29 | 12.40 | 13.70** |
| FTPP | 9.79 | 9.55 | 9.50* | 10.80** |
| FSPP | 100.83** | 96.82 | 86.17* | 100.45 |
| USPP | 11.28** | 11.21 | 10.57 | 8.50* |
| Pan/$m^2$ | 48.63 | 43.92* | 46.58 | 55.25** |
| BY | 4487.94 | 3778.33 | 3021.67* | 5600.00** |
| HI | 0.36** | 0.36** | 0.33* | 0.36** |
| PSht | 2.09 | 2.73** | 2.71 | 1.29* |
| GY | 2774.22 | 2471.39 | 2402.39* | 3236.15** |

** = highest value, * = lowest value, DM = days to 85% maturity, PH = plant height, PL = panicle length, TTPP = number of total tillers per plant, FTPP = number of fertile tillers per plant, FSPP = number of filled spikelets per panicle, USPP = number of unfilled spikelets per panicle, Pan/$m^2$ = number of panicles per meter square, BY = biomass yield, HI = harvest index, PSht = panicle shattering, GY = grain yield (kg $ha^{-1}$).

### 4.6.3. Genetic divergence analysis

The standardized Mahalanobis $D^2$ statistics showed that there is high genetic distance and highly significant variation at $P<0.01$ and $P<0.05$ among the four clusters (Table 11). The maximum squared distance was found between cluster three and four ($D^2 = 313.86$) followed by cluster two and four ($D^2 = 189.27$). Maximum genetic recombination is expected from the parents selected from divergent clusters groups. Therefore, maximum recombination and segregation of progenies is expected from crosses involving parents selected from cluster three and four followed by cluster two and four. The minimum squared distance was found between cluster two and three ($D^2 = 25.41$) followed by cluster one and two ($D^2 = 29.40$) and cluster one and four ($D^2 = 83.21$), indicating that genotypes in these clusters were not

genetically diverse or there was little genetic diversity between these clusters. This signifies that crossing of genotypes from these clusters might not give higher heterotic value in $F_1$ and narrow range of variability in the segregating $F_2$ population.

Table 11: Intra and inter-cluster values of generalized square distance ($D^2$) among four clusters constructed from 36 upland rice genotypes

| Clusters | Cluster I | Cluster II | Cluster III | Cluster IV |
|---|---|---|---|---|
| **Cluster I** | **1.50**$^{ns}$ | 29.40** | 97.29** | 83.21** |
| **Cluster II** | | **1.75**$^{ns}$ | 25.41** | 189.27** |
| **Cluster III** | | | **4.96**$^{ns}$ | 313.86** |
| **Cluster IV** | | | | **0.00**$^{ns}$ |

$X^2$ = 24.72 and 19.67 at 1% and 5% probability level, respectively, ** = highly significant, ns = non-significant, bold values are intra-cluster distance.

### 4.6.4. Principal component analysis

The principal component analysis revealed four principal components PC1, PC2, PC3 and PC4 with eigenvalues greater than one (Table 12). They have accounted for 70.54% of the total variation among genotypes for the twelve quantitative characters. Khare *et al*. (2014)reportedthat the combination of the first four principal components accounted for 77.13% of total variation of all the characters. The relative magnitude of eigenvectors from the first principal component (PC1) was 35% showing that all characters except plant height and number of filled spikelets per panicle had high loading and most contributing characters for the total variation. The second principal component (PC2) contributed 14.94% of the total variation. The major contributing characters for the variation in the second principal components (PC2) were days to 85% maturity, plant height, number of total tillers per plant, number of fertile tillers per plant, number of filled spikelets per panicle, number of unfilled spikelets per panicle, biomass yield and panicle shattering. In the same way, 11.62% of the total variability among the tested genotypes accounted for the third principal component (PC3) originated from variation in plant height, panicle length and number of total tillers per plant. The fourth principal component (PC4) contributed 8.98% of the total variation. Number of unfilled spikelets per panicle and harvest index expressed highest loads in principal component four (PC4). The positive and negative weight shows the presence of positive and

negative correlation trends between the components and the variables. Therefore, the above mentioned characters with high positive or negative loads contributed more to the variation and they were the ones that most differentiated the clusters.

Table 12: Eigenvectors and Eigenvalues of the first four principal components (PCs) for 12 characters of 36 upland rice genotypes

| **Characters** | | **PCA 1** | **PCA 2** | **PCA 3** | **PCA 4** |
|---|---|---|---|---|---|
| DM | | 0.47 | 0.40 | 0.11 | 0.09 |
| PH | | -0.11 | 0.54 | 0.70 | 0.01 |
| PL | | 0.59 | 0.12 | 0.63 | -0.13 |
| TTPP | | 0.43 | -0.55 | 0.55 | -0.02 |
| FTPP | | 0.79 | -0.41 | 0.21 | -0.08 |
| FSPP | | 0.19 | 0.71 | -0.17 | -0.01 |
| USPP | | -0.65 | 0.35 | 0.25 | -0.48 |
| Pan/$m^2$ | | 0.80 | -0.12 | -0.06 | 0.14 |
| BY | | 0.50 | 0.45 | -0.03 | -0.001 |
| HI | | 0.69 | -0.11 | -0.21 | -0.35 |
| PSht | | -0.71 | -0.29 | 0.27 | -0.02 |
| GY | | 0.89 | 0.24 | -0.13 | 0.12 |
| Eigen value | | 4.55 | 1.94 | 1.51 | 1.17 |
| Proportion (%) | 35 | | 14.94 | 11.62 | 8.98 |
| Cumulative (%) | 35 | | 49.94 | 61.56 | 70.54 |

DM = days to 85% maturity, PH = plant height, PL = panicle length, TTPP = number of total tillers per plant, FTPP = number of fertile tillers per plant, FSPP = number of filled spikelets per panicle, USPP = number of unfilled spikelets per panicle, Pan/$m^2$ = number of panicles per meter square, BY = biomass yield, HI = harvest index, PSht = panicle shattering, GY = grain yield (kg $ha^{-1}$).

# 5. SUMMARY AND CONCLUSION

Rice is the most important food crop and energy source for about half of the world's population. In Ethiopia, rice production has started a few decades ago and now it is important cereal crop cultivated in different parts of the country.However, in the country, rice production remains less productive (2.8 t $ha^{-1}$), compared to the World's average (4.4 t $ha^{-1}$), mainly due to shortage of improved varieties. To develop high yielding rice varieties and therebyto increase the productivity of rice, information on the extent and pattern ofgenetic variability present in the rice genotypes and associations between yield and yield related characters becomes a pre-requisite for any breeding strategy and variety improvement program. Therefore, in order to generate such information, thirty six upland rice genotypes were evaluated using simple lattice design at two locations (Gojeb and Guraferda), Southwestern Ethiopia with the objective ofestimating the extent of genetic variation and association among grain yield and yield related characters.

The combined analysis of variance revealed that, the genotypes were significantly different for all the characters studied, except days to 50% heading, panicle weight, thousand seed weight, lodging incidence and reaction to major rice diseases (leaf blast and brown spot). This indicates the existence of considerable amount of variation among the tested genotypes. The genotype × location interaction effects were also significant for days to 85% maturity, plant height, number of fertile tillers per plant, number of unfilled spikelets per panicle, biomass yield, panicle shattering and grain yield, indicates that differential response of genotypes under the two locations for these characters.

The estimates of phenotypic coefficient of variation (PCV) were slightly higher than that of genotypic coefficient of variation (GCV) for most of the characters studied, indicates the presence of slight environmental influence on the phenotypic expression of these characters.Higher phenotypic coefficient of variation (PCV) and moderate genotypic coefficient of variation (GCV) values were showed by panicle shattering. High heritability estimates were observed for number of panicles per meter square and plant height. However, low heritability estimates were observed for grain yield and panicle shattering indicates the predominance of non-additive gene effects in the inheritance of these characters.Among the

studied characters,number of total tillers per plant, number of fertile tillers per plant, number of panicles per meter square, biomass yield and harvest Index had moderate values of genetic advances as percent of mean. High heritability coupled with moderate genetic advance as percent of mean was observed for number of panicles per meter square, indicates additive genes governed the inheritance of this character and therefore, selection based on this character is may be effective for further improvement of the crop in Southwestern Ethiopia, while low heritability coupled with low genetic advance as percent of mean was observed for grain yield and panicle shattering, indicates governance of non-additive gene actions and greater influence of environment in the expression of these characters and therefore selection based on these characters are may not be effective in further improvement of the crop.

The result of correlation coefficient showed that, grain yield had positive and significant phenotypic and genotypic associations with days to 85% maturity, panicle length, number of fertile tillers per plant, number of panicles per meter square, biomass yield and harvest index, indicates in Southwestern Ethiopia grain yield of upland rice can be improved by selecting genotypes having higher performances for these positively and significantly associated characters. Phenotypic and genotypic correlation coefficients of various characters were partitioned in to direct and indirect effects by using path coefficient analysis and revealed that harvest index had the highest positive direct effect on grain yield at genotypic level. The genotypic correlation of this character with grain yield was positive and significant, signified that there is true association between this character and grain yield and should be given prior attention in practicing selection aimed at the improvement of grain yield of upland rice.

The genotypes were partitioned into four distinct groups based on their similarities in characteristics, this makes the genotypes to be moderately divergent. There was statistically approved differences between clusters. The maximum squared distance was found between cluster three and four ($D^2$=313.86) followed by cluster two and four ($D^2$=189.27). Therefore maximum recombination and segregation of progenies is expected from crosses involving parents selected from cluster three and four followed by cluster two and four. The principal component analysis revealed four principal components PC1, PC2, PC3 and PC4 with eigenvalues greater than one, have accounted for 70.54% of the total variation.

Based on genotypic coefficient of variation, broad sense heritability and genetic advance as percent of mean estimates, number of panicles per meter square, number of fertile tillers per plant, biomass yield and harvest index were important yield contributing characters. Particularly, number of panicles per meter square and harvest index had the maximum positive direct effect on grain yield with the highest genotypic correlation coefficient. Therefore, from the present study it can be concluded that, for increasing rice grain yield in Southwestern Ethiopia, a genotype should possess more number of paniclesper meter square and high grain to biomass ratio. The result suggests that these two characters are important yield contributing characters and selection on these characters would be most effective.

Generally, the present study indicated that there was no sufficient genetic variation present for the characters studied in rice genotypes Therefore, it recommended that broadening the genetic bases of rice germplasms by hybridization and introduction of more rice germplasmsfrom International Rice Research Institute and African Rice Center may be requiredfora successful breeding program in Southwestern Ethiopia. In addition, in order to give confirmative results, further studies in more locations and years, supported with molecular breeding approach should be conducted on rice genetic variability and character association.

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# 7. APPENDICES

Appendix Table 1: Homogeneity test according to Hartley (1950), ratio of largest to smallest mean squares of error

| Characters | Mean square of error at Gojeb | Mean square of error at Guraferda | Ratio of largest to smallest mean squares of error | F-tabulated | |
|---|---|---|---|---|---|
| | | | | 5% | 1% |
| DH | 5.45 | 4.34 | 1.26 | 1.53 | 1.84 |
| DM | 7.59 | 8.94 | 1.18 | 1.53 | 1.84 |
| PH | 8.01 | 12.41 | 1.55 | 1.53 | 1.84 |
| PL | 1.22 | 0.97 | 1.26 | 1.53 | 1.84 |
| TTPP | 2.59 | 2.53 | 1.02 | 1.53 | 1.84 |
| FTPP | 2.03 | 1.92 | 1.06 | 1.53 | 1.84 |
| FSPP | 137.37 | 147.09 | 1.07 | 1.53 | 1.84 |
| USPP | 1.83 | 3.17 | 1.73 | 1.53 | 1.84 |
| PW | 1.65 | 2.04 | 1.24 | 1.53 | 1.84 |
| Pan/$m^2$ | 43.46 | 52.02 | 1.20 | 1.53 | 1.84 |
| BY | 426610.89 | 435866.67 | 1.02 | 1.53 | 1.84 |
| HI | 0.002 | 0.0033 | 1.65 | 1.53 | 1.84 |
| TSW | 5.54 | 7.95 | 1.44 | 1.53 | 1.84 |
| LB | 22.37 | 13.02 | 1.72 | 1.53 | 1.84 |
| BS | 17.04 | 14.45 | 1.18 | 1.53 | 1.84 |
| LI | 0.37 | 0.31 | 1.19 | 1.53 | 1.84 |
| PSht | 0.26 | 0.29 | 1.12 | 1.53 | 1.84 |
| GY | 78076.29 | 131230.33 | 1.68 | 1.53 | 1.84 |

DH = days to heading, DM = days to maturity, PH = plant height, PL = panicle length, TTPP = number of total tillers per plant, FTPP = number of fertile tillers per plant, FSPP = number of filled spikelets per panicle, USPP = number of unfilled spikelets per panicle, PW = panicle weight, Pan/$m^2$ = number of panicles per meter square, BY = biomass yield, HI = harvest index, TSW = thousand seed weight, LB = leaf blast, BS = brown spot, LI = lodging incidence, PSht = panicle shattering, GY = grain yield (kg $ha^{-1}$).

Appendix Table 2: Analysis of variance summary for 18 yield and yield related characters at Gojeb

| Characters | Mean square | | | | | | CV (%) | Mean | Efficiency relative to RCBD |
|---|---|---|---|---|---|---|---|---|---|
| | Replication(1) | Treatments(35) | | Blocks with in rep(Adj) (10) | Error | | | | |
| | | Adj | Un-adj | | Intra block (25) | RCBD(35) | | | |
| DH | 17.01 | 9.15 | 10.04 | 9.83 | 5.45 | 6.70 | 2.86 | 81.63 | 109.09 |
| DM | 7.35 | 15.91* | 17.72 | 6.33 | 7.59 | 7.23 | 2.37 | 116.37 | 95.25 |
| PH | 15.87 | 28.14** | 33.99 | 11.55 | 8.01 | 9.02 | 3.44 | 82.35 | 103.55 |
| PL | 1.23 | 2.37* | 2.68 | 0.82 | 1.22 | 1.11 | 5.12 | 21.60 | 90.46 |
| TTPP | 3.29 | 4.50 | 4.68 | 2.56 | 2.59 | 2.58 | 13.65 | 11.80 | 99.68 |
| FTPP | 3.21 | 5.39** | 5.42 | 1.94 | 2.03 | 2.00 | 15.30 | 9.31 | 98.75 |
| FSPP | 319.20 | 244.17 | 285.01 | 130.95 | 137.37 | 135.53 | 12.08 | 97.00 | 98.67 |
| USPP | 4.01 | 4.42** | 5.53 | 1.66 | 1.83 | 1.78 | 12.70 | 10.65 | 97.39 |
| PW | 7.74 | 1.85 | 2.48 | 1.49 | 1.65 | 1.60 | 8.31 | 15.45 | 97.16 |
| Pan/$m^2$ | 0.00 | 79.40 | 84.10 | 88.05 | 43.46 | 56.2 | 13.99 | 47.14 | 112.97 |
| BY | 50138.89 | 759679.84 | 822893 | 85358.89 | 426610.89 | 329110 | 16.60 | 3933.61 | 77.14 |
| HI | 0.03 | 0.005** | 0.005 | 0.01 | 0.002 | 0.003 | 12.56 | 0.36 | 127.72 |
| TSW | 0.01 | 9.47 | 8.14 | 9.34 | 5.54 | 6.62 | 8.44 | 27.89 | 107.16 |
| LB | 15.77 | 29.23 | 33.69 | 6.11 | 22.37 | 17.72 | 22.39 | 21.13 | 79.24 |
| BS | 79.13 | 28.01 | 29.47 | 14.64 | 17.04 | 16.35 | 15.85 | 26.03 | 95.97 |
| LI | 0.61 | 0.54 | 0.61 | 0.28 | 0.37 | 0.35 | 21.83 | 2.79 | 92.88 |
| PSht | 0.43 | 2.23** | 2.71 | 0.29 | 0.26 | 0.27 | 20.53 | 2.47 | 100.51 |
| GY | 126690.7 | 307418.12** | 368052 | 23518.29 | 78076.29 | 62488 | 11.11 | 2515.06 | 80.03 |

The numbers in the brackets indicates degree of freedom,DH = days to heading, DM = days to maturity, PH = plant height, PL = panicle length, TTPP = number of total tillers per plant, FTPP = number of fertile tillers per plant, FSPP = number of filled spikelets per panicle, USPP = number of unfilled spikelets per panicle, PW = panicle weight, Pan/$m^2$ = number of panicles per meter square, BY = biomass yield, HI = harvest index, TSW = thousand seed weight, LB = leaf blast, BS = brown spot, LI = lodging incidence, PSht = panicle shattering, GY = grain yield (kg $ha^{-1}$).

Appendix Table 3: Analysis of variance summary for 18 yield and yield related characters at Guraferda

| Characters | Mean square | | | | | | CV (%) | Mean | Efficiency relative to RCBD |
|---|---|---|---|---|---|---|---|---|---|
| | Replication(1) | Treatments(35) | | Blocks with in rep(Adj) (10) | Error | | | | |
| | | Adj | Un-adj | | Intra block (25) | RCBD(35) | | | |
| DH | 4.50 | 6.98 | 7.68 | 4.80 | 4.34 | 4.47 | 2.57 | 80.97 | 100.28 |
| DM | 5.56 | 20.09* | 22.20 | 4.69 | 8.94 | 7.72 | 2.53 | 118.11 | 86.41 |
| PH | 191.43 | 69.21** | 73.45 | 24.67 | 12.41 | 15.92 | 4.16 | 84.65 | 112.26 |
| PL | 7.61 | 1.92* | 1.98 | 0.99 | 0.97 | 0.98 | 4.59 | 21.46 | 100.02 |
| TTPP | 0.04 | 4.41 | 5.79 | 3.46 | 2.53 | 2.79 | 12.57 | 12.66 | 102.61 |
| FTPP | 0.98 | 4.38* | 4.94 | 3.22 | 1.92 | 2.29 | 13.82 | 10.02 | 107.03 |
| FSPP | 101.29 | 198.99 | 262.79 | 221.90 | 147.09 | 168.46 | 12.27 | 98.85 | 104.47 |
| USPP | 8.41 | 4.50 | 4.67 | 1.23 | 3.17 | 2.61 | 15.45 | 11.51 | 82.57 |
| PW | 0.02 | 2.33 | 2.12 | 2.12 | 2.04 | 2.06 | 9.66 | 14.79 | 100.04 |
| Pan/$m^2$ | 227.56 | 87.84 | 108.50 | 29.31 | 52.02 | 45.52 | 15.60 | 46.22 | 87.53 |
| BY | 1729800.00 | 1070316.19** | 1194234 | 507273.33 | 435866.67 | 456269 | 15.47 | 4268.33 | 100.63 |
| HI | 0.02 | 0.0056 | 0.006 | 0.0015 | 0.0033 | 0.003 | 16.3 | 0.35 | 84.72 |
| TSW | 7.30 | 8.83 | 9.06 | 3.25 | 7.95 | 6.60 | 9.68 | 29.13 | 83.09 |
| LB | 2.80 | 20.41 | 23.78 | 11.36 | 13.02 | 12.54 | 16.63 | 21.70 | 96.35 |
| BS | 24.49 | 17.32 | 18.41 | 24.02 | 14.45 | 17.18 | 13.85 | 27.45 | 106.77 |
| LI | 0.44 | 0.35 | 0.29 | 0.44 | 0.31 | 0.35 | 19.8 | 2.80 | 103.6 |
| PSht | 0.07 | 2.29** | 2.43 | 0.39 | 0.29 | 0.32 | 23.36 | 2.31 | 102.37 |
| GY | 21302.54 | 189634.73 | 305103 | 271446.81 | 131230.33 | 171292 | 13.20 | 2744.71 | 113.74 |

The numbers in the brackets indicates degree of freedom, DH = days to heading, DM = days to maturity, PH = plant height, PL = panicle length, TTPP = number of total tillers per plant, FTPP = number of fertile tillers per plant, FSPP = number of filled spikelets per panicle, USPP = number of unfilled spikelets per panicle, PW = panicle weight, Pan/$m^2$ = number of panicles per meter square, BY = biomass yield, HI = harvest index, TSW = thousand seed weight, LB = leaf blast, BS = brown spot, LI = lodging incidence, PSht = panicle shattering, GY = grain yield (kg $ha^{-1}$).

Appendix Table 4: Combined analysis of variance summary for 18 yield and yield related characters of 36 upland rice genotypes

| Source of variation | DF | Mean Square | F- value | Probability |
|---|---|---|---|---|
| **Days to 50% Heading (DH)** | | | | |
| Location | 1 | 15.34 | 2.52 | 0.12 |
| Rep(Loc) | 1 | 19.51 | 3.20 | 0.08 |
| Block(Rep) | 10 | 2.52 | 0.41 | 0.93 |
| Genotype | 35 | 9.55 | 1.57 | 0.06 |
| Location* Genotype | 35 | 7.01 | 1.15 | 0.31 |
| Error | 60 | 6.10 | | |
| **Days to 85% maturity (DM)** | | | | |
| Location | 1 | 108.51 | 13.09 | 0.0006 |
| Rep(Loc) | 1 | 12.84 | 1.55 | 0.22 |
| Block(Rep) | 10 | 2.64 | 0.32 | 0.97 |
| Genotype | 35 | 22.61 | 2.73 | 0.0003 |
| Location* Genotype | 35 | 13.91 | 1.68 | 0.039 |
| Error | 60 | 8.29 | | |
| **Plant height (PH)** | | | | |
| Location | 1 | 190.44 | 16.21 | 0.0002 |
| Rep(Loc) | 1 | 158.76 | 13.51 | 0.0005 |
| Block(Rep) | 10 | 16.78 | 1.43 | 0.19 |
| Genotype | 35 | 79.67 | 6.78 | <.0001 |
| Location* Genotype | 35 | 19.72 | 1.68 | 0.04 |
| Error | 60 | 11.75 | | |
| **Panicle length (PL)** | | | | |
| Location | 1 | 0.75 | 0.70 | 0.41 |
| Rep(Loc) | 1 | 7.47 | 6.95 | 0.01 |
| Block(Rep) | 10 | 0.84 | 0.78 | 0.64 |
| Genotype | 35 | 2.98 | 2.77 | 0.0003 |
| Location* Genotype | 35 | 1.51 | 1.40 | 0.12 |
| Error | 60 | 1.08 | | |
| **Number of total tillers per plant(TTPP)** | | | | |
| Location | 1 | 26.52 | 10.17 | 0.0023 |
| Rep(Loc) | 1 | 2.01 | 0.77 | 0.38 |
| Block(Rep) | 10 | 3.19 | 1.22 | 0.30 |
| Genotype | 35 | 6.14 | 2.36 | 0.0017 |
| Location* Genotype | 35 | 2.67 | 1.02 | 0.46 |
| Error | 60 | 2.61 | | |
| **Number of fertile tillers per plant (FTPP)** | | | | |
| Location | 1 | 18.20 | 8.70 | 0.005 |
| Rep(Loc) | 1 | 3.87 | 1.85 | 0.18 |
| Block(Rep) | 10 | 2.47 | 1.18 | 0.32 |
| Genotype | 35 | 6.11 | 2.92 | 0.0001 |
| Location* Genotype | 35 | 3.67 | 1.75 | 0.03 |
| Error | 60 | 2.09 | | |

Appendix Table 4 *(Continued)*

| | | | | |
|---|---|---|---|---|
| **Number of filled spikelets per panicle(FSPP)** | | | | |
| Location | 1 | 123.58 | 0.80 | 0.38 |
| Rep(Loc) | 1 | 390.06 | 2.51 | 0.12 |
| Block(Rep) | 10 | 132.27 | 0.85 | 0.58 |
| Genotype | 35 | 324.73 | 2.09 | 0.006 |
| Location* Genotype | 35 | 165.40 | 1.07 | 0.41 |
| Error | 60 | 155.29 | | |
| **Number of unfilled spikelets per panicle(USPP)** | | | | |
| Location | 1 | 27.04 | 11.60 | 0.001 |
| Rep(Loc) | 1 | 0.40 | 0.17 | 0.68 |
| Block(Rep) | 10 | 1.40 | 0.60 | 0.81 |
| Genotype | 35 | 5.74 | 2.46 | 0.001 |
| Location* Genotype | 35 | 3.96 | 1.70 | 0.04 |
| Error | 60 | 2.33 | | |
| **Panicle weight(PW)** | | | | |
| Location | 1 | 15.80 | 8.96 | 0.004 |
| Rep(Loc) | 1 | 3.45 | 1.96 | 0.17 |
| Block(Rep) | 10 | 2.25 | 1.28 | 0.26 |
| Genotype | 35 | 2.56 | 1.45 | 0.102 |
| Location* Genotype | 35 | 1.82 | 1.03 | 0.45 |
| Error | 60 | 1.76 | | |
| **Number of panicles per meter square (Pan/$m^2$)** | | | | |
| Location | 1 | 30.25 | 0.67 | 0.415 |
| Rep(Loc) | 1 | 113.78 | 2.53 | 0.12 |
| Block(Rep) | 10 | 86.32 | 1.92 | 0.06 |
| Genotype | 35 | 120.29 | 2.68 | 0.0004 |
| Location* Genotype | 35 | 47.55 | 1.06 | 0.42 |
| Error | 60 | 44.95 | | |
| **Biomass yield per plot (BY)** | | | | |
| Location | 1 | 4033402.78 | 9.76 | 0.003 |
| Rep(Loc) | 1 | 1184469.44 | 2.87 | 0.10 |
| Block(Rep) | 10 | 268592.78 | 0.65 | 0.77 |
| Genotype | 35 | 1128445.63 | 2.73 | 0.0003 |
| Location* Genotype | 35 | 686545.63 | 1.66 | 0.04 |
| Error | 60 | 413372.20 | | |
| **Harvest index (HI)** | | | | |
| Location | 1 | 0.00007 | 0.03 | 0.87 |
| Rep(Loc) | 1 | 0.0004 | 0.15 | 0.70 |
| Block(Rep) | 10 | 0.0042 | 1.57 | 0.14 |
| Genotype | 35 | 0.0067 | 2.49 | 0.0009 |
| Location* Genotype | 35 | 0.0036 | 1.35 | 0.15 |
| Error | 60 | 0.0027 | | |

Appendix Table 4 *(Continued)*

| | | | | |
|---|---|---|---|---|
| **Thousand seed weight (TSW)** | | | | |
| Location | 1 | 55.95 | 8.38 | 0.01 |
| Rep(Loc) | 1 | 3.34 | 0.50 | 0.48 |
| Block(Rep) | 10 | 6.25 | 0.94 | 0.51 |
| Genotype | 35 | 10.48 | 1.57 | 0.06 |
| Location* Genotype | 35 | 7.06 | 1.06 | 0.42 |
| Error | 60 | 6.68 | | |
| **Leaf Blast (LB)** | | | | |
| Location | 1 | 11.61 | 0.69 | 0.41 |
| Rep(Loc) | 1 | 15.94 | 0.95 | 0.33 |
| Block(Rep) | 10 | 5.27 | 0.31 | 0.97 |
| Genotype | 35 | 26.55 | 1.58 | 0.06 |
| Location* Genotype | 35 | 25.02 | 1.49 | 0.09 |
| Error | 60 | 16.78 | | |
| **Brown Spot (BS)** | | | | |
| Location | 1 | 72.35 | 4.45 | 0.04 |
| Rep(Loc) | 1 | 7.79 | 0.48 | 0.49 |
| Block(Rep) | 10 | 19.75 | 1.21 | 0.30 |
| Genotype | 35 | 24.90 | 1.53 | 0.07 |
| Location* Genotype | 35 | 21.97 | 1.35 | 0.15 |
| Error | 60 | 16.27 | | |
| **Lodging Incidence (LI)** | | | | |
| Location | 1 | 0.00054 | 0.00 | 0.97 |
| Rep(Loc) | 1 | 1.04 | 3.30 | 0.07 |
| Block(Rep) | 10 | 0.53 | 1.67 | 0.11 |
| Genotype | 35 | 0.50 | 1.60 | 0.06 |
| Location* Genotype | 35 | 0.42 | 1.32 | 0.17 |
| Error | 60 | 0.32 | | |
| **Panicle Shattering (PSht)** | | | | |
| Location | 1 | 0.92 | 3.13 | 0.08 |
| Rep(Loc) | 1 | 0.07 | 0.25 | 0.62 |
| Block(Rep) | 10 | 0.29 | 0.98 | 0.47 |
| Genotype | 35 | 2.47 | 8.38 | <.0001 |
| Location* Genotype | 35 | 2.12 | 7.21 | <.0001 |
| Error | 60 | 0.29 | | |
| **Grain yield per hectare (GY)** | | | | |
| Location | 1 | 1898539.52 | 17.08 | 0.0001 |
| Rep(Loc) | 1 | 125946.91 | 1.13 | 0.29 |
| Block(Rep) | 10 | 151322.26 | 1.36 | 0.22 |
| Genotype | 35 | 288979.76 | 2.60 | 0.001 |
| Location* Genotype | 35 | 226956.50 | 2.04 | 0.01 |
| Error | 60 | 111151.56 | | |

Appendix Table **5**: Mean performance of 36 upland rice genotypes for 9 yield and yield related characters tested at two locations

| **Genotypes** | **DH** | **DM** | **PH** | **PL** | **TTPP** | **FTPP** | **FSPP** | **USPP** | **PW** |
|---|---|---|---|---|---|---|---|---|---|
| ART15 8-10-36-4-1-1-B-B-1 | 81.75 | 119.25 $^{b-c}$ | 85.35$^{c-h}$ | 23.15$^{a}$ | 12.65$^{b-h}$ | 11.4$^{b}$ | 97.9$^{a-j}$ | 11.2$^{a-f}$ | 16.48 |
| ART15 10-17-46-2-2-2-B-B-2 | 82.25 | 117.75 $^{b-f}$ | 78.55$^{k-m}$ | 22.05$^{a-g}$ | 12.7$^{b-f}$ | 10.85$^{b-c}$ | 110.5$^{a-c}$ | 10.35$^{b-i}$ | 15.55 |
| ART16 9-16-21-1-B-2-B-B-1 | 80.25 | 117.75$^{b-f}$ | 83.9$^{d-j}$ | 20.8$^{e-i}$ | 10.6$^{f-j}$ | 8.5$^{f-i}$ | 105.55$^{a-g}$ | 11.65$^{a-e}$ | 15.83 |
| ART16 9-29-10-2-B-1-B-B-1 | 80.5 | 117.75 $^{b-g}$ | 78.45$^{k-m}$ | 20.55$^{h-i}$ | 12.6$^{b-i}$ | 10$^{b-h}$ | 106.4$^{a-f}$ | 12.25$^{a-c}$ | 14.35 |
| ART16-4-1-21-2-B-2-B-1-1 | 83.75 | 118.75 $^{b-d}$ | 79.85$^{j-m}$ | 19.6$^{i}$ | 11.2$^{f-j}$ | 8.25$^{g-i}$ | 90.25$^{e-k}$ | 11.75$^{a-e}$ | 15.80 |
| ART16-4-13-1-2-1-1-B-1-1 | 80.5 | 119.5 $^{b-c}$ | 80.45$^{i-l}$ | 21.75$^{a-g}$ | 12.05$^{c-j}$ | 10.4$^{b-f}$ | 103.05$^{a-h}$ | 9.25$^{f-i}$ | 15.93 |
| ART16-5-10-2-3-B-1-B-1-2 | 82.25 | 114 $^{f-g}$ | 91$^{a-b}$ | 20.8$^{e-i}$ | 11.95$^{c-j}$ | 8.1$^{h-i}$ | 97.15$^{a-j}$ | 11.55$^{a-e}$ | 14.00 |
| ART16-9-1-9-2-1-1-B-1-1 | 82.5 | 117.75 $^{b-f}$ | 75.15$^{m}$ | 22$^{a-g}$ | 14.55$^{a-b}$ | 10.35$^{b-f}$ | 77$^{k-l}$ | 10.85$^{b-h}$ | 14.18 |
| ART16-9-4-18-4-2-1-B-1-1 | 81.25 | 115 $^{d-g}$ | 82.95$^{d-k}$ | 22.75$^{a-c}$ | 11.8$^{d-j}$ | 9.7$^{b-i}$ | 93$^{c-k}$ | 11.35$^{a-f}$ | 14.63 |
| ART16-9-4-18-4-2-1-B-1-2 | 80.25 | 118 $^{b-f}$ | 81.8$^{f-k}$ | 23$^{ab}$ | 14.6$^{a-b}$ | 13.9$^{a}$ | 96.8$^{a-j}$ | 9.75$^{d-i}$ | 14.30 |
| ART16-9-6-18-1-1-2-B-1-1 | 80.75 | 119.75 $^{b}$ | 86.55$^{b-f}$ | 22.8$^{a-c}$ | 12$^{c-j}$ | 10.25$^{b-g}$ | 111.5$^{a-b}$ | 11.35$^{a-f}$ | 16.50 |
| ART16-9-9-25-2-1-1-B-2-1 | 81.5 | 117.25 $^{b-g}$ | 79.3$^{j-m}$ | 20.8$^{e-i}$ | 12.45$^{b-j}$ | 10.55$^{b-e}$ | 83.8$^{j-l}$ | 9.65$^{e-i}$ | 14.83 |
| ART16-9-9-25-2-1-1-B-2-2 | 81.25 | 115.75 $^{b-g}$ | 80.35$^{i-l}$ | 21.2$^{e-g}$ | 12.85$^{b-f}$ | 10.25$^{b-g}$ | 100.25$^{a-j}$ | 10.65$^{b-i}$ | 14.98 |
| ART16-9-29-16-1-1-1-B-1-1 | 80.75 | 115 $^{d-g}$ | 81.15$^{h-l}$ | 21.35$^{c-h}$ | 12.05$^{c-j}$ | 10.4$^{b-f}$ | 86.35$^{h-l}$ | 11.9$^{a-d}$ | 14.13 |
| ART16 15-10-1-1-B-1-B-B-1 | 78.25 | 115 $^{d-g}$ | 86.05$^{c-g}$ | 20.55$^{h-i}$ | 11.3$^{f-j}$ | 8.85$^{d-i}$ | 106.4$^{a-f}$ | 11.95$^{a-c}$ | 14.48 |
| ART16 15-10-1-1-B-1-B-B-2 | 79.75 | 117 $^{b-g}$ | 79.8$^{j-m}$ | 21$^{e-i}$ | 10.45$^{g-j}$ | 8.3$^{g-i}$ | 112.05$^{a}$ | 11.95$^{a-c}$ | 15.78 |
| ART16-13-11-1-2-B-2-B-2-1 | 81.75 | 115.75 $^{b-g}$ | 75.5$^{m}$ | 20.7$^{f-i}$ | 11.6$^{d-j}$ | 8.7$^{e-i}$ | 71.25$^{l}$ | 12.15$^{a-c}$ | 13.85 |
| ART16-16-1-14-3-1-1-B-1-2 | 84.25 | 125.25 $^{a}$ | 93.85$^{a}$ | 23$^{a-b}$ | 10.3$^{j}$ | 8.55$^{e-i}$ | 103.35$^{a-h}$ | 12.05$^{a-c}$ | 15.30 |
| ART16-16-11-25-1-B-1-B-1-2 | 79.25 | 118.25 $^{b-e}$ | 93.45$^{a}$ | 22.8$^{a-c}$ | 15.8$^{a}$ | 10.75$^{b-d}$ | 93$^{c-k}$ | 12.35$^{a-b}$ | 14.18 |
| ART16-17-7-18-1-B-1-B-1-1 | 79.5 | 115.5 $^{c-g}$ | 87.45$^{b-d}$ | 21.6$^{b-h}$ | 11.8$^{d-j}$ | 9.05$^{c-i}$ | 88.35$^{g-l}$ | 9.65$^{e-i}$ | 14.08 |
| ART16-21-5-12-3-1-1-B-2-1 | 82.25 | 116 $^{b-g}$ | 81.25$^{g-k}$ | 20.6$^{g-i}$ | 11.45$^{f-j}$ | 8.55$^{e-i}$ | 99.2$^{a-j}$ | 12.3$^{a-c}$ | 15.03 |
| ART16-9-29-12-1-1-2-B-1-1 | 78.5 | 114.75 $^{d-g}$ | 86.9$^{b-e}$ | 20.75$^{e-i}$ | 14.15$^{a-c}$ | 11.25$^{b}$ | 106.05$^{a-f}$ | 12$^{a-c}$ | 15.05 |
| ART16-9-14-16-2-2-1-B-1-2 | 78 | 116.5 $^{b-g}$ | 81.9$^{f-k}$ | 22.2$^{a-e}$ | 11.25$^{f-j}$ | 8.65$^{c-i}$ | 102.9$^{a-h}$ | 10.95$^{b-f}$ | 15.73 |
| ART16-9-33-2-1-1-1-B-1-2 | 83.25 | 116.5 $^{b-g}$ | 86.5$^{b-f}$ | 20.9$^{e-i}$ | 10.35$^{i-j}$ | 9$^{c-i}$ | 109.95$^{a-c}$ | 12.3$^{a-c}$ | 16.05 |
| ART16-9-122-33-2-1-1-B-1-1 | 82.5 | 117.25 $^{b-g}$ | 87.2$^{b-d}$ | 21.6$^{b-h}$ | 12.25$^{c-j}$ | 9.1$^{c-i}$ | 91.45$^{d-k}$ | 10.2$^{b-i}$ | 14.23 |
| ART15-19-5-4-1-1-1-B-1-1 | 81.25 | 116.25 $^{b-g}$ | 85.8$^{c-h}$ | 22.15$^{a-f}$ | 15.4$^{a}$ | 10.35$^{b-f}$ | 84.5$^{i-l}$ | 10.15$^{c-i}$ | 14.13 |
| ART16-5-9-22-2-1-1-B-1-2 | 83.5 | 116.5 $^{b-g}$ | 85.15$^{c-i}$ | 20.95$^{e-i}$ | 10.4$^{h-j}$ | 8.15$^{h-i}$ | 103.9$^{a-h}$ | 11.45$^{a-e}$ | 15.95 |
| ART16-21-4-7-2-2-2-B-2-2 | 82 | 125.75 $^{a}$ | 78.85$^{k-m}$ | 21.95$^{a-h}$ | 13.7$^{a-e}$ | 10.75$^{b-d}$ | 100.45$^{a-j}$ | 8.5$^{i}$ | 16.05 |

Appendix Table 5*(Continued)*

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| ART16-9-16-21-1-2-1-B-1-1 | 83.75 | 117.75 $^{b-f}$ | 85.45$^{c-h}$ | 22.05$^{a-g}$ | 12.15$^{c-j}$ | 8.15$^{h-i}$ | 102.7$^{a-h}$ | 11.45$^{a-e}$ | 14.00 |
| ART15-13-2-2-2-1-1-B-1-2 | 79.75 | 117.25 $^{b-g}$ | 86.15$^{c-f}$ | 22.6$^{a-d}$ | 13.85$^{a-d}$ | 11.5$^{b}$ | 101.95$^{a-i}$ | 9.05$^{g-i}$ | 16.40 |
| ART15-16-45-1-B-1-1-B-1-2 | 83 | 118 $^{b-f}$ | 82.2$^{e-k}$ | 20.9$^{e-i}$ | 11$^{f-j}$ | 7.75$^{i}$ | 89.25$^{f-k}$ | 12.2$^{a-c}$ | 15.30 |
| ART16-5-10-2-3-B-1-B-1-1 | 79.75 | 116.75 $^{b-g}$ | 89.5$^{a-c}$ | 21.4$^{c-h}$ | 12.05$^{c-j}$ | 9.15$^{c-i}$ | 94.2$^{b-k}$ | 12.1$^{a-c}$ | 14.70 |
| ART16-4-1-21-2-B-2-B-1-2 | 81.25 | 114.5 $^{e-g}$ | 85.55$^{c-h}$ | 21.45$^{c-h}$ | 12.25$^{c-j}$ | 8.75$^{d-i}$ | 107.95$^{a-d}$ | 12.2$^{a-c}$ | 15.70 |
| NERICA-12 | 83 | 115.75 $^{b-g}$ | 87.5$^{b-d}$ | 22.1$^{a-f}$ | 10.9$^{f-j}$ | 9.15$^{c-i}$ | 97.1$^{a-j}$ | 13.15$^{a}$ | 16.23 |
| NERICA-4 | 79.75 | 113.25 $^{g}$ | 76.35$^{l-m}$ | 20.55$^{h-i}$ | 11.6$^{d-j}$ | 10.25$^{b-g}$ | 92.25$^{d-k}$ | 8.6$^{i}$ | 15.73 |
| ADET | 83 | 118 $^{b-f}$ | 78.75$^{k-m}$ | 20.7$^{f-i}$ | 12.05$^{c-j}$ | 10.4$^{b-f}$ | 107.65$^{a-e}$ | 8.7$^{h-i}$ | 15.03 |
| **Mean** | **81.30** | **117.24** | **83.50** | **21.53** | **12.23** | **9.67** | **97.93** | **11.08** | **15.12** |

DH = days to heading, DM = days to maturity, PH = plant height, PL = panicle length, TTPP = number of total tillers per plant, FTPP = number of fertile tillers per plant, FSPP = number of filled spikelets per panicle, USPP = number of unfilled spikelets per panicle, PW = panicle weigh.

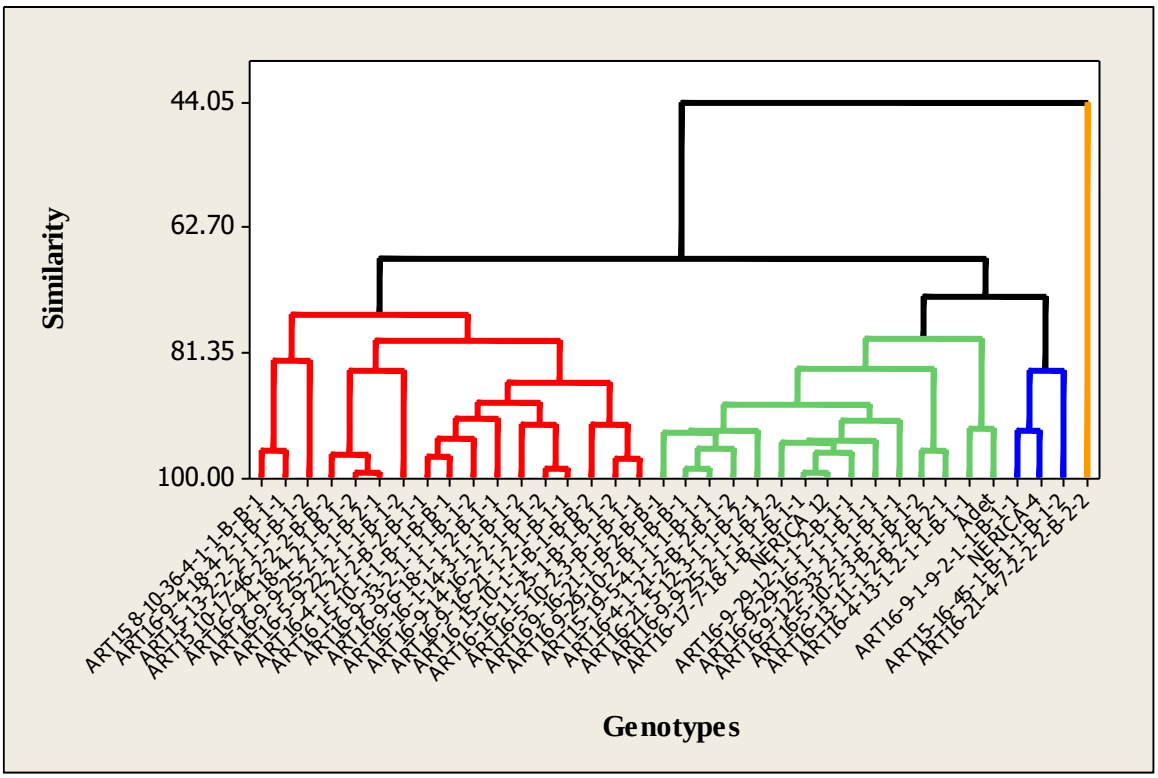
Appendix Table 6:Mean performances of 36 upland rice genotypes for 9 yield and yield related characters tested at two locations

| Genotypes | Pan/m$^2$ | BY | HI | TSW | LB | BS | LI | PSht | GY |
|---|---|---|---|---|---|---|---|---|---|
| ART15 8-10-36-4-1-1-B-B-1 | 50.75$^{b-h}$ | 4155$^{b-i}$ | 0.42$^{a-c}$ | 27.72 | 12.04 (20.06) | 15.74 (23.22) | 6.25 (2.57) | 5.25 (2.10)$^{d-e}$ | 3147.2$^{a-c}$ |
| ART15 10-17-46-2-2-2-B-B-2 | 43.75$^{e-k}$ | 4935$^{a-c}$ | 0.43$^{a-b}$ | 27.7 | 12.96 (20.85) | 20.37 (26.52) | 7.5 (2.80) | 2.25 (1.58)$^{e-g}$ | 2934.1$^{b-f}$ |
| ART16 9-16-21-1-B-2-B-B-1 | 39.75$^{j-k}$ | 3550$^{i-k}$ | 0.38$^{a-e}$ | 29.43 | 21.30 (27.43) | 28.70 (32.32) | 7.5 (2.80) | 2.25 (1.58)$^{e-g}$ | 2547.8$^{e-i}$ |
| ART16 9-29-10-2-B-1-B-B-1 | 42.75$^{f-k}$ | 3705$^{f-j}$ | 0.36$^{a-g}$ | 26.92 | 16.67 (23.63) | 24.08 (28.86) | 8.75 (3.02) | 8.25 (2.62)$^{d-c}$ | 2474.9$^{f-j}$ |
| ART16-4-1-21-2-B-2-B-1-1 | 40.75$^{j-k}$ | 4595$^{b-f}$ | 0.33$^{d-h}$ | 25.39 | 29.63 (32.94) | 25.00 (29.58) | 7.5 (2.80) | 3 (1.87)$^{e-g}$ | 2636.4$^{d-i}$ |
| ART16-4-13-1-2-1-1-B-1-1 | 52$^{b-f}$ | 3640$^{g-j}$ | 0.40$^{a-d}$ | 31.16 | 11.11 (19.34) | 18.52 (25.44) | 6.25 (2.57) | 1.5 (1.29)$^{f-g}$ | 3072.9$^{b-d}$ |
| ART16-5-10-2-3-B-1-B-1-2 | 45$^{d-k}$ | 3720$^{f-j}$ | 0.31$^{e-h}$ | 27.06 | 14.81 (22.30) | 22.22 (27.71) | 11.25 (3.37) | 15 (3.94)$^{a}$ | 1979.5$^{k}$ |
| ART16-9-1-9-2-1-1-B-1-1 | 47.25$^{c-j}$ | 3170$^{h-k}$ | 0.31$^{e-h}$ | 25.7 | 20.37 (26.51) | 25.93 (30.53) | 7.5 (2.80) | 15 (3.94)$^{a}$ | 2337.2$^{h-k}$ |
| ART16-9-4-18-4-2-1-B-1-1 | 48.5$^{c-j}$ | 4190$^{b-i}$ | 0.40$^{a-d}$ | 28.73 | 12.04 (20.06) | 18.52 (25.44) | 7.5 (2.80) | 3 (1.87)$^{d-f}$ | 3034.5$^{b-d}$ |
| ART16-9-4-18-4-2-1-B-1-2 | 65.5$^{a}$ | 4845$^{a-d}$ | 0.40$^{a-d}$ | 28.54 | 12.04 (20.06) | 16.67 (23.50) | 7.5 (2.80) | 2.25 (1.58)$^{e-g}$ | 2949$^{b-e}$ |
| ART16-9-6-18-1-1-2-B-1-1 | 55.25$^{b-c}$ | 4425$^{b-i}$ | 0.40$^{a-d}$ | 28.06 | 11.11 (19.34) | 17.59 (24.73) | 7.5 (2.80) | 0.75 (1.00)$^{g}$ | 2865.9$^{b-g}$ |
| ART16-9-9-25-2-1-1-B-2-1 | 59$^{a-b}$ | 4845$^{a-d}$ | 0.39$^{a-d}$ | 33.06 | 11.11 (19.14) | 18.52 (25.27) | 6.25 (2.57) | 1.5 (1.29)$^{f-g}$ | 2947.9$^{b-e}$ |
| ART16-9-9-25-2-1-1-B-2-2 | 46.25$^{c-k}$ | 3855$^{e-j}$ | 0.38$^{a-e}$ | 27.32 | 12.04 (20.06) | 19.45 (26.06) | 7.5 (2.80) | 3 (1.87)$^{d-f}$ | 2465.3$^{f-j}$ |
| ART16-9-29-16-1-1-1-B-1-1 | 47$^{c-k}$ | 3960$^{d-j}$ | 0.38$^{a-f}$ | 29.39 | 17.59 (24.00) | 24.07 (28.94) | 7.5 (2.80) | 15 (3.94)$^{a}$ | 2335.6$^{h-k}$ |
| ART16 15-10-1-1-B-1-B-B-1 | 47.75$^{c-j}$ | 4520$^{b-g}$ | 0.37$^{a-g}$ | 27.68 | 12.04 (20.06) | 19.45 (26.06) | 7.5 (2.80) | 3 (1.87)$^{d-f}$ | 2675.8$^{c-i}$ |
| ART16 15-10-1-1-B-1-B-B-2 | 41.25$^{i-k}$ | 4460$^{b-h}$ | 0.35$^{b-g}$ | 29.71 | 13.89 (21.13) | 21.30 (27.34) | 7.5 (2.80) | 12 (3.42)$^{a-b}$ | 2356.2$^{h-k}$ |
| ART16-13-11-1-2-B-2-B-2-1 | 42.5$^{g-k}$ | 3805$^{e-j}$ | 0.32$^{e-h}$ | 30.8 | 13.89 (21.51) | 25.00 (29.87) | 7.5 (2.80) | 12 (3.42)$^{a-b}$ | 2048.4$^{j-k}$ |
| ART16-16-1-14-3-1-1-B-1-2 | 50.25$^{b-i}$ | 4140$^{b-i}$ | 0.32$^{e-h}$ | 30.71 | 13.89 (21.64) | 25.00 (29.92) | 11.25 (3.42) | 3 (1.87)$^{d-f}$ | 2798.6$^{b-h}$ |
| ART16-16-11-25-1-B-1-B-1-2 | 43.25$^{f-k}$ | 4225$^{b-i}$ | 0.32$^{e-h}$ | 27.58 | 13.89 (21.64) | 23.15 (28.54) | 11.25 (3.42) | 9 (2.91)$^{b-c}$ | 2400.6$^{g-k}$ |
| ART16-17-7-18-1-B-1-B-1-1 | 43.5$^{e-k}$ | 3960$^{d-j}$ | 0.31$^{f-h}$ | 27.49 | 12.96 (20.85) | 19.45 (25.93) | 8.75 (3.02) | 9 (2.91)$^{b-c}$ | 2499.4$^{e-j}$ |
| ART16-21-5-12-3-1-1-B-2-1 | 43.25$^{g-k}$ | 3570$^{h-k}$ | 0.35$^{c-h}$ | 28.47 | 12.96 (20.85) | 20.37 (26.72) | 7.5 (2.80) | 12 (3.42)$^{a-b}$ | 2315.1$^{i-k}$ |
| ART16-9-29-12-1-1-2-B-1-1 | 45$^{d-k}$ | 4070$^{c-j}$ | 0.34$^{d-h}$ | 28.33 | 14.81 (22.30) | 22.22 (27.73) | 7.5 (2.61) | 7.5 (2.33)$^{c-e}$ | 2457.6$^{g-j}$ |
| ART16-9-14-16-2-2-1-B-1-2 | 47$^{c-k}$ | 4325$^{b-i}$ | 0.39$^{a-d}$ | 29.19 | 13.89 (21.64) | 18.52 (25.39) | 8.75 (3.02) | 3 (1.87)$^{d-f}$ | 2657.5$^{d-i}$ |
| ART16-9-33-2-1-1-1-B-1-2 | 47$^{c-k}$ | 4690$^{b-e}$ | 0.28$^{h}$ | 27.93 | 12.04 (20.14) | 19.44 (26.10) | 8.75 (3.02) | 3 (1.87)$^{d-f}$ | 2763.7$^{c-i}$ |
| ART16-9-122-33-2-1-1-B-1-1 | 39.75$^{j-k}$ | 3830$^{e-j}$ | 0.35$^{c-h}$ | 28.84 | 12.96 (20.98) | 19.45 (26.06) | 7.5 (2.80) | 3 (1.87)$^{d-f}$ | 2657.8$^{d-i}$ |
| ART15-19-5-4-1-1-1-B-1-1 | 41.5$^{h-k}$ | 3685$^{g-j}$ | 0.38$^{a-f}$ | 29.27 | 14.81 (22.43) | 22.22 (28.09) | 7.5 (2.61) | 8.25 (2.62)$^{c-d}$ | 2494.2$^{e-j}$ |
| ART16-5-9-22-2-1-1-B-1-2 | 43.25$^{f-k}$ | 5000$^{a-b}$ | 0.31$^{e-h}$ | 27.58 | 14.81 (22.43) | 22.23 (28.05) | 8.75 (2.97) | 12 (3.42)$^{a-b}$ | 2486.2$^{e-j}$ |
| ART16-21-4-7-2-2-2-B-2-2 | 55.25$^{b-c}$ | 5600$^{a}$ | 0.36$^{b-g}$ | 30.28 | 9.26 (17.63) | 15.74 (23.27) | 3.75 (1.94) | 1.5 (1.29)$^{f-g}$ | 3236.2$^{a-b}$ |

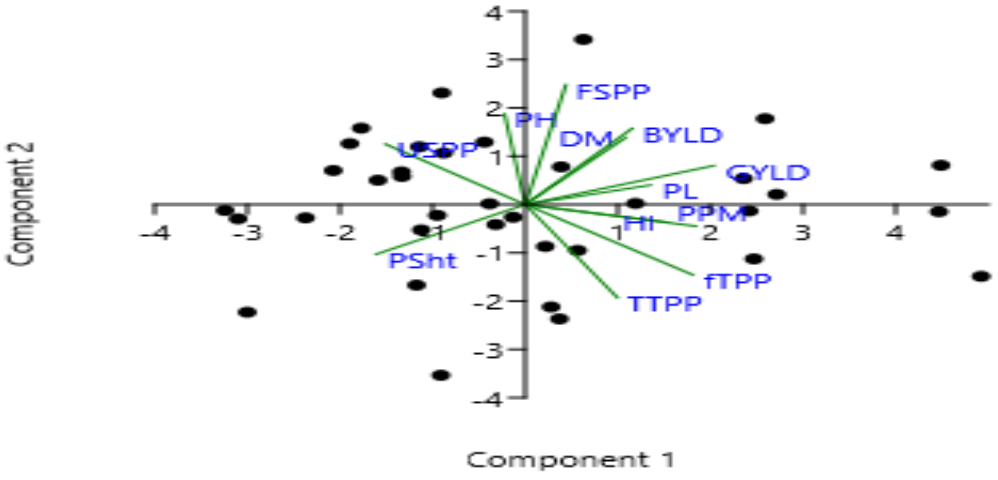
Appendix Table 6 *(Continued)*

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| ART16-9-16-21-1-2-1-B-1-1 | 44.75$^{d-k}$ | 4310$^{b-i}$ | 0.31$^{e-h}$ | 27.63 | 12.96 (20.85) | 20.37 (26.72) | 10 (3.19) | 9 (2.91)$^{b-c}$ | 2624.9$^{d-i}$ |
| ART15-13-2-2-2-1-1-B-1-2 | 54$^{b-d}$ | 4400$^{b-i}$ | 0.45$^{a}$ | 30.56 | 8.34 (16.71) | 10.19 (17.96) | 2.5 (1.53) | 1.5 (1.29)$^{f-g}$ | 3562.7a |
| ART15-16-45-1-B-1-1-B-1-2 | 39.75$^{j-k}$ | 2720$^{k}$ | 0.30$^{g-h}$ | 28.42 | 11.11 (19.34) | 20.37 (26.81) | 8.75 (2.97) | 8.25 (2.62)$^{c-d}$ | 2328.1$^{h-k}$ |
| ART16-5-10-2-3-B-1-B-1-1 | 44.75$^{d-k}$ | 4235$^{b-i}$ | 0.31$^{e-h}$ | 25.87 | 12.04 (20.06) | 23.15 (28.59) | 7.5 (2.80) | 9 (2.91)$^{b-c}$ | 2322.4$^{i-k}$ |
| ART16-4-1-21-2-B-2-B-1-2 | 37.75$^{k}$ | 3745$^{f-j}$ | 0.31$^{e-h}$ | 27.16 | 13.89 (21.77) | 22.22 (28.09) | 7.5 (2.80) | 7.5 (2.33)$^{c-e}$ | 2365.6$^{h-k}$ |
| NERICA-12 | 41.5$^{h-k}$ | 3975$^{d-j}$ | 0.42$^{a-c}$ | 29.2 | 12.96 (20.85) | 20.37 (26.72) | 8.75 (3.02) | 12 (3.42)$^{a-b}$ | 2494.9$^{e-j}$ |
| NERICA-4 | 52.75$^{b-e}$ | 3175$^{j-k}$ | 0.37$^{b-g}$ | 28.44 | 11.11 (19.34) | 18.52 (25.39) | 7.5 (2.80) | 2.25 (1.58)$^{e-g}$ | 2541.9$^{e-i}$ |
| ADET | 51.25$^{b-g}$ | 3605$^{h-k}$ | 0.34$^{d-h}$ | 29.11 | 12.96 (20.98) | 18.52 (25.35) | 5 (2.35) | 12 (3.42)$^{a-b}$ | 2861.9$^{b-g}$ |
| **Mean** | **46.68** | **4100.97** | **0.35** | **28.51** | **13.79 (21.41)** | **20.63 (26.74)** | **7.71 (2.80)** | **6.60 (2.39)** | **2629.89** |

Data's in the bracket indicated transformed according to arc sign and square root transformation methods,Pan/$m^2$ = number of panicles per meter square, BY = biomass yield, HI = harvest index, TSW = thousand seed weight, LB = leaf blast, BS = brown spot, LI = lodging incidence, PSht = panicle shattering, GY = grain yield (kg $ha^{-1}$).




Appendix Figure 1: Dendrogram indicating the genetic relationship of 36 upland ricegenotypesevaluated over the two locations at Southwestern Ethiopia.




Appendix Figure 2: Biplot scores of the first two principal components.