

**GENOTYPE X ENVIRONMENT INTERACTION AND STABILITY
ANALYSIS IN UPLAND RICE (*Oryza sativa* L.) VARIETIES IN
ETHIOPIA**

MSc THESIS

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**AUGUST 2019
HARAMAYA UNIVERSITY, HARAMAYA**

**Genotype x Environment Interaction and Stability Analysis in Upland Rice
(*Oryza sativa* L.) Varieties in Ethiopia**

**A Thesis Submitted to the School of Plant Sciences,
Postgraduate Programs Directorate
HARAMAYA UNIVERSITY**

**In Partial Fulfillment of the Requirements for the Degree of
MASTER OF SCIENCE IN PLANT BREEDING**

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**August 2019
Haramaya University, Haramaya**

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DEDICATION

I dedicate this thesis manuscript to my father Abebe Belete and my beloved brothers and sisters for nursing me with affection and love and for their dedicated partnership in the success of my life.

STATEMENT OF THE AUTHOR

I declare that this thesis is my bonafide work and that all sources of materials for this thesis have been duly acknowledged. This thesis has been submitted in partial fulfillment of the requirements for MSc degree in Plant Breeding at Haramaya University and is shelved at the University Library to be made available to users under rules of the Library. I solemnly declare that this thesis is not submitted to any other institution anywhere for the award of any academic degree, diploma, or certificate.

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BIOGRAPHICAL SKETCH

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ACKNOWLEDGEMENTS

First and above all, I would like to thank the almighty God with His mother virgin St. Mary for gave me strength and made me stand firm in my all ups and downs during my research work. I express my sincere gratitude to my major advisor Dr. Wassu Mohammed for his guidance, much helpful advice, useful discussion and careful supervision of my thesis research. Grateful acknowledgement is extended to my co-advisor, Dr. Abush Tesfaye, for his constructive advice, useful criticism and enthusiastic effort in preparation of the manuscript.

I am thankful to the Ethiopian Institute of Agricultural Research (EIAR) for giving me the opportunity to pursue my education and for providing me with the required financial support. My deepest gratefulness goes to Pawe Agricultural Research center for their support in field trial management and arrangement of the necessary facilities. I am sincerely grateful to Mr. Mulugeta Bitew, Ms. Atsedemariam Tewachew, Mr. Desalegn Wondifraw, Mr. Mesganaw Nuru and staff of cereal crops research team, for generously sharing their technical expertise and providing the necessary assistance.

I am deeply indebted to Fogera National Rice Research and Training Center for providing me with seeds of different genotypes and associated information for my work. I thank specially Mr. Abebaw Dessie, rice research coordinator for his encouragement and valuable comments on the study. I would like also to give special thanks to Mr. Tadesse Lakew, Mr. Kifle Yohannes, for their support in preparing the seed and send to other centers, planting and managing my Woreta site and timely execution of the study. I would like to give deeply indebted to Jimma research center especially to Dr. Leta and Mr. Tsegaw for your technical support. At the same level I would like to give my deep thanks to Tepi research center especially to Mr. Mekonent, and Mr. Tefera Abebe for their technical support. I would like to give deep thanks to Maitsebri research center especially to Mr. Alemu Reda for his grateful support. Finally, I would like to great thanks for all members of Pawe, Woreta, Jimma, Tepi and Maitsebri research center, Rice Research Section Technical staffs, for their technical support and timely execution of the study. I am also grateful to the Haramaya University for hosting my MSc. Study. The author extends his respect, appreciation and thanks to many other individuals who directly or indirectly contributed to the success of this thesis.

ACRONYMS AND ABBREVIATIONS

ANOVA	Analysis of Variance
AMMI	Additive Main Effects and Multiplicative Interaction
ASV	AMMI Stability Value
BARC	Bako Agricultural Research Center
CSA	Central Statistics Agency
EMA	Ethiopian Mapping Authority
FAO	Food and Agriculture Organization
FAOSTAT	Food and Agriculture Organization Statistics
FNRTC	Fogera National Rice and Training Center
GoE	Government of Ethiopia
GGE	Genotype, Genotype by Environment
GEI	Genotype by Environment Interaction
IPCA	Interaction Principal Component Analysis
IRRI	International Rice Research Institute
MARC	Melkassa Agricultural Research Center
MoA	Ministry of Agriculture
MoARD	Ministry of Agriculture and Rural Development
NERICA	New Rice for Africa
PARC	Pawe Agricultural Research Center
SNNPR	Southern Nations Nationalities and Peoples Region
SOPAR	Somalia Pastoral and Agro-pastoral Research
WARDA	West African Rice Development Association

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Genotype x Environment Interaction and Stability Analysis in Upland Rice (*Oryza sativa* L.) Varieties in Ethiopia

ABSTRACT

In Ethiopia, rice variety development program was started recently but many rice varieties were recommended for production. However, little information is available about the yield potential of varieties over diverse environments. This research was conducted to assess the magnitude of environment (E) and genotype x environment interaction (GEI) effects on yield and yields related traits, stability of the rice varieties for yield and to evaluate and stratify rice testing environments in Ethiopia. Twenty rice varieties were evaluated at six sites during 2016/17 in randomized complete block design with three replications. The combined analysis of variance over environments showed significant differences among genotypes (G), environments (E) and significant effect of GEI on phenology, growth traits, yield components and grain yield of varieties. Analysis of variance from Additive Main Effects and Multiplicative Interaction (AMMI) model revealed that G, E and GEI contributed 3.03 to 33.58, 25.69 to 72.02, and 7.09 to 30.36 %, respectively, to the total sum squares of traits. The E and GEI had a higher contribution than G to most of the traits, and GEI had larger contribution than G and E to the variations of varieties for yield. The interaction principal component axis one (IPC1) and two (IPC2) contributed 37.94 to 88.85 and 8.92 to 87.13% to sum squares of GEI, respectively. The varieties had mean yield of 3.509 t ha⁻¹, and 9 and 11 varieties had mean yield lower and higher than the average yield of genotypes, respectively. The stability parameters of regression coefficient (b_i) and deviation from regression (S^2_{di}) from Eberhart and Russell's (ER's), IPCA1, IPCA 2, AMMI stability value (ASV) from AMMI model, GGE biplot, Francis and Kannenberg's coefficient of variability (CV), Lin and Binns's cultivar performance measure (P_i), Shukla's stability variance (δ^2_i), Wricke's ecovalence (W_i), Finlay and Wilkinson's (b_i), Nassar and Huehn's mean Absolute rank difference (Si^1) and variance of ranks (Si^2) were used evaluate the stability of genotypes for yield. NERICA-3, Hidasse and Chewaqa varieties had 15.99, 15.7 and 15.42% higher yield than average yield of genotypes, respectively, and identify as responsive to changing environments, selected as the first four best genotypes across poor to most favorable environments and GGE biplot identified as ideal and stable varieties suggested to be used for production across environments. NERICA-12 and ADET varieties had 12.85 and 8.29% higher yield, respectively, than average yield of genotypes and identify as most stable by most of the stability parameters and considered as wide adaptable varieties. NERICA-4, NERICA-13 and Getachew varieties had 11.97, 10.83 and 5.7% yield advantages over the average yield of genotypes, identified as stable varieties by most of the stability parameters and selected as the first four best genotypes at poor to average environments suggested to be used in these environments. The GGE biplot identified Pawe and Tepi as most discriminating environments, Manbuk and Maitsebri identified as average environments and Woreta as representative environments that could be used as test environments to develop varieties at different stages of breeding activities. The stability parameters from ER's and AMMI models had positive and significant rank correlations with most of the stability parameters and yield and considered as sufficient to evaluate the stability of genotypes for yield. In conclusion, it is suggested to conduct the experiment over seasons to certain the results due to the significant effect of GEI

and its larger contribution to the variations of varieties for yield and other traits.

Keywords: AMMI, Discriminating & Representative environments, GGE-biplot and Rank correlation.

1. INTRODUCTION

Rice belongs to the genus *Oryza* with two cultivated, viz. the Asian rice, *Oryza sativa* L. and the African rice, *Oryza glaberrima* Steud and 22 wild species (Martin *et al.*, 2006). Rice is a diploid species ($2n=24$), and self-pollinated crop with up to 3% natural out-crossing that may occur depending on the cultivar and the environment (Poehlman and Sleper, 1995). It is the second most important cereal crop next to wheat in worldwide. It is by far the most economically important food crop in many of developing countries. It provides two third of the calories intake more than three billion people in Asia and one third of calories nearly for 1.5 billion people in Africa and Latin America. In Africa, the economic importance of rice has steadily increased over the past two decades (FAO, 1995).

In recognition to its importance, the Government of Ethiopia (GoE) has developed national strategy for rice research to promote the rice sector to ensure food security (MoARD, 2010). Rice was introduced and tested initially at different areas of Ethiopia, such as Gambella, Pawe, and Woreta nearly in the beginning of 1970s. However, due attention was given in the mid-1990s (Meron, 2016). Since, the mid-1990s, about 22 upland rice varieties have been released in regions where rain-fed rice is cultivated (Amhara, Tigray, Oromia, South NNPR, Gambella and Benshangule Gumuze Regions) (MoARD, 2010). The national average yield of rice in Ethiopia is 2.81 ton/ha (CSA, 2017), which is much lower than the world's average rice yield of 4.6 ton/ha (FAOSTAT, 2017).

Regarding the ecological zones important for growing rice, the rain fed upland rice can be grown in the altitudinal range of 1000 to 2000 meter above sea level (Shahi, 1994). Around 250,000 hectares in the near future and about 1 million hectares in the distant future are expected to come under cultivation. Ethiopia has a huge potential for rice production which is estimated to be about 30 million hectares (MoARD, 2010). Upland rice is cultivated in tropical and sub-tropical rain fed environments in aerobic soils without impounding water. However, production in high altitudes is limited due to extended vegetation period that may not be supported with the extended rainfall. The cold weather can be a stress because it induces pollen or spikelet sterility. Therefore, it is important to identify cold tolerant genotypes capable to cope the environment and produce stable grain yield (Shrestha, 2012).

Ethiopia is vulnerable to climate changes. It has been long experiencing the variation of weather conditions both from season to season and from place to place in the same season over relatively small areas. The country is known to have great environmental variations (EMA, 1988). This variation of the weather is mainly pronounced both in amount and rainfall distribution. In such weather conditions, it is not only average performance of crop genotypes is important in crop improvement programs but also the magnitude of genotype x environment interaction is important. This is because, one cultivar may have the highest yield in some environments and the other cultivar may excel in others and can be referred as inconsistent performance of genotypes (Bose *et al.*, 2015; Oladosu *et al.*, 2017; Taddesse *et al.*, 2017; Akter *et al.*, 2019). Increased concern with the importance of homeostasis in living organisms has stimulated plant breeders' awareness for the need to develop well-buffered cultivars. This has led to a greater emphasis on phenotypic stability in breeding programs and enabled understanding and usefulness of versions of stability methods (Lin *et al.*, 1986).

The effect of genotype x environment interaction (G x E) is statistically non additive indicating that differences in yield among cultivars depend on the environment (Zali and Farshadfar, 2011). Therefore, selection procedures based on the mean yield of cultivars in a given environment are less efficient (Hopkins *et al.*, 1995). This has forced breeders to conduct multi-location trials to reduce G x E interactions which will help in selecting cultivars with a better stability across a wide range of environments to predict genotypic behavior (Eberhart and Russell, 1966). A number of statistical procedures have been developed over the years to analyze genotype x environment interaction and yield stability over environments. Among a number of different approaches, the regression model initially proposed by Finlay and Wilkinson (1963) and latter improved by Eberhart and Russell (1966), and Additive Main effects and Multiplicative Interaction (AMMI) model (Gauch, 1988; Zobel, 1996; Gauch and Zobel, 1996) are mostly used.

The nationally coordinated rice research has been launched very recently in 1985 as compared to other cereal crops. However, the rice improvement project was capable in releasing about twenty two upland rice varieties with short period of time. These varieties were evaluated at locations in different regions during verification trials for release. The varieties were not evaluated across contrasting environments throughout the country. Among few studies, Teferi

(2009) was evaluated nine varieties at different locations in Northwestern Ethiopia. He reported the differential response of rice varieties for yield at different locations due to significant effects of genotype x environment interaction. The significant effect of genotype x environment interaction on rice varieties yield was reported by Tadesse *et al.* (2017) and Girma (2018).

In the presence of significant effect of genotype x environment interactions (GEI) on yield performance of rice genotypes, it is necessary to evaluate varieties in contrasting environments in the country. To our knowledge, all the released rice varieties had not yet been evaluated in contrasting environments of rice growing regions of the country except each varieties were evaluated at different locations of each recommendation domain during variety development process. For instances, NERICA-1 and 2, Chewaqa and Pawe-1, NERICA-4 and SUPERICA-1 varieties were released in Somalia, Bako and Pawe, respectively, after evaluating in different locations of each region. Therefore, it is important to determine stability of genotypes that have stable performance across environments of the country or varieties that perform best in specific environment. This would give a good opportunity to farmers in selecting suitable varieties to their specific areas. Moreover, the GEI study allows to group environments depending on the suitability for rice production that helps breeders where to test genotypes to develop stable varieties without yield penalty in the country. Developing varieties with best performing in specific area for specific purpose may be preferred but it is not feasible in developing countries like Ethiopia where resources are in scarce. Utilizing specific varieties for each pocket area of the country can request huge resources investment in doing research. In such cases, there is no doubt that the stability of a variety to be released is more important than high yield in specific area (Tadesse *et al.*, 2017; Oladosu *et al.*, 2017; Akter *et al.*, 2019). Therefore, this study was initiated with the following objectives:

- To determine the effect of genotype, environment and genotype x environment interaction on grain yield and yield related traits in upland rice varieties;
- To stratify rice testing environments based on the performance of rice varieties, and
- To determine the stability of upland rice varieties with reasonable yield across environments in Ethiopia

2. LITERATURE REVIEW

2.1. Taxonomy, Origin and Distribution of Rice

Rice (*Oryza sativa* L. $2n = 2x = 24$) belongs to the genus *Oryza*, tribe *Oryzeae*, sub-family *Bambusoideae* or *Ehrhartoideae*, and family *Poaceae* or *Gramineae* (Garris *et al.*, 2004). The two commonly cultivated rice species are the Asian rice (*Oryza sativa* L.) and the African rice (*O. glaberrima* (Huang *et al.*, 2012). The Asian rice species is distributed in many parts of the world, genetically more diverse and can be easily modified than African rice while African rice, *O. glaberrima* is grown in small scale farms in West Africa (Vaughan, 1989; Vaughan *et al.*, 2008; Sanni *et al.*, 2013). It is developed from the cross between *O. longistaminata* and *O. barthii* while *O. rufipogon* and *O. nivara* gave rise to *O. sativa*.

Rice was first domesticated in the region of the Yangtze River valley in China (Normile, 1997; Vaughan *et al.*, 2008; Huang *et al.*, 2012). The cultivated rice species originated from a common ancestor with AA genome. According to Dogara and Jumare (2014), perennial and annual ancestors of *O. sativa* are classified into three groups, Indica, Japonica and Javanica on the basis of genetic affinity. Indica and Japonica rices have a different origin. Indicas were domesticated in Eastern India and Japonicas in South China. Indica rice was dispersed throughout the tropics and subtropics from India and Japonica was moved Northward from South China to the temperate ecotype, then later Southward: Southeast of Asia, West Africa, Brazil and then became tropical ecotypes.

2.2. Rice Production in Ethiopia

Rice is one of the most strategic crops in Africa, and particularly in Ethiopia (Kijima *et al.*, 2008; Meron, 2016). Ethiopia has immense potentials for growing rice crop. Rice is grown under widely varying conditions of altitude and climate. It grows from sea level to as high as 3000 meters and it needs a hot and humid climate. The area of production of rice in the country has been increasing over the past few years. It is reported that the potential rice production area in Ethiopia is estimated to be about thirty million hectares (MoARD, 2010). Ethiopia has tremendous potential to increase the area under rice and is looking for partnerships to make use

of this land (EUCORD, 2012). In Ethiopia, in 2017, about 48,418.09 ha of land was cultivated to with the total production of 1,360,007.26 Quintals (CSA, 2017).

Rice is among the most important cereal crops grown in different parts of Ethiopia as food crop. Cognizant of the stated importance of rice and existing potential for its production, government establish national steering committee comprises of different stakeholders to make sure that the country will benefit from the crop (MoARD, 2009).

Amongst of the target commodities that have received due emphasis in promotion of agricultural production, rice is considered as the “Millennium crop” expected to contribute to ensuring food security in the country. Even though, it is a recent introduction to the country, rice has shown promise as to be among the major crops that can immensely contribute towards ensuring food security in Ethiopia. The country has vast suitable ecologies for rice production along with the possibility of growing it where other food crops do not do well (Teshome and Dawit, 2011; Meron, 2016).

2.3. Genotype x Environment Interaction

An individual's phenotype (P) is the product of the genotype (G) of the individual, the environment (E) that the individual is exposed to, and the interaction that occurs between the genotype of the individual and the environment (Lee *et al.*, 2003; Alberts, 2004).

From the plant breeders' point of view, environment is a general term that covers conditions under which plants grow and may involve locations, years, management practices or a combination of these factors. Every factor that is a part of the environment of a plant has the potential to cause differential performance which is associated with genotype x environment interaction (Fehr, 1991). Allard and Bradshaw (1964) classified environmental variables as unpredictable and predictable factors. The unpredictable factors include the fluctuating features of the location such as rainfall, relative humidity, temperature, etc., whereas the predictable factors are those factors which are under human control which include planting date, row spacing, plant population and rates of nutrient application. Both factors provide a greater range of environmental conditions to test genotypes (Eberhart and Russell, 1966). Unpredictable environmental factor is more difficult and often leads to large genotype x year and genotype x year x location interactions (Allard and Bradshaw, 1964). Selection of stable cultivars that perform

consistently across environments can reduce the magnitude of these interactions. The contribution of predictable environmental fluctuations to genotype x environment can be reduced by allocating specific cultivars to specific environments.

When assessing grain yield from a set of cultivars in a multi-environment trial, changes are commonly observed in the relative yield performance of cultivars with respect to each other across sites. This differential yield response of cultivars from one environment to another is called GEI and can be studied, described, and interpreted by statistical models (Crossa *et al.*, 1990; Vargas *et al.*, 1999).

Developing crop cultivars that perform well across a wide range of environmental conditions has been a major challenge to plant breeders long ago. In practice, genotype x environment interaction complicates the identification of superior genotypes (Allard and Bradshaw, 1964). For plant breeders, large genotype x environment interaction impedes progress from selection and has important implications for testing and cultivar release.

Genotype x environment interactions are generally considered to be a hindrance to crop improvement in a target region (Kang, 1998). Moreover, the genotype x environment interaction effects may be added to environmental effects in determining the temporal and spatial instability of crop yields. Temporal stability, in particular, negatively affects farmers' income and for staple crops in developing countries, contributes to food insecurity at the national and household level. The G x E interactions may also offer opportunities for selecting and using genotypes that show positive interaction with the location. It also prevailing environmental conditions (exploitation of specific adaptation) or genotypes characterized by low frequency of low yields or crop failure (exploitation of yield stability) (Annicchiarico, 2002).

Statistically, G x E interactions are detected as a significantly different pattern of responses among the genotype across environments and biologically, this will occur when the contributions (or level of expression) of the genes regulating the trait differ among environments (Basford and Cooper, 1998).

The ability of some crop varieties to perform well over a wide range of environmental conditions has long been appreciated by the agronomists and plant breeders. Finlay and Wilkinson, (1963)

pointed out that in meeting the demands for varieties better adapted to changing conditions, the plant breeder is faced with the choice of breeding either for closely defined ecological conditions or for more extensive conditions that include a considerable range of environments. Clearly the latter approach requires the development of varieties possessing wide adaptability. Even in a uniform edaphic environment a considerable degree of general adaptability will be important, because of the marked fluctuation of climatic conditions from season to season. Knowledge of the extent of $G \times E$ interaction and stability of the performance of genotypes across environments is absolutely essential to the plant breeder. The former will help him to decide whether he will aim at widely adapted varieties or the specifically adapted ones while the latter will help him in recommending the final release (Nassir, 2013; Luguterh *et al.*, 2016).

2.4. Statistical Methods to Measure $G \times E$ Interaction

A combined analysis of variance procedure is the most common method used to identify the existence of $G \times E$ from replicated multi-location trials. If the $G \times E$ variance is found to be significant, one or more of the various methods for measuring the stability of genotypes can be used to identify the stable genotype(s). A wide range of methods is available for the analysis of $G \times E$ and can be broadly classified into four groups: the analysis of components of variance, stability analysis, multivariate methods and qualitative methods. Of these four groups only the first three will be considered in this paper.

2.4.1. Conventional Analysis of Variance

Consider a trial in which the yield of genotypes (G) is measured in environments (E) each with replicates (R). The classic model for analyzing the total yield variation contained in GER observations is the analysis of variance (ANOVA). The within environment residual mean square measures the error in estimating the genotype means due to differences in soil fertility and other factors, such as shading and competition from one plot to another. After removing the replicate effect when combining the data, the $G \times E$ observations are partitioned into two sources: (a) additive main effect for genotypes and environments and (b) non additive effects due to $G \times E$ (Fisher, 1918, 1925).

The major restriction in this analysis is that the error variances over environments should be homogeneous to test for genotypic differences. If error variances are heterogeneous, this

analysis is open to criticism as the F-test of the G x E mean squares against the pooled error variances is biased towards significant results. One of the main problems of the combined analysis of variance of multi-location trials is that it does not explore any underlying structure within the observed non-additivity (G x E) effects. The analysis of variance fails to determine the pattern of response of genotypes and environments. The valuable information contained in (G-1) (E-1) degrees of freedom is particularly wasted if no further analysis is done. Since the non-additive structure of the data matrix has a non-random (pattern) and random (noise) component. The advantage of the additive model is lost if the pattern component of the non-additive structure is not further partitioned into functions of one variable each (Crossa, 1990). Analysis of variance of multi-location trials is useful for estimating variance components related to different sources of variation, including genotypes and G x E. In general, variance component methodology is important in multi-location trials since errors in measuring the yield performance of a genotype arise largely from G x E (Fisher, 1918, 1925).

2.4.2. Additive Main Effects and Multiplicative Interaction (AMMI)

The additive main effects and multiplicative interaction (AMMI) model (Gauch, 1992) is one of the most widely used statistical tool (method) to measure G x E. It can be used to understand and structure interactions between genotypes and environments. In its essence, the AMMI model applies the singular value decomposition (SVD) to the residuals of an additive two-way analysis of variance (ANOVA) model as applied to the GEI table of means (Gauch, 2013). The two main purposes of AMMI analysis of a yield trial's treatment design are: (i) understanding complex GEI, which includes delineating mega-environments and selecting genotypes to exploit narrow adaptations; and (ii) increasing accuracy to improve recommendations, repeatability, selections, and genetic gains. The main purposes of an experimental design are assigning experimental units to treatments, quantifying errors, and gaining accuracy (Gauch, 2013). The additive main effects and multiplicative interaction (AMMI) method integrates analysis of variance and principal components analysis into a unified approach (Gauch, 1988). According to Zobel *et al.*, (1988) and Crossa *et al.*, (1990) it can be used to analyses multi-location trials. Zobel *et al.*, (1988) pointed out that, considering the three traditional models, analysis of variance (ANOVA) fails to detect a significant interaction component, principal component analysis (PCA) fails to identify and separate the significant genotype and

environment main effects, linear regression models account for only a small portion of the interaction sum of squares.

The AMMI model combines the analysis of variance for the genotype and environment main effects with principal components analysis of the genotype environment interaction (Bose *et al.*, 2014; Luguterh *et al.*, 2016; Taddesse *et al.*, 2017). It has proven useful for understanding complex G x E. The results can be graphed in a useful biplot that shows both main and interaction effects for both the genotypes and environments (Oladosu *et al.*, 2017; Taddesse *et al.*, 2017). AMMI combines analysis of variance (ANOVA) into a single model with additive and multiplicative parameters. The AMMI method is used for three main purposes. The first is model diagnoses, AMMI is more appropriate in the initial statistical analysis of yield trials, because it provides an analytical tool of diagnosing other models as sub cases when these are better for particular data sets (Gauch, 1988). Secondly, it clarifies the G x E and summarizes patterns and relationships of genotypes and environments (Zobel *et al.*, 1988; Crossa *et al.*, 1990). The third use is to improve the accuracy of yield estimates. Gains have been obtained in the accuracy of yield estimates that are equivalent to increasing the number of replicates by a factor of two to five (Zobel *et al.*, 1988; Crossa, 1990). Such gains may be used to reduce testing cost by reducing the number of replications, to include more treatments in the experiments, or to improve efficiency in selecting the best genotypes.

AMMI is ordinarily the model of first choice when main effects and interaction effects are both important and the most common cause with yield trials (Mandel, 1971). If, for example, only main effects (additive structure) are present in the data, then the AMMI can be reduced to an ANOVA model. Whereas, if non-additive structure is only present then the PCA model is reflected. AMMI results can be readily used to diagnose these and others sub cases (Gabriel, 1978). The pattern portion of G x E sum of squares captured by the regression approach (heterogeneity among regressions) can at best capture only the amount of G x E sum of squares modeled by the simplest AMMI model. Therefore, AMMI analysis can potentially glean more patterns from the G x E than the regression approach (Sneller *et al.*, 1997). In addition, the AMMI analysis can be applied to data sets where regression analysis may be inappropriate.

2.4.3. Regression Models

Among these methods, the regression of mean yield on the environmental mean model (Yates and Cochran, 1938; Mandel, 1971; Finlay and Wilkinson, 1963) has wide application. Joint regression, in which genotype response is regressed on an environmental index, is a method where the interaction is analyzed more aggressively by considering not only genotype and environmental regressions but also joint regression. Within the framework of joint regression analysis, the sensitivity of a cultivar to environmental change is estimated from the slope of its regression coefficient of 1.0 and a residual mean square from regression model of zero. From a review work made by Becker and Leon, (1988) and Lin *et al.* (1986) it was found that the linear regression within the framework of joint regression analysis, the sensitivity of a cultivar to environmental change is estimated from the slope of its regression coefficient of 1.0 and a residual mean square from regression model of zero. From a review work made by Becker and Leon (1988) and Lin *et al.* (1986) it was found that the linear regression coefficient was considered as the best estimate of stability or responsiveness. However, Westcott (1986), Gauch and Zobel (1996) and other authors have shown the use of regression to evaluate cultivar performance to be deficient in many ways. As a result alternative models have been suggested, including a non-parametric approach Nassar and Huhn (1987) and the application of additive main effects and multiplicative interaction effects (AMMI) model.

Eberhart and Russell (1966) also reported the varieties having regression coefficient $b_i > 1$ are better adapted to favorable environmental conditions. In the case when $b_i < 1$, they perform better in low yielding environments. If $b_i = 1$, then the varieties are characterized by average adaptability to different environments. Cultivars with variance $S^2 d_i = 0$ are the most stable, whereas a high value of $S^2 d_i$ indicates low stability.

2.5. Stability Analysis

Stability of yield of a cultivar across a range of production environments is very important for variety recommendation. The cultivars must have the genetic potential for superior performance under ideal growing conditions, and must also produce acceptable yields under less favorable environments. Therefore, a stable genotype can be referred to as the one that is capable of utilizing the resources available in high yielding environments and has a mean performance that

is above average in all environments or can be described as the consistent performance of genotypes in different agro ecologies (Allard and Bradshaw, 1964; Eberhart and Russell, 1966). However, in Ethiopia, information on the extent and pattern of GEI and performance stability on rice is scanty.

Genotype x environment interactions are important sources of variation in any crop. The term stability is sometimes used to characterize a genotype which shows a relatively constant yield independent of change in environmental conditions. On the basis of this idea, genotypes with a minimal variance for yield across different environments are considered to be stable (Kaya *et al.*, 2003; Mulugeta *et al.*, 2016). The basic cause of differences between genotypes in their yield stability is the wide occurrence of G x E, i.e. the ranking of the genotype depends on the particular environmental conditions where it is grown.

In order to identify stable genotypes, the G x E must be partitioned into stability statistics that are assigned to each genotype evaluated across a range of environments. Stability indices have allowed researchers to identify widely adapted genotypes for use in breeding programs and have helped to improve recommendations to growers (Bose *et al.*, 2012; Krishnamurthy *et al.*, 2015). Although, it is important to detect such interactions by conducting yield trials over a series of environments, this alone gives no measure of the stability of individual genotypes. Hence, stability measurements are important since they give an indication of the adaptability of genotypes to general or specific conditions (Lin *et al.*, 1986; Luguterh *et al.*, 2016).

The statistical analysis of G x E has received considerable attention in plant breeding and crop production and a number of different methods have been proposed (Lin *et al.*, 1986; Westcott, 1986; Becker and Leon, 1988). The AMMI model, a combination of ANOVA main effects for genotypes and environments and multiplicative interaction effects, has been recommended as a superior to linear regression and principal components analysis (Crossa *et al.*, 1990).

2.5.1. Estimation of Stability Parameters

2.5.1.1. Cultivar performance measure (P_i) Lin and Binn's model

Lin and Binns' (1988) methodology is a good alternative for the assessment of cultivar performance in GEI. Their method does not have limitations inherent to the use of regression.

It characterizes the genotypes with a single parameter (P_i) by associating stability and productivity, and defines a superior cultivar as one with a performance near the maximum in various environments (Lin and Binns, 1988). This definition of superiority is similar to the breeder's objective, since a superior cultivar should be among the most productive in the greatest possible number of environments (Faria *et al.*, 1997). A genotype with small P_i is superior to the one with larger P_i value.

The values estimated from Lin and Binns' (1988) cultivar superiority (performance) measure are the squares of the differences between an entry mean and the maximum mean at a location, summed and divided by twice the number of locations. Checks need not be common at all locations. Genotypes with the smallest values tend to have larger yields and also be more stable.

2.5.1.2. Wricke's ecovalence (W_i)

Wricke (1962) defined the concept of ecovalence as the contribution of each genotype to the GEI sum of squares. The ecovalence (W_i) or stability of the i^{th} genotype is its interaction with the environments, squared and summed across environments. Genotypes with a low (W_i) value have smaller deviations from the overall mean across environments and are thus more stable. According to the meaning of ecovalence, the stable genotype possesses a low ecovalence.

2.5.1.3. Shukla's stability variance ($\delta^2 i$)

Shukla (1972) defined the stability variance of genotype i as its variance across environments after the main effects of environmental means have been removed. Since the genotype main effect is constant, the stability variance is thus based on the residual ($GEI_j + e_{ij}$) matrix in a two-way classification. A genotype is called stable if its stability variance ($\delta^2 i$) is equal to the environmental variance ($\delta^2 e$) which means that $\delta^2 i = 0$. A relatively large value of ($\delta^2 i$) will thus indicate greater instability of genotype i . With $\delta^2 i$, a genotype has stable trait expression when its contribution to GEI is small. The $\delta^2 i$ encompasses both GEI pattern and residual or noise. As the stability variance is the difference between two sums of squares, it can be negative, but negative estimates of variances are common in variance component problems. Negative estimates of $\delta^2 i$ may be taken as equal to zero as usual (Shukla, 1972). The stability variance is

a linear combination of the ecovalence, and therefore both W_i and δ^2_i are equivalent for ranking purposes (Lin *et al.*, 1986; Sneller *et al.*, 1997; Alberts, 2004).

2.5.1.4. Francis and Kannenberg's coefficient of variation (CV_i)

In the static or biological concept of stability phenotypic stability is simply the variance of a genotype across environments (Ferreira and Fernandes, 2016). This concept of stability is identical with type 1 stability as defined by Becker and Leon (1988), who suggest that it is particularly useful if the environmental range is small. A modified version of the static concept, based upon the coefficient of variation, has been used by Francis and Kannenberg, (1978).

The mean CV analysis introduced by Francis and Kannenberg, (1978) was designed to aid in studies on the physiological basis of yield stability. He introduced a simple graphical approach to assess performance and stability concurrently. It measures the performance and CV for each genotype over all environments and the mean yield plotted against the CV. It was found to characterize genotypes in groups rather than individually. Until the present time, a number of researchers are using this stability measure to study the homeostasis or buffering ability of different rice genotypes across various environmental conditions (Kiliç *et al.*, 2010; Krishnamurthy *et al.*, 2015; Oladosu *et al.*, 2017).

2.5.1.5. Eberhart and Russell's joint regression model

According to the joint linear regression model which was developed by Finlay and Wilkinson, (1963) and modified by Eberhart and Russell (1966), a stable genotype is one with a high mean yield, regression coefficient equals to one ($b_i=1$) and deviation from regression equals to zero ($S^2_{di}=0$). A genotype with b_i value less than 1.0 has above average stability and is especially adaptable to low-performing environments. A genotype with b_i value greater than 1.0 has below average stability and is especially adaptable to high performing environments and a genotype with b_i value equal to 1.0 has average stability and is well or poorly adaptable to all environments depending on high or low mean performance (Finlay and Wilkinson, 1963).

Eberhart and Russell (1966) stressed that the most important stability parameters appeared to be the deviation from linear regression mean square because all types of gene action were involved

in this parameter. Regression analysis should be used with caution when the data set includes results from only a few high or low yielding locations (Crossa, 1990).

2.5.1.6. Regression coefficient (b_i) and deviation mean square (S^2_{di})

Stability analysis provides a general summary of the response patterns of genotypes to environmental changes. Freeman (1973) termed the main type of stability analysis, joint regression analysis or joint linear regression (JLR). It involves the regression of the genotypic means on an environmental index. Joint regression analysis provides a means of testing whether the genotypes have characteristic linear responses to changes in environments. Joint regression analysis was first proposed by Yates and Cochran (1938) and then widely used and reviewed by various authors (Lin *et al.*, 1986; Crossa, 1990).

Joint linear regression (JLR) is a model used for analyzing and interpreting the non-additive structure (interaction) of two-way classification data. According to Finlay and Wilkinson, (1963) determined the regression coefficient by regressing variety mean on the environmental mean and plotting the obtained genotype regression coefficients against the genotype mean yields. Finlay and Wilkinson (1963) defined a genotype with $b_i = 0$ as stable, while Eberhart and Russell (1966) defined a genotype with $b_i = 1$ to be stable. Perkins and Jinks (1966) proposed an equivalent statistical analysis whereby the observed values are adjusted for environmental effects before the regression. Eberhart and Russell (1966) proposed pooling the sum of squares for environments and $G \times E$ and subdividing it into a linear effect between environments (with $E-1$ d.f), a linear effect for genotype $\times$ environment (with $E-2$ d.f). In effect the residual mean squares from the regression model across environments is used as an index of stability and a stable genotype is one in which the deviation from regression mean squares (S^2_{di}) is small.

According to Kenga *et al.* (2003) the mean square due to deviations from regression (S^2_{di}) indicates the degree of reliance that can be placed up on linear regression. In fact, S^2_{di} reveals a non-linear response of varieties (non-predictive). When the deviations are significant, the genotype stability is specified by a joint consideration of both η and b_i . The regression approach has been shown to be the most useful for geneticists (Freeman, 1973; Westcott, 1986) but it should be noted that these authors have pointed out several statistical and biological limitations and criticisms. Crossa (1990) concluded that in trying to determine which genotype is superior

with the regression approach, plant breeders have difficulty reaching a compromise between the mean yield, slope and deviation from regression, because the genotype's response to environments is intrinsically multivariate and regression tries to transform it into a univariate problem (Lin *et al.*, 1986).

2.5.1.7. AMMI stability value and interaction principal components (IPCA_s)

Stability methods have been used in both univariate and multivariate statistics (Lin *et al.*, 1986). Among the multivariate methods, the additive main effects and multiplicative interaction (AMMI) analysis is widely used for GEI investigation. This method has been effective because it captures a large portion of the GEI sum of squares; it clearly separates main and interaction effects and often provides meaningful interpretation of data to support a breeding program such as genotype stability (Gauch and Zobel, 1997). The AMMI model combines ANOVA for the genotype and environment main effects with principal components analysis of GEI (Gauch and Zobel, 1997). Therefore, based on the AMMI model (IPCA₁ and IPCA₂) the AMMI stability value (ASV) has been used. This ASV is comparable with the methods used by Shukla, Eberhart, and Russell for genotype stability (Purchase *et al.*, 2000).

2.6. Genotype x Environment Interaction in Rice

In Ethiopia, rice breeding research has entirely relied on introduction of rice germplasm from exotic resources such as Africa rice and IRRI. The breeding research efforts are made to develop improved and high yielding upland rice varieties mainly through multi-environment evaluation of rice genotypes. However, the incidence of G x E interaction complicates the selection of a rice variety with superior performance and adaptability to diverse environments (Tadesse *et al.*, 2017; Oladosu *et al.*, 2017; Girma, 2018).

The G x E interaction may arise when specified genotypes are grown in diverse environments (Zobel, 1996). It is important for breeders to identify specific genotypes adapted or stable to different environment(s), thereby achieving quick genetic gain through screening of genotypes for high adaptation and stability under varying environmental conditions prior to their release as cultivars. The general rice breeding scheme includes evaluating a number of genotypes at various stages and testing selected ones at several locations. The multi-location testing,

however, usually results in genotype by environment interactions that often complicate the interpretation of results obtained and reduce efficiency in selecting the best genotypes (Annicchiarico and Perenzin, 1994). This interaction is the result of changes in cultivar's relative performance across environments, due to differential responses of the genotypes to various edaphic, climatic and biotic factors (Suchit *et al.*, 2011; Bose *et al.*, 2014).

Information on genotype x environment interaction leads to successful evaluation of stable genotype, which could be used for general cultivation. Yield is a complex quantitative character and is greatly influenced by environmental fluctuations; hence, the selection for superior genotypes based on yield per se at a single location in a year may not be very effective (Suchit *et al.*, 2011; Shrestha, 2012). Thus, evaluation of rice genotypes for stability of performance under varying environmental conditions for yield has become an essential part of any breeding program.

2.7. Stability of Rice Genotypes

In Ethiopia, thirteen upland genotypes were tested in three location Pawe, Woreta and Metema (Teferi, 2009). The combined analysis of variance indicated highly significant ($P < 0.01$) genotypic, environmental, and G x E interaction effects on days of maturity, field grains per panicle, 1000 seed weight and grain yield. But the other parameters like plant height, days to heading and fertile tillers per plant shown non-significant ($P > 0.01$) genotypic, environmental and G x E interaction effects. The significance of genotypic effect is an indication of performance difference among genotypes (Tadesse *et al.*, 2017; Oladosu *et al.*, 2017; Girma, 2018). Although more than 900 rice varieties have been released in India, many of them were no longer cultivated within a few years due to inconsistent performance in diverse environments and only a few varieties with stable performance continue under cultivation after 15 to 20 years of their release. Analysis of genotype interaction with seasons and other agro-ecological conditions would help to get information on the adaptability and stability performance of genotypes.

The G x E interaction (GEI) reduces the association between phenotypic and genotypic values and leads to bias in the estimates of gene effects and combining ability for various characters

that are sensitive to environmental fluctuations less amenable to selection. Identification of superior genotypes through GEI became complicated for a range of environments to determine their true genetic potential (Yaghotipoor and Farshadar, 2007). The importance of GEI in national cultivar evaluation and breeding programs has been demonstrated in almost all major crops (Najafian *et al.*, 2010; Mulugeta *et al.*, 2016; Oladosu *et al.*, 2017).

3. MATERIALS AND METHODS

3.1. Description of Experimental Sites

The experiment was conducted at six locations during 2016/2017 main cropping season in Ethiopia. These locations are different in soil type, altitude, latitude, longitude, mean annual temperature and rainfall. Hence, each location was considered as an individual environment. The descriptions of test environments indicated in Table-1.

Table 1. Description of the test locations/environments

Location	Altitude (masl)	Latitude (⁰ North)	Longitude (⁰ East)	Soil type	Min.T (⁰ C)	Max.T (⁰ C)	Rain fall (mm)
Pawe	1120	11 ⁰ 19' N	36 ⁰ 24' E	Cambisol	16.3	32.6	1587
Manbuk	1210	12 ⁰ 23' N	36 ⁰ 24' E	Cambisol	15.5	29.5	1557
Woreta	1810	11 ⁰ 58' N	37 ⁰ 41' E	Vertisol	11.5	27.9	1300
Maitsebri	1350	13 ⁰ 05' N	38 ⁰ 08' E	Vertisol	15.7	36.6	1296.5
Jimma	1753	7 ⁰ 46' N	36 ⁰ 0' E	Fluvisol	9.0	28.0	1561.0
Tepi	1200	7 ⁰ 3' N	35 ⁰ 18' E	Nitosols	15.0	30.0	1522.1

Source; (EIAR, 2016), The Min. and Max. T (⁰C), are the average 10 years minimum and maximum temperature in ⁰C of each location, respectively, whereas RF (mm) the amount of 10 years average rainfall.

3.2. Genotypes

Twenty released upland rice varieties were tested in six main rice growing regions of Ethiopia under rain fed conditions. These varieties were originally introduced from International Rice Research Institute (IRRI), Africa Rice, West Africa Rice Development Association (WARDA) and Madagascar. The varieties introduced from WARDA were designated by NERICA (New Rice for Africa) whereas the others were from IRRI, Africa Rice and Madagascar. These NERICA varieties have combined traits of both parents like high yield potential, early maturity, drought tolerance, pest and disease resistance, shorter growth duration, early vigor, resistance to lodging, good tillering ability and compact panicle (Kijima *et al.*, 2008; Manneh *et al.*, 2007). On the other hand, genotypes obtained from IRRI have resistance to various pests and diseases, highly aromatic and productive. New released (Fogera-1) variety was included in this study as a standard check.

Table 2. Descriptions of genetic materials used in the study

Name & code of variety	Year of release	Breeding center	Origin
Hidasse (WAB515-B-16A1-2)	2012	FNRRTC	African Rice
Getachew (AD-01)	2007	FNNRTC	IRRI
Andassa (AD-012)	2007	FNRRTC	IRRI
Tana (AD-048)	2007	FNRRTC	IRRI
NERICA-3(WAB-450-IB-P-28-HB)	2006	PARC	WARDA
NERICA-4(49WAB-450-IB-P-9/1)	2006	PARC	WARDA
SUPERICA-1(WAB-4507)	2006	PARC	WARDA
Pawe-1(M-55)	1999	PARC	WARDA
Kokit (IRAT-209)	2000	FNRRTC	IRRI
Chewaqa (YINLU20)	2013	BARC	NA
NERICA-12	2013	FNRRTC	WARDA
NERICA-13	2014	MARC	WARDA
NERICA-2	2007	SOPAR	WARDA
NERICA-14	2010	FNRRTC	IRRI
NERICA -1	2007	SOPAR	WARDA
ADET(WAB450-1-B-P-462-HB)	2014	FNRRTC	WARDA
FOFIFA-4129	NA	FNRRTC	IRRI
FOFIFA-3737	2010	FNRRTC	Madagascar
FOFIFA-3730	NA	FNRRTC	Madagascar
Fogera-1(check)	2015	FNRRTC	NA

Seed source = Fogera National Rice Research and Training Center. FNRRTC= Fogera National Rice Research and Training Center, BARC= Bako Agricultural Research Center, PARC= Pawe Agricultural Research Center, MARC= Melkassa Agricultural Research Center, SOPAR= Somalia Pastoral and Agro-pastoral Research, IRRI= International Rice Research Institute, WARDA = West African Rice Development Association and NA = Not available

3.3. Experimental Design and Trial Management

The experiment was conducted in six locations of Ethiopia using randomized complete block design (RCBD) with three replications during main cropping season (2016/17). The size of experimental plot was 1.2 m long and 5 m wide (6 m²), with six rows which are 0.2 m apart each other. The spacing between the two adjacent blocks and the spacing between the plots was 1m and 0.3 m, respectively. The seeds was sown in rows by drilling manually at a rate of 60 kg ha⁻¹ basis. The fertilizer was applied at a rate of 64 Urea and 46 P₂O₅ kg ha⁻¹. All P₂O₅ and one-third Nitrogen were applied during planting while the second and the third one-third splits of

nitrogen from urea fertilizer were applied at tillering and at panicle initiation stages, respectively. All other agronomic practices were applied during the growing stages at all sites as per the recommendation made for rice production.

3.4. Data Collection

Data was collected and recorded for yield and yield related traits on plot and plant basis using Standard Evaluation System for rice (IRRI, 2014) from the middle four harvestable rows. Crop phenology (number of days to emergence, heading, flowering and maturity), growth of the crop (plant height, panicle length, number of fertile tillers per plant and number of unfertile tillers per plant), grain yield and yield related traits (number of filled grains per panicle, number of unfilled grains per panicle, thousand-grain weight, grain yield per plot, and biological yield), respectively. Biomass yield and grain yield data were collected on plot base from the central four rows. On the other hand, number of tillers per plant, number of effective tillers per plant, panicle length and plant height were taken on plant basis from randomly selected and tagged plants from the central four rows.

3.4.1. Phenology Traits

Days to 50% emergence: was registered as the number of days from sowing up to the date on which 50% of the plants emerged in each plot by visual observation.

Days to heading (DH): was registered as the numbers of days from sowing to days to 50% of the plants in each plot attained heading.

Days to flowering (DF): the number of days from sowing date to the date on which 50% of plants in the middle four rows of each plot attained flowering. It was judged by field visual observation.

Days to Maturity (DM): was taken as the number of days from sowing date to the date on which 80% of plants in the middle four rows attained maturity (Bioversity International, 2007). It was judged by field visual observation when the straws and the panicles of the crop changed to yellowish color.

3.4.2. Growth Traits

Plant height (cm) (PH): was measured the height of the plant in centimeter started from the base of the main stem to the tip of the panicle and recorded as the average of five randomly selected plants from the middle four rows of the plot.

Panicle length (PL): was measured the length of the panicle in centimeter started from the node on which the first panicle branch starts to the tip of the panicle as the average of five randomly selected plants from the middle four rows of the plot.

Number of fertile tillers per plant (NFTP): was counted the fertile tillers by taking the average number of fertile tillers from five randomly selected sample plants from the middle four rows of the plot.

Number of unfertile tillers per plant (NUFTP): was counted the unfertile tillers by taking the average number of unfertile tillers from five randomly selected sample plants from the middle four rows of the plot.

3.4.3. Grain Yield and Yield Components

Number of filled grains per panicle (NFGP): was taken the number of filled grains from the middle four rows of the main panicle of the plant from average of five randomly selected plants in the plot.

Number of unfilled grains per panicle (NUFGP): was registered the number of unfilled grains from the middle four rows of the main panicle of the plant from average of five randomly selected plants in the plot.

Thousand-grain weight (TGW): was measured the weight in gram of 1000 grains from bulked grains, which collected from the middle four rows of each plot and recorded on 14% seed moisture basis.

Grain yield per plant (GY/g): Grain yield in grams obtained from the central four rows of each plot and converted to kilograms per hectare and adjusted at 14% moisture content (Tadesse *et al.*, 2017).

Above ground biomass yield (BY/g): total biomass in gram of all the plants in all the four rows of each plot was measured at harvest after sun dried for two days.

Harvest index (HI %): calculated as the ratio of weight of grain yield in gram obtained from the middle four rows of each plot to the total weight of above ground biomass yield of the middle four rows of each plot expressed in percent and measured at harvest.

3.5. Data Analysis

3.5.1. Analysis of Variance

The plot mean values were subjected to ANOVA of the RCBD for each individual environment and combined analysis of variance over environments was computed for grain yield and other traits. Genotypes were assumed fixed whereas locations as random effects. Bartlett's chi-square test was used to assess homogeneity of error variances prior to combine analysis over environments. A SAS statistical software program (SAS Institute, 2004) was used for the ANOVA of both individual environments and the combined analysis. GEI was determined using combined ANOVA, which partitions the total variance into genotype, environment, GEI and error. Significance levels of these components were determined by using F- test.

The linear model used for individual site analysis was:

$$Y_{ijk} = \mu + G_i + R_j + BK_j + \varepsilon_{ijk}$$

Where:

Y_{ijk} = the observed value of trait from the i^{th} genotype from the k^{th} block nested in the j^{th} replicate,

μ = the overall mean,

G_i = the effect of i^{th} genotype,

R_j = the effect of the j^{th} replication and BK_j is the effect k^{th} block nested within the j^{th} replicate

ε_{ijk} = random error term.

Table 3. Skeleton ANOVA of a single environment

Source of variation	Degree of freedom	Mean square	Expected mean square
Replication	r-1	MSr	$\sigma^2_e + g\sigma^2_r$
Genotypes	g-1	MSg	$\sigma^2_e + r\sigma^2_g$
Error	(r-1)(g-1)	MSe	σ^2_e

Where, r = number of replications; g = number of genotypes; MSr = mean square due to replications; MSg = mean square due to genotypes; MSe = mean square of error; σ^2_g , σ^2_r and σ^2_e are variances due to genotype, replication and error, respectively.

The linear model used for combined analysis was:

$$Y_{ij} = \mu + G_i + E_j + GE_{ij} + \varepsilon_{ij}$$

Where: μ is the overall mean, G_i , E_j and GE_{ij} represent the effect of the genotype, environment, and genotype-environment interaction, respectively; and ε_{ij} is the average of the random errors associated with the i^{th} plot that receives the i^{th} genotype in the j^{th} environment.

Table 4. Skeleton ANOVA for mixed model analysis of variance (fixed- genotype and random-environments)

Source of variation	DF	MS	Expected mean square	F-ratios
Total	egb-1			
Environments (E)	e-1	MS_E	$\sigma_e^2 + G\sigma_{B(E)}^2 + BG\sigma_E^2$	$MS_E/MS_{B(E)}$
Block(environments)	(b-1)*e	$MS_{B(E)}$	$\sigma_e^2 + G\sigma_{B(E)}^2$	$MS_{B(E)}/MS_e$
Genotypes (G)	g-1	MS_G	$\sigma_e^2 + B\sigma_{G \times E}^2 + EB\sigma_G^2$	$MS_G/MS_{G \times E}$
G x E	(g-1)* (e-1)	$MS_{G \times E}$	$\sigma_e^2 + B\sigma_{G \times E}^2$	MS_{GE}/MS_e
Error	e(g-1)(b-1)	MS_e	σ_e^2	

Note that: DF = degree of freedom, MS = Mean squares, B = Blocks, g = genotypes= environments, b=blocks, MS_E = mean squares due to environments, $MS_{B(E)}$ = mean squares due to Block (Environments), MS_G = Mean squares due to genotypes, $MS_{G \times E}$ = Mean squares due to G x E and MS_e = Mean squares due to error.

3.5.2. Stability Analyses

Joint linear regression analysis proposed by Eberhart and Russell, (1966) (b_i and S^2d_i) Coefficient of Variation (CV) of (Francis and Kannenberg, 1978), cultivar superiority measure (P_i) of Lin and Binn's (1988), Shukla (1972) stability variance (δ^2_i), Wricke (1962) ecovalence (W_i) and AMMI stability value (ASV) of Purchase *et al.* (2000) were used for estimating stability of the genotypes. The genotype x environment interaction analysis using Eberhart and Russell (1966) model were computed using SPAR two statistical software, while GenStat statistical software used for AMMI (Gauch and Zobel, 1996) model. In addition, environment index and ranking were conducted using Eberhart and Russell (1966) and AMMI (Gauch and Zobel, 1996) models, respectively. Accordingly, regression coefficient (b_i) and deviation from linear regression (S^2d_i) from Eberhart and Russell (1966) model, and from AMMI model, interaction principal component axes (IPCA) scores of genotype and environment and AMMI biplot were computed as per the established standard procedures for each model. Spearman's rank correlation between the different stability parameters was also computed. Stability analysis was conducted using means of genotypes at each environment. Significance levels of these components were determined by using F- test.

i) **Eberhart and Russell's joint linear regression** analysis is described as:

$$Y_{ij} = \mu + \beta_i I_j + \delta_{ij} \quad (i = 1, 2, \dots, v \text{ and } j = 1, 2, \dots, n)$$

Where,

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

μ = mean of all the genotypes over all the environments,

β_i = the regression coefficient of the i^{th} variety on the environmental index,

I_j = the environmental index,

δ_{ij} = the deviation from regression of the i^{th} genotype at the j^{th} environment,

v = number of genotypes and

n = number of environments

The two stability parameters used in this model and their computation are discussed as follows:

ii) **Regression coefficient (β_i)** is the regression of the performance of each genotype under different environments and is estimated as:

$$\beta_i = \frac{\sum_j Y_{ij} I_j}{\sum_j I_j^2}$$

Where,

$\sum_j Y_{ij} I_j$ = the sum of products and

$\sum_j I_j^2$ = the sum of squares.

2) Mean square deviation ($\delta^2 d_i$) from linear regression is estimated as:

$$\sigma^2_{d_i} = \left[\frac{\sum_j \hat{\delta}_{ij}^2}{n-2} \right] - \frac{S_e^2}{r}$$

Where,

$$\sum_j \hat{\delta}_{ij}^2 = \left[\sum_j Y_{ij}^2 - \frac{Y_{i.}^2}{v} \right] - \left[\frac{\left(\sum_j Y_{ij} I_j \right)^2}{\sum_j I_j^2} \right]$$

S_e^2 = estimate of mean square of error from the combined analysis and

r = the number of replications within environment.

iii) **Lin and Binns' (1988) cultivar superiority measure (P_i)** was obtained as:

$$P_i = \frac{\sum (Y_{ij} - M_j)^2}{2n}$$

Where,

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

P_i = superiority index of the i^{th} cultivar,

M_j = maximum response obtained among all the cultivars in the j^{th} environment, and

n = number of environments

This expression was further partitioned into:

$$P_i = \frac{[n(\bar{Y}_i - \bar{M})^2 + \sum_j^n (Y_{ij} - \bar{Y}_i - M_j + \bar{M})^2]}{2n}$$

Where,

$$\overline{M} = \frac{\sum_j M_j}{n},$$

$\overline{M}$ = mean of the maximum response in the s environments.

$\overline{Y}_i$ = the genotype and environment mean deviations, respectively, and

According to Lin and Binns (1988), the first part of the Pi expression quantifies the genetic deviation and the second quantifies the GEI.

iv) Shukla (1972) stability variance is estimated as follows:

$$\sigma^2_i = \frac{1}{(v-1)(v-2)(n-1)} [v(v-1) \sum_{j=1}^n (Y_{ij} - \overline{Y}_i - \overline{Y}_j + \overline{Y}_{..})^2 - \sum_{i=1}^v \sum_{j=1}^n (Y_{ij} - \overline{Y}_i - \overline{Y}_j + \overline{Y}_{..})^2]$$

Where,

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

$\overline{Y}_i$ and $\overline{Y}_j$ = the genotype and environment mean deviations, respectively, and

$\overline{Y}_{..}$ = the overall mean

v = number of genotypes and

n = number of environments

v) Wricke (1962) ecovalence (W_i) or stability of the i^{th} genotype is its interaction with the environments, squared and summed across environments and expressed as:

$$W_i = \sum_j (Y_{ij} - \overline{Y}_i - \overline{Y}_j + \overline{Y}_{..})^2$$

Where,

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

$\overline{Y}_i$ and $\overline{Y}_j$ = the genotype and environment mean deviations, respectively, and

$\overline{Y}_{..}$ = the overall mean

vi) AMMI model as described by Zobel *et al.* (1988) is estimated as:

$$Y_{ij} = \mu + \alpha_i + I_j + \sum_{n=1}^N \lambda_n \xi_{in} \eta_{jn} + \theta_{ij}$$

Where,

μ = grand mean,

α_i = genotypic effect,

I_j = environmental effect (index),

λ_n = the eigenvalue of the IPCA axis, n ,

ξ_{in} and η_{jn} = genotype and environment IPCA scores for the IPCA axis, and

θ_{ij} = residual.

As stated by Alberts (2004) since, AMMI model does not make provision for a quantitative stability measure, AMMI stability value (ASV) Purchase *et al.* (2000) measure was computed in order to quantify and rank genotypes according to their yield stability.

The ASV can be estimated using the following formula:

$$\text{AMMI Stability Value (ASV)} = \sqrt{\left[\frac{\text{IPCA1sumofsquares}}{\text{IPCA2sumofsquares}} (\text{IPCA1score})^2 + [\text{IPCA1score}]^2 \right]}$$

The ASV is the distance from zero in a two dimensional scatter gram of IPCA1 (Interaction Principal Component Analysis axis 1) scores against IPCA2 score. Since the IPCA1 score contributes more to G x E sum of squares; it has to be weighted by the proportional difference between IPCA1 and IPCA2 scores to compensate for the relative contribution of IPCA1 and IPCA2 to total G x E sum of squares. The distance from zero is then determined by using the theorem of Pythagoras.

vii) GGE bi-plot analysis

The G and GE are the two sources of variation that are relevant to mega-environment analysis, genotype evaluation, and test-environment evaluation; they must be considered simultaneously for these purposes. Both GGE bi-plot analysis and AMMI analysis combine rather than separate G and GE in mega-environment analysis and genotype evaluation; AMMI graphs for these purposes are also “GGE” graphs (Zerihun, 2011; Oladosu *et al.*, 2017). Test environment evaluation has not been a research topic in AMMI analysis. GGE bi-plot is able to show the best genotype with the highest yield in a quadrant containing identical locations (mega-environments), genotype average performance and stability, ideal genotype and ideal location to increase yield and specific location. Visualization of GGE bi-plot is very useful to evaluate and find the most stable genotypes and it is effective method only if the GEI is significant (Yan and Tinker, 2006; Oladosu *et al.*, 2017). The analysis was performed using GenStat version 16 and Plant Breeding Tools version 1.4 software.

3.5.3. Comparison of Stability Measures

The Spearman's coefficient of rank correlation (r_s) as determined by Steel and Torrie (1980) is used to examine the degree of correlation between the above stability analyses (Alberts, 2004). By considering t genotypes arranged in the same following order to two stability parameters, X_i indicates the ranking order (or number) of the i^{th} genotype for the first parameter, Y_i , indicates the ranking order of the i^{th} genotype of the second parameter, then $d_i = X_i - Y_i$ ($i = 1, 2, 3 \dots t$) and Spearman's rank correlation coefficient (r_s) can be described as:

$$r_s = \frac{6 \sum d_i^2}{t(t^2 - 1)}$$

The significance of r_s was tested by means of Student's t test

Where,

$$t = \frac{r_s \sqrt{t-2}}{\sqrt{1-r_s^2}}, \text{ with } t-2 \text{ degrees of freedom.}$$

4. RESULTS AND DISCUSSION

4.1. Analysis of Variance

The analysis of variance (ANOVA) for each location was conducted. The results of ANOVA revealed the presence of highly significant ($P < 0.01$) differences among the upland rice genotypes for all traits at all locations, except non-significant difference among genotypes for grain yield was observed at Tepi (Appendix Table 1). This indicated the presence of performance variation among the tested genotypes for yield and yield related traits that may allow identifying genotype(s) for high yield and other desirable traits. Other workers also reported significant differences among upland rice genotypes evaluated at various locations in Ethiopia (Yussouf *et al.*, 2010; Taddesse *et al.*, 2017; Oladosu *et al.*, 2017; Girma, 2018). The homogeneity of error variances was evident for all traits except days to heading, number of fertile tillers per plant, number of filled grain per panicle, number of unfilled grain per panicle, harvest index and thousand grain weight in which genotypes had significant differences from the F-ratio test. Therefore, a combined analysis of variance (ANOVA) had performed on the original (untransformed) data for the traits that homogeneity of error variances was evident; while data was transformed for the traits that homogeneity of error variances was not evident prior to conduct combined ANOVA over locations.

The combined analysis of variance over environments showed significant ($P < 0.01$) and highly significant ($P < 0.001$) mean squares of environment, genotypes, the interaction of genotype x environment (GEI) for days to heading, days to maturity, panicle length, plant height, number of unfertile tillers, number of filled grains per panicle, number of unfilled grains per panicle, harvest index and grain yield. However, the mean square for GEI were non-significant for number of fertile tillers per plant, biological yield and thousand grain weight, respectively, though the mean square for genotype and environment were significant. This indicated that the genotypes responded differently to the different environmental conditions. Thus, it suggested the need to conduct further GEI, and stability analyses to understand the nature of GEI, and stability of the performance of the genotypes across environments. Other works also reported the significant effects of genotypes, environments and GEI, on the performance of rice varieties in Ethiopia (Yussouf *et al.*, 2010; Bose *et al.*, 2015; Taddesse *et al.*, 2017; Girma, 2018).

The mean squares of environment and GEI were significant for days to maturity, plant height, panicle length, number of unfertile tillers per plant, biological yield and grain yield. The error variance for these traits were detected homogenously and the F-test less than three (Appendix Table 2). This suggested the performances of genotypes could be compared on the basis of pooled mean values. While, the mean squares of environment and GEI were non-significant for number of fertile tillers per plant, number of filled grains per panicle, number of unfilled grains per panicle, harvest index and thousand grain weight. The error variance for these traits were detected heterogenously and the F-test greater than three (Appendix Table 2). This suggested the performance of genotypes was evaluated based on mean values of genotypes for the traits in each location (Table 5).

Table 5. Mean squares from combined analysis of variance for 12 traits of 20 upland rice genotypes evaluated across six environments, during 2016/2017 cropping season

Source of variation	Rep(Env) (12)	Environment (5)	Genotype (19)	G x L (95)	Pooled error (228)	CV (%)
DH	282.3(0.83)	1805.02** (5.46)	620.97** (1.84)	63.82** (0.18)	21.31(0.00)	5.7
DM	47.93(0.096)	14192.06** (28.30)	556.24** (1.039)	155.91** (0.286)	7.10(0.015)	2.2
PL (cm)	4.55(0.002)	409.48** (0.222)	12.93** (0.01)	2.13** (0.001)	1.35(0.001)	6.0
PH (cm)	169.77(0.01)	12239.63** (0.33)	1053.96** (0.027)	116.92** (0.003)	43.42(0.001)	7.6
NFTPP	33.15(0.703)	768.755** (24.84)	15.44** (0.478)	3.52(0.096)	3.32(0.095)	25.3
NUFTPP	0.012(0.23)	33.79** (9.89)	1.28** (0.269)	0.57** (0.118)	0.01(0.09)	12.78
NFGPP	2049.1(0.15)	18406.7** (1.44)	487** (0.043)	183.2** (0.015)	113.3(0.01)	12.1
NUFGPP	249.02(5.88)	4243.71** (97.01)	49.86(0.82)	36.59** (0.41)	11.77(0.21)	39.2
HI	0.012(0.02)	1.15** (0.80)	0.06** (0.06)	0.01** (0.01)	0.01(0.004)	18.6
BIO(kg/ha)	105540912(0.22)	584582596** (1.98)	43153524** (0.09)	10332994(0.023)	8542128(0.01)	29.7
TGW (g)	30.75(0.006)	442.23** (0.084)	106.04** (0.024)	10.03(0.002)	7.83(0.001)	9.8
GY (kg/ha)	5855984.3(0.10)	8209859.7** (0.19)	3446901** (0.10)	1320290** (0.05)	485968(0.01)	19.8

* and ** significant at $P < 0.05$ and $P < 0.01$, respectively. Number in parenthesis represent degree of freedom for the respective source of variation, DH = days to heading, DM = days to maturity, PL = panicle length, PH = plant height, NFTPP = number of fertile tillers per plant, NUFTPP = number of unfertile tillers per plant, NFGPP = number of filled grains per panicle, NUGPP = number of unfilled grains per panicle, HI = harvest index, BIO = biological yield, TGW = Thousand grain weight and GY (kg/ha) = grain yield.

4.2. Mean Performance of Genotypes

4.2.1. Phenology Traits

The mean performance of 20 rice genotypes for days to heading and maturity are presented in (Table 6). The error variances for days to heading was detected as heterogeneous with F-test (Appendix Table 1), therefore, the comparison of genotypes performances were conducted for each location. The error variance for days to maturity was homogenous and comparison of genotypes performances was conducted on the basis of pooled mean over locations.

The environment mean of the genotypes for days to heading was 80.18, 76.3, 86.1, 73.2, 81.02 and 87.43 at Pawe, Manbuk, Woreta, Maitsebri, Jimma and Tepi, respectively. Four genotypes Pawe-1(88days), Tana (84 days), Chewaqa (85 days) and Andassa (84 days) had late days to heading, whereas, NERICA-2 and NERICA-14 (75 days) and ADET and NERICA-3 (76 days) had early days to heading at Pawe. At Manbuk, genotypes Pawe-1 (87days), Tana (80 days) and Fogera-1 (80 days) had late heading, whereas genotypes NERICA-14 (71 days), NERICA-3 (73 days) and NERICA-2 (73 days) had early days to 50% heading. At Woreta, Pawe-1 (124 days), Chewaqa (102 days) and Getachew (96 days) had maximum late to 50% heading. While, five genotypes NERICA-2 and FOFIFA-4129 (72 days), FOFIFA-3737 (74 days), NERICA-14 (76 days), NERICA-1 (79 days) had the earliest days to 50 % days to heading. The maximum days to heading was recorded at this environment. At Maitsebri, genotypes Getachew (86 days), Tana (83 days) and FOFIFA-3730 (82 days) had the latest days to heading, whereas genotypes NERICA-14 (63 days), FOFIFA-3737 and FOFIFA-4129 (67 days) and NERICA-2 (68 days) had the early days to 50% heading. At Jimma, genotypes Pawe-1 (93 days), Andassa and Tana (91 days) and SUPERICA-1 (90 days) had late days to heading, whereas NERICA-2 and NERICA-14 (63 days) and NERICA-1 (67days) had the earliest days to 50 % heading. Similarly, at Tepi, genotypes Pawe-1 (104 days), NERICA-12 (96 days) and Chewaqa (95 days) had latest days to 50 % heading, while genotype NERICA-14 (79 days), NERICA-1 (80 days) and FOFIFA-4129 (82 days) had early days to 50 % heading. Generally, most of the genotypes had earliest days to 50% heading indicating that the genotypes had good traits for earliest and good for future genotypes improvement especially for late heading genotypes. Tefera *et al.* (2017) and Mulugeta *et al.* (2016) in Ethiopia evaluated 34 and 22 rice genotypes, respectively,

and reported the presence of significant variations among genotypes for days to 50% heading ranging from 82.5 to 110 days and 67.3 to 87.3 for days to flowering, respectively.

The genotypes, Pawe-1, Chewaqa and Getachew had maximum maturity period of 142, 126 and 123 days, respectively, with significant differences among the mean values of the genotypes. The genotype NERICA-14 and NERICA-2 were identified earliest maturity with 116 and 117 days of mean maturity over locations. Eight genotypes had above grand mean days to maturity. This indicated that those genotypes grouped as late maturing genotypes when compare to the rest tested genotypes. Whereas, the rest 12 genotypes including the check (Fogera-1) had mean days to maturity lower than the overall mean of genotypes indicating majority of the genotypes were early maturing.

Osman *et al.* (2012) and Mulugeta *et al.* (2016) evaluated 13 and 22 rice genotypes, respectively, and found that genotypes had variation in days to maturity in the range between 88 to 110 and 104 to 115 days, respectively. Similarly, Atsedemariyam *et al.* (2018) and Tefera *et al.* (2017) evaluated 23 and 34 rice genotypes, respectively, and reported the presence of significant variations among genotypes for days to heading, flowering and maturity.

Table 6. Mean performance of 20 rice genotypes for days to heading and days to maturity evaluated across six environments, during 2016/2017 cropping season

Genotype	Days to Heading						Mean	Days to Maturity
	E1	E2	E3	E4	E5	E6		
Hidasse	81 ^{bcd}	74.7 ^{d-f}	83.7 ^{ef}	72 ^{cd}	82 ^{a-d}	86 ^{b-f}	79.8	119.1 ^{ghi}
Getachew	83.7 ^{ab}	79.7 ^{bc}	96 ^c	86.3 ^a	87 ^{abc}	93 ^{bcd}	87.7	122.9 ^{cd}
Andassa	84.3 ^{ab}	79 ^{b-d}	92.3 ^c	78.3 ^{cd}	91 ^{ab}	91 ^{b-e}	86.1	122.2 ^{cd}
Tana	84.3 ^{ab}	80 ^b	90 ^d	83.3 ^{ab}	91 ^{ab}	89.7 ^{b-f}	86.4	122.9 ^{cd}
NERICA-3	75.7 ^d	72.7 ^{ef}	82.7 ^{ef}	71 ^d	76 ^{bcd}	84.7 ^{c-f}	77.1	118.2 ^{g-j}
NERICA-4	76.7 ^{cd}	75 ^{c-f}	83.3 ^{ef}	70.3 ^d	75 ^{cd}	86.7 ^{b-f}	77.8	119.6 ^{fgh}
SUPERICA-1	81 ^{b-d}	77 ^{b-e}	83.7 ^{ef}	73.3 ^{cd}	90 ^{abc}	83.7 ^{def}	81.3	120.2 ^{efg}
Pawe-1	88.7 ^a	87 ^a	124 ^a	73.3 ^{cd}	93 ^a	104.3 ^a	95.1	142.4 ^a
Kokit	77 ^{cd}	74.7 ^{d-f}	82.7 ^{ef}	72.7 ^{cd}	81 ^{a-d}	84.7 ^{c-f}	78.8	120.1 ^{efg}
Chewaqa	84.7 ^{ab}	79.7 ^{bc}	102 ^b	80 ^{ab}	87 ^{abc}	95 ^{abc}	88.1	126.4 ^b
NERICA-12	79 ^{b-d}	74.7 ^{d-f}	85.7 ^c	71.3 ^d	85 ^{abc}	96.3 ^{ab}	82.1	121.8 ^{cde}
NERICA-13	76.3 ^d	75 ^{c-f}	81.7 ^f	71 ^d	81.7 ^{a-d}	86.7 ^{b-f}	78.7	119.8 ^{fg}
NERICA-2	75 ^d	73 ^{ef}	72 ⁱ	68.3 ^{de}	66.3 ^d	81.3 ^{ef}	72.7	116.6 ^j
NERICA-14	75 ^d	71.3 ^f	76 ^h	63.3 ^e	66.3 ^d	79.3 ^f	71.9	116.3 ^j
NERICA -1	83 ^{a-c}	75 ^{b-f}	79 ^g	73 ^{cd}	66.7 ^d	80.7 ^{ef}	76.3	121.4 ^{def}
ADET	75.7 ^d	74 ^{ef}	82 ^f	70 ^d	74.3 ^{cd}	84 ^{def}	76.72	119 ^{ghi}
FOFIFA-4129	79.3 ^{b-d}	73.7 ^{ef}	72 ⁱ	67.3 ^{de}	83 ^{abc}	82 ^{ef}	76.22	117.56 ^{ij}
FOFIFA-3737	79.3 ^{b-d}	75 ^{c-f}	74 ^{hi}	67.3 ^{de}	76.7 ^{bcd}	85 ^{c-f}	76.22	117.67 ^{hij}
FOFIFA-3730	83.7 ^{ab}	80 ^b	95.3 ^c	82 ^{ab}	88 ^{abc}	89 ^{b-f}	86.33	123.61 ^c
Fogera-1	80.3 ^{b-d}	74 ^{ef}	83.7 ^{ef}	70.3 ^d	79.3 ^{a-d}	85.3 ^{c-f}	78.83	119.78 ^{fg}
Mean	80.2 ^a	76.3 ^c	86.1 ^a	73.2 ^d	81 ^b	87.4 ^a	80.70	121.39
LSD (5%) EM				1.66				1.75

Mean values shared similar letter(s) in each column had non-significant difference at $P < 0.05$. LSD= Least significant difference at $P < 0.05$, E1=Pawe, E2= Manbuk, E3= Woreta, E4= Maitsebri, E5= Jimma, E6= Tepi

4.2.2. Growth Traits

The pooled mean values comparison from combined analysis of variances for plant height, panicle length and number of unfertile tiller per plant revealed that significant difference among genotypes (Table 7). In contrary, the number of fertile tillers per plant was showed non-significant difference among genotypes due to the error variance were detected as heterogeneous with F-test (Appendix Table-1). Therefore, the comparison of the genotypes performances were conducted for each location in Table 7. The genotypes showed a wide range of variation for plant height, panicle length and number of unfertile tiller per plant which ranged from 77.1cm to 99.6cm, 17.1cm to 20.34cm and 0.36 to 1.11, respectively.

The genotypes Tana, FOFIFA-3730, Getachew and Andassa had significantly highest plant height, whereas, four genotypes NERICA-14, NERICA-1, Kokit and Pawe-1 were showed lowest mean values of plant height. Generally, eight genotypes were showed long plant height above the overall mean, whereas 12 genotypes were showed short plant height lower than the overall mean. This indicated that the majority of the tested genotypes had short plant height. Akinwale *et al.* (2011) also reported plant height showed significant difference among the genotypes and it ranged from 86.06cm to 107.66cm.

A wide range of variability was observed in panicle length ranged from 17.1cm to 20.34cm with a mean value of 19.25cm. Five genotypes (FOFIFA-3730, NERICA-13, Getachew, Tana and Chewaqa) had significantly highest mean values of panicle length with significant differences among the mean values. Genotype Pawe-1 was recorded the lowest mean value of panicle length (17.1 cm). Ten genotypes out of 20 were recorded more than the overall gran mean. This indicated that half of the genotypes had longest panicle length among the tested genotypes. Osman *et al.* (2012) reported plant height and panicle length were ranged from 71 to 102cm and 18 to 22 cm, respectively, with mean of 85 and 20cm, respectively. Naeem *et al.* (2015) also reported panicle length ranged from 20 cm to 29.87 cm and Mazid *et al.* (2013) also evaluated 41 rice genotypes and reported significant variation between genotypes for plant height and panicle length with mean value of 84.23cm and 19.62 cm, respectively.

The genotypes had wide variation of number of unfertile tillers per plant range from 0.29 to 1.29 with the gran mean value of 0.789. Four genotypes (NERICA-2, Getachew, Andassa and NERICA-14) had high number of unfertile tillers per plant with the mean value of (1.29, 1.24, 1.22 and 1.02), respectively. Whereas, three genotypes (Fogera-1, NERICA-4 and SUPERICA-1) had the lowest number of unfertile tillers per plant with the mean value of 0.29, 0.41 and 0.44, respectively. This indicated that those genotypes had good tillering capacity and had good trait to resist unfertile problem. Therefore, this genotypes will be recommended for rice breeding program to improve tiller fertility problems. Osman *et al.* (2012) reported number of fertile tillers was ranged from 4.83 to 10.27 with mean of 7.5 and Teferi, (2009) also reported number of unfertile tillers was range from 0.5 to 1.0 with mean of 0.7, respectively.

The genotypes were showed the non-significant difference for the number of fertile tillers per plant. The genotypes showed significant environment with the environment mean values of 6.34, 5.26, 3.62, 4.67, 11.01, and 12.28 at Pawe, Manbuk, Woreta, Maitsebri, Jimma and Tepi, respectively. Environment Tepi and Jimma had maximum number of fertile tillers than others. At Pawe (FOFIFA-3730, Chewaqa, Andassa), at Manbuk (Andassa, Tana, FOFIFA-3730), at Woreta (Andassa, FOFIFA-3730, Chewaqa and Getachew), at Maitsebri (Tana, Getachew and Andassa), at Jimma (FOFIFA-3730, Andassa, Tana and ADET), at Tepi (Chewaqa, Getachew and FOFIFA-3730) had the highest number of fertile tillers per plant. Whereas, genotypes (Pawe-1, NERICA-12, FOFIFA-3737) at Pawe, (Kokit, FOFIFA-4129, Hidasse) at Manbuk, (NERICA-3, Pawe-1, ADET and NERICA-2) at Woreta, (NERICA-3, SUPERICA-1, NERICA-13, FOFIFA-4129 and 3730) at Maitsebri, (Hidasse, NERICA-1 and Pawe-1) at Jimma, and (SUPERICA-1, NERICA-3 and Andassa) had the lowest number of fertile tillers per plant, with the respective environments. Three genotypes, Getachew, Chewaqa and FOFIFA-3730 had maximum number of fertile tillers at Tepi (E6), whereas NERICA-3, Pawe-1, ADET and NERICA-2 had the lowest number of fertile tillers among the genotypes at Woreta (E3). Generally, most of the tested environments (Pawe, Manbuk, Woreta and Maitsebri) were recorded the minimum number of fertile tillers indicating that the ability of the tested genotypes to produce more tillers were low. Therefore, better to search more germplasm that had high tillering capacity and made selection to overcome the problem.

Table 7. Mean performance of 20 rice genotypes for growth traits evaluated across six environments, during 2016/2017 cropping season in Ethiopia

Genotype	Plant height (cm)	Panicle length (cm)	Number of unfertile tillers per plant	Number of fertile tillers per plant						Mean
				E1	E2	E3	E4	E5	E6	
Hidasse	82 ^{c-g}	19.4 ^{c-f}	0.91 ^{cd}	4.7 ^{cd}	4.07 ^c	3.7 ^{abc}	4.2 ^c	8.4 ^c	10.5 ^{bc}	5.93
Getachew	98.9 ^a	20.3 ^{ab}	1.24 ^a	6.3 ^{a-d}	6.13 ^{a-c}	4.3 ^{ab}	5.7 ^{ab}	11.8 ^{abc}	16.2 ^a	8.4
Andassa	96.7 ^a	19.9 ^{a-d}	1.22 ^a	8.9 ^{ab}	8.53 ^a	5.1 ^a	5.7 ^{ab}	13.3 ^{ab}	9.93 ^c	8.58
Tana	99.6 ^a	20.1 ^{abc}	0.86 ^{cde}	6.9 ^{a-d}	7.33 ^{ab}	3.9 ^{abc}	6 ^a	12.5 ^{abc}	13 ^{abc}	8.26
NERICA-3	83.7 ^{cde}	18.7 ^{fgh}	0.84 ^{ef}	6.8 ^{a-d}	5.07 ^{bc}	2.7 ^c	3.9 ^c	11.7 ^{abc}	9.3 ^c	6.59
NERICA-4	82 ^{c-g}	19.1 ^{d-h}	0.39 ^k	5.5 ^{b-d}	4.67 ^{bc}	3.7 ^{abc}	4.6 ^{bc}	10.2 ^{bc}	10.5 ^{bc}	6.52
SUPERICA-1	90.8 ^b	19.1 ^{d-h}	0.48 ^j	6.1 ^{b-d}	4.8 ^{bc}	3.5 ^{bc}	4.1 ^c	10.7 ^{abc}	9.1 ^c	6.37
Pawe-1	78.9 ^{efg}	17.1 ⁱ	0.59 ^{hi}	3.9 ^d	5.73 ^{a-c}	3.1 ^{bc}	5.1 ^{abc}	9.5 ^{bc}	13.1 ^{abc}	6.71
Kokit	78.6 ^{efg}	18.5 ^{fgh}	0.69 ^g	7.3 ^{a-d}	3.73 ^c	3.7 ^{abc}	4.7 ^{bc}	9.7 ^{bc}	12.7 ^{abc}	6.98
Chewaqa	95.4 ^a	20 ^{abc}	0.56 ⁱ	8.2 ^{a-c}	5.33 ^{bc}	4.2 ^{ab}	4.5 ^{bc}	11.2 ^{abc}	16.1 ^{ab}	8.26
NERICA-12	90.4 ^b	19.9 ^{a-d}	0.84 ^{def}	4.5 ^{cd}	4.7 ^{bc}	3.8 ^{abc}	4.3 ^c	10.6 ^{bc}	11.9 ^{abc}	6.63
NERICA-13	85.3 ^{cd}	20.3 ^{ab}	0.83 ^{ef}	5.5 ^{b-d}	4.7 ^{bc}	3.3 ^{bc}	4.1 ^c	11.6 ^{abc}	13 ^{abc}	7.02
NERICA-2	80.8 ^{d-g}	19.6 ^{a-e}	1.29 ^a	6.3 ^{a-d}	4.5 ^{bc}	3.13 ^{bc}	4.7 ^{bc}	10.3 ^{bc}	11.7 ^{abc}	6.8
NERICA-14	77.1 ^g	19.4 ^{b-f}	1.02 ^b	7.5 ^{a-d}	5.5 ^{bc}	3.7 ^{abc}	4.3 ^c	10.1 ^{bc}	12.3 ^{abc}	7.2
NERICA -1	78.5 ^{fg}	18.3 ^h	0.78 ^f	7.1 ^{a-d}	5.3 ^{bc}	3.6 ^{abc}	4.3 ^c	9.5 ^{bc}	11.6 ^{abc}	6.9
ADET	82.6 ^{c-f}	19.2 ^{c-g}	0.64 ^{gh}	4.7 ^{cd}	4.3 ^{bc}	3.1 ^{bc}	4.7 ^{bc}	12.2 ^{abc}	12.7 ^{abc}	6.9
FOFIFA-4129	82.3 ^{c-f}	18.41 ^{gh}	0.80 ^{ef}	5.9 ^{b-d}	4.1 ^c	3.3 ^{bc}	4.1 ^c	9.9 ^{bc}	10.1 ^c	6.2
FOFIFA-3737	86.87 ^{bc}	18.31 ^h	0.80 ^{ef}	4.5 ^{cd}	4.7 ^{bc}	3.3 ^{bc}	4.1 ^c	10.9 ^{abc}	12.9 ^{abc}	6.73
FOFIFA-3730	99.57 ^a	20.34 ^a	0.92 ^c	9.9 ^a	6.8 ^{a-c}	4.1 ^{abc}	5.8 ^{ab}	14.9 ^a	15.7 ^{ab}	9.53
Fogera-1	83.06 ^{c-f}	18.97 ^{e-h}	0.29 ^l	6.3 ^{a-d}	5.3 ^{bc}	3.5 ^{bc}	4.53 ^{bc}	11.2 ^{abc}	13.2 ^{abc}	7.33
Mean	86.66	19.25	0.798	6.34 ^c	5.26 ^d	3.62 ^e	4.67 ^d	11.01 ^b	12.28 ^a	7.2
LSD (5%)	4.33	0.76	0.067	LSD (5%) EM= 0.6559						

Mean values shared similar letter(s) in each column had non-significant difference at $P < 0.05$. LSD= Least significant difference at $P < 0.05$, E1=Pawe, E2= Manbuk, E3= Woreta, E4= Maitsebri, E5= Jimma, E6= Tepi, EM= Environment mean

4.2.3. Yield and Yield Component Traits

The mean performance of 20 rice genotypes for number of filled grain per panicle, number of unfilled grain per panicle, harvest index, thousand grain weight, biological yield and grain yield are presented in Table 10, 11 and 12, respectively. The error variances for all traits except biological yield and grain yield were detected as heterogeneous with F-test (Appendix Table 1), therefore, the genotypes comparison of performances were conducted for each location. The error variance for biological yield and grain yield were homogeneous with F-test (Appendix Table 2), therefore, the genotype comparison were conducted based on pooled mean.

The environment mean values for number of filled grains per panicle of the genotypes were 109.61, 103.67, 70.15, 66.12, 85.46 and 92.13 grams, at Pawe, Manbuk, Woreta, Maitsebri, Jimma and Tepi, respectively. At Pawe, five genotypes, Hidasse (96.1g), Fogera-1(93.7g), NERICA-12 (93.4g), NERICA-4 (92.9g) and NERICA-13 (92.6g) had the maximum number of filled grains per panicle, whereas genotypes Kokit (94.3g), FOFIFA-3730 (100.7g) and Tana (103.7g) had the lowest number of filled grains per panicle with significant difference between the mean values. Genotype Hidasse was the only genotype that had high number of filled grains per panicle than the standard check (Fogera-1), while, the rest of the genotypes had less number of filled grains per panicle than the check. At Manbuk, ADET (115g), Hidasse (114.7g) and Fogera-1 (114g) had maximum number of filled grains per panicle, whereas, Kokit (94.7g), Tana (90.9g) and NERICA-14 (91.9g) had lowest number of filled grains per panicle. At Woreta, three genotypes Chewaqa (81.4g), NERICA-13 (80.1g) and Hidasse (79.9g) had maximum filled grains per panicle, whereas, Pawe-1 (53.7g), FOFIFA-4129 (60.2g), NERICA-2 (64.3g) and NERICA-14 (64.3g) had the lowest filled grains per panicle with non-significant difference between mean values, respectively. At Maitsebri, Getachew (74.5g), Fogera-1 (72.1g) and FOFIFA-3730 (71.7g) had maximum number of filled grains per panicle, whereas, Kokit (57g), Pawe-1 (57.8g), NERICA-14 (59.1g) had the lowest value, respectively, with non-significant difference between mean values. At Jimma, Kokit (100g), NERICA-3 (96g) and NERICA-14 (94.1g) had maximum field grains per panicle. While, genotypes Pawe-1(47g) and Andassa (71.5g) had the lowest filled grains per panicle with non-significant difference between them. Hidasse (115.5g) and NERICA-4 (113.2g) had maximum filled grains per panicle, while, FOFIFA-3730 (67.4g), Andassa (71.9g) and Pawe-1 (73.2g) had the lowest filled grains per

panicle with non-significant difference between the mean values, respectively, at Tepi. Tadesse *et al.* (2017) and Akinwale *et al.* (2011) evaluated 16 and 20 rice genotypes and reported significant difference among the genotypes for number of filled grains per panicle with mean value of 97.7 and 125.25grams, respectively.

The environment mean values for number of unfilled grains per panicle of the genotypes were 5.49, 4.07, 4.4, 1.83, 24.23 and 12.25 grams at Pawe, Manbuk, Woreta, Maitsebri, Jimma and Tepi, respectively. Genotypes, FOFIFA-3730 (9.1g), Tana (8.3g) and NERICA-1 (8.1g) at Pawe; NERICA-3 (3g), Kokit (3.3g) and FOFIFA-3730 (3.7g) at Manbuk; Pawe-1(6.3g), Tana (5.7g) and NERICA-2 (5.6g) at Woreta; NERICA-2 (3.5g) and Getachew (2.9g) at Maitsebri; Pawe-1 (54.4g), Getachew (31.6g) and Andassa (30.7g) at Jimma and FOFIFA-3730 (18.7g), Andassa (16.8g) and Hidasse (16.53g) at Tepi; had the maximum number of unfilled grain per panicle in the perspective environments. The maximum number of unfilled grain per panicle was recorded at Jimma on genotype Pawe-1. Based on the result, 7 genotypes at Pawe, 8 genotypes at Manbuk, 6 genotypes at Woreta, 8 genotypes at Maitsebri, 4 genotypes at Jimma and 8 genotypes at Tepi had the mean value greater than the respective environment mean value. These indicated that most of the tested genotypes had the mean value greater than the respective environment mean value indicating that the majority of the genotypes had good filled grain per panicle, which is good opportunity for future rice breeding program to improve unfilled grain or infertility problems in rice. Atsedemariyam *et al.* (2018) evaluated 23 rice genotypes and reported significant difference among the genotypes with the mean value of 7.24gram.

Table 8. Mean performance of 20 rice genotypes for number of filled and unfilled grain per panicle and harvest index evaluated across six environments

Genotype	Number of filled grain/panicle							Number of unfilled grain/panicle						
	E1	E2	E3	E4	E5	E6	Mean	E1	E2	E3	E4	E5	E6	Mean
Hidasse	105 ^{a-d}	114.7 ^{ab}	79.9 ^{ab}	70.8 ^{abc}	90.1 ^{ab}	115.5 ^a	96.1	4.2 ^{d-f}	3 ^{ab}	3.8 ^{cd}	1.6 ^{b-e}	23.8 ^b	16.53 ^{ab}	8.8
Getachew	110 ^{a-c}	106.3 ^{a-c}	67.3 ^{cde}	74.5 ^a	79.5 ^{ab}	82.3 ^{bcd}	86.7	7.6 ^{a-c}	3.93 ^{ab}	4.1 ^{bcd}	2.9 ^{abc}	31.6 ^b	15.4 ^{abc}	10.9
Andassa	103.8 ^{b-d}	102.3 ^{a-c}	67.3 ^{cde}	67 ^{a-d}	71.5 ^b	71.9 ^{cd}	80.7	7.5 ^{a-d}	5.33 ^{ab}	4.1 ^{bcd}	2.7 ^{abc}	30.7 ^b	16.8 ^{ab}	11.2
Tana	103.7 ^{b-d}	90.9 ^c	77.3 ^{abc}	68.9 ^{a-d}	85.5 ^{ab}	80.9 ^{bcd}	84.5	8.3 ^{ab}	3.67 ^{ab}	5.7 ^{ab}	2.7 ^{abc}	22.6 ^b	14.3 ^{abc}	9.5
NERICA-3	108 ^{a-d}	108 ^{a-c}	70 ^{a-e}	60.9 ^{bcd}	96 ^{ab}	101 ^{abc}	90.7	3 ^f	7.47 ^a	3.5 ^d	2 ^{a-e}	19.5 ^b	10.7 ^{abc}	7.7
NERICA-4	110 ^{a-c}	100 ^{a-c}	75.4 ^{a-d}	68.5 ^{a-d}	90.3 ^{ab}	113.2 ^a	92.9	4.9 ^{b-f}	3 ^{ab}	4 ^{bcd}	2.5 ^{a-d}	20.3 ^b	8.1 ^c	7.1
SUPERICA-1	116 ^{ab}	101.4 ^{a-c}	73.7 ^{a-d}	66.9 ^{a-d}	83.7 ^{ab}	94.9 ^{a-d}	89.4	3.7 ^{ef}	3.27 ^{ab}	3.8 ^{cd}	1.9 ^{a-e}	18.8 ^b	9.5 ^{bc}	6.8
Pawe-1	112.2 ^{a-c}	103 ^{a-c}	53.7 ^f	57.8 ^{cd}	47 ^c	73.2 ^{cd}	74.5	4.4 ^{c-f}	5.48 ^{ab}	6.3 ^a	0.9 ^{de}	54.4 ^a	8.6 ^{bc}	13.3
Kokit	94.3 ^d	94 ^{a-c}	68.8 ^{b-e}	57 ^d	100 ^a	96.4 ^{a-d}	85.1	3.3 ^f	2.13 ^b	3.1 ^d	1.9 ^{a-e}	22.2 ^b	9 ^{bc}	7.0
Chewaqa	114.6 ^{a-c}	107 ^{a-c}	81.4 ^a	63.5 ^{a-d}	88.6 ^{ab}	90.6 ^{a-d}	91.0	4.1 ^{ef}	3.93 ^{ab}	4.7 ^{a-d}	1.3 ^{b-e}	22.5 ^b	10.3 ^{bc}	7.8
NERICA-12	111.3 ^{a-c}	113 ^{a-c}	72.9 ^{a-d}	71 ^{abc}	86.5 ^{ab}	105.7 ^{ab}	93.4	5.1 ^{b-f}	4.3 ^{ab}	4.4 ^{bcd}	1.2 ^{b-e}	20.3 ^b	15 ^{abc}	8.4
NERICA-13	108 ^{a-d}	111 ^{a-c}	80.1 ^{ab}	62.8 ^{a-d}	87.1 ^{ab}	106.4 ^{ab}	92.6	4.7 ^{c-f}	3.5 ^{ab}	4.4 ^{bcd}	1.4 ^{b-e}	21.3 ^b	13.5 ^{abc}	8.1
NERICA-2	116.7 ^{ab}	101.9 ^{a-c}	64.3 ^{def}	70.9 ^{abc}	92 ^{ab}	81.8 ^{bcd}	87.9	6.9 ^{a-e}	4.3 ^{ab}	5.6 ^{abc}	3.5 ^a	22.2 ^b	15.3 ^{abc}	9.6
NERICA-14	109 ^{a-d}	91.9 ^{bc}	64.3 ^{ef}	59.1 ^{bcd}	94.1 ^{ab}	92.3 ^{a-d}	85.1	6.7 ^{a-e}	5.1 ^{ab}	4.2 ^{bcd}	1.5 ^{b-e}	21.6 ^b	12.5 ^{abc}	8.6
NERICA -1	108 ^{a-d}	99 ^{a-c}	67.5 ^{cde}	61.3 ^{bcd}	83.1 ^{ab}	95.3 ^{a-d}	85.8	8.1 ^{ab}	5.1 ^{ab}	4.3 ^{bcd}	1.13 ^{cde}	26.5 ^b	12.3 ^{abc}	9.6
ADET	110.1 ^{a-c}	115.9 ^a	69.4 ^{b-e}	71.7 ^{ab}	89.1 ^{ab}	95.2 ^{a-d}	92.0	3.9 ^{ef}	4.3 ^{ab}	3.5 ^d	1.7 ^{a-e}	20.9 ^b	12.4 ^{abc}	7.8
FOFIFA-4129	119.5 ^a	95.5 ^{a-c}	60.2 ^{ef}	64.4 ^{a-d}	85.1 ^{ab}	90.5 ^{a-d}	85.85	3.2 ^f	3.1 ^{ab}	3.8 ^{cd}	0.9 ^{de}	21.5 ^b	11 ^{abc}	7.26
FOFIFA-3737	111.4 ^{a-c}	98.4 ^{a-c}	68.6 ^{b-e}	61.5 ^{a-d}	93 ^{ab}	86.7 ^{a-d}	86.6	5.5 ^{b-f}	3.9 ^{ab}	4.2 ^{bcd}	0.7 ^e	19.9 ^b	10.1 ^{bc}	7.36
FOFIFA-3730	100.7 ^{cd}	104.1 ^{a-c}	68.4 ^{b-e}	71.7 ^{ab}	83.1 ^{ab}	67.4 ^d	82.57	9.1 ^a	3 ^{ab}	5.5 ^{abc}	2.9 ^{ab}	20.1 ^b	18.7 ^a	9.88
Fogera-1	119 ^a	114 ^{a-c}	72.5 ^{a-d}	72.1 ^{ab}	83.4 ^{ab}	101 ^{abc}	93.7	5.6 ^{b-f}	3.8 ^{ab}	3.9 ^{bcd}	1.13 ^{cde}	23.9 ^b	10.5 ^{abc}	8.16
EM	109.5 ^a	103.67 ^b	70.15 ^e	66.1 ^f	85.5 ^d	92.13 ^c	87.85	5.49 ^c	4.07 ^d	4.4 ^{cd}	1.83 ^e	24.23 ^a	12.52 ^b	8.75
LSD (5%)EM			3.8285								1.2344			

Mean values shared similar letter(s) in each column had non-significant difference at P<0.05. LSD= Least significant difference at P<0.05, E1=Pawe, E2= Manbuk, E3= Woreta, E4= Maitsebri, E5= Jimma, E6= Tepi, EM= environment mean

The mean performance of 20 upland rice genotypes for harvest index, thousand grain weight and above ground biological yield were presented in Table 10. The F-test >3 for harvest index and thousand grain weight. Therefore, the mean comparisons of these traits were conducted for each environment separately. While, F-test <3 for biological yield implies the error variance was detected homogenously and the mean comparison was conducted from the pooled error.

The genotypes mean values for harvest index were ranged from 0.24 to 0.46, 0.26 to 0.39, 0.19 to 1.20, 0.25 to 0.46, 0.26 to 0.46 and 0.14 to 0.38, at Pawe, Manbuk, Woreta, Maitsebri, Jimma and Tepi, respectively. Three genotypes (NERICA-4, NERICA-13 and Fogera-1) accounted the highest harvest index, while genotypes (FOFIFA-3730, Tana and Andassa) had the lowest harvest index with non-significant difference between the mean values at Pawe. At Pawe, only two genotypes (NERICA-4 and NERICA-13) had better harvest index than the standard check (Fogera-1). While, ten genotypes had harvest index greater than the environment mean. These indicating that half of the tested genotypes performed below the grand mean. NERICA-3, Hidasse and NERICA-13 had maximum harvest index, whereas, FOFIFA-3737, Andassa and Getachew had the lowest harvest index at Manbuk. Six genotypes had better harvest index from the check, while half of the genotypes had harvest index greater than the gran mean at Manbuk. Genotypes Kokit, NERICA-2 and NERICA-3 had the highest harvest index at Woreta. These genotypes had the maximum harvest index may be the environment more conducive for more biological yield than other environments. FOFIFA-3730, NERICA-13 and Kokit had highest harvest index, whereas Pawe-1, Andassa and FOFIFA-3730 were recorded the highest harvest index value at Maitsebri. In this environment, except two genotypes (FOFIFA-3730 had maximum and Pawe-1 had minimum) harvest index, the rest genotypes had the optimum harvest index. NERICA-13, Kokit and Hidasse had high harvest index, whereas genotypes Pawe-1, Andassa and FOFIFA-3730 had the lowest harvest index. Twelve genotypes out of 20 had harvest index above the gran mean. At Tepi, genotypes Kokit, Hidasse and NERICA-13 had the maximum harvest index. Generally, more than half of the tested genotypes had good harvest index, indicating that the majority of the tested genotypes had good biological and grain yield ability. Therefore, those genotypes suggested that good for future rice yield improvement program. Tefera *et al.* (2017) evaluated 36 rice genotypes for harvest index and reported in the range of 0.04 to 0.27.

Thousand grain weight also showed non-significant variation on genotypes with the environment mean values of 25.5, 27.7, 28.1, 27.3, 28.4 and 33.6 grams at Pawe, Manbuk, Woreta, Maitsebri, Jimma and Tepi, respectively. Genotypes, Pawe-1 (31.2g), FOFIFA-4129 (29.7g), FOFIFA-3730 (28.7g) and Kokit (28.5g) were counted the highest thousand grain weight at Pawe. Eight genotypes had thousand grain weight greater than the grand mean value (25.49g). Genotypes, Pawe-1(33g), FOFIFA-3730 and NERICA-13 (30.3g) were accounted the highest grain weight at Manbuk. Half of the tested genotypes were accounted more than the grand mean value of 27.71 gram. Genotypes, Pawe-1 (33.78g), NERICA-13 (33.98g) and SUPERICA-1 (32.28g) were accounted the highest grain weight at Woreta. Eight out of 20 genotypes were accounted more than the grand mean value (28.14g). Genotypes, NERICA-13 (33.5g) SUPERICA-1 (30.5g) and NERICA-12 (30g) were accounted maximum grain weight at Maitsebri. Half of the tested genotypes were accounted more than overall mean value (27.27g). Genotypes, Pawe-1 (32.78g), SUPERICA-1 (32.5g) and NERICA-13 (32.5g) had the maximum thousand grain weight at Jimma. Genotypes, SUPERICA-1 (43g), Fogera-1 (38.28g) and Pawe-1(38.8g) and Chewaqa (38g) had the maximum thousand grain weight at Tepi. Genotype SUPERICA-1 was the only genotypes gave higher thousand grain weight than the standard check Fogera-1 at this location. While, nine out of 20 genotypes had grain weight more than overall mean value (33.56g). Generally, the majority of the tested genotypes had thousand grain weight below the gran mean value, indicating that those genotypes had low performance on producing grain weight, which implies the need of searching and screening germplasm that had good grain weight in the future upland rice breeding program in Ethiopia. This finding in line with the previous finding of Tefera *et al.* (2017) and (Girma, 2018).

Table 9. Mean performance of 20 rice genotypes for harvest index and thousand grain weight evaluated across six environments, during 2016/2017 cropping season

Genotypes	Harvest index (%)							Thousand grain weight (g)						
	E1	E2	E3	E4	E5	E6	Mean	E1	E2	E3	E4	E5	E6	Mean
Hidasse	0.37 ^{a-d}	0.39 ^a	0.87 ^a	0.44 ^{ab}	0.44 ^{ab}	0.36 ^{ab}	0.48	23.3 ^e	26 ^{e-h}	26.9 ^{de}	26 ^{d-i}	28 ^{cd}	36 ^{ab}	27.6
Getachew	0.26 ^{e-g}	0.27 ^{cd}	0.57 ^{bc}	0.41 ^{abc}	0.31 ^{def}	0.24 ^{ab}	0.34	23.7 ^e	28 ^{b-e}	25.1 ^{fg}	28 ^{b-g}	27 ^{cd}	31 ^{ab}	27.1
Andassa	0.24 ^{fg}	0.27 ^{cd}	0.65 ^{abc}	0.38 ^{bc}	0.29 ^{ef}	0.21 ^{ab}	0.34	24.3 ^{de}	27 ^{c-g}	24.6 ^g	27 ^{b-h}	26 ^{cd}	27 ^b	26.1
Tana	0.24 ^{fg}	0.28 ^c	0.72 ^{abc}	0.39 ^{bc}	0.30 ^{ef}	0.21 ^{ab}	0.36	25 ^{cde}	28.2 ^{b-f}	24.8 ^g	27 ^{b-h}	27 ^{cd}	32 ^{ab}	27.38
NERICA-3	0.38 ^{a-d}	0.38 ^{ab}	0.77 ^{ab}	0.43 ^{ab}	0.42 ^{abc}	0.32 ^{ab}	0.49	23.7 ^e	25.5 ^{f-h}	26.5 ^{ef}	24.4 ^{f-i}	26 ^{cd}	28 ^b	25.55
NERICA-4	0.46 ^a	0.34 ^{abc}	0.74 ^{abc}	0.39 ^{bc}	0.38 ^{bcd}	0.3 ^{ab}	0.45	23.2 ^e	25 ^{gh}	28 ^{de}	24.1 ^{ghi}	27 ^{cd}	34 ^{ab}	26.76
SUPERICA-1	0.44 ^{ab}	0.3 ^{bcd}	0.67 ^{abc}	0.39 ^{bc}	0.38 ^{bcd}	0.29 ^{ab}	0.42	27 ^{bcd}	28.3 ^{b-d}	33.2 ^a	30.5 ^b	32.5 ^a	43 ^a	32.51
Pawe-1	0.31 ^{d-f}	0.31 ^{bcd}	0.19 ^d	0.25 ^d	0.26 ^f	0.20 ^b	0.25	31.2 ^a	33 ^a	33.7 ^a	27.7 ^{b-f}	32.7 ^a	38 ^{ab}	32.71
Kokit	0.4 ^{a-d}	0.35 ^{abc}	0.87 ^a	0.39 ^{bc}	0.44 ^{ab}	0.38 ^a	0.53	28.5 ^{ab}	28.2 ^{b-f}	30.3 ^c	29.3 ^{bc}	31 ^{ab}	37 ^{ab}	30.61
Chewaqa	0.33 ^{c-f}	0.35 ^{abc}	0.49 ^c	0.41 ^{abc}	0.35 ^{bcd}	0.14 ^{ab}	0.38	22.3 ^e	26 ^{e-h}	24.8 ^g	26 ^{c-i}	27 ^{cd}	38 ^{ab}	27.33
NERICA-12	0.43 ^{a-c}	0.35 ^{abc}	0.69 ^{abc}	0.43 ^{ab}	0.41 ^{abc}	0.33 ^{ab}	0.44	27 ^{bcd}	30.17 ^b	32 ^{ab}	29.9 ^b	31 ^{ab}	34 ^{ab}	30.67
NERICA-13	0.46 ^a	0.38 ^{ab}	0.73 ^{abc}	0.46 ^a	0.46 ^a	0.37 ^{ab}	0.52	27.8 ^{bc}	30.3 ^b	32.9 ^a	33.8 ^a	32.5 ^a	37 ^{ab}	32.45
NERICA-2	0.44 ^{ab}	0.34 ^{abc}	0.62 ^{abc}	0.44 ^{ab}	0.41 ^{abc}	0.34 ^{ab}	0.52	23 ^e	24.17 ^h	24.8 ^g	24 ^{hi}	25.5 ^d	31 ^{ab}	25.45
NERICA-14	0.35 ^{b-e}	0.32 ^{abcd}	0.70 ^{abc}	0.44 ^{ab}	0.38 ^{bcd}	0.33 ^{ab}	0.42	27 ^{bcd}	27 ^{c-g}	28.5 ^d	28 ^{bcd}	28 ^{bc}	30.4 ^b	28.19
NERICA -1	0.36 ^{a-e}	0.3 ^{bcd}	0.69 ^{abc}	0.35 ^c	0.31 ^{def}	0.24 ^{ab}	0.37	24.3 ^{de}	26.3 ^{d-h}	26.7 ^{ef}	25.1 ^{e-i}	26 ^{cd}	29.2 ^b	26.33
ADET	0.44 ^{ab}	0.34 ^{abc}	0.72 ^{abc}	0.43 ^{ab}	0.40 ^{abc}	0.31 ^{ab}	0.44	23.7 ^e	25 ^{gh}	27.5 ^{de}	23.3 ⁱ	26 ^{cd}	29.6 ^b	25.8
FOFIFA-4129	0.41 ^{a-d}	0.30 ^{bcd}	0.76 ^{abc}	0.42 ^{ab}	0.39 ^{abc}	0.31 ^{ab}	0.43	29.7 ^{ab}	30.3 ^b	31 ^{bc}	29 ^{bcd}	31 ^{ab}	32.7 ^{ab}	30.52
FOFIFA-3737	0.32 ^{d-f}	0.26 ^d	0.69 ^{abc}	0.4 ^{abc}	0.31 ^{def}	0.21 ^{ab}	0.37	28.7 ^{ab}	30.2 ^b	30.3 ^c	29.6 ^b	30 ^{ab}	33.2 ^{ab}	30.37
FOFIFA-3730	0.21 ^g	0.29 ^{cd}	0.66 ^{abc}	0.93 ^{bc}	0.29 ^{ef}	0.22 ^{ab}	0.35	22.5 ^e	29.8 ^{bc}	23.8 ^g	28 ^{b-g}	27 ^{cd}	32.9 ^{ab}	27.0
Fogera-1	0.45 ^{ab}	0.34 ^{abc}	0.69 ^{abc}	0.42 ^{ab}	0.4 ^{abc}	0.31 ^{ab}	0.48	23.8 ^e	25.3 ^{gh}	27.2 ^{de}	25.4 ^{e-i}	28 ^{cd}	38.2 ^{ab}	27.98
EM	0.36 ^c	0.32 ^d	0.68 ^a	0.4 ^b	0.37 ^c	0.29 ^e	0.42	25.5 ^d	27.7 ^{bc}	28.1 ^{bc}	27.3 ^c	28.4 ^b	33.6 ^a	28.43
LSD (5%) EM			0.027								1.01			

Note that; mean values shared similar letter(s) in each column had non-significant difference at P<0.05. LSD= least significant difference at P<0.05, E1= Pawe, E2= Manbuk, E3=Woreta, E4= Maitsebri, E5= Jimma, E6= Tepi, EM= environment mean

The genotypes had significant difference among the genotypes for biological yield with the grand mean value of 9831kg/ha. Four genotypes Getachew, FOFIFA-3730, Tana and Chewaqa had the maximum biological yield across the environments. Whereas, genotypes Kokit and NERICA-12 had the lowest biological yield. Nine genotypes had the biological yield above the overall mean value, indicating that the performance of the genotypes on biological yield was good, which may help for improving the biological yield. Mulugeta *et al.* (2016) evaluated 22 rice genotypes and reported the biological yield in the range between 2966.67 and 5533.33 kg/ha which showed wide range of variation among the varieties. Tefera *et al.* (2017) also evaluated 34 rice genotypes and reported biological yield showed significant difference among the tested genotypes.

The genotypes showed differential response to environments and the best performing genotypes at each environment differed. A total of 11 genotypes had mean grain yield greater than overall genotypes mean grain yield. Three genotypes NERICA-3, Hidasse and Chewaqa had the highest grain yield across the environment with the mean value of 4074.1, 4062.1 and 4053.6 kg/ha, respectively. In the contrary, genotypes Pawe-1 and Kokit had the lowest grain yield among the genotypes with the mean value of 2711.8 and 2770.2 kg/ha, respectively.

This inconsistency of genotypes performances across locations and it was an indication that the genotypes responded differently to different environmental conditions. The mean grain yield of genotypes across locations also differed that the highest mean yield was obtained from Jimma followed by Pawe and Manbuk. This indicated some locations were favorable for genotypes to produce yield above the average environment. Many authors reported differential performances of rice genotypes across environments (Bose *et al.*, 2014; Krishnamurthy *et al.*, 2015; Mulugeta *et al.*, 2016; Taddesse *et al.*, 2017; Girma, 2018) and in other crops such as in wheat (Kiliç *et al.*, 2010; Fentaw, 2011), sorghum (Adugna, 2007; Sintayehu and Tesfaye, 2017) and maize (Solomon *et al.*, 2008; Gami *et al.*, 2017).

Table 10. Mean performance of 20 rice genotypes for biological and grain yield evaluated across six environments, during 2016/2017 cropping season

Genotypes	Biological yield (kg/ha)	Grain yield (kg/ha)
Hidasse	9272.2 ^{cde}	4062.1 ^a
Getachew	12029.1 ^a	3713.7 ^{a-d}
Andassa	11233.4 ^{abc}	3328.3 ^{c-f}
Tana	11767 ^{ab}	3548.9 ^{a-e}
NERICA-3	9662.5 ^{b-e}	4074.1 ^a
NERICA-4	11001.8 ^{abc}	3929.7 ^a
SUPERICA-1	9529.3 ^{b-e}	3609.5 ^{a-e}
Pawe-1	10432 ^{a-d}	2711.8 ^h
Kokit	6370.5 ^f	2770.2 ^{gh}
Chewaqa	11713.4 ^{ab}	4053.6 ^a
NERICA-12	9255.8 ^{cde}	3801.1 ^{abc}
NERICA-13	8493.3 ^{def}	3891.7 ^{ab}
NERICA-2	7948.5 ^{ef}	3263.9 ^{d-g}
NERICA-14	8134.3 ^{ef}	3076.9 ^{e-h}
NERICA -1	10750 ^{a-d}	3184.3 ^{e-h}
ADET	9949 ^{a-e}	3960 ^a
FOFIFA-4129	8121.9 ^{ef}	3101.8 ^{e-h}
FOFIFA-3737	9830 ^{a-e}	3002.2 ^{fgh}
FOFIFA-3730	11964.8 ^a	3385.8 ^{b-f}
Fogera-1	9161.8 ^{cde}	3725.1 ^{a-d}
Mean	9831	3509.73
LSD (5%)	1919.6	457.87

Mean values shared similar letter(s) in each column had non-significant difference at $P < 0.05$. LSD= Least significant difference, GM= Grand mean.

4.3. Analysis of Variance for Grain Yield from ER's and AMMI Models

The combined analysis of variance (Table 5) showed that the mean square for genotype x location interaction was highly significant ($P < 0.01$) for grain yield (Table 7). The result indicated the inconsistent performance of genotypes across the test environments for yield suggested the need to conduct further GEI and thereby stability analyses to understand the nature of GEI and stability of the performance of genotypes across environments. Many workers reported the presence of significant GEI effect on grain yield of rice genotypes and suggested the need to conduct GEI and stability analyses (Ramezani and Torabi, 2014; Luguterh *et al.*, 2016; Oladosu *et al.*, 2017; Taddesse *et al.*, 2017; Girma, 2018; Akter *et al.*, 2019). Accordingly results of analysis of variance from Eberhart and Russell's Model (ER's) model in Table 11.

The analysis of variance from linear regression (ER's) model revealed that significant ($P \leq 0.05$) mean squares of G x E (linear) and pooled deviation (Table 11). The significant mean square for pooled deviation indicated that the variability of genotype for yield performance was partially unpredictable. The significant mean square for G x E (linear) indicated that the linearity was a considerable portion of GEI and the stability parameter "b" estimated by linear response to change in environment was not the same for all the genotypes. The significant mean squares of genotype, environment + (genotype x environment) and environment linear indicated the presence of significant differences among genotypes and environments for mean grain yield. The effect of genotype x environment interaction (G x E) is statistically non additive indicating that differences in yield among cultivars depend on the environment (Zali and Farshadfar, 2011). This is because, one cultivar may have the highest yield in some environments and the other cultivar may excel in others and can be referred as inconsistent performance of genotypes (Bose *et al.*, 2015; Oladosu *et al.*, 2017; Taddesse *et al.*, 2017; Akter *et al.*, 2019).

Eleven rice genotypes were evaluated at six environments in Western Ethiopia during 2015 and 2016 main cropping season. The analysis GEI indicated that mean square due to genotypes and interaction of genotype x environment (linear) were highly significant ($P < 0.01$) suggested the differences in yield performance among the genotypes under different environments (Girma, 2018). Mosavi *et al.* (2013) observed significant yield differences among rice genotypes, environment and genotype by environment interaction. The GEI reduces the association between phenotypic and genotypic values and leads to bias in the estimates of gene effects less amenable to selection (Farshadfar *et al.*, 2011). In the presence of significant GEI effect, the identification of superior genotypes for a range of environments is difficult because GEI complicated to determine their true genetic potential (Yaghotipoor and Farshadar, 2007). It was reported that the contribution of environmental effect was large to total variation (Blanche *et al.*, 2009). The importance of GEI in national cultivar evaluation and breeding programs has been demonstrated in almost all major crops (Najafian *et al.*, 2010; Zali and Farshadfar, 2011; Krishnamurthy *et al.*, 2015; Mulugeta *et al.*, 2016; Gami *et al.*, 2017).

Table 11. Joint regression analysis of variance (ER's model) for grain yield of 20 upland rice genotypes at six environments, during 2016/2017 cropping season in Ethiopia

Source of variation	DF	SS	MS
Total	119	77322665.56	
Genotype	19	21830372.01	1148967*
Environment+ (Genotype x Environment)	100	55492293.54	554922.94*
Environment linear	1	13683092.05	13683092***
G x E (linear)	19	14424601.22	759189.5*
Pooled deviation	80	27384600.28	342307.5*
Hidasse	4	1556588.65	389147.2
Getachew	4	383620.94	95905.24
Andassa	4	657271.64	164317.9
Tana	4	491821.38	122955.3
NERICA-3	4	2386204.3	596551.1
NERICA-4	4	2520333.58	630083.4*
SUPERICA-1	4	554529.69	138632.4
Pawe-1	4	7657829.66	1914457*
Kokit	4	248690.99	62172.75
Chewaqa	4	1419567.99	354892
NERICA-12	4	276084.84	69021.21
NERICA-13	4	1314647.91	328662
NERICA-2	4	2068472.03	517118
NERICA-14	4	411103.86	102776
NERICA -1	4	939917.43	234979.4
ADET	4	1069377.17	267344.3
FOFIFA-4129	4	592502.61	148125.7
FOFIFA-3737	4	330953.12	82738.28
FOFIFA-3730	4	770549.19	192637.3
Fogera-1	4	1734533.28	433633.3
Pooled error	240	60357477.7	251489.5

* and **, significant at $P < 0.05$ and $P < 0.01$, respectively. DF= Degree of freedom, SS= Sum of squares, MS= Mean square

The results of analysis of variance from Additive Main effects and Multiplicative Interaction (AMMI) model are presented in Table 12. The results from AMMI model analysis revealed highly significant ($P < 0.01$) mean squares for genotype, environment and G x E interaction effects for grain yield. The highest percentage (30.36%) of the total variation for grain yield was explained, by the genotype x environment interaction which was much greater than the sum of the genotype and environment contribution to the total sum square of yield. This result showed

that rice grain yield were significantly influenced by GEI. The magnitude of GEI as compared to environment and genotype suggested the possible existence of different mega-environments. This result in line with the previous finding of Zerihun (2011).

The mean squares for the first two interaction principal components (IPCA1 and IPCA2) were also highly significant ($P < 0.001$). The first two IPCA (IPCA 1 and IPCA2) axes were explained 55.12% and 28.40 % of the G x E interaction for grain yield, respectively, with their cumulative contribution of 83.52% of the total GEI. This indicated that the AMMI analysis with only two interaction principal component axes was the best predictive model, which is in agreement with previous results of the different authors (Das *et al.*, 2010; Bose *et al.*, 2015; Tadesse *et al.*, 2017; Girma, 2018; Akter *et al.*, 2019). The mean squares for IPCAs (IPCA3 and 4) were non-significant and may had small contribution of noise and, therefore, might not help to predict validation observations. This result in line with the previous findings (Mulugeta *et al.*, 2016; Tadesse *et al.*, 2017; Girma, 2018).

Table 12. AMMI analysis of variance for grain of 20 upland rice genotypes tested at six environments, during 2016/17 cropping season in Ethiopia

Source of variation	DF	SS	MS	Sum of square explained		
				%Total	% G x E	% G x E cumulative
Total	359	413.04				
Rep (Env)	12	70.272	5.856**			
Genotype (G)	19	65.493	3.447**	15.84		
Environment (E)	5	41.05	8.21**	9.94		
Interactions (G x E)	95	125.4	1.32**	30.36		
IPCA 1	23	69.115	3.005**		55.12	55.12
IPCA 2	21	35.616	1.696**		28.4	83.52
Residuals	228	110.808	0.486 ^{NS}	26.83		

ns, and **, nonsignificant, significant at $P < 0.01$, respectively. DF = Degree of freedom, SS = Sum of square, MS = Mean square, G = Genotype, E = Environment, G x E = Genotype by environment interaction, IPCA 1 and IPCA 2 = Interaction principal component axis one and two, respectively.

4.4. Stability Analyses for Grain Yield

4.4.1. Estimates of Stability Parameters from Eberhart and Russell's Model

A total of nine genotypes had mean grain yield lower than the genotypes average yield over environments. The seven genotypes (Kokit, FOFIFA-3737, NERICA-14, FOFIFA-4129, Andassa, FOFIFA-3730 and NERICA-1) had S^2di values non-significant from zero indicated the genotypes were stable for yield across environments. The two genotypes (NERICA-2 and Pawe-1) had significant S^2di values from zero, suggesting the genotypes were not stable for yield across environments. Among the nine genotypes, only two (Kokit and Andassa) had negative b_i values significant different from unity suggesting the genotypes were more performing at unfavorable environments. The other seven genotypes had positive b_i values significant different from unity indicated the genotypes were performed well at favorable environments (Table 12). However, all genotypes had mean yield lower than the overall mean yield of genotypes, which might indicate that these genotypes might not worth to further test to release to as new variety. According to Eberhart and Russell (1966) model, a stable genotype should have high yield, unit regression coefficient ($b_i=1$) and deviation from regression nearly equal to zero ($S^2di=0$). The desirable genotypes are expected not only stable in all environments, but also had desirable mean values (high mean values) (Zerihun, 2011; Parmar *et al.*, 2016).

A total of 11 genotypes had mean grain yield of higher than the genotypes overall mean yields. The seven genotypes (NERICA-12, Getachew, Tana, SUPERICA-1, ADET, NERICA-13 and Chewaqa) had S^2di values non-significant from zero, indicating that the genotypes were stable for yield across environments. The four genotypes (Hidasse, Fogera-1, NERICA-3 and NERICA-4) had significant S^2di values from zero suggested the genotypes were not stable for yield across environments. The two (Getachew and Tana) had negative b_i values significant different from unity suggested the genotypes were more performed at unfavorable environments. The other nine genotypes had positive b_i values significant different from unity indicated the genotypes were performed well at favorable environments. The 11 genotypes could be further evaluated to identify widely adaptable genotypes for in the test environments or/and adaptable for specific environment(s). The genotypes with b_i and S^2di values significantly different from unity and zero, respectively, suggested the genotypes had dynamic stability (not static stability) and were highly responsive to environments (Adugna and

Labuschagne, 2002; Alberts, 2004; Akcura and Kaya, 2008; Mut *et al.*, 2010; Bose *et al.*, 2014; Luguterh *et al.*, 2016; Oladosu *et al.*, 2017; Girma, 2018; Akter *et al.*, 2019).

The regression coefficient (b_i) measures the response of genotypes to environments. When the regression coefficient of the genotype is nonsignificant from unity ($b_i = 1$), the genotype is said to be average responsive suitable to both poor and good environments, while the b_i value of the genotype is significantly greater than from one/unity ($b_i > 1$), it is said the genotype is highly considered responsive to favourable environments and suitable only in good environment. Whereas, if the estimate of b_i value of the genotype b_i value is significantly less than one/unity ($b_i < 1$), it might indicate that the genotype is less responsive, and it is suitable to poor environment (Wachira *et al.*, 2002; Kiliç and Yağbasanlar, 2010). Accordingly, six genotypes (NERICA-3, Hidasse, Chewaqa, ADET, NERICA-4 and NERICA-13) had yield advantages of 10.86 to 15.99% overall genotypic mean and had positive b_i values ($b_i > 1$), indicated the genotypes were performing better under favorable environments. SUPERICA-1, Fogera-1 and NERICA-12 had also positive b_i values and yield advantages of 2.88, 6.3 and 8.29%, respectively. Therefore, these genotypes along with the six genotypes could be considered as candidate genotypes for favorable environments. Tana and Getachew varieties had yield advantages of 1.17 and 5.73% over mean yield of genotypes, respectively. These varieties also had negative b_i values suggested the varieties could be recommended for production under unworkable environments (Das *et al.*, 2010).

Generally, according to Wachira *et al.* (2002) regression coefficient (b_i) interpretation, nine genotypes (Hidasse, NERICA-3, NERICA-4, SUPERICA-1, Pawe-1, Chewaqa, ADET, FOFIFA-4129 and FOFIFA-3737) had significantly greater than unity/one ($b_i > 1$), indicated the genotypes were highly responsive above the average and suitable only in favorable environments. In the opposite, 11 genotypes including the standard check, had significantly less than unity/one ($b_i < 1$), indicated the genotypes were less responsive to environmental change and it is suitable to poor/unfavorable environments. No genotypes had b_i value equal to unity/one, which indicated that the tested genotypes were not responsive for both good and poor environments.

Table 13. Regression coefficients and deviations from regression from ER's model for grain yield of the 20 rice genotypes evaluated at six environments, during 2016/17 cropping season

No.	Genotype	Yield (t/ha)	Rank	bi	Rank	S ² di	Rank
1	Hidasse	4.06	2	1.756	16	0.227	15
2	Getachew	3.71	9	-0.245	3	-0.067	4
3	Andassa	3.33	13	-0.413	2	0.003	9
4	Tana	3.55	11	-0.468	1	-0.038	6
5	NERICA-3	4.07	1	2.134	18	0.436	18
6	NERICA-4	3.93	5	1.679	15	0.467	19
7	SUPERICA-1	3.61	10	2.395**	19	-0.024	7
8	Pawe-1	2.71	20	1.843	17	1.753	20
9	Kokit	2.77	19	-0.136	4	-0.100	1
10	Chewaqa	4.05	3	3.596**	20	0.196	14
11	NERICA-12	3.80	7	0.226	5	-0.093	2
12	NERICA-13	3.89	6	0.624	8	0.167	13
13	NERICA-2	3.26	14	0.640	9	0.354	17
14	NERICA-14	3.08	17	0.367	7	-0.059	5
15	NERICA -1	3.18	15	0.845	11	0.073	11
16	ADET	3.96	4	1.562	14	0.104	12
17	FOFIFA-4129	3.10	16	1.041	12	-0.014	8
18	FOFIFA-3737	3.00	18	1.524**	13	-0.078	3
19	FOFIFA-3730	3.39	12	0.702	10	0.030	10
20	Fogera-1	3.73	8	0.328	6	0.272	16

**, significant at P<0.01. bi= regression coefficient, S²di =deviation from the regression

4.4.2. Stability Parameters from AMMI Model

The IPCA1 and IPCA2 scores for each genotypes were calculated a stability parameters of AMMI model. Moreover, AMMI stability value (ASV) for each genotype was calculated and the rank was given from 1-20 in ascending order (from low to high value) to identify the most stable genotypes, since it considers both the IPCA1 and IPCA2 scores (Purchase et al., 2000). The mean grain yields and ASV of genotypes were ranked to identify the genotypes, with high yield and more stable over environments. The results are presented in Table 14.

The 11 genotypes had mean yield of higher than the overall genotypic mean yield, and all with high ASV rank ranging from 11 to 19 ranks except three genotypes with <10 rank (Getachew, NERICA-4 and Kokit). Based on mean yield, IPCAs and ASV, these genotypes could be grouped into three. The first group consists of four genotypes of 1-3 ranks for high yield (NERICA-3, Hidasse and Chewaqa) and one genotype (SUPERICA-1) ranking 10th for yield, and had negative IPCA1 and positive IPCA2, with high ASV of 13, 14, 18 and 19th ranks,

indicating the genotypes were less stable and high performing in unfavorable environments, since IPCA2 was positive and opposite to the negative sign of IPCA1. Zerihun, (2011) and Oladosu *et al.* (2017) evaluated 18 and 16 barley and rice genotypes at 11 and 8 environments, and grouped the genotypes stability based on grain yield, IPCA1, IPCA2 and ASV.

The second group consisted of three genotypes (ADET, NERICA-13 and NERICA-4) that ranked 4, 5 and 6th for grain yield, and both IPCAs had the same negative sign, and ASV of 6, 9 and 17, ranks and one genotype (Fogera-1) ranked 8th for yield, and both IPCA had the same positive sign and ASV rank of 12th . This indicated that the genotypes were equally performing both at favorable and unfavorable environments. The third group contained three genotypes (NERICA-12, Getachew and Tana) with mean yield ranks of 7, 9 and 11, and negative IPCA1 and positive IPCA2 values, and ASV ranks of 2, 10 and 11 indicating that genotypes had average or more than average stability, and high performing in unfavorable environments, since IPCA2 was positive and opposite to the negative sign of IPCA1. The remaining nine genotypes had ASV ranking of below 1 to 10, except few with 15, 16 and 20, but with mean yield lower than the grand genotypic mean yield indicating that the genotypes had not practical importance to be selected for high yield, though genotypes were relatively stable across environments. Taddess *et al.* (2017) and Girma (2018) also grouped the genotypes based on ASV, IPCA2 and IPCA1.

In this model, genotypes with least ASV or have smallest distance from the origin are considered as the most stable genotypes, whereas those which have highest ASV are considered as unstable (Purchase *et al.*, 2000). Accordingly, genotypes FOFIFA-4129, FOFIFA-3730 and NERICA-12 could be considered as the most stable genotypes with 1, 2 and 3rd ranks, whereas genotypes Pawe-1, Chewaqa and NERICA-3 were considered unstable genotypes with 20, 19 and 18th ranks (Table 14). Previously, different researchers used AMMI stability parameters to study the stability of grain yield and quality of different rice genotypes, across various environments (Nassir, 2013; Bose *et al.*, 2014; Luguterh *et al.*, 2016; Oladosu *et al.*, 2017).

Table 14. Stability parameters from AMMI model with mean grain yield ranks of 20 upland rice genotypes evaluated at six environments, during 2016/17 cropping season in Ethiopia

No	Genotype	Graph ID	Mean yield	IPCA1	IPCA2	ASV	Rank
1	Hidasse	1	4.06	-0.5789	0.0203	1.124	14
2	Getachew	2	3.71	0.4508	-0.2993	0.964	10
3	Andassa	3	3.33	0.5411	-0.3834	1.197	16
4	Tana	4	3.55	0.3223	-0.6305	1.023	11
5	NERICA-3	5	4.07	-0.7915	0.0176	1.536	18
6	NERICA-4	6	3.93	-0.7051	-0.2061	1.411	17
7	SUPERICA-1	7	3.61	-0.4566	0.4513	1.095	13
8	Pawe-1	8	2.71	0.8473	1.1516	2.970	20
9	Kokit	9	2.77	0.2482	-0.3982	0.640	7
10	Chewaqa	10	4.05	-0.8830	0.6422	2.126	19
11	NERICA-12	11	3.80	0.0030	-0.3887	0.157	2
12	NERICA-13	12	3.89	-0.2709	-0.4748	0.751	9
13	NERICA-2	13	3.26	0.5423	0.3518	1.176	15
14	NERICA-14	14	3.08	0.2451	-0.1581	0.501	5
15	NERICA -1	15	3.18	0.3213	0.2422	0.682	8
16	ADET	16	3.96	-0.2759	-0.0360	0.537	6
17	FOFIFA-4129	17	3.10	0.0112	0.1205	0.036	1
18	FOFIFA-3737	18	3.00	-0.2448	0.1508	0.498	4
19	FOFIFA-3730	19	3.39	0.1377	-0.2092	0.311	3
20	Fogera-1	20	3.73	0.5364	0.0360	1.042	12

The best four stable genotypes ranked based on AMMI presented in Table 15. In this study, the best adapted genotypes for each testing environment and other environments, with similar agro-ecological conditions with the testing environments were identified using the AMMI model. In this study, genotypes were responded differently to environmental fluctuation (have high GEI), and hence, the AMMI model allowed us to select, relatively, the best genotypes that suit to a specific environment. Accordingly, genotype Pawe-1 was the best at Pawe and ranked 19th at Jimma, whereas genotypes Fogera-1, NERICA-13, Chewaqa, Getachew and Hidasse were the best genotypes, which specifically adapted to Manbuk, Woreta, Jimma, Maitsebri and Tepi, respectively (Table 15).

The genotype Fogera-1 was identified as the best at four environments and had four favorable environments (Manbuk, Pawe, Maitsebri and Tepi). NERICA-3 was selected in one favorable environments (Tepi), and two unfavorable environment (Jimma and Woreta). Hidasse (G1) was selected at two favorable environments of Tepi and Manbuk and two unfavorable environments of Woreta and Jimma. This indicated the three genotypes were performing best in many

locations that other best four selections of AMMI and performing both under favorable and unfavorable environments. Genotype Getachew (G2) was selected at two favorable environments (Manbuk and Maitsebri), and similarly, genotype ADET (G16) was selected at two favorable environments (Manbuk and Tepi). This indicates that the two genotypes were performing well only at favorable environments that others best four selections of AMMI model. Genotype NERICA-4 (G6) was selected at two unfavorable environments (Jimma and Woreta). This indicates that the performance of the genotype was poor in many locations based on AMMI model selection. Genotype Chewaqa (G10) was selected at one favorable (Pawe) and at one unfavorable environment (Jimma). Genotypes: NERICA-2 (G13) and NERICA-12 (G11) were selected one favorable environment of Pawe and Maitsebri, respectively. This indicated that the genotypes were best at specific locations only at Pawe and Maitsebri, respectively, implies the performance of the genotypes were not consistence across the environments. Whereas, NERICA-13 (G12) was also selected at one unfavorable environment at Woreta. This indicated that the genotype performance across the environment was poor. Zerihun (2011) evaluated of 23 barely genotypes on 11 mega-environments and found that the classification of favorable and unfavorable and also the ideal environment based on the performance of the genotypes. Oladosu *et al.* (2017) and Bose *et al.* (2014) also evaluated 15 and 12 genotypes on 6 and 10 environments, respectively, and found that based on the genotypes performance classified the mega-environments to favorable, unfavorable and ideal environments.

Table 15. AMMI model best four upland rice genotypes selections for mean yield at different environments

Number	Environment	Mean (kg/ha)	IPCA2 Score	1	2	3	4
1	Jimma	4153	-54.63	G10	G5	G1	G6
3	Pawe	3603	25.81	G8	G20	G13	G10
5	Manbuk	3587	12.36	G20	G2	G16	G1
4	Tepi	3350	8.79	G1	G16	G20	G5
2	Maitsebri	3271	24.93	G2	G4	G20	G11
6	Woreta	3094	-17.26	G12	G6	G5	G1
Grand mean		3509.67					

Note: G1=Hidasse, G2= Getachew, G3= Andassa, G4= Tana, G5= NERICA-3, G6= NERICA-4, G7= SupERICA-1, G8= Pawe-1, G9= Kokit, G10= Chewaqa, G11= NERICA-12, G12= NERICA-13, G13= NERICA-2, G14= NERICA-14, G15= NERICA-1, G16= ADET, G17=FOFIFA-4129, G18= FOFIFA-3737, G19=FOFIFA-3730, G20= Fogera-1.

4.4.3. GGE Biplot Analysis

4.4.3.1. Which-won-where

In this study, the partitioning of genotype and genotype by environment interaction through GGE bi-plot analysis showed that, IPCA 1 and IPCA 2 explained 79.6% (PCA1 = 59.3% and PCA2 = 20.3%) of the total variation for grain yield (Figure 1). This moderate percentage variability of GGE accounted by the bi-plot indicated that there was strong and complex GEI in this multi-environment yield trial data. The GGE biplot was constructed by plotting the first two principal components, PC1 and PC2 referred to as the primary and secondary effects, respectively, derived from subjecting environment centered yield data to singular value decomposition (Yan *et al.*, 2000; Meimei *et al.*, 2014). GGE bi-plot is an effective tool for identification of the ideal environments, ideal genotypes and best genotypes and their adaptable environments. The biplot analysis of GEI provides the best way for visualizing the interaction patterns between genotypes and environments (Gauch and Zobel, 1996; Yan *et al.*, 2000) and to study the possible existence of different environment groups in a region (Yan and Kang, 2003) which a set of genotypes are grown.

The polygon view of the GGE bi-plot for grain yield of 20 rice genotypes is presented in Figure 1. A polygon view of GGE was formed by connecting the vertex genotypes with straight lines and the rest of the genotypes were placed within the polygon. There are five rays in, which divided the bi-plot into five sections. The bi-plot showed that eight vertex genotypes, NERICA-4 (G6), Pawe-1 (G8), Chewaqa (G10), NERICA-3 (G5), NERICA-13 (G12), Tana (G4), Andassa (G3) and Kokit (G9) located at the top of the polygon. The vertex genotypes in each sector are the best genotype at environments whose markers fall into the respective sector. These genotypes also had the largest distance from the origin indicated the genotypes were more responsive to the varying environments. On the other hand, the rest of 12 genotypes within the polygon and nearer to origin were less responsive than vertex genotypes (Yan *et al.*, 2001; Yan and Tinker, 2006).

The two environments, E5 (Jimma) and E3 (Woreta) were in which the genotypes had highest and lowest mean grain yield, respectively. The genotypes had mean yield above the average yield of the six environments at E1 (Pawe) and E2 (Manbuk) environments (Table 15). In these environments, G10 (Chewaqa) identified among the best four high yielding genotypes at Pawe (E1) and Jimma (E5), G5 (NERICA-3) was second, third and fourth ranking of high yield genotype at Jimma (E5), Woreta (E3), and Tepi (E6), respectively, and G6 (NERICA-4) was the second and fourth high yield ranking at Woreta (E3) and Jimma (E5). Therefore, E1, E4, E5 and E6 share two and three high yielding genotypes. The three environments, Pawe (E1), Manbuk (E4) and Jimma (E5) share same sector and Pawe (E1) and Jimma (E5) share same winner genotype G10 (Chewaqa), and Jimma (E5) and Tepi (E6) share same winner genotype G5 (NERICA-3). The environments at different sectors viz., E3 (Woreta) and E5 (Jimma) shared the same winner genotype G6 (NERICA-4), but G9 (Kokit) and G8 (Pawe-1) were winner at Woreta (E3). This indicated environments within the same sector or at different sectors share the same winning genotypes, and also environments in different sectors have different winning genotypes. Accordingly, E2 (Manbuk) and E6 (Tepi) shared different winning genotypes and G4 (Tana) and G12 (NERICA-13), respectively. Whereas, G3 (Andassa) was the winning genotype in sector five, but no environments included in this sectors. This indicted that the performance of the genotype was poor in all six environments. Meimei *et al.* (2014) reported the same findings by evaluated 165 full-sib families in each five sites, out of them 165, 173 and 103 families were the vertex families but not included in all five sites due to had poorest performance in this environments.

The “which-won-where” function of a GGE biplot is an extended use of the “pair-wise comparison” function described above. A polygon is first drawn on genotypes that are furthest from the biplot origin so that all other genotypes are contained within the polygon. The which-won-where view of the GGE biplot to show which genotypes performed best in which environments. According to Yan and Tinker (2006), the genotypes that are located on the vertices of the polygon performed either the best or the poorest in one or more environments. Yan *et al.* (2000) and Yan *et al.* (2003) reported as the polygon view of GGE biplot is the best way for the identification of winning genotypes with visualizing the interaction patterns between genotypes and environments. The GGE biplot has therefore, been used in crop genotypes trials to effectively identify the best-performing genotype(s) across environments, identify the best

genotypes for specific environments delineation, whereby specific genotypes can be recommended to specific environments and evaluate the yield and stability of genotypes (Yan and Kang, 2003; Yan and Tinker, 2006).

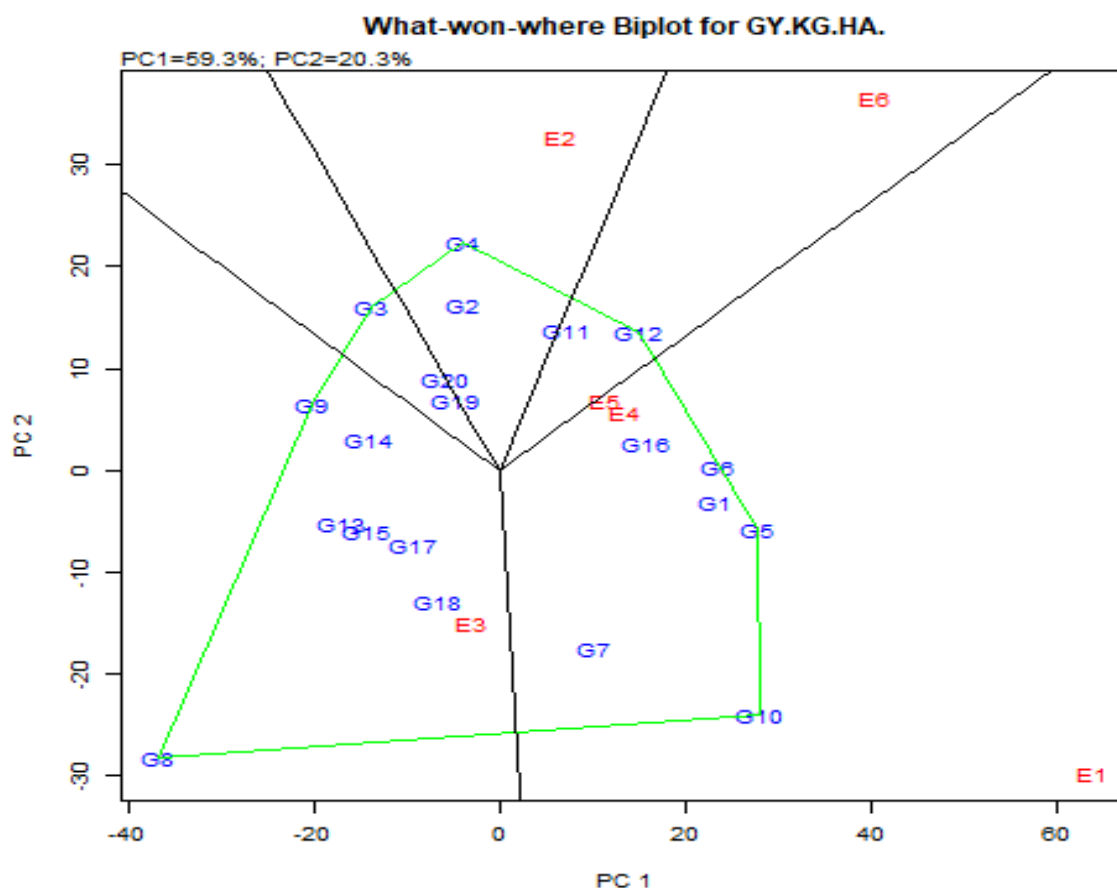


Figure 1. Polygon view of genotype-environment interaction for which-won-where view of the GGE biplot for 20 rice genotypes and six environments.

Note: The G1-G20 is the codes for the 20 rice genotypes in such a way, G1=Hidasse, G2=Getachew, G3=Andassa, G4=Tana, G5=NERICA-3, G6=NERICA-4, G7=Superica-1, G8=Pawe-1, G9=Kokit, G10=Chewaqa, G11=NERICA-12, G12=NERICA-13, G13=NERICA-2, G14=NERICA-14, G15=NERICA-1, G16=ADAT, G17=FOFIFA-4129, G18=FOFIFA-3737, G19=FOFIFA-3730, G20=Fogera-1, and E1-E6 are environment codes, E1=Pawe, E2=Manbuk, E3=Woreta, E4=Maitsebri, E5=Jimma and E6=Tepi.

4.4.3.2. Genotypes relative to an ideal genotype

The direction of arrow showed the ranking of genotypes in increasing order with respect to higher traits performance as indicated on the AEA abscissa. Therefore, genotype NERICA-3 (G5) was the “ideal” genotype and the highest mean grain yield. NERICA-3 is considered the most stable across variable environments. Genotypes closer to the ideal genotype NERICA-4 (G6), Hidasse (G1) and Chewaqa (G10) were also the stable ones, while genotypes Pawe-1 (G8), NERICA-2 (G13) and Kokit (G9) were far from the ideal genotypes. This indicated that those genotypes were unstable.

Genotype ADET (G16), NERICA-12 (G11) and NERICA-13 (G12) were closed to the average environment, indicating that these genotypes were performed best in the average environment like Manbuk and Maitsebri. Genotypes: Pawe-1 (G8), Kokit (G9), NERICA-2 (G13), and FOFIFA-3737 (G18) were far from the ideal genotypes and also had low grain yield among genotypes, whereas, genotype NERICA-3 (G5), Pawe-1 (G8), Hidasse (G1) and Chewaqa (G10) were closer to the ideal genotypes and had high grain yield, respectively. Genotype G5 (NERICA-3) was the only ideal and high yield genotype according to the GGE biplot graph in Figure 2. The genotypes that had long lines from the AEA were considered as unstable genotypes. Therefore, genotypes Chewaqa (G10), Tana (G4), Andassa (G3) and SUPERICA-1 (G7) had long lines which considered as unstable genotypes, whereas, genotypes FOFIFA-3737 (G18), NERICA-2 (G13), FOFIA-4129 (G17) and ADET (G16) had short lines which considered as stable genotypes. Generally, the genotype is more desirable and high yielder if it is located closer to the ideal genotype.

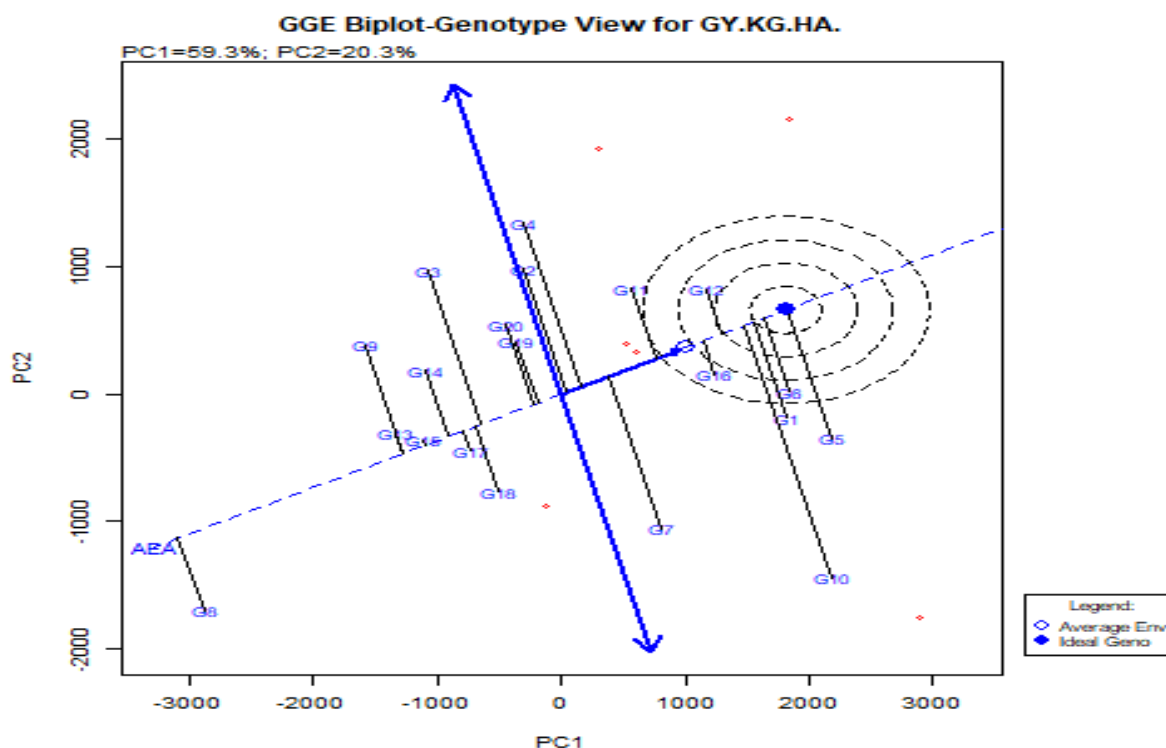


Figure 2. GGE-bi-plot showing the “ideal” genotype for grain yield

Note: G1=Hidasse, G2= Getachew, G3=Andassa, G4=Tana, G5= NERICA-3, G6= NERICA-4, G7= Superica-1, G8=Pawe-1, G9=Kokit, G10=Chewaqa, G11=NERICA-12, G12=NERICA-13, G13= NERICA-2, G14= NERICA-14, G15= NERICA-1, G16= ADAT, G17= FOFIFA-4129, G18= FOFIFA-3737, G19= FOFIFA-3730, G20= Fogera-1, E1=Pawe, E2= Manbuk, E3=Woreta, E4= Maitsebri, E5= Jimma and E6= Tepi

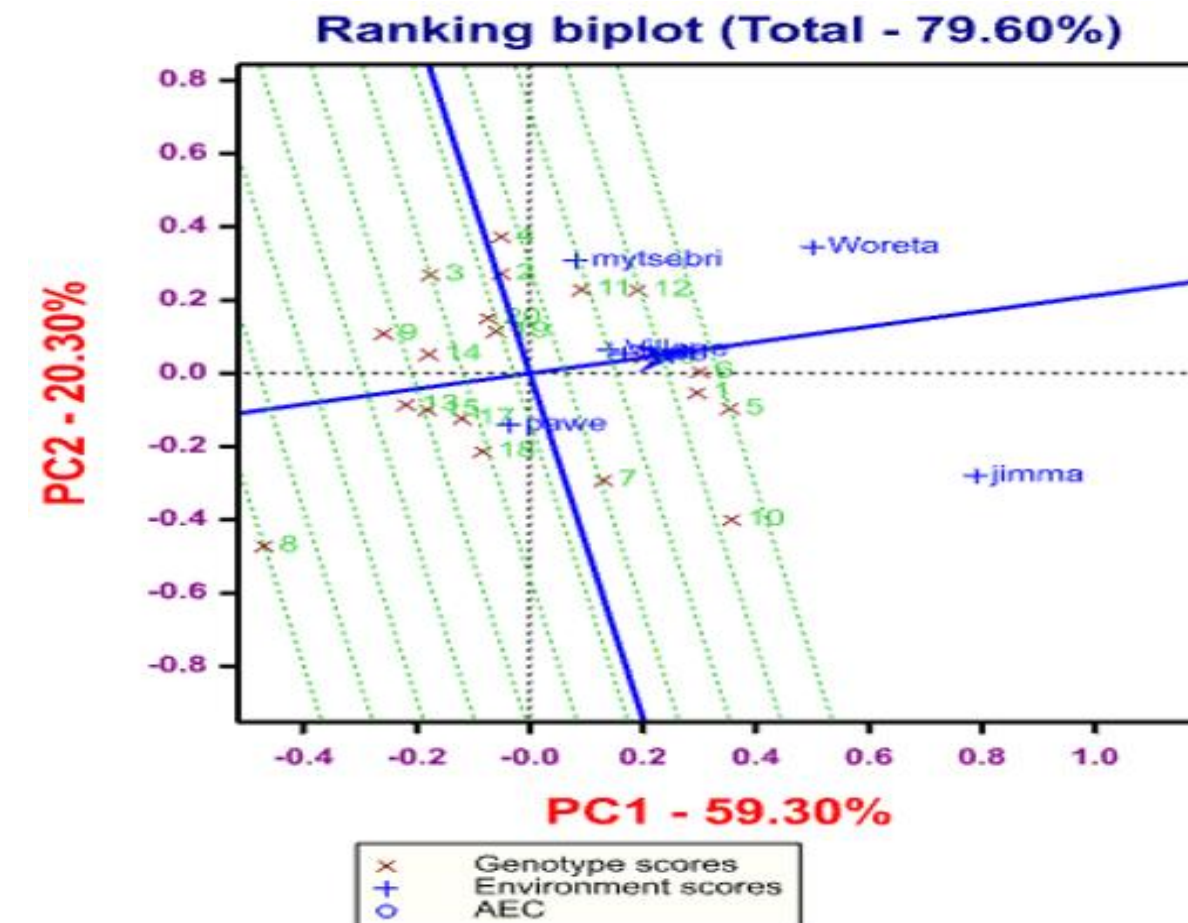


Figure 3. The average-environment coordination (AEC) views to rank genotypes relative to an ideal genotype (the center of the concentric circles).

4.4.3.3. Discriminating ability and representativeness of test environments

The GGE bi-plot environment view for grain yield (Figure 4) indicated that each environment was connected to the bi-plot origin using a vector to determine the discriminating ability of the test environments. Environments with longer vectors are known to be more discriminative of the genotypes than those with short vectors (Yan and Tinker, 2006; Sharma *et al.*, 2013). In this particular study, environments E1 and E6 had the longest environmental vectors, implying that they were most discriminating environments. Whereas, environment E4 and E5 had the shortest environmental vectors, implying that they were least discriminating environments. These environments also closed to the average environment axis, implies that those environments were more favorable or desirable environments for all genotypes. An environment is more desirable when located closer to the center of circle or to an ideal environment (Zerihun, 2011; Oladosu

et al., 2017). Hence, environments E6 and E1 had the longest vector with large IPCA, which near to the concentric circles, and hence, considered as an ideal environment in terms of being the most representative of the environments with the longest environmental vectors, implying their ability to discriminate varieties based on their genotypic performance. Similarly, Yan and Tinker (2006) and Rita *et al.* (2009) reported GGE-biplot classified the environments in to discriminate, lest discriminate and desirable environments based on the genotypes performance.

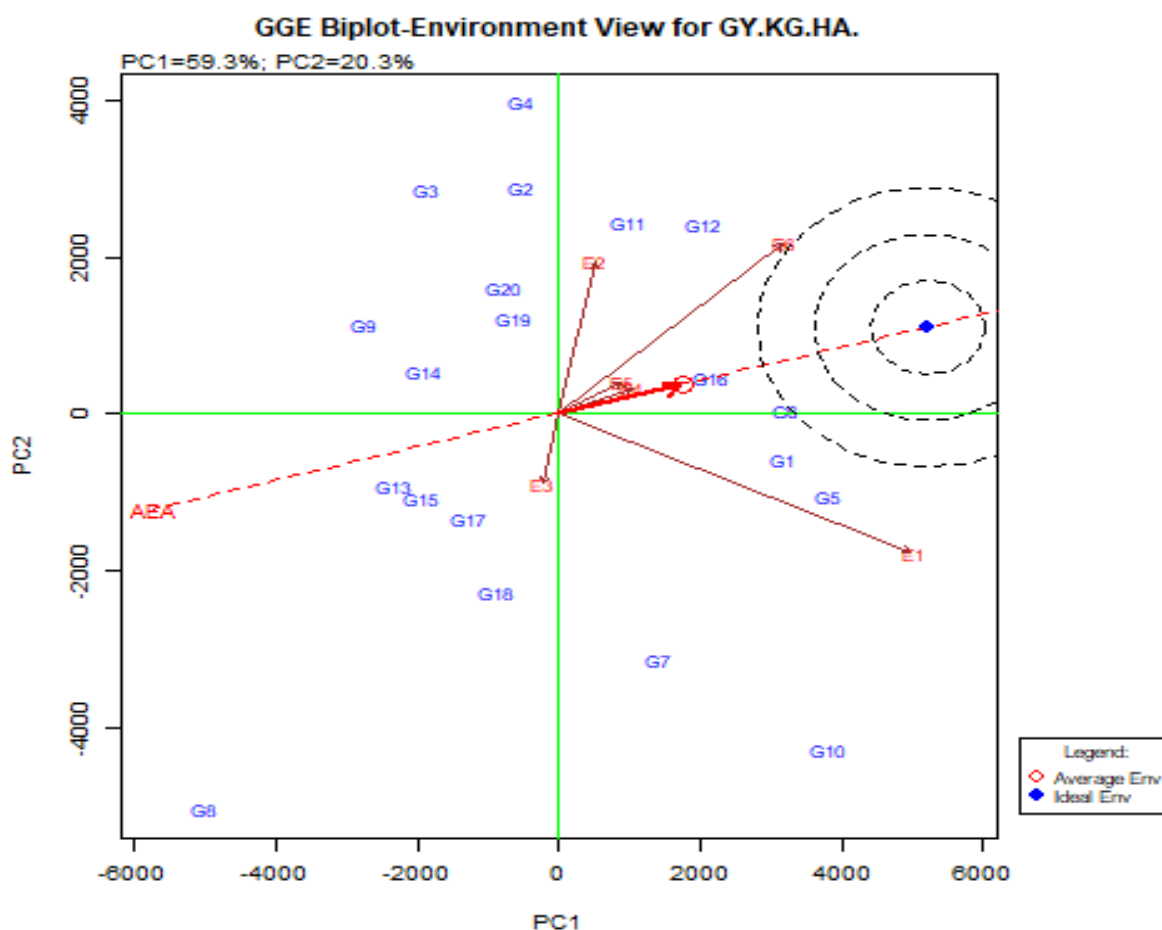


Figure 4. Average environment axis (AEA) in view of GGE bi-plot graph for grain yield.

Note: G1=Hidasse, G2= Getachew, G3=Andassa, G4=Tana, G5= NERICA-3, G6= NERICA-4, G7= Superica-1, G8=Pawe-1, G9=Kokit, G10=Chewaqa, G11=NERICA-12, G12=NERICA-13, G13= NERICA-2, G14= NERICA-14, G15= NERICA-1, G16= ADAT, G17= FOFIFA-4129, G18= FOFIFA-3737, G19= FOFIFA-3730, G20= Fogera-1, E1=Pawe, E2= Manbuk, E3=Woreta, E4= Maitsebri, E5= Jimma and E6= Tepi.

4.4.3.4. Comparison of environments

An environment with a small angle to the average environment axis (AEA) is more representative than other test environments. Being representative is the ability of the environment to allow the genotypes to perform more or less the same as they would do in any other environment in the study. Any two environments can be positively, negatively or not correlated if the angles between their vectors are less than 90° , more than 90° or equal to 90° , respectively (Yan and Tinker, 2006; Vishakha, 2017). In this study, the vector view of the GGE biplot (Figure 5) gives a succinct summary of the correlation among the environments. Thus, all the environments, which are found in the quadrant II were positively correlated to each other as the angle between them was less than 90° (i.e. acute angle), which was also true for environments in quadrant I. In addition to this, E2, E4, E5 and E6 were positively correlated with E1 quadrant III. In the contrary, there were negative correlation between E2 and E1 environments as the angle between them is slightly greater than 90° (i.e. obtuse angle), implying that the GEI moderately large. Similarly, there was a wide obtuse angle (180°) between E2 and E3 environments showing the strong grain yield correlation between the two environments. These indicating that there was a strong crossover of GEI. Zerihun (2011), Sharma *et al.* (2013) and Vishakha, (2017) reported the similar findings.

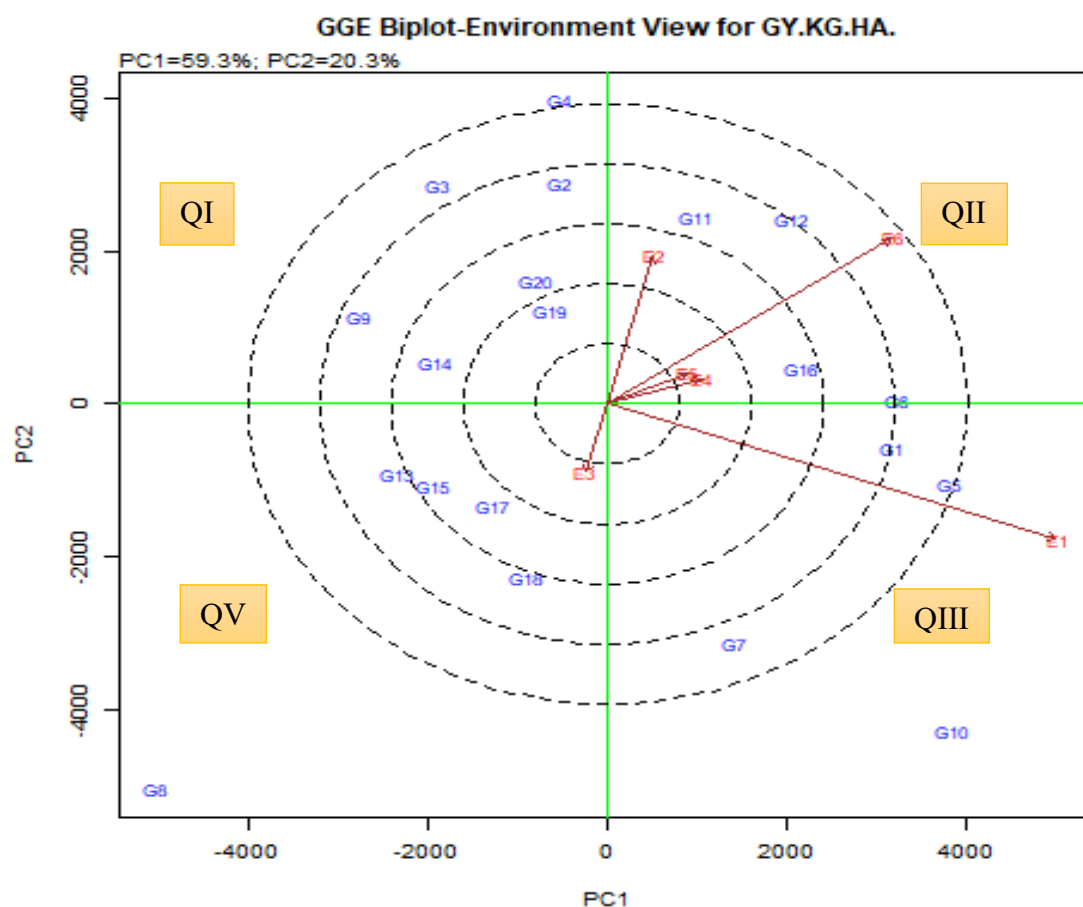


Figure 5. Average genotype axis (AGA) in view of GGE bi-plot graph for grain yield.

Note; G1=Hidasse, G2= Getachew, G3=Andassa, G4=Tana, G5= NERICA-3, G6= NERICA-4, G7= Superica-1, G8=Pawe-1, G9=Kokit, G10=Chewaqa, G11=NERICA-12, G12=NERICA-13, G13= NERICA-2, G14= NERICA-14, G15= NERICA-1, G16= ADAT, G17= FOFIFA-4129, G18= FOFIFA-3737, G19= FOFIFA-3730, G20= Fogera-1, E1=Pawe, E2= Manbuk, E3=Woreta, E4= Maitsebri, E5= Jimma and E6= Tepi.

4.5. Stability Analyses other than ER's AMMI and GGE Biplot Models

4.5.1. Lin and Binns's Cultivar Performance Measure (Pi)

The genotype with lowest Pi value would be the most stable genotypes among the genotypes in a given set of environments. Therefore, according to Lin and Binns, (1988) stability parameter genotypes NERICA-3, Hidasse, ADAT, NERICA-4 and Chewaqa had the lowest cultivar superiority value with high mean grain yield, indicating that these genotypes have wider adaptation. These stable genotypes had least contribution to the total variation of the genotype by environment interaction. While, genotypes Pawe-1, Kokit, NERICA-14, NERICA-2 and Andassa had the highest cultivar superiority value with lower mean grain yield were considered as unstable genotype and their contribution to the total variation due to GEI is high (Table 16). In general, the most productive genotypes tend to be the most stable as well. Different authors such as Aremu *et al.* (2007b); Parmar *et al.* (2016) and Oladosu *et al.* (2017) used this stability parameter to identify high yielding and stable rice genotypes, respectively.

4.5.2. Wricke's Ecovalence (Wi)

Wricke's (1962) defined the concept of ecovalence, to describe the stability of a genotype, as the contribution of each genotype to the genotype x environment interaction sum of squares. The ecovalence (Wi) or the stability of the i^{th} genotype is its interaction with environments, squared and summed across environments. Genotypes with low ecovalence have smaller fluctuations across environments and therefore are stable. Wricke's ecovalence was determined for each of the 20 genotypes evaluated at six locations (Table 16).

The stability of twenty rice genotypes in six environments were evaluated and the result showed that the relative stable genotypes were FOFIFA-3737, FOFIFA-4129 and NERICA-12 that had lowest ecovalence value and ranked 18th, 16th and 7th in mean grain yield performance across the environments, respectively (Table 16). Whereas, genotypes Pawe-1, Chewaqa and NERICA-3 had the highest ecovalence value and ranked 20th, 3rd and 1st in mean grain yield performance across the environment, respectively. These genotypes contribute highest amount of variation to the total genotype by environment interaction variance. Hence, these genotypes can be considered as unstable. In case of genotypes NERICA-3 and Chewaqa, even though, they

had highest yield performance, ranked the 1st and 3rd their highest ecovalence value made them undesirable and they could not be recommended for wider adaptation. This result in line to the previous finding of Oladosu *et al.* (2017) on different rice genotypes.

4.5.3. Shukla's Stability Variance (δ^2i)

According to Shukla (1972) stability analysis indicated (Table 16) the most stable and desirable genotypes were FOFIFA-3737, FOFIFA-4129 and NERICA-12 which had low Shukla's stability variance value and ranked 1th, 2th and 3rd in their yielding performance as compared to other genotypes in the test, respectively. Even though, genotypes NERICA-3 and Chewaqa showed high grain yield performance, their high Shukla's stability variance value made them undesirable for wider adaptation rather recommend for specific adaptation. The most unstable genotypes were NERICA-3, Chewaqa and Pawe-1 which ranked 18th, 19th and 20th of Shukla stability value for grain yield, respectively. World wide a number of researcher have been used this stability parameter to identify high yielding stable genotypes on different types of crop, for example, Oladosu *et al.* (2017) on rice genotypes, Kiliç *et al.* (2010) were used it on wheat genotypes and Farshadfar *et al.* (2013) on chickpea.

Table 16. Cultivar performance measure (P_i), Wricke's ecovalence (W_i) and Shukla's stability variance (δ^2_i) values of the 20 rice genotypes across environments

No	Genotype	Yield (t/ha)	Ranks	P_i	Ranks	W_i	Ranks	δ^2_i	Ranks
1	Hidasse	4.06	2	0.348	2	1.952	12	0.409	12
2	Getachew	3.71	9	1.165	10	1.442	10	0.295	10
3	Andassa	3.33	13	1.687	16	2.016	14	0.425	14
4	Tana	3.55	11	1.299	12	1.961	13	0.413	13
5	NERICA-3	4.07	1	0.326	1	3.264	18	0.702	18
6	NERICA-4	3.93	5	0.416	4	2.837	17	0.604	17
7	SUPERICA-1	3.61	10	0.656	7	1.887	11	0.394	11
8	Pawe-1	2.71	20	3.242	20	8.138	20	1.786	20
9	Kokit	2.77	19	2.429	19	1.13	7	0.226	7
10	Chewaqa	4.05	3	0.423	5	6.013	19	1.316	19
11	NERICA-12	3.80	7	0.734	8	0.685	3	0.127	3
12	NERICA-13	3.89	6	0.541	6	1.411	9	0.290	9
13	NERICA-2	3.26	14	1.746	17	2.157	16	0.453	16
14	NERICA-14	3.08	17	1.811	18	0.687	4	0.128	4
15	NERICA -1	3.18	15	1.669	15	0.956	6	0.188	6
16	ADET	3.96	4	0.367	3	1.284	8	0.260	8
17	FOFIFA-4129	3.10	16	1.518	13	0.594	2	0.108	2
18	FOFIFA-3737	3.00	18	1.557	14	0.519	1	0.092	1
19	FOFIFA-3730	3.39	12	1.238	11	0.832	5	0.160	5
20	Fogera-1	3.73	8	1.078	9	2.045	15	0.430	15

4.5.4. Francis and Kannenberg's Coefficient of Variability

The mean CV analysis introduced by Francis and Kannenberg (1978) was designed to aid in studies on the physiological basis of yield stability. They introduced a simple graphical approach to assess performance and stability concurrently. It measures the performance and CV for each genotype over all environments and the mean yield plotted against the CV. It was found to characterize genotypes in groups rather than individually (Francis and Kannenberg, 1978).

The stable genotype is the one that provides a high yield performance and consistent low CV. Therefore, genotypes ADET (G16), NERICA-12 (G11) and SUPERICA-1 (G7) which recorded higher mean grain yield and lower coefficient of variation can be considered as the second group of choice. Genotypes Hidasse (G1) and Chewaqa (G10) were fallen in the high grain yield mean performance while their high coefficient of variation could made them undesirable genotypes (Figure 6).

In other way round, genotypes SUPERICA-1 (G7) recorded very low coefficient of variation but due to their low yielding performance, they grouped in to undesirable genotypes. The most unstable genotype with low yield and high coefficient of variation (CV) were Pawe-1 (G8) and Kokit (G9) as shown in Figure 6. By using coefficient of variability as stability parameter, globally several stability works have been done to know the homeostasis or buffering ability of rice genotypes (Kadhem *et al.*, 2010; Das *et al.*, 2010).

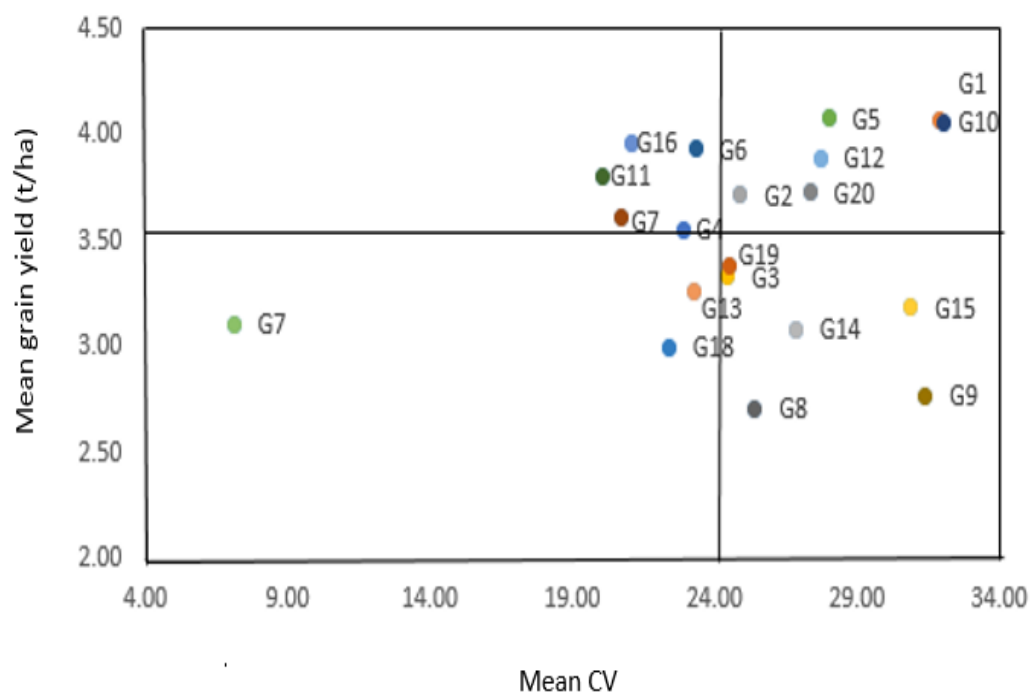


Figure 6. Coefficient of variability plotted against mean grain yield (t/ha) of tested genotypes.

Note: G1= Hidasse, G2= Getachew, G3= Andassa, G4= Tana, G5= NERICA-3, G6= NERICA-4, G7= SUPERICA-1, G8= Pawe-1, G9= Kokit, G10= Chewaqa, G11= NERICA-12, G12= NERICA-13, G13= NERICA-2, G14= NERICA-14, G15= NERICA -1, G16= ADET, G17= FOFIFA-4129, G18= FOFIFA-3737, G19= FOFIFA-3730, G20= Fogera-1

4.5.5. Finlay and Wilkinson's Joint Regression Analysis (bi)

According to Finlay and Wilkinson's (1963) regression model the genotype sensitivity estimate for grain yield was shown in Table 13. Genotypes Andassa, Tana, Getachew, Fogera-1 (standard check) and Kokit were observed the highest genotype sensitivity, whereas, genotype Chewaqa and NERICA-3 and SUPERICA-1 were observed the lowest genotype sensitivity across environment. Based on the result, genotype Andassa and Tana were ranked the first and the second from the most stable genotypes across the environment. This indicated that those genotypes more stable or the response of the genotypes for those environment were similar. This result concurred with the finding of Bose *et al.* (2012), Mulugeta *et al.* (2016), Tadesse *et al.* (2017), Oladosu *et al.* (2017) and Girma (2018). In the contrast, genotype Chewaqa was recorded the lowest one that means this genotypes responded differently across environment. This implies that genotype Chewaqa and NERICA-3 were adapted for specific environment (not stable across environments).

4.5.6. Nassar and Huehn's Mean Absolute Rank Difference and Variance of Ranks

According to Nassar and Huhn's (1987) non-parametric stability measure for grain yield of 20 rice genotypes evaluated under six different environments in Ethiopia is indicated on (Table 17). According to this stability procedure, genotypes Hidasse, ADAT, NERICA-12 and Getachew that had low estimates of Si^1 and Si^2 with higher grain yield performance were considered as the most desirable and stable genotypes, whereas Kokit, NERICA-14 and Andassa were stable but undesirable genotypes because of their low yield performance (lower than mean grain yield) in both mean absolute rank difference and variance of ranks. This result indicated that as there were potential to adapt across environments. This implies that these four genotypes (Hidasse, ADAT, NERICA-12 and Getachew) could recommended for all six environments based on this stability measures, whereas those genotypes did not show stability across environment could be recommend for specific environment. In the previous time, different authors reported similar results on different rice genotypes (Huehn, 1990; Akcura and Kaya, 2008; Mohammad *et al.*, 2010; Mut *et al.*, 2010).

Table 17. Mean absolute rank difference (Si^1) and variance of ranks (Si^2)

No.	Genotype	Yield (t/ha)	Rank	Si^1	Rank	Si^2	Rank
1	Hidasse	4.06	2	4.40	3	15.07	5
2	Getachew	3.71	9	4.733	5	14.97	4
3	Andassa	3.33	13	5.20	8	18.67	7
4	Tana	3.55	11	6.333	14	29.37	15
5	NERICA-3	4.07	1	6.467	16	30.97	17
6	NERICA-4	3.93	5	6.867	19	31.77	18
7	SUPERICA-1	3.61	10	6.20	13	25.37	11
8	Pawe-1	2.71	20	6.667	18	46.67	20
9	Kokit	2.77	19	2.533	1	4.27	1
10	Chewaqa	4.05	3	6.60	17	30.3	16
11	NERICA-12	3.80	7	4.733	6	15.77	6
12	NERICA-13	3.89	6	6.067	12	27.1	13
13	NERICA-2	3.26	14	7.20	20	34.4	19
14	NERICA-14	3.08	17	4.60	4	14.3	3
15	NERICA -1	3.18	15	6.00	11	25.2	10
16	ADET	3.96	4	4.333	2	13.37	2
17	FOFIFA-4129	3.10	16	5.867	9	23.2	9
18	FOFIFA-3737	3.00	18	4.933	7	19.07	8
19	FOFIFA-3730	3.39	12	6.40	15	26.8	12
20	Fogera-1(check)	3.73	8	5.867	10	27.47	14

4.6. Superman's Rank Correlation Coefficient for Stability Measures

Superman rank correlations were computed for genotypes ranking against their stability measures for all evaluated trait means. The values of Superman's correlation coefficient for all stability parameters including grain yield were presented in Table 19. The univariate stability parameters measures included coefficient of variation (Francis and Kannenberg, 1978), ecovalence (Wricke, 1962), stability variance (Shukla, 1972), deviation from regression (Eberhart and Russell, 1966), mean absolute rank difference (Si^1) and variance of rank (Nassar and Huhn, 1987) and AMMI stability value (Eberhart and Russell, 1966). In this study, trait mean was positively and highly significant correlated (Spearman) with only Shukla stability variance and ecovalence for all stability parameters evaluated except Finlay and Wilkinson's Joint Regression Analysis (bi) (Table 13). Bose *et al.* (2014) reported that statistical stability parameters provides information that cannot be quantified from the traits means. The value of ecovalence was significantly ($P < 0.001$) and positively correlated with Shukla stability variance for all stability parameters except regression slope shown non-significant correlation (Table 19),

these however, suggest that Wricke covalence and Shukla stability variance measured the same thing (Fentaw, 2011). Also, Wricke covalence was perfect positive correlation with Shukla stability variance. This indicated that these two stability models had the same stability measures and could be used one.

Based on univariate and multivariate stability parameters, rice genotypes were classified into three main categories. First group were genotypes having high stability along with high yield per hectare. These genotypes include ADET and NERICA-12 and are widely adapted to diverse environment conditions. The second group were genotypes that exhibited high yield per hectare but low stability, these genotypes NERICA-3 and Chewaqa were suitable for specific environments, Jimma and Pawe. The last group is genotypes with low yield per hectare and high stability which includes genotypes FOFIFA-4129 and FOFIFA-3737. The last genotypes group is more stable for breeding specific traits or perhaps has yield component compensation. The performance of these genotypes in comparison to the nationally recommended variety Fogera-1 indicates the importance of specific adaptation. However, the highest performing genotypes for yield per hectare were not the highest for all yield component traits. Therefore, there is room for further improvement because yield is a complex trait which is controlled by many traits such as tillers per plant, filled grains per panicle, grain weight per panicle. In general, breeding for stability of performance under variable conditions is a complex and difficult task because yield and yield components are greatly influenced by different factors such as environment which has a directly or indirectly effect. Therefore, evaluation of genotypes under different environments and adoption of simultaneous selection for yield and stability is a reliable selection criterion for any breeding program.

Table 18. The Superman's rank correlation coefficient for all stability measures including grain yield

	Yield	CV	P _i	W _i	δ^2_i	b _i	S ² di	Si ¹	Si ²	ASV
Yield	1									
CV	0.188 ^{ns}	1								
P _i	-0.952 ^{**}	-0.068 ^{ns}	1							
W _i	0.367 [*]	0.37 [*]	-0.217 ^{ns}	1						
δ^2_i	0.367 [*]	0.37 [*]	-0.217 ^{ns}	1 ^{**}	1					
b _i	0.528 ^{**}	0.064 ^{ns}	-0.684 ^{**}	0.083 ^{ns}	0.083 ^{ns}	1				
S ² di	0.382 [*]	0.308 [*]	-0.32 [*]	0.755 ^{**}	0.755 ^{**}	0.326 [*]	1			
Si ¹	0.083 ^{ns}	-0.008 ^{ns}	-0.045 ^{ns}	0.617 ^{**}	0.617 ^{**}	0.227 ^{ns}	0.644 ^{**}	1		
Si ²	0.12 ^{ns}	0.054 ^{ns}	-0.078 ^{ns}	0.684 ^{**}	0.684 ^{**}	0.197 ^{ns}	0.725 ^{**}	0.959 ^{**}	1	
ASV	0.313 [*]	0.418 ^{**}	-0.182 ^{ns}	0.962 ^{**}	0.962 ^{**}	0.149 ^{ns}	0.705 ^{**}	0.571 ^{**}	0.623 ^{**}	1

*, and **, significant at P<0.05, P<0.01 and P<0.001 respectively, ns= non-significant, CV= coefficient of variation, Pi=Cultivar performance measure, W_i= Wricke's ecovalence, δ^2_i =Shukla's stability variance, b_i= Finlay and Wilkinson's (1963) regression coefficient, S²di=deviation from regression, Si¹=mean absolute rank difference, Si²= rank of variance, ASV= AMMI stability value

4.7. Comparison of Stability Measures

Different parametric and non-parametric stability measures as well as grain yield were compared for stability ranking of the genotypes (Table 18). Even though, there was change in ranking order of genotypes from one stability parameter to another parameter, genotypes NERICA-12, FOFIFA-3737, ADET and FOFIFA-4129 had been the most stable genotypes by most of stability parameters, namely coefficient of variation (Francis and Kannenberg, 1978), ecovalence (Wricke, 1962), stability variance (Shukla, 1972), deviation from regression (Eberhart and Russell, 1966), mean absolute rank difference (Si^1) and variance of rank (Nassar and Huhn, 1987) and AMMI stability value (Eberhart and Russell, 1966). Such genotypes have better buffering capacity to environmental changes such as occurrence of disease, insect pests and adaptation across environments (Becker and Leon, 1988). This indicated that these genotypes had potential to adapt to multi-environment better than others. In contrast, genotypes Pawe-1, Chewaqa, NERICA-3, NERICA-4 and NERICA-2 had showed most unstable genotypes by most stability parameters of ecovalence (Wi), Shukla's stability variance (δ^2i), deviation from regression (S^2di), mean absolute rank difference (Si^1) and variance of rank (Si^2) and AMMI stability value (ASV). This indicated that these genotypes mostly adapted to specific environment.

Francis and Kannenberg's coefficient of variability (CV_i) showed a positive non-significant correlation with grain yield and negative non-significant correlation with cultivar superiority performance and mean absolute rank difference (Si^1), whereas it had a highly positive significant correlation ($r=0.72^{**}$) with mean square deviation. But it had positive non-significant correlation with Finlay and Wilkinson's regression coefficient (bi) and variance of ranks (Si^2).

Lin and Binns's (P_i) method showed a highly significant negative rank correlation ($r = -0.95^{**}$) with mean grain yield. This indicates that high yielding and responsive genotypes like, NERICA-3, Hidasse, Chewaqa and ADET tended to have lower P_i value, which is in harmony with the work of Kiliç *et al.* (2010) on wheat and Oladosu *et al.* (2017) on rice genotypes. Besides, the presence of this significant negative rank correlation between mean grain yield and cultivar superiority measure (P_i) indicates that neither of these parameters alone could be sufficient for rice genotype stability assessment and recommendation.

This result seems to have similar idea with the definition of Lin and Binns (1988), they define cultivar superiority measure as the deviation of a specific genotype's performance from the performance of the best genotype in a trial (a stable genotype is one that performs in tandem with the environment). This procedure appears to be considerably more of a genotype performance measure, rather than a stability measure over sites.

The Wricke's ecovalence had a positive perfect rank correlation ($r=1.00$) with Shukla's stability variance and highly significant positive rank correlation ($r= 0.96$) with ASV. It had highly significant positive correlation with deviation from regression (S^2di), mean absolute rank difference (Si^1) and variance of ranks (Si^2). It had also positive non-significant rank correlation with Finlay and Wilkinson's regression coefficient (bi) as shown in Table (19). The presence of positive but non-significant rank correlation between W_i and b_i indicates that the regression coefficient (bi) was non-significantly the same from unity. Conversely, ecovalence had negative rank correlation with cultivar superiority performance (P_i), and a positive significant rank correlations with grain yield and coefficient of variability (CV_i).

Shukla's stability variance had a highly significant positive rank correlation with deviation from regression, mean absolute rank difference (Si^1), variance of ranks (Si^2) and ASV. These correlation rank had the same value and rank with stability measure of Wricke's ecovalence. The occurrence of perfect significant correlation between Shukla's stability variance and Wricke's ecovalence indicates that these two parameters were equivalent for genotype ranking purposes. In line with this result Kiliç *et al.* (2010) and Fentaw, (2011) reported the ranking equivalency of these two stability measurements in wheat genotypes. Conversely, Shukla's stability variance had non-significant negative rank correlation with cultivar superiority measure and significant positive correlation with gran yield and coefficient of variability (CV_i) (Table 19).

Finlay and Wilkinson's regression coefficient (bi) had a positive significant rank correlation with deviation from regression (S^2di), whereas the rest stability measures showed a positive non-significant rank correlation with mean absolute rank difference (Si^1), variance of ranks (Si^2) and AMMI stability value (ASV). In other way round, it had showed a negative highly significant rank correlation ($r=-0.684^{**}$) with cultivar superiority performance and a positive significant rank correlations with grain yield. While it had a positive but non-significant rank

correlation with coefficient of variation and Wricke's ecovalence. This result disagree with the finding of Tadesse *et al.* (2017).

Deviation from regression (S^2_{di}) showed a highly significant positive rank correlation ($r=0.65^{**}$) with AMMI stability value (ASV) and also had a significant positive rank correlation with mean absolute rank difference (Si^1) and variance of ranks (Si^2). Conversely, deviation from regression showed a negative significant rank correlation with cultivar superiority performance and positive significant rank correlation with grain yield, coefficient of variation, Wricke's ecovalence, Shukla's stability variance and Finlay and Wilkinson's regression coefficient (bi) were showed.

Nassar and Huehn's mean absolute rank difference (Si^1) and variance of ranks (Si^2) showed a highly significant positive rank correlation with each other. In line with this finding, highly significant positive rank correlation among the above two non-parametric approaches was reported on wheat genotypes by different authors (Huehn, 1990; Akcura and Kaya, 2008; Mohammad *et al.*, 2010; Mut *et al.*, 2010). These two non-parametric approaches also had non-significant positive rank correlation with grain yield and Finlay and Wilkinson's regression coefficient (bi), whereas it had a negative non-significant rank correlation with cultivar superiority performance (Pi). Both mean absolute rank difference (Si^1) and variance of ranks (Si^2) showed similar correlation trends with different stability measures. This confirms that the similarity of mean absolute rank difference (Si^1) and variance of ranks (Si^2). Consequently, only one of these stability measures would be enough to identify stable genotypes in a rice breeding program.

Spearman's rank correlation coefficient (Steel and Torrie, 1980) was also determined for each of the possible pair wise comparisons of the ranks of the different stability measures. The result of spearman's rank correlation coefficient (Table 19) showed a negative highly significant rank correlation ($r= -0.952^{**}$) between grain yield and cultivar superiority measure. Similarly, Kiliç *et al.* (2010) and Mohammadi and Amri (2008) were reported that the presence of negative highly significant correlation among yield and cultivar superiority performance (Pi) stability measure on rice genotypes. Grain yield also had a significant positive rank correlations with Wricke's ecovalence, Shukla's stability variance (δ^2_i), Finlay and Wilkinson regression

coefficient (b_i), deviation from regression (S^2_{di}) and AMMI stability value, whereas grain yield had positive but non-significant rank correlation with mean absolute rank difference (Si^1), variance of ranks (Si^2) and coefficient of variation (CV). Previous findings of Oladosu *et al.* (2017) on rice varieties and Fentaw (2011) on wheat genotypes reported similar results.

Table 19. Ranks of 20 rice genotypes based on different stability parameters

Genotype	Yield	R	CV	R	Pi	R	Wi	R	δ^2_i	R	bi	R	S ² di	R	Si ¹	R	Si ²	R	ASV	R
Hidasse	4.06	2	31.91	18	0.348	2	1.952	12	0.409	12	1.756	16	0.227	15	4.4	3	15.07	5	1.124	14
Getachew	3.71	9	24.91	11	1.165	10	1.442	10	0.295	10	-0.245	3	-0.067	4	4.73	5	14.97	4	0.964	10
Andassa	3.33	13	24.47	9	1.687	16	2.016	14	0.425	14	-0.412	2	0.003	9	5.2	8	18.67	7	1.197	16
Tana	3.55	11	22.89	6	1.299	12	1.961	13	0.413	13	-0.468	1	-0.038	6	6.33	14	29.37	15	1.023	11
NERICA-3	4.07	1	27.99	16	0.326	1	3.264	18	0.702	18	2.133	18	0.436	18	6.47	16	30.97	17	1.536	18
NERICA-4	3.93	5	23.32	8	0.416	4	2.837	17	0.604	17	1.679	15	0.467	19	6.87	19	31.77	18	1.411	17
SUPERICA-1	3.61	10	20.72	3	0.656	7	1.887	11	0.394	11	2.395	19	-0.024	7	6.2	13	25.37	11	1.095	13
Pawe-1	2.71	20	25.43	12	3.242	20	8.138	20	1.786	20	1.843	17	1.753	20	6.67	18	46.67	20	2.97	20
Kokit	2.77	19	31.42	19	2.429	19	1.13	7	0.226	7	-0.136	4	-0.100	1	2.53	1	4.27	1	0.64	7
Chewaqa	4.05	3	32.01	20	0.423	5	6.013	19	1.316	19	3.596	20	0.196	14	6.6	17	30.3	16	2.126	19
NERICA-12	3.80	7	20.08	2	0.734	8	0.685	3	0.127	3	0.226	5	-0.093	2	4.73	6	15.77	6	0.157	2
NERICA-13	3.89	6	27.69	15	0.541	6	1.411	9	0.290	9	0.624	8	0.167	13	6.07	12	27.1	13	0.751	9
NERICA-2	3.26	14	23.29	7	1.746	17	2.157	16	0.453	16	0.640	9	0.354	17	7.2	20	34.4	19	1.176	15
NERICA-14	3.08	17	26.86	13	1.811	18	0.687	4	0.128	4	0.367	7	-0.059	5	4.6	4	14.3	3	0.501	5
NERICA -1	3.18	15	30.89	17	1.669	15	0.956	6	0.188	6	0.845	11	0.073	11	6.0	11	25.2	10	0.682	8
ADET	3.96	4	21.09	4	0.367	3	1.284	8	0.260	8	1.562	14	0.104	12	4.33	2	13.37	2	0.537	6
FOFIFA-4129	3.10	16	7.11	1	1.518	13	0.594	2	0.108	2	1.0405	12	-0.014	8	5.87	9	23.2	9	0.036	1
FOFIFA-3737	3.00	18	22.40	5	1.557	14	0.519	1	0.092	1	1.5236	13	-0.078	3	4.93	7	19.07	8	0.498	4
FOFIFA-3730	3.39	12	24.48	10	1.238	11	0.832	5	0.160	5	0.7022	10	0.030	10	6.4	15	26.8	12	0.311	3
Fogera-1	3.73	8	27.34	14	1.078	9	2.045	15	0.430	15	0.3281	6	0.272	16	5.87	10	27.47	14	1.042	12

Where, CV= coefficient of variation, Pi=Cultivar performance measure, Wi= Wricke's ecovalence, δ^2_i =Shukla's stability variance, bi= Finlay and Wilkinson's (1963) regression coefficient, Sdi²=deviation from regression, Si¹=mean absolute rank difference, Si²= rank of variance, ASV= AMMI stability value, R= rank

5. SUMMARY AND CONCLUSIONS

The Government of Ethiopia has developed national strategy for rice research understanding the role of the crop for food security. The crop is cultivated in most of the regional states in Ethiopia. Since, the mid-1990s, considerable number of upland rice varieties has been recommended for production in regions where rain-fed rice is cultivated in Ethiopia. The recommendation of varieties and introduction of new genotypes alone might not be important to increase the yield of rice in the country rather the distribution and availability of varieties in rice growing areas is important. This required conducting a multi-location evaluation of genotypes and identifying genotypes of wide adaptable or adaptable to specific area which is one of the critical steps in breeding. This research was conducted with objectives of estimating the magnitude of environmental and genotype x environment interaction (GEI) effects on yield and yield related traits, stability of the rice varieties for yield under diverse agro ecologies and evaluating and stratifying of rice testing environments in Ethiopia. Twenty rice varieties were tested at six different sites (Pawe, Manbuk, Woreta, Maitsebri, Jimma and Tepi) during 2016/17 cropping season in experiment laid out in randomized complete block design with three replications. Data for crop phenology, growth traits, yield components and yield were collected and subjected to various data analysis methods.

The data collected for crop phenology, growth traits, yield components and yield were subjected to analysis of variance for each environment. The results from each location analysis of variance showed that the genotypes had significant differences for all traits except for stand count at harvest. Prior conducting combined analysis of variance, the count data (days to heading and days to maturity, number of fertile tillers per plant, number of unfertile tillers per plant, number of filled grain per panicle and number of unfilled grain per panicle) square root transformed, percentage data (harvest index) subjected to arcsine transformation and measured data (panicle length, plant height, biological yield biological yield, thousand grain weight and grain yield) log transformed. The combined analysis of variance over environments showed that the presence of significant differences among genotypes (G), environments (E) and significant effect of GEI on all phenology, growth, yield components and grain yield. Thus the data were further subjected to GEI analyses of Eberhart and Russell's (ER's), and Additive Main effects and Multiplicative

Interaction Model (AMMI) models as well as Genotype and Genotype x Environment (GGE) biplot. The stability of genotypes for yield was evaluated by stability parameters from ER's, AMMI, GGE biplot, Francis and Kannenberg's coefficient of variability (CV), Lin and Binns's cultivar performance measure (Pi), Shukla's stability variance (δ^2_i), Wricke's ecovalence (Wi), Finlay and Wilkinson's (bi), Nassar and Huehn's mean Absolute rank difference (Si^1) and variance of ranks (Si^2).

The partitioning of sources of variation from AMMI model analysis of variance showed that the contribution of genotypes (G), environments (E) and genotype x environment interaction (GEI) for crop phenology, growth and yield component were in the range between 3.03 and 33.58, 25.69 and 72.02 and 7.09 and 17.26 % respectively. The contribution of E was higher than G and GEI for total variations of all phenology, growth and yield component except days to heading that the contribution of G was greater than E and GEI. The contribution of GEI was also higher than G for total variations of all phenology, growth and yield component except days to heading, panicle length and plant height. The interaction principal component axis one (IPC1) and two (IPC2) were significant and IPC1 and IPC2 contributed 37.94 to 88.85 and 8.92 to 87.13% to sum squares of GEI, respectively. This indicated that the environment and the GEI had a higher contribution than genetic factors to the observed variations among genotypes for phenology, growth and yield components. The contribution of G, E and GEI to the total sum square of yield was 15.12, 9.94 and 30.36 %, respectively. The IPC1 and IPC2 mean squares were significant and IPC1 and IPC2 contributed 55.12 and 28.4 % to the total sum squares of GEI, respectively. This suggested that the yield of genotype(s) vary across environments.

The three high yielding varieties, NERICA-3 released in 2006, Hidasse released in 2012 and Chewaqa released in 2013 had 15.99, 15.7 and 15.42% higher yield, respectively, than average yield of genotypes and identify as responsive to changing environments. Fogera-1 released in 2015 and used as check variety had 6.27% higher yield over the average yield of genotypes. NERICA-3 and Hidasse were selected as the first four best genotypes at Tepi (most favorable environment) and Jimma and Woreta (most unfavorable environments), besides Hidasse was identified one of the first four best genotypes at Manbuk (average environment), and Chewaqa selected as the first four best genotypes at Pawe (favorable environment) and at Jimma

(unfavorable environment). Fogera-1 was identified one of the first four best genotypes at Manbuk, Pawe, Maitsebri and Tepi. Therefore, these varieties could be recommended for production across environments and most preferably for environments the varieties produced high yield.

The two varieties, NERICA-12 released in 2013 and ADET released in 2014 had 12.85 and 8.29% higher yield, respectively, than average yield of genotypes and identify as most stable by most of the stability parameters and considered as wide adaptable varieties. The three, varieties, NERICA-4 released in 2006, NERICA-13 released in 2014 and Getachew released in 2007 had 11.97, 10.83 and 5.7% yield advantages over the average yield of genotypes at six environments, respectively. NERICA-4 and NERICA-13 selected among the first four best genotypes at Woreta, besides NERICA-4 was one of the four best genotypes at Jimma and identified as stable by GGE biplot. Getachew variety was selected as one of the first four best genotypes at Maitsebri and Manbuk both that were considered as average environments. These varieties could be recommended for average to poor environments.

The genotypes had delayed days to heading and maturity at Pawe and Tepi, and the genotypes had significantly highest mean performances for biological yield, number of filled grain per panicle and number of fertile tillers per plant. At Tepi, the genotypes had also mean number of fertile tillers per plant as equal as at Pawe and the genotypes also had highest mean performance at Tepi for thousand grain weight. The genotypes had significantly early maturity at Manbuk, and at this location had significantly highest mean performance for number of unfilled grain per panicle. The mean performance of genotypes for panicle length was significantly highest at Jimma. Moreover, the genotypes had highest mean grain yield at Jimma, and at Pawe and Manbuk the genotypes mean yield was above the average yield of six environments while the mean yield of genotypes at Tepi, Maitsebri and Woreta was lower than the average yield of six environments. The GGE biplot identified Pawe and Tepi as most discriminating environments, Manbuk and Maitsebri identified as average environments and Woreta as representative environments.

Superman's rank correlation coefficient for nine stability measures and grain yield showed that P_i from Lin and Binns's cultivar performance measure with yield and b_i showed a negative and

significant rank correlation while ASV from AMMI model had positive significant rank correlation with yield, CV, W_i , δ^2_i , S^2_{di} , Si^2 , and S^2_{di} . δ^2_i with W_i had perfect positive significant correlation, Shukla's stability variance (δ^2_i) and W_i with S^2_{di} , Si^1 and Si^2 showed positive significant rank correlation. Thus S^2_{di} and ASV stability parameters from Eberhart and Russell's and AMMI models, respectively, were better parameters to evaluate the stability of genotypes for yield since the parameters showed positive and significant rank correlation with most of the parameters and yield.

The research generated information to be implemented as to the preferences of users, however, it could be concluded, i) the importance of varieties evaluation over diverse environments was verified from the larger contribution of GEI than genotype (genetic factor) to the observed variations among varieties for yield components and yield, ii) NERICA-3, Hidasse and Chewaqa could be used for production across environments because these were high yielding varieties, identified as first four best genotypes in poor, favorable and unfavorable environments and GGE biplot considered as stable genotypes, ii) Pawe and Tepi sites could be used for multi-location test as discriminating environments, and the identified representative environment, Woreta site could be used to evaluate large number of genotypes during first stages of breeding, and iii) The stability parameters from Eberhart and Russell's and AMMI models could be considered as sufficient to evaluate the stability of genotypes for yield. However, it is recommended to conduct the experiment over seasons, because a one season data is not sufficient for recommendation of varieties, testing sites, and stability parameters that the larger contribution of GEI to the variations of varieties for yield components and yield make difficult and complicated the decision to be made.

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7. APPENDICES

Appendix Table 1. Analysis of variance for grain yield and yield related traits of 20 upland rice genotypes evaluated at six locations, during 2016/2017 cropping season in Ethiopia

Location	Source of variation	DH	DM	PL (cm)	PH (cm)	NFTPP	NUFTPP	NFGPP
Pawe	Replication (2)	19.32	110.52	3.00	377.58	4.11	0.002	77.97
	Genotype (19)	46.37**	39.31**	2.71 ^{NS}	107.44 ^{NS}	7.33*	0.482**	113.74*
	Residual (38)	11.19	8.34	3.40	100.76	3.73	0.013	57.75
Manbuk	Replication (2)	13.4	6.72	0.03	17.72	5.68	0.0001	330.43
	Genotype (19)	39.82**	36.45**	2.35**	317.88**	4.23 ^{NS}	0.116**	173.18 ^{NS}
	Residual (38)	6.52	8.70	0.78	60.14	2.43	0.008	134.62
Woreta	Replication (2)	1.05	11.47	6.58	431.33	4.02	0.009	461.24
	Genotype (19)	427.27**	1042.38**	4.76**	185.11**	0.84 ^{NS}	0.179**	140.96**
	Residual (38)	2.56	9.17	0.81	13.36	0.57	0.004	37.16
Maitsebri	Replication (2)	37.72	21.65	9.55	20.09	0.28	0.011	111.62
	Genotype (19)	103.69**	16.28 ^{NS}	8.46**	373.18**	1.27**	0.111**	85.85*
	Residual (38)	12.77	8.95	0.95	17.94	0.44	0.005	43.71
Jimma	Replication (2)	872.27	3.02	6.39	53.31	15.16	0.043	185.5
	Genotype (19)	211.03**	151.12**	2.57**	320.81**	6.66 ^{NS}	1.316**	363.24*
	Residual (38)	65.07	0.82	0.94	34.42	4.79	0.025	167.98
Tepi	Replication (2)	750.07	134.21	1.76	118.58	169.62	0.008	11128.02
	Genotype (19)	111.89**	50.24**	2.75*	334.13**	12.69 ^{NS}	1.93**	525.99**
	Residual (38)	29.75	6.6	1.22	33.91	7.98	0.006	238.31
F-ratio		25.42	11.18	4.36	7.54	18.14	6.25	6.41

Ns, * and **, non-significant, significant at $P < 0.05$ and $P < 0.01$, respectively. Number in parenthesis represent degree of freedom for the respective source of variation, and F-ratio= the ratio of highest to lowest error mean squares. DH= days to heading, DM= days to maturity, PL= panicle length (cm), PH= plant height (cm), NFTPP= number of fertile tillers per plant, NUFTPP= number of unfertile tillers per plant, NFGPP= number of filled grain per panicle, NUFGPP= number of unfilled grain per panicle, F-ratio= ratio for larger to smaller error mean square

Appendix Table 1. Continued

Location	Source of variation	NUFGPP	SC	HI	BIO (kg/ha)	TSW (g)	GY(kg/ha)
Pawe	Replication (2)	38.64	786.07	0.002	1634375	2.62	120902.68
	Genotype (19)	10.58**	194.99 ^{NS}	0.02**	19605866.2**	20.91**	824340.8**
	Residual (38)	3.00	282.08	0.003	2517050.4	2.42	338339.91
Manbuk	Replication (2)	11.83	5357.6	0.01	1746875	0.50	230747.89
	Genotype (19)	4.2 ^{NS}	165.80 ^{NS}	0.004**	7850657.9*	16.73**	459063.24*
	Residual (38)	6.07	185.16	0.002	3937664.5	2.00	231454.88
Woreta	Replication (2)	0.58	4472.52	0.03	52899473.2	2.88	9152718.10
	Genotype (19)	2.03**	2431.01 ^{NS}	0.062**	4749709.3*	30.77**	2581083.44**
	Residual (38)	0.83	2886.22	0.018	2454082.3	0.92	458787.85
Maitsebri	Replication (2)	1.56	6882.95	0.002	192527	0.93	258746.9
	Genotype (19)	1.94**	152.75 ^{NS}	0.01**	6986520.5**	20.51**	1155321.18**
	Residual (38)	0.82	181.14	0.001	2297535.8	3.26	413122.89
Jimma	Replication (2)	205.69	5965.25	0.004	48159723.6	6.25	4840888.82
	Genotype (19)	186.28**	250.25 ^{NS}	0.01**	29319600.8**	17.68**	4534995.17**
	Residual (38)	42.08	179.25	0.002	8701476.2	1.84	707947.20
Tepi	Replication (2)	1236.32	68192.6	0.03	528612500	171.3	20531901.4
	Genotype (19)	27.79 ^{NS}	1727.01 ^{NS}	0.01 ^{NS}	26306140 ^{NS}	49.6 ^{NS}	493548.16 ^{NS}
	Residual (38)	17.84	960.89	0.01	31344956	36.53	766156.48
F-ratio		51.32	16.10	18	13.64	39.70	3.31

Ns,*, and **, non-significant, significant at $P<0.05$ and $P<0.01$, respectively. Number in parenthesis represent degree of freedom for the respective source of variation, and F-ratio= the ratio of highest to lowest error mean squares. SC= stand count, HI= harvest index, BIO= above ground biological yield (kg/ha), TSW= thousand grain weight (gram), GY= grain yield (kg/ha), F-ratio= ratio for larger to smaller error mean square

Appendix Table 2. Transformed data analysis of variance for yield and yield related traits of 20 upland rice genotypes at six locations, during 2016/2017 cropping season

Location	Source of variation	DH	DM	PL (cm)	PH (cm)	NFTPP	NUFTPP	NFGPP
Pawe	Replication (2)	0.059	0.25	0.0012	0.007	0.131	0.03	0.005
	Genotype (19)	0.142**	0.08**	0.001 ^{NS}	0.002 ^{NS}	0.27*	0.22*	0.01*
	Residual (38)	0.03	0.02	0.002	0.002	0.141	0.08	0.003
Manbuk	Replication (2)	0.046	0.016	0.00	0.00	0.26	0.03	0.022
	Genotype (19)	0.126**	0.08**	0.001**	0.01**	0.18 ^{NS}	0.15*	0.01 ^{NS}
	Residual (38)	0.02	0.02	0.001	0.001	0.12	0.07	0.01
Woreta	Replication (2)	0.003	0.03	0.01	0.02	0.25	0.15	0.05
	Genotype (19)	1.13**	1.92**	0.004**	0.007**	0.05 ^{NS}	0.08 ^{NS}	0.02*
	Residual (38)	0.01	0.02	0.001	0.001	0.04	0.1	0.004
Maitsebri	Replication (2)	0.12	0.05	0.01	0.00	0.15	0.03	0.01
	Genotype (19)	0.34**	0.04 ^{NS}	0.01**	0.01**	0.06**	0.085 ^{NS}	0.01*
	Residual (38)	0.04	0.02	0.001	0.001	0.023	0.09	0.01
Jimma	Replication (2)	2.66	0.01	0.002	0.002	0.33	0.04	0.01
	Genotype (19)	0.66**	0.25**	0.001**	0.01**	0.14 ^{NS}	0.17**	0.04**
	Residual (38)	0.19	0.01	0.001	0.001	0.1	0.06	0.01
Tepi	Replication (2)	2.1	0.23	0.00	0.002	3.23	1.11	0.83
	Genotype (19)	0.31**	0.08**	0.001**	0.01**	0.24 ^{NS}	0.15 ^{NS}	0.23**
	Residual (38)	0.07	0.01	0.001	0.001	0.14	0.14	0.02
F-ratio		19	2.0	2.0	2.0	6.13	2.33	6.67

* and **, significant at $P < 0.05$ and $P < 0.01$, respectively. Number in parenthesis represent degree of freedom for the respective source of variation, and F-ratio= the ratio of highest to lowest error mean squares. DH= days to heading, DM= days to maturity, PL= panicle length (cm), PH= plant height (cm), NFTPP= number of fertile tillers per plant, NUFTPP= number of unfertile tillers per plant, NFGPP= number of filled grain per panicle, F-ratio= ratio for larger to smaller error mean square

Appendix Table 2. Continued

Location	Source of variation	NUFGPP	HI	BIO (kg/ha)	TSW (g)	GY(kg/ha)
Pawe	Replication (2)	0.105	0.002	0.004	0.001	0.002
	Genotype (19)	1.79*	0.014*	0.034*	0.01**	0.013**
	Residual (38)	0.45	0.002	0.01	0.002	0.01
Manbuk	Replication (2)	0.57	0.004	0.001	0.00	0.004
	Genotype (19)	0.178 ^{NS}	0.003**	0.01*	0.004**	0.01*
	Residual (38)	0.27	0.001	0.01	0.001	0.02
Woreta	Replication (2)	0.032	0.092	0.51	0.00	0.15
	Genotype (19)	0.11*	0.065**	0.07*	0.01*	0.25**
	Residual (38)	0.05	0.01	0.022	0.001	0.01
Maitsebri	Replication (2)	0.102	0.00	0.00	0.00	0.004
	Genotype (19)	0.27**	0.004**	0.02**	0.01**	0.02**
	Residual (38)	0.12	0.00	0.01	0.001	0.01
Jimma	Replication (2)	2.71	0.003	0.06	0.002	0.04
	Genotype (19)	1.39**	0.01**	0.04**	0.004**	0.05**
	Residual (38)	0.42	0.001	0.01	0.0004	0.01
Tepi	Replication (2)	30.04	0.02	0.75	0.03	0.37
	Genotype (19)	0.47 ^{NS}	0.01 ^{NS}	0.03 ^{NS}	0.01 ^{NS}	0.01 ^{NS}
	Residual (38)	0.28	0.01	0.024	0.006	0.024
F-ratio		9	10	2.4	15	2.4

NS, * and **, non-significant, significant at $P < 0.05$ and $P < 0.01$, respectively. Number in parenthesis represent degree of freedom for the respective source of variation, and F-ratio= the ratio of highest to lowest error mean squares. NUGFPP= number of unfilled grain per panicle, HI= harvest index, BIO= biological yield (kg/ha), TSW= thousand grain weight (gram), GY= grain yield (kg/ha). F-ratio= ratio for larger to smaller error mean square

Appendix Table 3. Combined analysis of variance for grain yield and yield related traits of 20 upland rice genotypes evaluated at six locations, during 2016/2017 cropping season in Ethiopia

Source of variation	Phenology traits							
	Days to heading				Days to maturity			
	SS	MS	%TSS	% GxE	SS	MS	%TSS	% GxE
Total (359)	35133.2				98533.39			
Rep (Env) (12)	3387.63	282.3	9.64		575.17	47.93	0.58	
Genotypes (G) (19)	11798.5	620.9**	33.58		10568.56	556.24**	10.73	
Environments(E) (5)	9025.11	1805**	25.69		70960.29	14192.1**	72.02	
G x E (95)	6062.94	63.8**	17.26		14811.38	155.91**	15.03	
IPCA1(23)	3505	152.4**		57.81	12842	558**		86.70
IPCA2(21)	1387	66**		22.88	1171	56**		7.91
Error (228)	4859.03	21.33	13.83		1618.17	7.097	1.64	

Source of variation	Growth traits											
	Panicle length (cm)				Plant height (cm)				Number of unfertile tillers/ plant			
	SS	MS	%TSS	% GxE	SS	MS	%TSS	% GxE	SS	MS	%TSS	% GxE
Total (359)	2858.9				104269				250.1			
Rep (Env) (12)	54.63	4.55	1.91		2037.23	169.8	1.95		9.36	0.78	3.74	
Genotypes (G) (19)	245.75	12.93**	8.60		20025.2	1054**	19.21		14.89	0.78**	5.96	
Environments(E) (5)	2047.4	409.5**	71.61		61198.1	12240**	58.69		160.1	32**	64.03	
G x E (95)	202.68	2.13**	7.09		11107.4	116.9**	10.65		26.6	0.28*	10.64	
IPCA1(23)	76.9	3.34**		37.94	4773	208**		42.97	18.08	0.79**		67.97
IPCA2(21)	67	3.19**		33.06	2955	141**		26.60	8.11	0.38**		30.49
Error (228)	308.44	1.35	10.79		9900.83	43.42	9.50		47.88	0.21	19.15	

* and ** significant at $P < 0.05$ and $P < 0.01$, respectively. Rep (Env) = replication with in environment, MS= mean square, %TSS = percentage of total sum of square, the value in the bracket indicates the degree of freedom.

Appendix Table 3. Continued

Source of variation	Yield components											
	Number of filled grain/panicle				Number of unfilled grain/panicle				Harvest index (%)			
	SS	MS	%TSS	% GxE	SS	MS	%TSS	% GxE	SS	MS	%TSS	% GxE
Total (359)	169102				31315.1				15.78			
Rep (Env) (12)	24589.6	2049.1	14.54		2988.3	249.02	9.54		0.63	0.05	3.99	
Genotypes (G) (19)	9253.7	487**	5.47		947.4	49.86**	3.03		1.83	0.09**	11.6	
Environments(E) (5)	92033.5	18407**	54.42		21218.5	4243.7**	67.76		9.06	1.81**	57.4	
G x E (95)	17402.8	183.2**	10.29		3476.5	36.59**	11.10		2.13	0.02**	13.5	
IPCA1(23)	8380	364**		48.15	2980	129.6**		85.72	1.884	0.08**		88.45
IPCA2(21)	4750	226**		56.68	335	16 ^{NS}		11.24	0.168	0.008		8.92
Error (228)	25822.3	113.26	15.27		2684.4	11.77	8.57		0.076	0.002		

*, ** Significant at $P < 0.05$ and $P < 0.01$, respectively. Rep (Env) = replication with in environment, MS= mean square, %Total SS = percentage of total sum of square, the value in the bracket indicates the degree of freedom.

Appendix Table 4. Mean value of grain yield and yield related traits of 20 upland rice genotypes evaluated at Pawe on station, during 2016/2017 cropping season in Ethiopia

Genotype	DH	DM	PL(cm)	PH(cm)	NFTPP	NUFTPP	NFGPP	NUFGPP	HI	BIO(kg/ha)	TSW(g)	GY(kg/ha)
1	80.7 ^{bcd}	109 ^{b-e}	21.5 ^a	100.5 ^{ab}	4.7 ^{cd}	0.20 ^{ghi}	105 ^{a-d}	4.2 ^{d-f}	0.37 ^{a-d}	10333 ^{b-d}	23.3 ^e	3780.4 ^{a-c}
2	83.67 ^{ab}	114 ^{bc}	21.8 ^a	101.9 ^{ab}	6.3 ^{a-d}	1.18 ^b	110 ^{a-c}	7.6 ^{a-c}	0.26 ^{e-g}	14333 ^a	23.7 ^e	3757.9 ^{a-c}
3	84.33 ^{ab}	113 ^{b-e}	22.6 ^a	102.4 ^{ab}	8.9 ^{ab}	1.43 ^a	103.8 ^{b-d}	7.5 ^{a-d}	0.24 ^{fg}	14583 ^a	24.3 ^{de}	3521.7 ^{a-d}
4	84.33 ^{ab}	112 ^{b-e}	20.9 ^a	99.8 ^{ab}	6.9 ^{a-d}	0.49 ^{ef}	103.7 ^{b-d}	8.3 ^{ab}	0.24 ^{fg}	13167 ^{ab}	25 ^{cde}	3517.1 ^{a-d}
5	75.67 ^d	107.3 ^e	21.7 ^a	95.3 ^{ab}	6.8 ^{a-d}	0.75 ^d	108 ^{a-d}	3.0 ^f	0.38 ^{a-d}	9500 ^{c-e}	23.7 ^e	3597.5 ^{a-d}
6	76.67 ^{cd}	110 ^{b-e}	20.8 ^a	94.7 ^{ab}	5.5 ^{b-d}	0.32 ^{fg}	110 ^{a-c}	4.9 ^{b-f}	0.46 ^a	7583 ^{d-f}	23.2 ^e	3468.8 ^{a-d}
7	81 ^{b-d}	108.3 ^{c-e}	22.5 ^a	105.7 ^{ab}	6.1 ^{b-d}	0.22 ^{ghi}	116 ^{ab}	3.7 ^{ef}	0.44 ^{ab}	9167 ^{c-f}	27 ^{bcd}	4013.3 ^{a-c}
8	88.67 ^a	123.7 ^a	21.4 ^a	97 ^{ab}	3.9 ^d	0.07 ⁱ	112.2 ^{a-c}	4.4 ^{c-f}	0.31 ^{d-f}	14333 ^a	31.2 ^a	4462.1 ^a
9	77 ^{cd}	108 ^{de}	19.7 ^a	87.5 ^b	7.3 ^{a-d}	0.20 ^{ghi}	94.3 ^d	3.3 ^f	0.4 ^{a-d}	6250 ^f	28.5 ^{ab}	2501.3 ^d
10	84.67 ^{ab}	113 ^{b-e}	21.7 ^a	98 ^{ab}	8.2 ^{a-c}	0.07 ⁱ	114.6 ^{a-c}	4.1 ^{ef}	0.33 ^{c-f}	10667 ^{b-d}	22.3 ^e	3517.1 ^{a-d}
11	79.3 ^{b-d}	112 ^{b-e}	20.8 ^a	105.4 ^{ab}	4.5 ^{cd}	0.30 ^{fgh}	111.3 ^{a-c}	5.1 ^{b-f}	0.43 ^{a-c}	8083 ^{c-f}	27 ^{bcd}	3492.5 ^{a-d}
12	76.3 ^d	107.7 ^{de}	22.4 ^a	97.1 ^{ab}	5.5 ^{b-d}	0.50 ^{ef}	108 ^{a-d}	4.7 ^{c-f}	0.46 ^a	7167 ^{ef}	27.8 ^{bc}	3165.8 ^{cd}
13	75 ^d	109 ^{b-e}	22.8 ^a	106.5 ^{ab}	6.3 ^{a-d}	0.98 ^c	116.7 ^{ab}	6.9 ^{a-e}	0.44 ^{ab}	10083 ^{c-e}	23.0 ^e	4363.8 ^{ab}
14	75 ^d	110 ^{b-e}	22.3 ^a	104.4 ^{ab}	7.5 ^{a-d}	0.65 ^{de}	109 ^{a-d}	6.7 ^{a-e}	0.35 ^{b-e}	8250 ^{c-f}	27 ^{bcd}	2916.3 ^{cd}
15	83 ^{a-c}	114.7 ^b	20.1 ^a	99.3 ^{ab}	7.1 ^{a-d}	0.4 ^{fg}	108 ^{a-d}	8.1 ^{ab}	0.36 ^{a-e}	10750 ^{bc}	24.3 ^{de}	3862.9 ^{a-c}
16	75.7 ^d	110 ^{b-e}	21.5 ^a	93.1 ^{ab}	4.7 ^{cd}	0.0 ⁱ	110.1 ^{a-c}	3.9 ^{ef}	0.44 ^{ab}	8833 ^{c-f}	23.7 ^e	3820.8 ^{a-c}
17	79.3 ^{b-d}	110 ^{b-e}	20.7 ^a	96.3 ^{ab}	5.9 ^{b-d}	0.37 ^{fg}	119.5 ^a	3.2 ^f	0.41 ^{a-d}	9667 ^{c-e}	29.7 ^{ab}	3785 ^{a-c}
18	79.3 ^{b-d}	112 ^{b-e}	20.3 ^a	94.2 ^{ab}	4.5 ^{cd}	0.0 ⁱ	111.4 ^{a-c}	5.5 ^{b-f}	0.32 ^{d-f}	10250 ^{b-e}	28.7 ^{ab}	3287.5 ^{b-d}
19	83.7 ^{ab}	113 ^{b-d}	23.3 ^a	112.9 ^a	9.9 ^a	0.73 ^d	100.7 ^{cd}	9.1 ^a	0.21 ^g	14500 ^a	22.5 ^e	3055.8 ^{cd}
20	80.3 ^{b-d}	112 ^{b-e}	21.6 ^a	107.7 ^a	6.3 ^{a-d}	0.10 ^{hi}	119 ^a	5.6 ^{b-f}	0.45 ^{ab}	10250 ^{b-e}	23.83 ^e	4586.7 ^a
Mean	80.18	111.52	21.52	99.98	6.34	0.45	109.61	5.49	0.37	10387.5	25.49	3603.27
CV (%)	4.17	2.59	8.57	10.04	30.47	25.5	6.93	31.5	14.74	15.27	6.11	16.14
LSD	5.53	4.77	3.05	16.59	3.19	0.18	12.56	2.86	0.09	2622.4	2.57	961.45

Note; DH= days to heading, DM= days to maturity, PL= panicle length (cm), PH= plant height (cm), NFTPP= number of fertile tillers per plant, NFGPP= number of filled grain per panicle, NUFGPP= number of unfilled grain per panicle, HI= harvest index, BIO= above ground biological yield (kg/ha), TSW= thousand grain weight (gram), GY= grain yield (kg/ha).

Appendix Table 5. Mean value of grain yield and yield related traits of 20 upland rice genotypes evaluated at Manbuk, during 2016/2017 cropping season in Ethiopia

Genotype	DH	DM	PL(cm)	PH(cm)	NFTPP	NUFTPP	NFGPP	NUFGPP	HI	BIO(kg/ha)	TSW(g)	GY(kg/ha)
1	74.7 ^{d-f}	106 ^{de}	20.2 ^a	92.7 ^{d-f}	4.07 ^c	0.28 ^{def}	114.7 ^{ab}	3 ^{ab}	0.39 ^a	10583 ^{b-e}	26 ^{e-h}	4090.8 ^a
2	79.7 ^{bc}	111 ^{b-d}	20.1 ^a	111.9 ^{ab}	6.13 ^{a-c}	0.38 ^{cde}	106.3 ^{a-c}	3.93 ^{ab}	0.27 ^{cd}	15083 ^a	28.3 ^{b-e}	4054.2 ^a
3	79 ^{b-d}	111 ^{b-d}	19.5 ^{a-d}	114.7 ^a	8.53 ^a	0.63 ^{ab}	102.3 ^{a-c}	5.33 ^{ab}	0.27 ^{cd}	14083 ^{ab}	27.3 ^{c-g}	3778.3 ^{ab}
4	80 ^b	110 ^{b-d}	20.1 ^a	115.9 ^a	7.33 ^{ab}	0.29 ^{def}	90.9 ^c	3.67 ^{ab}	0.28 ^c	13667 ^{abc}	28.2 ^{b-f}	3805 ^{ab}
5	72.7 ^{ef}	104 ^e	19 ^{a-e}	104 ^{a-d}	5.07 ^{bc}	0.50 ^{bc}	108 ^{a-c}	7.47 ^a	0.38 ^{ab}	11083 ^{b-e}	25.5 ^{f-h}	4096.3 ^a
6	75 ^{c-f}	105.7 ^{de}	19 ^{a-e}	93.5 ^{d-f}	4.67 ^{bc}	0.06 ^{gh}	100 ^{a-c}	3 ^{ab}	0.34 ^{abc}	11667 ^{a-e}	25 ^{gh}	3878.8 ^{ab}
7	77 ^{b-e}	109 ^{b-e}	18 ^{c-e}	95.1 ^{c-f}	4.8 ^{bc}	0.23 ^{efg}	101.4 ^{a-c}	3.27 ^{ab}	0.3 ^{bcd}	10917 ^{b-e}	28.3 ^{b-d}	3243.3 ^{a-c}
8	87 ^a	118 ^a	18 ^{c-e}	89.9 ^{def}	5.73 ^{a-c}	0.43 ^{cd}	103 ^{a-c}	5.48 ^{ab}	0.31 ^{bcd}	11000 ^{b-e}	33 ^a	3371.3 ^{a-c}
9	74.7 ^{d-f}	109 ^{b-e}	17.5 ^e	80.2 ^f	3.73 ^c	0.52 ^{bc}	94 ^{a-c}	2.13 ^b	0.35 ^{abc}	8583 ^e	28.2 ^{b-f}	3055.4 ^{bc}
10	79.7 ^{bc}	113 ^{bc}	19.7 ^{a-c}	109.5 ^{a-c}	5.33 ^{bc}	0.06 ^{gh}	107 ^{a-c}	3.93 ^{ab}	0.35 ^{abc}	11833 ^{a-e}	25.7 ^{e-h}	4069.6 ^a
11	74.7 ^{d-f}	107 ^{c-e}	19.8 ^{ab}	97.7 ^{b-e}	4.7 ^{bc}	0.21 ^{efg}	113 ^{a-c}	4.3 ^{ab}	0.35 ^{abc}	10000 ^{c-e}	30.167 ^b	3561.3 ^{a-c}
12	75 ^{c-f}	108 ^{b-e}	19.8 ^{ab}	92.9 ^{def}	4.7 ^{bc}	0.12 ^{fgh}	111 ^{a-c}	3.5 ^{ab}	0.38 ^{ab}	9500 ^{de}	30.333 ^b	3542.9 ^{a-c}
13	73 ^{ef}	106.3 ^{de}	20 ^a	98.4 ^{b-e}	4.5 ^{bc}	0.41 ^{cd}	101.9 ^{a-c}	4.3 ^{ab}	0.34 ^{abc}	10583 ^{b-e}	24.167 ^h	3586.7 ^{a-c}
14	71.3 ^f	103.7 ^e	19 ^{a-e}	83.2 ^{ef}	5.5 ^{bc}	0.43 ^{cd}	91.9 ^{bc}	5.1 ^{ab}	0.32 ^{abcd}	10917 ^{b-e}	27 ^{c-g}	3421.3 ^{a-c}
15	75 ^{b-f}	107 ^{c-e}	18.3 ^{b-e}	94.5 ^{def}	5.3 ^{bc}	0.7 ^a	99 ^{a-c}	5.1 ^{ab}	0.3 ^{bcd}	12083 ^{a-e}	26.3 ^{d-h}	3597.5 ^{a-c}
16	74 ^{ef}	106.3 ^{de}	19 ^{a-e}	97.7 ^{b-e}	4.3 ^{bc}	0.44 ^{cd}	115.9 ^a	4.3 ^{ab}	0.34 ^{abc}	11000 ^{b-e}	25 ^{gh}	3665 ^{a-c}
17	73.7 ^{ef}	107 ^{c-e}	18 ^{c-e}	93.9 ^{def}	4.1 ^c	0.44 ^{cd}	95.5 ^{a-c}	3.1 ^{ab}	0.30 ^{bcd}	9250 ^{de}	30.3 ^b	2807 ^c
18	75 ^{c-f}	107 ^{c-e}	17.9 ^{de}	97.3 ^{b-e}	4.7 ^{bc}	0.63 ^{ab}	98.4 ^{a-c}	3.9 ^{ab}	0.26 ^d	10917 ^{b-e}	30.2 ^b	2772 ^c
19	80 ^b	113.3 ^b	19 ^{a-e}	116.6 ^a	6.8 ^{a-c}	0.47 ^{bc}	104.1 ^{a-c}	3 ^{ab}	0.29 ^{cd}	12917 ^{a-d}	29.8 ^{bc}	3715.4 ^{a-c}
20	74 ^{ef}	107 ^{c-e}	19.5 ^{a-d}	95.5 ^{c-e}	5.3 ^{bc}	0.03 ^h	114 ^{a-c}	3.8 ^{ab}	0.34 ^{abc}	10833 ^{b-e}	25.3 ^{gh}	3625.4 ^{a-c}
Mean	76.25	108.58	19.04	98.75	5.27	0.37	103.67	4.07	0.32	11325	27.71	3586.88
CV (%)	3.35	2.72	4.65	7.85	29.65	25.15	11.19	60.48	12.53	17.52	5.10	13.41
LSD	4.22	4.88	1.46	12.82	2.58	0.16	19.18	4.07	0.07	3280	2.34	795.21

Note; DH= days to heading, DM= days to maturity, PL= panicle length (cm), PH= plant height (cm), NFTPP= number of fertile tillers per plant, NFGPP= number of filled grain per panicle, NUFGPP= number of unfilled grain per panicle, HI= harvest index, BIO= above ground biological yield (kg/ha), TSW= thousand grain weight (gram), GY= grain yield (kg/ha).

Appendix Table 6. Mean value of grain yield and yield related traits of 20 upland rice genotypes evaluated at Woreta, during 2016/2017 cropping season in Ethiopia

Genotype	DH	DM	PL(cm)	PH(cm)	NFTPP	NUFTPP	NFGPP	NUFGPP	HI	BIO (kg/ha)	TSW(g)	GY(kg/ha)
1	83.7 ^{ef}	111 ^{de}	16.9 ^{abc}	70.9 ^{def}	3.7 ^{abc}	0.20 ^{ef}	79.9 ^{ab}	3.8 ^{cd}	0.87 ^a	5030 ^{abc}	26.9 ^{de}	4138 ^{abc}
2	96 ^c	128.7 ^c	16.7 ^{a-d}	79.7 ^{abc}	4.3 ^{ab}	0.033 ^h	67.3 ^{cde}	4.1 ^{bcd}	0.57 ^{bc}	6740 ^a	25.1 ^{fg}	3426 ^{a-f}
3	92.3 ^c	126 ^c	15.7 ^{a-e}	79.3 ^{abc}	5.1 ^a	0.84 ^a	67.3 ^{cde}	4.1 ^{bcd}	0.65 ^{abc}	5333 ^{abc}	24.6 ^g	3168 ^{a-f}
4	90 ^d	125 ^c	16.7 ^{a-d}	85.1 ^a	3.9 ^{abc}	0.07 ^{gh}	77.3 ^{abc}	5.7 ^{ab}	0.72 ^{abc}	5555 ^{abc}	24.8 ^g	3611 ^{a-f}
5	82.7 ^{ef}	109.7 ^e	14.8 ^e	69.3 ^{efg}	2.7 ^c	0.35 ^{cd}	70 ^{a-e}	3.5 ^d	0.77 ^{ab}	4432 ^{a-d}	26.5 ^{ef}	234.5 ^{ab}
6	83.3 ^{ef}	109.7 ^e	15.9 ^{a-e}	71.6 ^{def}	3.7 ^{abc}	0.15 ^{fg}	75.4 ^{a-d}	4 ^{bcd}	0.74 ^{abc}	5609 ^{ab}	28.1 ^{de}	4391.4 ^a
7	83.7 ^{ef}	113 ^{de}	15.9 ^{a-e}	79.2 ^{abc}	3.5 ^{bc}	0.52 ^b	73.7 ^{a-d}	3.8 ^{cd}	0.67 ^{abc}	4518 ^{a-d}	33.2 ^a	2983 ^{b-f}
8	124 ^a	184 ^a	11.7 ^f	50.3 ^h	3.1 ^{bc}	0.32 ^{cd}	53.7 ^f	6.3 ^a	0.19 ^d	1823 ^d	33.7 ^a	177.1 ^g
9	82.7 ^{ef}	116 ^d	15.5 ^{b-e}	73.1 ^{cde}	3.7 ^{abc}	0.62 ^b	68.8 ^{b-e}	3.1 ^d	0.87 ^a	2459 ^{cd}	30.3 ^c	2707.9 ^{def}
10	102 ^b	135.7 ^b	16.8 ^{abc}	71.5 ^{def}	4.2 ^{ab}	0.32 ^{cd}	81.4 ^a	4.7 ^{a-d}	0.49 ^c	5767 ^{ab}	24.8 ^g	2817.7 ^{def}
11	85.7 ^e	116.7 ^d	17.4 ^a	80.9 ^{ab}	3.8 ^{abc}	0.83 ^a	72.9 ^{a-d}	4.4 ^{bcd}	0.69 ^{abc}	5810 ^{ab}	32.2 ^{ab}	385 ^{a-e}
12	81.7 ^f	111 ^{de}	17 ^{ab}	77.2 ^{bcd}	3.3 ^{bc}	0.18 ^f	80.1 ^{ab}	4.4 ^{bcd}	0.73 ^{abc}	4470 ^{a-d}	32.9 ^a	4030 ^{a-d}
13	72 ⁱ	100 ^f	15 ^{de}	63 ^g	3.13 ^{bc}	0.03 ^h	64.3 ^{def}	5.6 ^{abc}	0.62 ^{abc}	2461 ^{cd}	24.8 ^g	2372 ^f
14	76 ^h	100 ^f	16.1 ^{a-e}	65.3 ^{fg}	3.7 ^{abc}	0.07 ^{gh}	64.3 ^{ef}	4.2 ^{bcd}	0.70 ^{abc}	3603 ^{bcd}	28.5 ^d	2564.3 ^{ef}
15	79 ^g	113 ^{de}	14.7 ^e	64.6 ^{fg}	3.6 ^{abc}	0.0 ^h	67.5 ^{cde}	4.3 ^{bcd}	0.69 ^{abc}	3701 ^{a-d}	26.7 ^{ef}	2466.1 ^f
16	82 ^f	109.3 ^e	15.1 ^{cde}	68.8 ^{efg}	3.1 ^{bc}	0.33 ^{cd}	69.4 ^{b-e}	3.5 ^d	0.72 ^{abc}	4965 ^{abc}	27.5 ^{de}	3536 ^{a-f}
17	72 ⁱ	101.3 ^f	14.7 ^e	69.8 ^{efg}	3.3 ^{bc}	0.38 ^c	60.2 ^{ef}	3.8 ^{cd}	0.76 ^{abc}	3808 ^{a-d}	31 ^{bc}	2859.3 ^{c-f}
18	74 ^{hi}	101.3 ^f	14.8 ^e	73.9 ^{cde}	3.3 ^{bc}	0.20 ^{ef}	68.6 ^{b-e}	4.2 ^{bcd}	0.69 ^{abc}	4127 ^{a-d}	30.3 ^c	2706.7 ^{def}
19	95.3 ^c	127.7 ^c	16.4 ^{a-e}	77.7 ^{bcd}	4.1 ^{abc}	0.30 ^{cde}	68.4 ^{b-e}	5.5 ^{abc}	0.66 ^{abc}	4200 ^{a-d}	23.8 ^g	2800.4 ^{def}
20	83.7 ^{ef}	111.3 ^{de}	15.4 ^{b-e}	68 ^{efg}	3.5 ^{bc}	0.25 ^{def}	72.5 ^{a-d}	3.9 ^{bcd}	0.69 ^{abc}	3630 ^{a-d}	27.2 ^{de}	3036 ^{b-f}
Mean	86.10	117.58	15.66	71.96	3.62	0.30	70.15	4.35	0.68	4401.96	28.14	3094.1
CV (%)	1.86	2.58	5.76	5.08	20.8	20.58	8.69	20.96	20.12	35.59	3.41	21.89
LSD	2.64	5.0	1.49	6.04	1.24	0.10	10.08	1.51	0.22	2589.4	1.58	1119.6

Note; DH= days to heading, DM= days to maturity, PL= panicle length (cm), PH= plant height (cm), NFTPP= number of fertile tillers per plant, NFGPP= number of filled grain per panicle, NUFGPP= number of unfilled grain per panicle, HI= harvest index, BIO= above ground biological yield (kg/ha), TSW= thousand grain weight (gram), GY= grain yield (kg/ha).

Appendix Table 7. Mean value of grain yield and yield related traits of 20 upland rice genotypes evaluated at Maitsebri, during 2016/2017 cropping season in Ethiopia

Genotype	DH	DM	PL(cm)	PH (cm)	NFTPP	NUFTPP	NFGPP	NUFGPP	HI	BIO (kg/ha)	TSW(g)	GY(kg/ha)
1	72 ^{cd}	107 ^{bc}	15.9 ^{efg}	71.1 ^e	4.2 ^c	0.36 ^f	70.8 ^{abc}	1.6 ^{b-e}	0.44 ^{ab}	6583 ^{ef}	26 ^{d-i}	2900 ^{cde}
2	86.3 ^a	113 ^a	19.3 ^{ab}	102.4 ^a	5.7 ^{ab}	0.37 ^f	74.5 ^a	2.9 ^{abc}	0.41 ^{abc}	9283 ^{a-e}	28 ^{b-g}	3792 ^{a-d}
3	78.3 ^{cd}	112.7 ^a	18.9 ^{abc}	98.5 ^a	5.7 ^{ab}	0.55 ^{cd}	67 ^{a-d}	2.7 ^{abc}	0.38 ^{bc}	9600 ^{a-d}	27 ^{b-h}	3675 ^{a-d}
4	83.3 ^{ab}	112 ^a	20.1 ^a	105.5 ^a	6 ^a	0.77 ^a	68.9 ^{a-d}	2.7 ^{abc}	0.39 ^{bc}	10575 ^a	27 ^{b-h}	4083 ^{abc}
5	71 ^d	108 ^{abc}	16 ^{d-g}	74.9 ^{cde}	3.9 ^c	0.42 ^{ef}	60.9 ^{bcd}	2 ^{a-e}	0.43 ^{ab}	6500 ^{ef}	24.4 ^{f-i}	2825 ^{cde}
6	70.3 ^d	109 ^{abc}	16.4 ^{d-g}	73.2 ^{de}	4.6 ^{bc}	0.22 ^h	68.5 ^{a-d}	2.5 ^{a-d}	0.39 ^{bc}	7842 ^{a-f}	24.13 ^{ghi}	3050 ^{a-e}
7	73.3 ^{cd}	110 ^{abc}	15.5 ^{fgh}	79.8 ^{bcd}	4.1 ^c	0.32 ^{fgh}	66.9 ^{a-d}	1.9 ^{a-e}	0.39 ^{bc}	7292 ^{c-f}	30.5 ^b	2835 ^{cde}
8	73.3 ^{cd}	112 ^{ab}	13.9 ^h	70.3 ^e	5.1 ^{abc}	0.43 ^{def}	57.8 ^{cd}	0.9 ^{de}	0.25 ^d	10333 ^{ab}	27.7 ^{b-f}	2633.3 ^{de}
9	72.7 ^{cd}	109 ^{abc}	15.9 ^{efg}	74.9 ^{cde}	4.7 ^{bc}	0.43 ^{def}	57 ^d	1.9 ^{a-e}	0.39 ^{bc}	6900 ^{def}	29.3 ^{bc}	2683.3 ^{de}
10	80 ^{ab}	112 ^{ab}	17.9 ^{bcd}	83.8 ^b	4.5 ^{bc}	0.35 ^{fg}	63.5 ^{a-d}	1.3 ^{b-e}	0.41 ^{abc}	7456 ^{b-f}	26 ^{c-i}	3075 ^{a-e}
11	71.3 ^d	111 ^{abc}	16.7 ^{d-g}	81.7 ^{bc}	4.3 ^c	0.73 ^{ab}	71 ^{abc}	1.2 ^{b-e}	0.43 ^{ab}	9008 ^{a-f}	29.9 ^b	3808 ^{a-d}
12	71 ^d	109 ^{abc}	7.5 ^{b-e}	79 ^{bcd}	4.1 ^c	0.60 ^c	62.8 ^{a-d}	1.4 ^{b-e}	0.46 ^a	8850 ^{a-f}	33.8 ^a	4067 ^{abc}
13	68.3 ^{de}	106 ^c	17.3 ^{c-f}	72.9 ^{de}	4.7 ^{bc}	0.78 ^a	70.9 ^{abc}	3.5 ^a	0.44 ^{ab}	6467 ^{ef}	24 ^{hi}	4067 ^{abc}
14	63.3 ^e	105.3 ^c	17.4 ^{cde}	71.7 ^{de}	4.3 ^c	0.37 ^f	59.1 ^{bcd}	1.5 ^{b-e}	0.44 ^{ab}	6850 ^{def}	27.7 ^{bcd}	3025 ^{b-e}
15	73 ^{cd}	110 ^{abc}	16.3 ^{d-g}	72.5 ^{de}	4.3 ^c	0.73 ^{ab}	61.3 ^{bcd}	1.13 ^{cde}	0.35 ^c	7908 ^{a-f}	25.1 ^{e-i}	2666.3 ^{de}
16	70 ^d	108 ^{abc}	16.9 ^{d-g}	76 ^{b-e}	4.7 ^{bc}	0.62 ^{cb}	71.7 ^{ab}	1.7 ^{a-e}	0.43 ^{ab}	9675 ^{a-d}	23.3 ⁱ	4216.7 ^{ab}
17	67.3 ^{de}	110 ^{abc}	15.2 ^{gh}	77 ^{b-e}	4.1 ^c	0.50 ^{cde}	64.4 ^{a-d}	0.9 ^{de}	0.42 ^{ab}	6392 ^{ef}	28.9 ^{bcd}	2700 ^{de}
18	67.3 ^{de}	108 ^{abc}	15.1 ^h	78 ^{b-e}	4.1 ^c	0.52 ^{cde}	61.5 ^{a-d}	0.7 ^e	0.4 ^{abc}	6075 ^f	29.6 ^b	2408.3 ^e
19	82 ^{ab}	113 ^a	20 ^a	99.5 ^a	5.8 ^{ab}	0.10 ⁱ	71.7 ^{ab}	2.9 ^{ab}	0.93 ^{bc}	9733 ^{a-d}	28 ^{b-g}	3850 ^{a-d}
20	70.3 ^d	109 ^{abc}	15.7 ^{efg}	75.5 ^{cde}	4.53 ^{bc}	0.23 ^{gh}	72.1 ^{ab}	1.13 ^{cde}	0.42 ^{ab}	10183 ^{abc}	25.4 ^{e-i}	4283.3 ^a
Mean	73.23	109.70	16.88	80.94	4.67	0.47	66.12	1.83	0.40	8175.29	27.27	3270.89
CV (%)	4.88	2.73	5.79	5.23	14.17	14.32	10.0	49.49	8.31	18.54	6.62	19.65
LSD	5.91	4.94	1.61	7.00	1.09	0.11	10.93	1.49	0.06	2505.4	2.98	1062.4

Note; DH= days to heading, DM= days to maturity, PL= panicle length (cm), PH= plant height (cm), NFTPP= number of fertile tillers per plant, NFGPP= number of filled grain per panicle, NUFGPP= number of unfilled grain per panicle, HI= harvest index, BIO= above ground biological yield (kg/ha), TSW= thousand grain weight (gram), GY= grain yield (kg/ha).

Appendix Table 8. Mean value of grain yield and yield related traits of 20 upland rice genotypes evaluated at Jimma, during 2016/2017 cropping season in Ethiopia

Genotype	DH	DM	PL(cm)	PH(cm)	NFTPP	NUFTPP	NFGPP	NUFGPP	HI	BIO(kg/ha)	TSW(g)	GY(kg/ha)
1	82 ^{a-d}	135 ^{bc}	22.5 ^{a-e}	66 ^{e-h}	8.4 ^c	2.63 ^{cd}	90.1 ^{ab}	23.8 ^b	0.44 ^{ab}	12603 ^{bcd}	27.6 ^{cd}	5551 ^{abc}
2	87 ^{abc}	134 ^{bc}	23.3 ^{abc}	81.7 ^{bc}	11.8 ^{abc}	2.8 ^{bc}	79.5 ^{ab}	31.6 ^b	0.31 ^{def}	10735 ^{b-e}	27.1 ^{cd}	3307.8 ^{fg}
3	91 ^{ab}	135 ^{bc}	22.5 ^{a-e}	73.3 ^{b-e}	13.3 ^{ab}	3.63 ^a	71.5 ^b	30.7 ^b	0.29 ^{ef}	9301 ^{cde}	26.1 ^{cd}	2768.9 ^g
4	91 ^{ab}	134 ^{bc}	22.6 ^{a-e}	77.4 ^{bcd}	12.5 ^{abc}	3.07 ^b	85.5 ^{ab}	22.6 ^b	0.30 ^{ef}	10972 ^{b-e}	27.4 ^{cd}	3288.2 ^{ef}
5	76 ^{bcd}	134 ^{bc}	21.5 ^{cde}	64.7 ^{e-h}	11.7 ^{abc}	2.13 ^e	96 ^{ab}	19.5 ^b	0.42 ^{abc}	14127 ^{bc}	25.6 ^{cd}	5962.1 ^{ab}
6	75 ^{cd}	134 ^{bc}	22.2 ^{b-e}	64.9 ^{e-h}	10.2 ^{bc}	1.47 ^{hi}	90.3 ^{ab}	20.3 ^b	0.38 ^{bcd}	15810 ^{ab}	26.8 ^{cd}	5581.5 ^{abc}
7	90 ^{abc}	135 ^{bc}	23.1 ^{a-d}	83.2 ^b	10.7 ^{abc}	1.3 ⁱ	83.7 ^{ab}	18.8 ^b	0.38 ^{bcd}	14117 ^{bc}	32.5 ^a	5354.5 ^{a-d}
8	93 ^a	166 ^a	2.8 ^e	69.3 ^{d-g}	9.5 ^{bc}	1.67 ^{gh}	47 ^c	54.4 ^a	0.26 ^f	10433 ^{b-e}	32.7 ^a	2715.8 ^g
9	81 ^{a-d}	133 ^c	22.8 ^{a-d}	60.5 ^{fgh}	9.7 ^{bc}	2.07 ^e	100 ^a	22.2 ^b	0.44 ^{ab}	6031 ^e	30.6 ^{ab}	2627.8 ^g
10	87 ^{abc}	134 ^{bc}	24.3 ^a	96.9 ^a	11.2 ^{abc}	1.77 ^{fg}	88.6 ^{ab}	22.5 ^b	0.35 ^{bcd}	19558 ^a	27.3 ^{cd}	6786.6 ^a
11	85 ^{abc}	134.3 ^{bc}	23.5 ^{ab}	71.4 ^{c-f}	10.6 ^{bc}	2.45 ^d	86.5 ^{ab}	20.3 ^b	0.41 ^{abc}	10133 ^{b-e}	30.7 ^{ab}	4180.8 ^{c-g}
12	81.7 ^{a-d}	133.7 ^{bc}	23.5 ^{ab}	66.3 ^{e-h}	11.6 ^{abc}	1.93 ^{efg}	87.1 ^{ab}	21.3 ^b	0.46 ^a	10640 ^{b-e}	32.5 ^a	4817.4 ^{b-f}
13	66.3 ^d	134.7 ^{bc}	22 ^{b-e}	57.4 ^h	10.3 ^{bc}	3.07 ^b	92 ^{ab}	22.2 ^b	0.41 ^{abc}	7430 ^{de}	25.5 ^d	3042.2 ^g
14	66.3 ^d	134.3 ^{bc}	21.9 ^{b-e}	58.3 ^h	10.1 ^{bc}	2.43 ^d	94.1 ^{ab}	21.6 ^b	0.38 ^{bcd}	8353 ^{cde}	28.2 ^{bc}	3168.2 ^g
15	66.7 ^d	135 ^{bc}	20.8 ^e	56.1 ^h	9.5 ^{bc}	2.5 ^d	83.1 ^{ab}	26.5 ^b	0.31 ^{def}	11557 ^{b-e}	26.3 ^{cd}	3287.9 ^{fg}
16	74.3 ^{cd}	35.3 ^b	21.7 ^{b-e}	62.2 ^{e-h}	12.2 ^{abc}	2.10 ^e	89.1 ^{ab}	20.9 ^b	0.40 ^{abc}	13554 ^{bc}	25.8 ^{cd}	5310.1 ^{a-e}
17	83 ^{abc}	133.7 ^{bc}	21.7 ^{b-e}	63 ^{e-h}	9.9 ^{bc}	2.63 ^{cd}	85.1 ^{ab}	21.5 ^b	0.39 ^{abc}	9782 ^{cde}	30.5 ^{ab}	3743.3 ^{efg}
18	76.7 ^{bcd}	134.3 ^{bc}	21.4 ^{de}	72.2 ^{cde}	10.9 ^{abc}	2.0 ^{ef}	93 ^{ab}	19.9 ^b	0.31 ^{def}	13444 ^{bc}	30.4 ^{ab}	4126.2 ^{c-g}
19	88 ^{abc}	134.3 ^{bc}	23.1 ^{a-d}	80.5 ^{bc}	14.9 ^a	2.6 ^{cd}	83.1 ^{ab}	20.1 ^b	0.29 ^{ef}	13439 ^{bc}	27.2 ^{cd}	3849 ^{d-g}
20	79.3 ^{a-d}	134.3 ^{bc}	22.4 ^{b-e}	62.9 ^{e-h}	11.2 ^{abc}	0.87 ^j	83.4 ^{ab}	23.9 ^b	0.4 ^{abc}	8907 ^{cde}	28 ^{cd}	3596.2 ^{fg}
Mean	81.02	135.92	22.39	69.40	11.01	2.25	85.46	24.23	0.37	11546.2	28.43	4153.26
CV (%)	9.96	0.67	4.33	8.45	19.89	7.11	15.17	26.77	10.77	25.55	4.78	20.26
LSD	13.33	1.50	1.60	9.70	3.62	0.26	21.42	NS	0.07	4875.80	2.24	1390.80

Note; DH= days to heading, DM= days to maturity, PL= panicle length (cm), PH= plant height (cm), NFTPP= number of fertile tillers per plant, NFGPP= number of filled grain per panicle, NUFGPP= number of unfilled grain per panicle, HI= harvest index, BIO= above ground biological yield (kg/ha), TSW= thousand grain weight (gram), GY= grain yield (kg/ha).

Appendix Table 9. Mean value of grain yield and yield related traits of 20 upland rice genotypes evaluated at Tepi, during 2016/2017 cropping season in Ethiopia

Genotype	DH	DM	PL(cm)	PH(cm)	NFTPP	NUFTPP	NFGPP	NUFGPP	HI	BIO (kg/ha)	TSW(g)	GY(kg/ha)
1	86 ^{b-f}	145.7 ^{b-e}	19.3 ^{ab}	90.9 ^{d-g}	10.5 ^{bc}	1.80 ^d	115.5 ^a	16.53 ^{ab}	0.36 ^{ab}	10500 ^a	35.71 ^{ab}	3912.8 ^a
2	93 ^{bcd}	137 ^g	20.7 ^{ab}	116 ^a	16.2 ^a	2.67 ^a	82.3 ^{bcd}	15.4 ^{abc}	0.24 ^{ab}	16000 ^a	31 ^{ab}	3944 ^a
3	91 ^{b-e}	135.7 ^g	19.9 ^{ab}	112.2 ^{ab}	9.93 ^c	0.23 ^{kl}	71.9 ^{cd}	16.8 ^{ab}	0.21 ^{ab}	14500 ^a	27.2 ^b	3058.1 ^a
4	89.7 ^{b-f}	143.7 ^{def}	20.2 ^{ab}	113.9 ^a	13 ^{abc}	0.45 ^{ij}	80.9 ^{bcd}	14.3 ^{abc}	0.21 ^{ab}	16667 ^a	31.9 ^{ab}	3397.3 ^a
5	84.7 ^{c-f}	146 ^{a-e}	19.2 ^b	93.9 ^{d-g}	9.3 ^c	0.86 ^g	101.1 ^{abc}	10.7 ^{abc}	0.32 ^{ab}	12333 ^a	27.7 ^b	3729.1 ^a
6	86.7 ^{b-f}	148.7 ^{a-d}	20.8 ^{ab}	94.1 ^{d-g}	10.5 ^{bc}	0.17 ^l	113.2 ^a	8.1 ^c	0.3 ^{ab}	17500 ^a	33.5 ^{ab}	3207.9 ^a
7	83.7 ^{def}	146 ^{a-e}	19.8 ^{ab}	102 ^{bcd}	9.1 ^c	0.28 ^{kl}	94.9 ^{a-d}	9.5 ^{bc}	0.29 ^{ab}	11167 ^a	42.9 ^a	3227.9 ^a
8	104.3 ^a	150 ^{ab}	17.1 ^c	96.9 ^{c-f}	13.1 ^{abc}	0.63 ^h	73.2 ^{cd}	8.6 ^{bc}	0.20 ^b	14667 ^a	38.0 ^{ab}	2911.4 ^a
9	84.7 ^{c-f}	145 ^{cde}	19.9 ^{ab}	95.5 ^{c-f}	12.7 ^{abc}	0.32 ^{jk}	96.4 ^{a-d}	9 ^{bc}	0.38 ^a	8000 ^a	36.7 ^{ab}	3045.3 ^a
10	95 ^{abc}	150.7 ^a	19.9 ^{ab}	112.7 ^a	16.1 ^{ab}	0.78 ^g	90.6 ^{a-d}	10.3 ^{bc}	0.14 ^{ab}	15000 ^a	37.8 ^{ab}	4055.8 ^a
11	96.3 ^{ab}	149 ^{abc}	21.5 ^a	105.3 ^{abc}	11.9 ^{abc}	0.54 ^{hi}	105.7 ^{ab}	15 ^{abc}	0.33 ^{ab}	12500 ^a	34 ^{ab}	3907 ^a
12	86.7 ^{b-f}	148.7 ^{a-d}	21.4 ^{ab}	99.4 ^{cde}	13 ^{abc}	1.64 ^e	106.4 ^{ab}	13.5 ^{abc}	0.37 ^{ab}	10333 ^a	37.4 ^{ab}	3727.1 ^a
13	81.3 ^{ef}	143 ^{ef}	20.5 ^{ab}	86.4 ^{fgh}	11.7 ^{abc}	2.43 ^b	81.8 ^{bcd}	15.3 ^{abc}	0.34 ^{ab}	10667 ^a	31.3 ^{ab}	3377.1 ^a
14	79.3 ^f	144.7 ^{c-f}	20 ^{ab}	79.6 ^h	12.3 ^{abc}	2.18 ^c	92.3 ^{a-d}	12.5 ^{abc}	0.33 ^{ab}	10833 ^a	30.4 ^b	3366.5 ^a
15	80.7 ^{ef}	148.3 ^{a-d}	19.5 ^{ab}	84.1 ^{gh}	11.6 ^{abc}	0.32 ^{jk}	95.3 ^{a-d}	12.3 ^{abc}	0.24 ^{ab}	18500 ^a	29.2 ^b	3225 ^a
16	84 ^{def}	147 ^{a-e}	20.9 ^{ab}	97.5 ^{c-f}	12.7 ^{abc}	0.35 ^{jk}	95.2 ^{a-d}	12.4 ^{abc}	0.31 ^{ab}	11667 ^a	29.6 ^b	3211.2 ^a
17	82 ^{ef}	142.7 ^{ef}	20.2 ^{ab}	93.4 ^{d-g}	10.1 ^c	0.45 ^{ij}	90.5 ^{a-d}	11 ^{abc}	0.31 ^{ab}	9833 ^a	32.7 ^{ab}	2715.9 ^a
18	85 ^{c-f}	142.7 ^{ef}	20.4 ^{ab}	105.2 ^{abc}	12.9 ^{abc}	1.42 ^f	86.7 ^{a-d}	10.1 ^{bc}	0.21 ^{ab}	14167 ^a	33.2 ^{ab}	2712.2 ^a
19	89 ^{b-f}	140 ^{fg}	20.3 ^{ab}	110.3 ^{ab}	15.7 ^{ab}	1.31 ^f	67.4 ^d	18.7 ^a	0.22 ^{ab}	17000 ^a	32.9 ^{ab}	3044.4 ^a
20	85.3 ^{c-f}	145 ^{cde}	19.2 ^b	88.7 ^{e-h}	13.2 ^{abc}	0.26 ^{kl}	101.3 ^{abc}	10.5 ^{abc}	0.31 ^{ab}	11167 ^a	38.2 ^{ab}	3223.1 ^a
Mean	87.43	145.03	20.03	98.98	12.28	0.95	92.13	12.52	0.29	13150.0	33.56	3349.96
CV (%)	6.24	1.77	5.52	5.89	23.01	8.44	16.76	33.74	30.77	42.58	18.01	26.13
LSD	9.02	4.25	1.83	9.63	4.67	0.05	25.52	6.98	0.15	NS	9.99	NS

Note; DH= days to heading, DM= days to maturity, PL= panicle length (cm), PH= plant height (cm), NFTPP= number of fertile tillers per plant, NFGPP= number of filled grain per panicle, NUFGPP= number of unfilled grain per panicle, HI= harvest index, BIO= above ground biological yield (kg/ha), TSW= thousand grain weight (gram), GY= grain yield (kg/ha).

