GENETIC VARIABILITY AND CHARACTER ASSOCIATION IN RAIN FED LOWLAND RICE (*Oryza sativa* L.) GENOTYPES AT PAWE AND FOGERA, ETHIOPIA

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GENETIC VARIABILITY AND CHARACTER ASSOCIATION IN RAIN FED LOWLAND RICE (*Oryza sativa* L.) GENOTYPES AT PAWE AND FOGERA, ETHIOPIA

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DEDICATION

I dedicate this thesis to the memory of my family for nursing me with affections and loves and their partnership for the success of my life.

STATEMENT OF THE AUTHOR

By my signature below, I declare and affirm that this thesis is my work. I have followed all ethical and technical principles of scholarship in the proposition, data collection, data analysis and compilation of this thesis. Any scholarly matter that is included in the thesis has been given recognition through citation. This thesis is submitted in partial fulfillment of the requirements for the award of a Master of Science Degree at Jimma University. The thesis is deposited in the library of Jimma University and will be made available to borrowers under the rule of the library. I declare that this has not been submitted to any other institution anywhere for the award of any academic degree, diploma or certificate.

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ABBREVATIONS AND ACRONYMS

ANOVA	Analysis of Variance
CSA	Central Statistical Authority
CV	Coefficient of Variation
FAO	Food and Agricultural Organization
IRRI	International Rice Research Institute
MoARD	Ministry of Agriculture and Rural Development
NRDSE	National Rice Development Strategies
NRRDSE	National Rice Research and Development Strategy of Ethiopia
OECD	Organization for Economic Cooperation and Development
SSA	Sub Saharan Africa
WARDA	West Africa Rice Development Association

GENETIC VARIABILITY AND CHARACTER ASSOCIATION IN RAIN FED LOWLAND RICE (*Oryza sativa* L.) GENOTYPES AT PAWE AND FOGERA, ETHIOPIA

ABSTRACT

The national average yield of rice is low which is mainly attributed to shortage of improved varieties. The present study consists of 36 rice genotypes that were evaluated at two locations, namely Fogera and Pawe with the objectives of identifying high yielding and well adapted varieties assessing genetic variability and character association for the 14 traits. The experiments were conducted using simple lattice design across two locations during the 2015 cropping season. Combined analysis of variance revealed statistically significant differences ($p<0.05$) indicating the existence of genetic variability among the 36 genotypes for all the traits studied. Genotype x location interactions were significant for days to maturity, plant height, panicle length, culm length, flag leaf length, number of filled spikelets per panicle, number of total spikelets per panicle, days to heading, biomass yield, paddy yield and harvest index. Significant differences were observed for paddy yield that ranged from 6759.00 to 2886.00 kg ha^{-1} with overall mean value of 5370.0 kg ha^{-1}. Higher PCV and GCV values were exhibited by plant height, culm length, number of unfilled spikelets per panicle, biomass yield and paddy yield. The highest heritability was recorded for culm length followed by plant height, biomass yield and panicle length. High to medium heritability coupled with high GCV and high genetic advance as percentage of mean were exhibited for plant height, biomass yield , paddy yield and number of unfilled spikelets per panicle. High genetic advances as percent of means were recorded by plant height, culm length, biomass yield, paddy yield and number of unfilled spikelets per panicle. Clustering of genotypes were not associated with their geographical origin, instead of the genotypes were mainly grouped based on morphological significances. The Mahalanobis D^2 statistics revealed that 36 genotypes were grouped into five distinct clusters, and the chi-square test for the five clusters indicated the presence of highly significant difference ($p<0.01$) among the clusters, confirming that the studied genotypes were divergent. Principal component (pc) showed that the first four PCs having eigen values greater than one accounted about 79.23% of the total variation. Grain yield exhibited significant ($P<0.05$) and positive genotypic correlation with days to heading, days to maturity, number of filled spikelets per panicle, number of fertile tillers per plant, harvest index, number of total spikelets per panicle and biomass yield. Path coefficient analysis showed that biomass yield followed by harvest index, number of total spikelets per panicle and plant height exhibited the highest direct effects on grain yield. These characters can be considered for indirect selection for paddy yield. This study was carried out only for one season at two locations. Hence, it is advisable to repeat the study at more number of locations and seasons in major rice-growing areas by including additional genotypes to come up with sound conclusion and in the future, molecular analysis techniques should be employed to confirm the genotypic diversity in this study.

Key words: correlation, *heritability*, *Oryza sativa* (rice), principal component, variability

1. INTRODUCTION

Rice is a self-pollinated cereal crop belonging to the family *Gramineae* (synomym-*Poaceae*) under the order *Cyperales* and class monocotyledon having chromosome number 2n=24 (Hooker, 1979). The genus *Oryza* is known to consist of two cultivated species i.e. Asian rice (*O. sativa*, 2n=24=AA) and African rice (*O. glaberrima*, 2n=24=AA) and 22 wild species (2n=24, 48) (Singh *et al*., 2015). The river valleys of Yangtze, Mekon River area in China could be the primary center of origin of *Oriza sativa* (Zhao, 2011; Gross and Zhao, 2014). *Oryza glaberrima* is indigenous to the upper valley of the Niger River and it is cultivated only in western tropical Africa (Ansari, *et al.*, 2015).

The government of Ethiopia named as rice *millennium crop* and ranked it among the priority commodities of the country to attain food security (NRRDSE, 2010; Asefa *et al*., 2011). It is also considered as one of the best and the cheapest alternative technology available to farmers for efficient utilization of their scarce resources, especially the land and water in swampy and water logged environments (Mulugeta, 2000; Mulugeta and Gebrekidan, 2005). Rice is source of income and employment opportunities for rice farmers. It is used in the preparation of local foods such as *injera*, *dabbo*, *genffo*, *kinchie* and *shorba* and local beverages like t*ela* and *areki* (Heluf and Mulugeta, 2006; Asefa *et al*., 2011). The straw is mainly used as fuel, feed stuff, fertilizer and industrial raw material (Liu *et al*., 2011).

Rice is the second most-produced cereal in the world after wheat and representing a staple food source for more than half of the world's population (Luz *et al*., 2016). The world's average production (kg/ha) has doubled during the last 25 years, largely due to the use of improved technology such as high yielding varieties (Rahman *et al*., 2012). The global production of paddy rice in 2014 was about 740.96 million tones and the cultivated area is estimated as 163.24 million hectares. From the total production, Asia accounts the largest production totaling to about 144.25 million tones whereas Africa produces approximately 11.58 million tons (FAOSTAT, 2015). In 2014, average yield of rice for high producing countries 6.69, 6.75, 9.52, 5.75, 5.13 and 8.48 ton ha^{-1} for Japan, China, Egypt, Vietnam,

Indonesia and USA, respectively, (FAOSTAT, 2015). In Ethiopia, in 2014, about 46, 823ha of land was cultivated to with the total production of 1, 318, 218.53 tons (CSA, 2015).

Currently, Fogera, Gambella, Metema, and Pawe plains located in the northern, northwestern, and western regions of Ethiopia are becoming a major rice producing areas in Ethiopia (Mulugeta, 1999; 2000). Furthermore, based on GIS information and agro-ecological requirements of rice, the potential rain fed rice production area in Ethiopia is estimated to be about 30 million hectares (MoARD, 2010; Assefa *et al*., 2011). Of which 5.6 million ha is found to be highly suitable, and 25 million ha is suitable to rain fed up land rice while 3.7 million ha is potential available area for lowland irrigated rice in the country (NRRDSE ,2010; Dawit , 2015).

The national average paddy yield of rice in Ethiopia is 2.81 ton/ha (CSA, 2015; FAOSTAT, 2015), which is much lower than the world's average rice yield of 4.54 ton/ha (FAOSTAT, 2015). This is due to insect pest and diseases occurrence (rice blast and brown spot), weeds and environmental fluctuations (Reda *et al*., 2012; Lakew *et al.,* 2014). In addition, poor agronomic practices; human and institutional capacity and shortage of adapted to different agro-ecologies are the major rice production constraints in the country (Tesfaye *et al.,* 2005; MoARD, 2010; NRRDSE, 2010).

Rice is believed to be introduced to Ethiopia in 1970s (Gebrekidan and Seyoum, 2006) and research on the crop was started in 1985 (NRDSE, 2009; NRRDSE, 2010). Since then, to alleviate some of the constraints to rice production by developing improved varieties researchers studied genetic variability in rice which is pre-requisite for rice breeding program since the development of an effective rice breeding program is dependent up on the existence of genetic variability and character association. Therefore, before launching any breeding program, survey of genetic variability with the help of suitable parameters such as genotypic coefficient of variation, heritability estimates and genetic advance are absolutely necessary to start an efficient breeding program (Mishra *et al*., 1988; Atta *et al*., 2008).

For instance, Mulgeta (2015) studied 22 released upland rice varieties and Mulugeta *et al*. (2012) investigated the genetic variability and character association of 14 upland rice genotypes using morphological characterization. Moreover, Fentie *et al*. (2014) evaluated 12 upland rice genotypes using morphological characterization. All researchers reported that the existence of adequate genetic variability and character association among the tested materials. Several other researchers also reported association between different yield and yield related traits along with high values of heritability and genetic advance for grain, 1000 grain weight, number of fertile tillers per plant, number of grains per panicle, panicle length, biomass yield and plant height in rice. Traits such as plant height, number of fertile tillers per plant, panicle length showed a positive significant association with grain yield both at genotypic and phenotypic levels (Sabesan *et al*., 2009; Nandan *et al*., 2010 ; Rai *et al*., 2014).

However, limited attention has been given to studies on genetic variability and character association of grain yield and yield related traits in introduced rain fed lowland rice genotypes to improve the grain yield in the study areas. Therefore, keeping in view these urgent needs, the present investigation has been undertaken to assess the extent of genetic variability and character association among thirty-four rain fed lowland rice genotypes with two check varieties for yield and yield related traits to increase productivity and bridge the yield gap between national average and available the potentials. The current study was conducted with the following objectives:

(i) To assess the extent of genetic variability for grain yield and related traits to identify high yielding and well adapted varieties in rain fed lowland rice genotypes.
(ii) To estimate the association for grain yield and related traits to partitioning the correlation coefficients into direct and indirect effects in rice genotypes.

2. LITERATURE REVIEW

2.1. General Description of Rice

The most commonly cultivated species of *O. sativa* is further classified into sub species namely, *indica*, *japonica* and *javanica* (Machunde, 2013). It is grown worldwide including in Asian, North and South American, European Union, Middle Eastern and African countries. *O. glaberrima* is grown solely in West African countries. There is close similarity between the two species: the only differences are in glume pubescence, ligule size and color of pericarp which is red in *Oryza glaberrima*. Interestingly, intermediate forms between the two species occur (Usha and Pandey, 2007).

The wild species are widely distributed in the humid tropics and subtropics of Africa, Asia, Central and South America, and Australia (Chang, 1976). Vaughan (1994) described 24 distinct species in the genus *Oryza* and classified them into four species complexes; *O. sativa* complex, *O. officinalis* complex, *O. meyeriana* complex and *O. ridleyi* complex. *O. schlechteri* was thought to be extinguished, but recently recollected from Papua New Guniea by Vaughan (1994). *O. sativa* complex comprises two cultigen; *Oryza sativa* (indica and japonica rice) and *O. glaberrima* (African cultivated rice) and six wild species (Singh and Khush, 2000).

Coleoptiles and roots first emerge from the germinating rice seeds. Seedlings differentiate leaves from the growing point of the main culm and tiller buds in the axil of leaves. Panicles primordial differentiate at the top of culms. At heading time, panicles come out of flag leaf sheaths. Flowering takes place in spikelets on a panicle, followed by pollination on stigmata and fertilization in ovules. Embryo and endosperm mature in the ovule and become a seed for the next generation. Rice plants are very easily propagated by seeds or tiller buds (OCED, 1999). The leaf consists of a blade, a sheath and a ligule and auricle at the junction between blade and sheath. The culm consists of nodes and hollow internodes. The spikelet has six stamens and the ovary has two branched stigma. The seed consists of embryo, endosperm, pericarp and testa enclosed by a palea and a lemma with an apiculus on the top of the lemma (OECD, 1999).

2.2. Genetic Variability , Heritability and Expected Genetic Advance

2.2.1. Genetic variability

Variation is the occurrence of differences among the individuals due to the differences in their genetic composition and/or the environment in which they were raised (Allard, 1960; Falconer and Mackay, 1996). In addition, the magnitude of genetic variability present in the base population of any crop species is also pivotal to crop improvement which must be exploited by plant breeders for yield improvement (Idahosa *et al*., 2010). The success of a breeding program depends upon the magnitude of variability existing in the germplasm. Genetic variability is of immense importance because it could be transmitted to the progeny and the proper management of this diversity could produce permanent gain in the performance of the plant (Welsh, 1981). According to Asins (2002), genetic variation is the raw material used by plant breeders to improve traits and characteristics of interest for producers and consumers. The genetic variability is the real measure for variability concealed in a population, since it is a result of additive and non-additive gene effects (Machunde, 2013). Thus, genetic variability is pre-requisite for improving any crop plant. The information about the nature and extent of variation coupled with the knowledge of character association are helpful for improving the grain yield through selection. Heritability and genetic advance of grain yield and its components help to assess the genetic gain through selection (Kumar, 2011).

Phenotypic variability is the observable variation present in a character in a population, it includes both genotypic and environmental of variation and as a result, its magnitude differs under different environmental conditions. Genotypic variation, on the other hand, is the component of variation which is due to the genotypic differences among individuals within a population and is the main concern of plant breeders (Singh, 2001). The amount of variation present in a population is measured and expressed in terms of variance (Falconer and Mackay, 1996). Moreover, genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are useful in detecting the amount of variability present in the germplasm (Idris *et al*., 2012). Genotypic coefficient of variation (GCV) measures the variability of any trait. The extent of the environmental influence on any trait is indicated by the magnitude of the differences between the genotypic and phenotypic

coefficients of variation. Large differences reflect high environmental influence, while small differences reveal high genetic influence (Allard, 2000; Osman *et al*., 2012).

Selection for yield may not be much satisfying unless other yield attributing traits are taken into consideration (Akinwale *et al.,* 2011). The assessment of variability for grain yield and its component characters is of utmost importance before planning for an appropriate breeding strategy for genetic improvement. Genetic variability for agronomic traits is the key component of breeding programs for broadening the gene pool of rice. Plant breeders commonly select for yield components which indirectly increase yield.

The genetic basis of changes associated with the process of rice domestication was studied in detail (Xiong *et al*., 1999). Studies in rice using advanced backcross QTL analysis provided evidence that certain regions of rice genome are likely to harbour genes of interest for plant improvement (Xiao *et al*., 1998; Moncada *et al*., 2001). Generally, Falconer and Mackay (1996) indicates the three ways of assessing the existence of variability in breeding population; (1) by using simple measures of variability, such as range, mean, variance, standard deviation, coefficient of variability and standard error (2) by estimating the various components of variance and (3) by measuring the genetic diversity e.g. D^2 statistics.

Akinwale *et al.* (2011) estimated the phenotypic and genotypic coefficients of variation, in rice and significantly differed for days to 50% heading, days to maturity, plant height, panicle length, number of tillers per plant,1000 grains weight and grain yield, which implies that the genotypes constitute a pool of germplasm with adequate genetic variability. An investigation also conducted by J*aved et al.* (2015) in fifteen advanced breeding lines of rice. The yield attributing traits like plant height, panicle length, filled spikelet, unfilled spikelet, tillers per plant, thousand grains weight and yield per plant showed significant variability.

An attempt made by Sarwar *et al*. (2015) to assess genetic variability for important agro-morphological traits in forty-two a-man rice (harvested in the month of November and December) genotypes. the analysis of variance revealed significant variation for plant height, total tillers per plant, effective tillers per plant, days to 50% flowering, panicle length, filled grains per panicle, unfilled grains per panicle, days to maturity, thousand grains weight and

yield per plant studied indicates the existence of variation among the genotypes. The PCV values were slightly higher than the respective GCV values for all the characters except number of unfilled grains per panicle indicating that the characters were less influenced by the environment.

Shahriar *et al*. (2014) conducted an experiment with thirty advanced transplanted a-man rice breeding lines along with four checks. The analysis of variance indicated that the differences among genotypes for all the traits studied were highly significant. A wide range of variation observed among 34 rice genotypes for nine yield contributing traits. Phenotypic coefficients of variation (PCV) were higher than genotypic coefficients of variation (GCV) for plant height, panicle length, effective tillers per hill, number of filled grains per panicle, number of unfilled grain per panicle, days to maturity,1000 grain weight and yield per plot indicating that the measured traits interacted with the environment to some extent.

2.2.2. Heritability

According to Falconer and Mackay (1996), heritability is defined as the measure of the correspondence between breeding values and phenotypic values. Heritability is classified into broad and narrow sense (Acquaah, 2012). Heritability in the broad sense is defined as the proportion of phenotypic variance that is attributable to an effect for the whole genotype, comprising the sum of additive, dominance and epistatic effects (Nyquist 1991; Falconer; Mackay 1996). Moreover, it is the relative magnitude of genotypic and phenotypic variance for the traits and it gives an idea of the total variation accounted to genotypic effect (Allard, 1960). This gives an idea of the total variation ascribable to genotypic effects, which are exploitable portion of variation. The importance of broad sense heritability in plant breeding is limited because it does not give the clear estimate of the fixable genetic variance for selection. On the other hand, narrow sense heritability is the ratio of additive genetic variance to the total phenotypic variance and it gives the best estimate of heritable variance which can be fixed by selection (Falconer and Mackay, 1996; Sleper and Poehlman, 2006; Piepho and Mohring, 2007).

Heritability is often used by plant breeders to quantify the precision of single field trials or of series of field trials and a key parameter in quantitative genetics because it determines the

response to selection. Thus, heritability plays a predictive role in breeding, expressing the reliability of phenotype as a guide to its breeding value. It is the breeding value which determines how much of the phenotype would be passed onto the next generation (Tazeen *et al*., 2009). Therefore, high heritability helps in effective selection for a particular character, which also is classified as low (below 30%), medium (30-60%) and high (above 60%) (Robinson *et al*. ,1949; Falconer and Mackay, 1996).

There is a direct relationship between heritability and response to selection, which is referred to as genetic advance. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone (Larik *et al*., 2000; Bisne*et al*., 2009; Mohsin *et al*., 2009). Moreover, heritability and genetic advance when calculated together would prove more useful in predicting the resultant effect of selection on phenotypic expression (Johnson *et al*., 1955). Therefore, heritability of a trait is an important in determining its response to selection. It was found out earlier that genetic improvement of plant for quantitative traits requires reliable estimates of heritability in order to plan efficient breeding program. The progress in breeding for yield and its contributing characters of any crop is polygenically controlled, environmentally influenced and determined by the magnitude and nature of their genetic variability (Fisher, 1981). It is very difficult to judge whether observed variability is highly heritable or not. Moreover, knowledge of heritability is essential for selection based improvement, as it indicates the extent of transmissibility of a character into future generations (Sabesan *et al*., 2009).

High heritability values indicate that the characters under study are less influenced by environment in their expression. The plant breeder may make selection safely on the basis of phenotypic expression of these characters in the individual plant by adopting simple selection methods. Characters having high heritability indicates the scope of genetic improvement of these characters through selection. Similar results have been reported by Sarawgi *et al*. (2000) and Gannaman (2001). Moreover, Johnson *et al*. (1955) suggested that higher heritability estimates along with higher genetic advance would be more useful for selecting the best individual. Therefore, the estimation of heritability for any trait requires the partitioning of the observed variation between genetic effects and environmental effects (Cockerhem, 1963). However, when the phenotypic variability is large, traits with high

heritability values are subject to large genetic gains per generation when selection is applied (Nyquist, 1991).

Different researchers estimated broad sense heritability for different rice plant traits and the reports are available. Kathikeyan *et al*. (2010) recorded estimates heritability, 99.8% for days to flowering, 99.2% for days to maturity, 87.3% for plant height, 79.8% for panicle length, 88.8% for number of fertile florets per plant, 97.6% for 1000 grain weight and 73.2% for grain yield plant. Fentie *et al*. (2014) reported high broad sense heritability for thousand seed weight, days to maturity, days to 50% heading and biomass yield (kg/ha) and medium heritability reported for plant height, grain yield (kg/ha), number of filled grains per panicle and number of spikelet per panicle. Akinwale *et al*. (2011) registered high to medium heritability for days to heading, days to maturity, plant height, grain yield and number of grains per panicle. Bisne *et al*. (2009) also observed high heritability for days to heading, plant height, panicle length, effective tillers per plant, number of filled spikelets per panicle, total number of spikelets per panicle, 1000 grain weight and harvest index.

Yadav *et al*. (2010) conducted an experiment with forty rice genotypes. These authors observed high heritability for traits like plant height (98.8%), biological yield (97.1%), harvest index (95.8%), number of spikelets per panicle (94.4%), flag leaf length (92.5%), panicle length (89.4%) and days to 50 % flowering (87.6%). Mulegeta *et al*. (2012) evaluated fourteen upland rice genotypes with eleven characters to estimates the phenotypic and genotypic variability. The broad sense heritability values were varied from 25.82 to 92.17% and highest heritability values were recorded for 50% flowering, days to 85% maturity, plant height, panicle length, spikelets per panicle and 1000 grain weight.

2.2.3. Genetic advance (GA)

Genetic advance measures the expected genetic progress that would result from selecting the best performing genotypes for a character being evaluated (Allard, 1999). The estimate of genetic advance as per cent of mean provides more reliable information regarding the effectiveness of selection in improving the traits. Genetic advance denotes the improvement in the genotypic value of the new population over the original population (Ghosh and Sharma, 2012). Moreover, genetic advance provides information on expected genetic gain resulting from selection of superior individuals (Satheeshkumar and Saravanan, 2012).

According to Allard (2000), genetic advance under selection is a genotypic value, which depends on three things such as genetic variability, heritability or masking effect of non-genetic variability on the genetic variability and the selection intensity applied. Genetic progress would increase with increase in the variance. Therefore, the utility of estimates of heritability is increased when they are used in conjunction with the selection differential, the amount by which the mean of the selected lines exceeds the mean of the entire group (Johnson *et al*., 1955). Generally, genetic advance gives clear picture and precise view of segregating generations for possible selection. Higher estimates of heritability coupled with better genetic advance confirms the scope of selection in developing new genotypes with desirable characteristics (Ajmal *et al.*, 2009).

Many researchers reported different findings in rice. For instance, Rai *et al*. (2014) reported that high heritability coupled with high genetic advance as percent mean for grain yield per plant, biological yield per plant, flag leaf length, number of spikelets per panicle, and harvesting index. Osman *et al.* (2012) evaluated thirteen genotypes of upland rice to estimate the genotypic and phenotypic variability. The highest genotypic coefficient of variation and genetic advance were recorded for number of tillers per plant and plant height. Shahriar *et al*. (2014) evaluated thirty advanced long-stemmed transplanted (T-aman) rice *(Oryza sativa L.)* breeding lines along with four checks, the highest genetic advance was recorded for number of filled grain per panicle (28.7) followed by number of unfilled grain per panicle and the lowest for days to maturity (0.83) among yield contributing traits. The genetic advance as percent of mean was the highest in case of unfilled grain per panicle while it was the lowest for days to maturity.

Genetic advance in 24 rice genotypes evaluated by Patel *et al.* (2012) and the highest genetic advance as percentage of mean was observed for number of unfilled spikelet panicle^{-1}. The estimates of genetic advance as percentage of mean (>30%) were also observed for other characters for total number of tillers per plant, total number of spikelets panicle^{-1} and number of filled grain panicle^{-1}. Anbanandan *et al.* (2009) also observed genetic advance for the characters *viz.*, number of productive tillers plant^{-1}, 1000 grain weight and grain yield plant^{-1} in both F3 and F4 generations of four crosses of rice genotypes.

2.2.4. Correlation(r) and path coefficient analysis

2.2.4.1. Phenotypic and genotypic character associations

The degree of association between two characters is measured by the correlation coefficient. Therefore, correlation is helpful in determining the component characters of a complex trait like yield. Such studies are useful in disclosing the magnitude and direction of these relationships between the different characters and grain yield as well as among characters themselves (Falconer and Mackay, 1996).

Character of crop plant are generally correlated to each other. There are three types of correlations phenotypic, genotypic, and environmental correlations. The phenotypic correlation measures the extent to which the two observed characters are linearly related. Genetic correlation is the association of breeding values (additive genetic variance) of the two characters. The genetic causes of correlation are mainly pleiotropic effects of genes affecting different characters. Pleiotropy is the property of a gene whereby it affects two or more characters, so that if the gene is segregating it causes simultaneous variation in the two genetic correlations determines the degree of association between character and how they may enhance selection (Falconer and Mackay, 1996). According to Falconer (1985) correlation between different traits is generally due to the presence of linkage disequilibrium, pleiotropic gene actions and epistatic effect of different genes, environment also plays an important role in the correlation. In some cases, environment affects both the traits simultaneously in the same direction or sometimes in different directions. Genetic and environmental causes of correlation combine together and give phenotypic correlation. The dual nature of phenotypic correlation makes it clear that the magnitude of genetic correlation cannot be determined from phenotypic correlation. According to Johansson *et al*. (1955) studies on genotypic and phenotypic correlations among characters of crop plants are useful in planning, evaluating and setting selection criteria for the desired characters in breeding programme.

Breeding strategy in rice mainly depends upon the degree of associated characters as well as its magnitude and nature of variation (Prasad *et al*., 2001; Zahid *et al*., 2006). Thus, complete knowledge on interrelationship of plant character like grain yield with other characters is of

paramount importance to the breeder for making improvement in complex quantitative character like grain yield for which direct selection is not much effective. Hence, association analysis was undertaken to determine the direction of selection and number of characters to be considered in improving grain yield (Idris *et al*., 2012). Correlation coefficient measures the strength and direction of a linear association between two variables. It ranges from -1 to +1. Correlation value (r = 1) implies perfect (100%) correlation, where both traits vary hand in hand, (r = -1) means there is 100 % correlation between two characters, but they vary in opposite direction, and (r = 0) carries the implication that there is no correlation at all between the two characters (Falconer and Mackay 1996).

The relationship between rice grain yield and yield component traits has been studied widely at a phenotypic level. Idris *et al*. (2012) observed positive phenotypic and genotypic correlation coefficient between grain yield and number of filled grains per panicle, harvest index, panicle length and number of grains per panicle. Hairmansis *et al*. (2010) recorded a positive and significant association of grain yield with number of filled grain per panicle and number of spikelets per panicle. Ullah *et al*. (2011) obtained that grain yield was positive and significant associated with panicle length.

2.2.4.2. Path coefficient analysis

Path coefficient analysis is simply a standardized partial regression coefficient and as such measures the direct and indirect effect for one variable upon another and permits the separation of the correlation coefficient into components of direct and indirect effect (Dewey and Lu, 1959). Moreover, using path coefficient analysis, it is easy to determine which yield component is influencing the yield substantially. The information obtained by this technique helps in indirect selection for genetic improvement of yield of rice and measures the relative importance of each trait. Yield component analysis is of fundamental importance to determine the direct and indirect contributions towards yield. Path analysis provides clear picture of character associations for formulating efficient selection strategy. Since, the correlation coefficient alone is inadequate to interpret the cause and effect of relationships among the traits and ultimately with yield. Because, path coefficient analysis furnishes information of influence of each contributing traits to yield directly as well as indirectly and also enables

breeders to rank the genetic attributes according to their contribution (Cyprien and Kumar, 2011). As the yield is polygenically controlled and also influenced by its component characters, direct selection for yield is often misleading. Path analysis has been used by plant breeders to assist in identifying traits that are useful as selection criteria to improve crop yield (Milligan *et al*., 1990).

Generally, path coefficient analysis is a statistical technique of partitioning the correlation coefficients into its direct and indirect effects, so that the contribution of each character to yield could be estimated. It is used in plant breeding programs to determine the nature of the relationships between yield and yield components that are useful as selection criteria to improve the crop yield (Mohamed *et al.*, 2012). Since grain yield is a complex trait, indirect selection through correlated, less complex and easier measurable traits would be an advisable strategy to increase the grain yield. Efficiency of indirect selection depends on the magnitude of correlations between yield and target yield components (Bhatti *et al*., 2005). Breeding strategy in rice mainly depends upon the degree of associated characters as well as its magnitude and nature of variation (Zahid *et al*., 2006).

The goal of the path analysis is to accept descriptions of the correlation between the traits, based on a model of cause and effect relationship and to estimate the importance of the affecting traits on a specific trait (Cyprien and Kumar, 2011). Correlation together with path analysis would give a better insight into cause and effect relationship between different pairs of characters (Jayasudha and Sharma, 2010). Knowledge of correlation between yield and its contributing characters are basic and foremost endeavor to find out guidelines for plant selection. Partitioning of total correlation into direct and indirect effect by path coefficient analysis helps in making the selection more effective (Priya and Joel, 2009).

Path analysis was used by several researchers to determine the effects of important yield components. Surek and Beser (2003) studies correlation and path coefficient analysis for some yield related traits in rice (*Oryza sativa* L.) they reported that the number of filled grains per panicle, number of productive tillers per square meter, biological yield and harvest index recorded a direct positive effect on grain yield, and they had a positive indirect effect via each

other except between biological yield and harvest index and between the number of productive tillers per square meter and the number of filled grains per panicle.

Mamun *et al.* (2012) reported that days to heading had the maximum positive direct effect on grain yield followed by number of filled grain yield per panicle in rice crop. The direct effect revealed that the characters viz., days to heading and number of filled grain yield per panicle had high positive correlation with grain yield per hill, suggesting thereby, good scope for the improvement of grain yield by selecting plant types bearing higher days to harvesting in combination with high filled grain per panicle. Mulugeta *et al. (*2012) reported that the grain yield per panicle (2.226) exhibited maximum positive direct effect on grain yield followed by das to 50% flowering (1.465), panicle length (0.641) and plant height (0.087) in rice.

2.2.5. Genetic divergence

Genetic divergence is the statistical distance between genotypes. It is determined by using cluster analysis in to different groups (Singh and Chaudhary, 1999). It is the major tool that used in estimating genetic distances is multivariate analysis. Genetic distance measures based on phenotypic characters are one of the main multivariate techniques used to provide criteria for choosing parents (Bertan *et al*., 2007). According to Vivekananda and Subramanian (1993) genetic divergence is an efficacious tool for an effective choice of parents for hybridization and breeding program. In addition, it is a source of variation, the raw material for crop improvement work, essential to decrease crop vulnerability to abiotic and biotic stresses, ensure long term selection gain in genetic improvement and promote rational use of genetic resources (Messmer *et al*., 1993). Sharma and Koutu (2011) stated that study of genetic divergence among the plant materials is a vital tool to the plant breeders for an efficient choice of parents for plant improvement. Genetically diverse parents are likely to contribute desirable segregants and/or to produce high heterotic crosses. Parents identified on the basis of divergence for any breeding program would be more promising.

Initiation of a hybridization program for improvement of rice requires knowledge of genetic diversity in order to get greatest likelihood of recovering promising segregants. Nevertheless, this beginning information (genetic variability) criterion cannot be successfully used for

discrimination between parents without knowledge of genetic divergence (Ahmed and Borah, 1999). Success in recombination breeding depends on the suitable exploitation of genotypes as parents for obtaining high heterotic crosses and transgressive segregants. For this, the presence of genetic variability in a base population is essential so research should be done for creating of variation. The crosses between parents with maximum genetic divergence are generally the most responsive for genetic improvement (Arunachalam, 1981).

Moreover, one of the main approaches to rice breeding is crossing and subsequent selection. Desirable parental selection is the first and most important step in crop improvement program through hybridization. In order to be benefited from transgressive segregation, genetic dissimilarity between parental genotypes is an essential element (Joshi *et al.,* 2004). In inclusion, genetically divergent parents in any breeding programme is essential to create new genetic stocks and genetic diversity is the most important tool in the hands of the plant breeder in choosing the right type of parents for hybridization programme (Garg *et al.*, 2011).

Evaluation of genetic diversity is important for the source genes of particular traits within the available germplasm (Roy and Panwar, 1993). Thousands of rice cultivars have been evolved through selection from the cultivated material many centuries ago, which are well adapted to the local environments. Many of those rice cultivars had good quality characteristics and higher yield potential under biotic and abiotic stress environments. Since the dawn of civilization, thousands of locally adapted genotypes of aromatic rice have evolved through human selection (Singh *et al.*, 2000). Thus, the study of genetic divergence among the plant materials is an important tool to the plant breeders for an efficient selection of the diverse parents for their potential use in a rice breeding program for the improvement of the rice production. Parents identified on the basis of divergence for any breeding program would be more promising (Kwon *et al*., 2002).

The D^2 technique is based on multivariate analysis developed by Mahalanobis (1936) that had been found to be a potent tool in quantifying the degree of divergence in germplasm. Therefore, the use of Mahalanobis D^2 statistics for estimating genetic divergence has been emphasized by many workers (Shukla *et al*., 2006; Ramya and Senthilkumar, 2008). Other several workers have also emphasized the importance of genetic divergence for the selection

of desirable parents (Murthy and Arunachalam, 1996; Rahman, 1997). Generally, the D^2 statistics is one of the powerful tools to assess the relative contribution of different component traits to the total diversity; it helps to quantify the degree of divergence between populations and to choose genetically diverse parents for obtaining desirable recombination.

Ovung *et al. (*2012) assessed 70 genotypes of rice with 13 agro morphological characters for their genetic divergences and they found high divergence among the genotypes. They observed maximum inter-cluster distance suggesting that the genotypes constituted in different clusters may be used as parents for future hybridization program. Lavanya *et al*. (2014) also evaluated 32 elite rice genotypes with 13 characters and they found high inter cluster distance among other cluster. Rai *et al.* (2014*)* evaluated 40 high yielding rice genotypes observed high inter cluster distance among the genotypes. They suggested that these lines may be utilized in further breeding program for the exploitation of hybrid vigor.

2.2.6. Principal component analysis (PCA)

Principal component analysis is one of the multivariate statistical techniques PCA is a powerful tool for investigating and summarizing underling trends in complex data structures (Legendre and Legendre, 1998). According to Ogunbodede (1997) which identifies plant characters that contribute most to the variation within a group of entries. It is also a common ordination numerical technique, which reduces the dimensions of multivariate data by removing inter-correlation among variables (characters on which units are to be compared), and enables multi-dimensional relationship to be plotted on two or three principal axes (Hayman, 1967). PCA chooses independent or orthogonal axes, which are minimally correlated and represents linear combination of the original characters (Clifford and Stephenson, 1975). In addition, the relative discriminating power for axes and their associated characters are measured by eigen values and factor scores, respectively. A large number of variables are often measured by plant breeders, some of which may not be of sufficient discriminatory power for germplasm evaluation, characterization and management. In such case, principal component analysis may be used to reveal patterns and eliminate redundancy in data sets as morphological and physiological variations routinely occur in crop species (Adams, 1995).

Therefore, knowledge of the nature, extent and organization of this variation could be useful for genetic improvement of crop species. Until a collection has been properly evaluated and its attributes become known to breeders, it has little practical use. Germplasm evaluation in the broad sense and in the context of genetic resources is the description of the material in a collection that covers the entire range of activities starting from the receipt of the new samples by the curator and growing of these for seed increase, characterization and preliminary evaluation and for further evaluation.

According to Sharman (1998) and Chahal and Gosal (2002) characters with largest absolute value closer to unity within the first principal component influence the clustering more than those with lower absolute value closer to zero. The positive and negative loading shows the presence of positive and negative correlation trends between the components and the variables. The characters, which load high positively or negatively, contributed more to the diversity and they were the ones that most differentiated the clusters. The first step in PCA is to calculate eigen values, which define the amount of total variation that is displayed on the PC axes. The first PC summarizes most of the variability present in the original data relative to all remaining PCs. The second PC explains most of the variability not summarized by the first PC and uncorrelated with the first and so on (Jollife, 1986).

Maji and Shaibu (2012) conducted research based on phenotypic diversity of growth character and yield components of 131 rice lines for detecting variation. They reported that PC1 explained 55% and PC2 accounted for 23% of the morphological variation. Worede *et al.* (2014) employed PCA for detecting variation in 24 rice genotypes and reported that the first five PCs explained 89.68 % of the total variation and out of which, the first and the second explained 44.52 %, 16.64 %, respectively, among 24 genotypes. The first PCs major contributor's traits were days to flowering, plant height, biomass yield, culm length and panicle length and in the second PCs total productive tillers per panicle were contributed. Similarly, Tuhina-Khatun *et al. (*2015) reported that the first four PCs accounted for about 72% of the total variation among 43 up land rice genotypes tested.

2.2.7. Cluster analysis (CA)

According to Kroonenberg *et al*. (1995) the main aim of using a cluster technique in the analysis of data from plant breeding trials is to group the varieties into several homogeneous groups such that those varieties within a group have a similar response pattern across the locations. It is reasonable to suppose that all the varieties in the trials will not behave completely independently of one another. For instance, those with similar genetic makeup would be expected to behave similarly. If the entire data array containing information on a (usually large) number of varieties can be reduced to the information on a (usually much fewer) number of groups of varieties (within which the varieties have a similar response pattern), then the task of the plant breeder to interpret the information is much simpler. The methods are often extended to genotype grouping in order to cluster entries that show similarity in one or more characters and thus guide in the choice of parents for hybridization (Nair *et al*., 1998).

There are two types of clustering methods: (1) distance-based methods, in which a pair wise distance matrix is used as an input for clustering analysis. The result can be visualized as a tree or dendrogram in which clusters may be identified; and (2) model based methods, in which observation from each cluster are assumed to be random draws from some parametric model, and inference about parameters corresponding to each cluster and cluster membership of each individual are performed jointly using maximum likelihood or Bayesian methods (Johnson and Wichern, 1992).

The other important aspect in clustering analysis is determining number of clusters or number of acceptance clusters. In essence, this involves deciding where to "cut" a dendogram to find the true or natural groups. Cubic clustering criterion (CCC), pseudo F (SPF) and t^2 (PST^2) statistics were used in determining the number of clusters in the data. It might be advisable to look for consensus among the three statistics that is, local peaks of the CCC and pseudo F statistics combined with a small value of the pseudo t^2 statistic and a larger pseudo t^2 for the next cluster fusion (Mohammadi *et al*., 2003). It must be emphasized that these criteria are appropriate only for compact or slightly elongated clusters, preferably clusters that are roughly multivariate normal.

Several workers grouped rice genotypes using cluster analysis. Baloch *et al*. (2016) classified 20 rice genotypes with 11 morphological characters into four main clusters and those genotypes showing wide genetic diversity among the tested genotypes. Khatun *et al. (*2015) grouped 43 upland rice genotypes into five major groups based on multivariate analysis. Moreover, Pandey *et al*. (2009) reported that by testing the 40 genotypes of rice based on relative magnitude of D^2 statistics grouped into seven clusters; each consists of variable number of genotypes.

3. MATERIALS AND METHODS

3.1. Description of the Study Areas

Field experiments were conducted in 2015 cropping season at two locations, namely, Pawe Agricultural Research Center and Fogera National Rice Research and Training Center. The locations are situated in north western part of Ethiopia in Benishagul-Gumuz and Amhara Region states, respectively.

Fogera National Rice Research and Training Center is located 607km from Addis Ababa (capital of Ethiopia) in the north western part of Ethiopia. Specifically, the experimental site is located at 11^{0}58' N latitude, 37° 41' E longitude and at an elevation of 1810m above sea level. Based on ten years' average meteorological data, the annual rainfall, and mean annual minimum and maximum temperatures are 1300mm, 11.5°C and 27.9°C, respectively. The soil type is black (Vertisol) with pH of 5.90.

Pawe Agricultural Research Center is located 578km away from Addis Ababa. The experimental site is lies at 13° 19' N latitude, 37° 24' E longitude and at an elevation of 1200m above sea level. The major soil type of the study site is well drained Nitisol with the pH value ranging from 5.3 to 5.5. Based on ten years' average meteorological data, the annual rainfall, mean annual minimum and maximum temperatures are 1587mm, 16.3°C and 32.6°C, respectively.

3.2. Experimental Materials

The present study comprised of 34 genotypes of rice along with two checks (Table 1). Among the tested genotypes 17 were from the medium maturing group whereas 19 were from the early maturing group. All genotypes were obtained from Fogera National Rice Research and Training Center and were introduced from Africa Rice Center (Table 1).

3.3. Experimental Design and Trial Management

The experiments were laid out in 6x6 simple square lattice design. The plot size was six rows of 5m length with 0.2m row spacing giving a total areas of $6m^2$ (standard plot size for rice variety trial). Spacing's of 1.0 m and 0.30 m were used between blocks and plots, respectively. For data collection, the middle four rows only were used for determination of grain yield and yield related traits (5 m × 0.8 m =4 m^2).

Planting was done by manual drilling at a rate of 36 g per plot on June 17 at Pawe and June 28 at Fogera in 2015 cropping season. Recommended fertilizer of Urea and DAP at the rate of 64 kg N ha^{-1} and 46 kg P_2O_5 ha^{-1} was applied to each plot. P_2O_5 was applied all at planting time whereas N was applied in three splits i.e. 1/3 at planting, 1/3 at tillering and the remaining 1/3 at panicle initiation according to the national rice fertilizer blanket recommendation at each location.

Weeding was done by hand two to three times starting from 25-30 days after sowing depending on infestation level. All other agronomic practices were applied as per the recommendation for rice production in the two locations during the growing season to raise a healthy rice crop.

Table 1. Description of rice genotypes used for the study

Number	Pedigree	Origin	Ecotype	Sources and maturity group
1	IR74052-184-3-3	IRRI	Lowland	2014 LRNVT-ES
2	YUNJING 23	CHINA	Lowland	2014 LRNVT-ES
3	WAB502-8-5-1	Africa rice	Lowland	2014 LRNVT-ES
4	PSBRC44	IRRI	Lowland	2014 LRNVT-ES
5	WAB376-B-10-H3	Africa rice	Lowland	2014 LRNVT-ES
6	IR 83222-F11-167	IRRI	Lowland	2014 LRNVT-ES
7	IR 83222-F11-18	IRRI	Lowland	2014 LRNVT-ES
8	IR 83222-F11-200	IRRI	Lowland	2014 LRNVT-ES
9	IR 83222-F11-209	IRRI	Lowland	2014 LRNVT-ES
10	IR 83222-F11-66	IRRI	Lowland	2014 LRNVT-ES
11	IR76999-52-1-3-2	IRRI	Lowland	2014 LRNVT-ES
12	IR 83249-F9-29	IRRI	Lowland	2014 LRNVT-ES
13	STEJAREE 45	IRRI	Lowland	2014 LRNVT-ES
14	CHOMRONG	Senegal	Lowland	2014 LRNVT-ES
15	WAB880-1-38-20-17-P1-HB	Africa rice	Lowland	2014 LRNVT-ES
16	WAB880-1-32-1-2-P1-HB	Africa rice	Lowland	2014 LRNVT-MS
17	IRAT112	Cote devoir	Lowland	2014 LRNVT-MS
18	WAS 161-B-6-B-B-1-B	Africa rice	Lowland	2014 LRNVT-MS
19	WAB 326-B-B-7-H1	Africa rice	Lowland	2014 LRNVT-MS
20	IR 83372-B-B-115-4	IRRI	Lowland	2014 LRNVT-MS
21	IR 83377-B-B-93-3	IRRI	Lowland	2014 LRNVT-MS
22	IR 83383-B-B-141-2	IRRI	Lowland	2014 LRNVT-MS
23	IR 83372-B-B-115-3	IRRI	Lowland	2014 LRNVT-MS
24	IR 83383-B-B-141-1	IRRI	Lowland	2014 LRNVT-MS
25	IR80420-B-22-2	IRRI	Lowland	2014 LRNVT-MS
26	IR80463-B-39-3	IRRI	Lowland	2014 LRNVT-MS
27	IR 72768-8-1-1	IRRI	Lowland	2014 LRNVT-MS
28	IR 75518-18-1-2-B	IRRI	Lowland	2014 LRNVT-MS
29	IR 75518-84-1-1-B	IRRI	Lowland	2014 LRNVT-MS
30	YUNLU N0.33	CHINA	Lowland	2014 LRNVT-MS
31	IR 81047-B-106-2-4	IRRI	Lowland	2014 LRNVT-MS
32	WAS 161-B-6-B-1 (NERICA-L-36)	Africa rice	Lowland	2014 LRNVT-MS
33	ARCCU16Bar-21-5-12-3-1-2-1	Africa rice	Lowland	2014 LRNVT-MS
34	ARCCU16Bar-13-2-16-2-1-1	Africa rice	Lowland	2014 LRNVT-MS
35	EDIGET (CHECK-1)	Africa rice	Lowland	Released
36	X-JIGNA (CHECK-2)	North Korea	Lowland	Local

LRNVT-ES= Lowland Rice National Variety Trial Early Set; LRNVT-MS= Lowland Rice National Variety Trial Medium Set; IRRI= international rice research institute Sources: Fogera National Rice Research and Training Center

3.3. Data Collected

Fourteen quantitative traits of morphological data at appropriate growth stage of rice plant were collected and recorded on plot and plant basis according to two rice descriptors (IRRI, 2002 and Bioversity International (2007).

3.3.1. On plot basis

Days to 50 % heading: Days to 50% heading was recorded as the number of days from seeding to the date on which the panicle tips when emerge in 50% of the plants in each plot of the central four rows of panicle have at least partially attained heading.

Days to 85 % maturity: Was registered as the number of days from sowing to the attainment of physiological maturity in 85% of the crop stands attained maturity. It was judged by field visual observation when the turning of the straw and panicle changed to light yellow or straw color.

Paddy yield per plot (g): The rough (paddy) rice yield was determined by harvesting the rice crop from the net middle plot area of $4m^2$ and threshed cleaned and weighed using an electronic sensitive balance and then adjusted to 14% moisture content by using rice moisture tester.

Thousand grains weight (g): paddy grains were measured by random taking of 1000 grains that were well developed, clean and sun dried , which were collected from the middle of four rows of each plot. Finally, the moisture content of the paddy yield was adjusted at 14% moisture content and weighed by using a sensitive balance.

Above ground biomass yield (gram per plot): The total above ground biomass yield produced from all the central four rows of each plot was measured at harvest after two days' sun dried.

Harvest index (%): The ratio of weight of dried paddy yield per plot in grams adjusted to 14 % moisture content obtained from the middle four rows of each plot to the dried total weight of above ground biological yield per plot expressed in percent. Harvest index of each of the genotype was computed using the following formula:

Harvest index=$\frac{\text{Economic grain yield per plot}}{\text{Biological yield per plot}}$ * 100

3.3.2. On plant basis

Plant height (cm): The height of the plant was measured started from the base of the main stem to the tip of the tallest panicle and data recorded by a meter rule on the main tiller of 5 randomly pre-tagged plants in the four central rows of each plot.

Panicle length (cm): The panicle length was measured from the five panicle lengths of the main tiller randomly pre- tagged plants in centimeter started from the basal node on which the first panicle branch starts to the tip of the panicle from the middle of four rows in each plot.

Culm length (cm): Culm length was measured from ground level to the base of the panicle (neck node) and recorded from average of five randomly selected pre-tagged plants, to the nearest centimeter from four middle rows in each plot.

Flag leaf length (cm): The flag leaf length was measured from the ligule to the tip of the blade on the pre-tagged five representative selected plants and was calculated average to the nearest cm after athesis.

Fertile tillers per plant: Number of fertile tillers per plant were taken by actual counts of the total number of tillers bearing panicles per plant by taking the average number of five randomly selected pre-tagged plants that bear panicle was registered at harvest

Number of filled spikelets per panicle: The number of spikelets was determined by counting only filled spikelets from five randomly selected panicles of five sample plants in each plot and averaged.

Number of total spikelet's per panicle: The number of spikelets was determined by counting all spikelets (filled and unfilled) from five randomly selected panicles of five sample plants in each plot and averaged.

Number of unfilled spikelets per panicle: The spikelets that was without kernel as determined by counting only unfilled spikelets from five randomly selected panicles of five sample plants in each plot and averaged.

3.4. Statistical Analysis

The data were subjected to analysis of variance, path analysis, cluster analysis, principal component analysis and phenotypic and genotypic correlations by using SAS 9.2 (SAS, 2008) and GENRES Statistical Software (PISS, 1994)7.01.

3.4.1. Analysis of Variance (ANOVA)

The relative efficiency of simple lattice design obtained was better than Randomized Complete Block Design (Appendix Table1 and 2) at two locations. Therefore, the data of the mean values all experimental units were subjected analysis of variance (ANOVA) based on simple lattice design. To perform a combined statistical analysis across location, test of homogeneity of error variances of each character for the two locations were performed by using F- test (the ratio of the largest to the smallest error variance) to the characters and the test showed homogeneity of the two locations for all characters that involved in the study. Therefore, the ANOVA was also run for the two locations separately and combined over the two locations since all characters showed homogeneity of error variance.

The analysis of variance (ANOVA) was done by using Proc GLM and Proc Lattice procedures for the data collected for grain yield and yield related traits were subjected based on simple lattice design by using SAS version 9.2 separately (SAS, 2008). Then after testing the ANOVA assumptions, Fisher's protected least significant difference (LSD) test at 5% and 1% level of significance was used for genotypes mean comparisons, whenever genotype differences were significant. Cluster analysis and principal analysis were done by using SAS version 9.2 (SAS, 2008) and Minitab 16.

ANOVA model for single location of Simple Lattice Design is:

$$Y_{ijklm} = \mu + \alpha i + \beta + \gamma(k) + \partial j + \pi m + \varepsilon ijklm$$

Where, Y_{ijklm}= response of Y trait from i^{th} genotypes, j^{th} replication

μ=overall mean effects, αi=effects of i^{th} level of treatments,

β= effects of j^{th} level of replications

$\gamma(k)$= effects of k^{th} level of blocks within replications (adjusted for treatments)

∂_l= effects of l^{th} level of intera block error

πm=effects of m^{th} level of randomized complete block error,

ε_{ijklm}=random error component.

ANOVA model for over location of Simple Lattice Design is:

$$Pitjk = \mu + lt + ri(t) + bj(i)(t) + gk + (gl)kt + \varepsilon itjk$$

Where, P_{itjk} is the phenotypic observation in the i^{th} replication, j^{th} incomplete block within replication i and location t and from the k^{th} genotype

μ is the overall grand mean

l_t is the effect of location t,

$r_{i(t)}$ is the effect of replicate i within location t,

$b_{j(i)(t)}$ is the effect of the incomplete block j within replication i and location t,

gk is the effect of the k^{th} genotype,

$(gl)_{kt}$ is the effect of interaction of k^{th} genotype and the t^{th} location

ε_{itjk} is the random error.

Table 2a. Skeleton for combined over locations of analysis variance (ANOVA) for simple lattice design

Sources of variation	**Df**	**SS**	**MS**	**F-value**	**Expect mean squares**
Replication (r)	r-1	SS_R	MS_R	MS_R/MS_E	$\sigma^2 + r\sigma^2_{gl}+gr\ \sigma^2_L$
Location	L-1	SSL	MS_L		
Blocks/location	r-1	MS B	SS_B	MSB/MSE	$\sigma^2e+ g\ \sigma\ ^2B/L$
Genotypes (G) - [Unadj.]	G^2-1	SS_G	MS_t	MS_G/MS_E	$\sigma^2g+ r\ \sigma^2gl+lr\ \sigma^2g$
- [adj.]	G^2-1	SS_G	MS_t	MS_G/MS_E	
Within replication (b) [adj.]	r(b-1)	SS_b	MS_b	MS_b/MS_e	
GxL	(g-1) (L-1)	SS_{GL}	SM_{GL}		$\sigma^2g+ r\ \sigma^2_{gl}$
Intra-block error (e)	(b-1) (rb-b-1)	Ss_e	MS_e		
Total	rb^2-1	SS_t			

Where, r = number of replication

G = number of genotypes

df = degree of freedom, b = block,

SS = Sum of squares, MS = mean squares, SSR and MSR are sums of squares and mean of replication, respectively.

SSG and MSG are sums of squares and mean of genotypes, respectively.

SSb and MSb are sums of squares and mean of blocks within replication, respectively. SSe and MSe are sums of squares and mean of intra-block error, respectively.

SSt is sum of squares of the total; σ^2g= variance due to genotypes, σ^2 GL= variance due to genotypes x locations interaction, σ^2L= variance due to locations, σ^2B/L= variance due to blocks within location.

Table 2b. Skeleton for individual location of analysis variance (ANOVA) for simple lattice design

Source of variance	**Df**			
Replication (r)	**r-1**	**SSR**	**MSr**	**MSR/MSE**
Genotypes (g) - [Un adj.]	g^2-1	SSg	MSg	MSg/MSE
- [adj.]	g^2-1	SSTg	MSg	MSg/MSE
Block within replication (b) [adj.]	r(b-1)	SSB	MSb	MSb/MSe
Intra-block error (e)	(b-1) (rb-b-1)	SSE	MSe	
Total	rb^2-1	SSg		

Where, r = number of replication, G = number of genotypes

df = degree of freedom, b = block, SS = Sum of squares, MS = mean squares, SSR and MSR are sums of squares and mean of replication, respectively

SSg and MSg are sums of squares and mean of genotypes, respectively

SSb and MSb are sums of squares and mean of blocks within replication respectively.

SSe and MSe are sums of squares and mean of intra-block error, respectively and SSt is sum of squares of the total.

3.4.2. Estimation of variance components

Components of variance, $\sigma^2 g$ = genotypic variance, $\sigma^2 p$ = phenotypic variance and $\sigma^2 e$ = error variances were calculated as suggested by Burton and Devane (1953) and Wricke Weber (1986) :

Environmental variance ($\sigma^2 e$) = $\mathbf{MSE / r}$. Where, MSE= error mean square and r= number of replications.

Genotypic variance ($\sigma^2 g$)= $\frac{\mathbf{MSG-MSgl}}{\mathbf{rl}}$

Where, $\sigma^2 g$= Genotypic variance, MSG= genotype mean square, MS_{gl} =mean square of genotype by location interaction= number of replication and l= number of locations.

Phenotypic variance ($\sigma^2 p$) = $\sigma^2 g + \sigma^2 gl + \sigma^2 e$ Where, $\sigma^2 g$ is genotypic variance, $\sigma^2 gl$ is genotype by location interactions , $\sigma^2 e$= Environmental variance) and r is number of replication.

Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was calculated as suggested by Burton and Devane (1953):

Phenotypic coefficient of variation (PCV) = $\frac{\sqrt{\sigma^2 p}}{\bar{x}}$ *100

Genotypic coefficient of variation (GCV) = $\frac{\sqrt{\sigma^2 g}}{\bar{x}}$ *100

Phenotypic variance ($\sigma^2 p$) = $\sigma^2 g$+ $\sigma^2 gl$ + $\sigma^2 e$, where, $\sigma^2 g$ is genotypic variance, $\sigma^2 gl$ is genotype by location interactions and $\sigma^2 e$ is environmental variance.

Where: $\sigma^2 p$ =Phenotypic variation; $\sigma^2 g$= Genotypic variation and

$\bar{x}$ = Grand mean of the characters under study.

Sivasubramanian and Madhavamenon (1973) GCV and PCV values were categorized as low (0–10%), moderate (10–20%) and high (20% and above)

3.4.2.1. Broad sense heritability ($H^2 b$)

Heritability in broad sense ($H^2 b$) was estimated according to the formula suggested by Johnson *et al.* (1955) and Hanson *et al.* (1956).

Heritability ($H^2 b$) = $\frac{\sigma^2 g}{\sigma^2 p+\sigma^2 gl/l+\sigma^2 e/rl}$*100

Where, $H^2 b$ =Heritability in broad sense

δ^2g= Genotypic variance , σ^2gl= the variance of genotypes by environmental interactions, σ^2e= the residual error variance δ^2p = Phenotypic variance= replication and l=locations

The Heritability was categorized as low (0-30%), moderate (30-60%) and high (60% and above) as given by Robinson *et al*. (1949).

3.4.2.2. Genetic advance under selection (GA)

The expected genetic advance for different characters under selection was estimated using the formula suggested by Lush (1949) and Johnson *et al*. (1955).

$$GA\ (\%) = K.H^2b \times \sigma p$$

Where, H^2b= Heritability in broad sense,σp = Phenotypic standard deviation

GA= Expected genetic advance and

k = the standardize selection differential at 5% selection intensity (K = 2.063)

3.4.2.3. Genetic advance as percent of mean

Genetic advance in percentage of mean was calculated using the formula given by Comstock and Robinson (1952).

$$\text{Genetic advance in percentage of mean} = \frac{\text{genetic advance} * 100}{\text{population mean}} = \text{GAM} = \frac{GA * 100}{\bar{x}}$$

Where, GAM=Genetic advance as percent of mean

GA= Genetic advance under selection and

$\bar{x}$= Grand Mean of the trait

Genetic advance as percent mean was categorized as low (0-10%), moderate (10-20% and (≥20%) as given by Johnson *et al*. (1955) and Falconer and Mackay (1996)

3.4.2.4. Correlation and path coefficient analysis

3.4.2.4.1. Correlation coefficient (r)

Genotypic coefficient of correlation (r_g) and phenotypic coefficient of correlation (r_p) were computed as per Robinson *et al*. (1955).

$r_g = \frac{Covg\ (X.Y)}{\sqrt{Var\ gX}.\sqrt{Var\ gY}}$

Where, Covg (XY) is genotypic covariance between characters X and Y

Var gX is genotypic variance of character X

Var gY is genotypic variance of character Y.

$r_p = \frac{Covp\ (X.Y)}{\sqrt{VarpX}.\sqrt{VarpY}}$

Where, Covp(XY) is phenotypic covariance between characters X and Y

Var pX is phenotypic variance of character X

Var pY is phenotypic variance of character Y.

The correlation coefficients were carried out to determine the degree of association of a character with yield and among the yield components. Estimates of genotypic and phenotypic correlation coefficients were compared against r-values given in Fisher and Yates (1963) table at g-2 degrees of freedom, at the probability levels of 0.05 and 0.01 to test their significance, where g is the number of genotypes. To test the significance of correlation coefficients, the following formula was adopted (Sharma, 1998):

Where, r is correlation coefficient; n is number of characters. To test the significance of correlation coefficient, the calculated t-value can be compared with tabulated t-value at (n-2) degree of freedom at 5% and 1% levels of probability (Snedecor and Cochran, 1981).

3.4.2.4.2. Path coefficient analysis

Path coefficient analysis was carried out by using GENRES Statistical Software Package (Pascal Intl Software Solutions, 1994) to study the direct and indirect contributions of the characters to the associations. The measure of direct and indirect effects of each trait on grain yield was estimated using a standardized partial regression coefficient known as path coefficient analysis, as suggested by Dewey and Lu (1959). Therefore, correlation coefficient of different characters with grain yield was partitioned into direct and indirect effects adopting the following formula:

$$riy = r1ip2 + \cdots r1ipi \ldots + rnipn$$

Where, riy=is correlation of i^{th} character with grain yield; r1ip2 is indirect effect of i^{th} character on grain yield through first character; rni is correlation between nth character and i^{th} character is the number of independent variables; pi is direct effect of i^{th} character on grain yield; pn is direct effects of character on grain yield.

The direct effects of different characters on grain yield were obtained by solving the following equations:

$$(riy) = (Pi)\ (rij);\ \text{and}\ (Pi) - 1\ (r1iPi)$$

Where, (Pi) is matrix of direct effect

(rij) is matrix of correlation coefficients among all the n^{th} component characters
(riy) is matrix of correlation of all component characters with gran yield

(r1iPi) is indirect effect of i^{th} character on grain yield through first character.

The contribution of the remaining unknown factors was measured as the residual factor R, which was calculated as given in Dewey and Lu (1959).

$$R = \sqrt{(1 - \sum rik.pkj)}$$

The analysis was based on all yield contributed traits influencing yield. The estimated values were compared with table values of the correlation coefficient to test the significance of the correlation coefficient prescribed by Fisher and Yates (1967).

3.4.2.5 . Cluster analysis (CA)

The fourteen morphological characters mean data values were standardized to have a mean of zero and variance of unity before cluster analysis to remove the biases due to differences in the scale of measurment by employing the average linkage method. Finally, the information was summarized by constructing a dendogerams. Hierarchical clustering was attempted by using paired group algorithm with Mahalanobis genetic distance (D^2). The Cubic clustering criterion (CCC), pseudo F (PSF) statistic and the pseudo T^2 (PST^2) statistic were examined by

using PROC clustering strategy to decide the numbers of clusters using SAS version 9.2 (SAS, 2008).

3.4.2.5.1. Genetic divergence analysis (D^2)

The generalized genetic distance between clusters was calculated using the generalized Mahalanobis' (1936) D^2 statistics equation by using SAS software program. Square distance (D^2) for each pair of genotypes combinations were computed using the following formula:

$$D_{ij}^2 = (xi - xj)s - 1(xi - xj)$$

Where, D^2ij = the distance between class i and j

Xi-xj =is the difference in the mean vectors of the two population (class i and j)

S-1= pooled error variance and covariance matrix.

The D^2 values obtained for pairs of clusters were considered as the calculated values of chi-square (x^2) and were tested for significance both at 1 and 5% probaplity levels against the tabulated value of x^2 for p degree of freedom , where p is the number of characters considred (Singh and Chaudhary, 1977).

3.4.2.5.2. Principal component analysis (PCA)

Principal components based on correlation matrix were calculated by following PRINCOMP procedure of SAS version 9.2 (SAS, 2008) to examined the contribution of each character for the total variation. The PCs with eigen values greater than one was select as proposed by Jeffers (1967). Correlations between the original traits and the respective PCs were calculated. The principal component analysis was computed using the following equation:

$$PC1 = b11(x1) + b12 + b1p = (XP)$$

Where,

pc1= the subjects score on pc1 (the first component extracted), b1p=the regression coefficient (weight) for observed variable p, as used in creating principal component 1 and xp=the subjects score on observed variable p.

4. RESULTS AND DISCUSSION

4.1. Analysis of Variance

The analysis of variance for all characters at Pawe and Fogera locations is presented in Appendix Table 1-2, respectively. The analysis of variance revealed that there were significant differences (P< 0.01) among 36 genotypes for all characters measured at two locations except for number of filled spikelets per panicle, fertile tillers per plant, number of total spikelets per panicle and harvest index at Pawe and number of unfilled spikelets per panicle (p< 0.05) were significant at Fogera. However number of unfilled spikelets per panicle and 1000 grain weight non-significant at both locations Pawe and Fogera , respectively.

The relative efficiency of simple lattice design obtained was better than randomized complete block design (greater than 80%) at the two locations. Therefore, the data of the mean values all experimental units were subjected to analysis of variance (ANOVA) based on simple lattice design. Test of homogeneity of error variances of each character were performed by using F- test and the test showed homogeneity of the two locations for all characters that involved in the study. Therefore, combined ANOVA was run over the two locations since all characters showed homogeneity of error variance.

The combined analysis of variance (ANOVA) revealed that mean squares due to genotypes were significant (P<0.05) for all traits studied (Table 3). Shahriar *et al*. (2014) also reported similar results in 34 rice genotypes for all the traits they studied. Satheeshkumar and Saravanan (2012); Osman *et al*. (2012) and Fentie *et al*. (2014) reported significance differences among rice genotypes evaluated in different locations. The result of the current study indicated that the genotypes evaluated possess acceptable amount of genetic variations with respect to the characters studied. This gives an opportunity for rice breeders to improve those traits through selection.

Mean squares due to genotype x location interactions were highly significant ($p< 0.01$) except number of unfilled grain yield per panicle and 1000 grain weight but for days to maturity, plant height, panicle length, culm length, flag leaf length, number of filled spikelets per panicle and number of total spikelets per panicle and significant ($P < 0.05$) for days to heading, biomass yield, paddy yield and harvest index (Table 3). These significance of genotype x location interactions implies that differential response of genotypes under the two locations for these traits. Similar finding was previous reported by Ogunbayo *et al*. (2014) for plant height, days to maturity, flag leaf length and panicle length.

Mean squares due to location was also significant ($p<0.05$) for days to heading, plant height, culm length, flag leaf length, number of filled spikelets per panicle, number of fertile tillers per panicle, harvest index, 1000 grain weight, biomass yield and number of total spikelets per panicle (Table 3). This indicates that the phenotypic expression of characters was different at the two locations.

Table 3. Mean square values from analysis of variance, and coefficient of variation (CV) for 14 traits of 36 rice genotypes evaluated at two locations (Pawe and Fogera) during the 2015/2016 main cropping season

	Mean squares					
Sources of variation	**Location**	**Rep**	**Genotypes**	**Location X Genotype**	**Intra block error**	**CV (%)**
DF	1	25	35	35	10	2.82
DH	2240.44**	16^{ns}	149.69**	13.003*	5.73^{ns}	
DM	3.67^{ns}	150.06^{ns}	199.89**	112.82**	28.51^{ns}	5.7
PH	17897.98**	64.80*	706.98**	140.71**	30.74*	4.71
PL	282.24**	0.04^{ns}	6.77**	2.34**	2.15*	5.52
CL	10760.61**	33.64^{ns}	670.62**	126.47**	30.95*	5.6
FLL	1622.75**	0.51^{ns}	32.95**	23.59**	8.84^{ns}	10.37
FSPP	16409.61**	294.69*	173.58**	110.67**	58.29^{ns}	6.48
USPP	0.56*	1.89*	0.25*	0.11^{ns}	0.09^{ns}	22.32
FTP	189.98**	38.65**	3.46**	2.83**	4.66**	15.99
NTSPP	11481.12**	377.00*	183.82**	125.48**	71.32^{ns}	6.61
TGW	201.24**	25.33^{ns}	17.85*	12.54^{ns}	2.50^{ns}	11.66
BY	44.11**	15.41*	7.55**	2.01*	1.64^{ns}	11.28
PY	524929.20^{ns}	118043.80^{ns}	3264619.3**	1490636.3*	936552.1^{ns}	13.96
HI	0.04**	0.024**	0.005**	0.0034*	0.002*	12.97

CV = Coefficient of Variation and DF= Degree of Freedom "*"= Significant at 5% probability level and "**"= Highly significant at 1% probability level and NS= Non- Significant. BY= Biomass Yield, DH= Days to Heading, CL= Culm Length, DM= Days to Maturity, FSPP = Filled Spikelets per panicle, FLL= Flag Leaf Length, FTP= Fertile Tiller per plant, PY= Paddy Yield kg ha^{-1} , HI= harvest Index , NTSPP= Number of Total Spikelets Per Panicle, PH= Plant Height, PL= Panicle Length, TGW= Thousand Grain Weight, UGY= Unfilled spikelets per panicle.

4.2. Range and Mean Values

4.2.1. Crop phenology

The grand mean of days to heading was 98.06 with a range of 82.5 to 110.0 (Table 4). The maximum days to heading (110.0 days) were recorded in the genotype PSBRC44 and the earliest was recorded in CHOMRONG genotype (82.5 days). Mulugeta (2015) also reported the variability among the genotypes for days to heading. The grand mean of maturity days was 133.38 with a maximum maturity period of 145 days that was registered for IR 75518-84-1-1-B genotype and the early maturity days was (116.5 days) which was recorded by CHOMRONG genotype. Among 36 genotypes, 44.4% exhibited days to maturity lower than the overall mean indicating that those genotypes were earlier maturing as compared to the others. On the one hand, as compared to the standard check variety (Ediget) 30.5 % of the genotypes showed earlier maturity period. However, only 8.3% of genotypes were earlier maturing than the local check variety (X-Jigna). This suggested the chance of selecting early genotypes which can escape terminal moisture stress.

4.2.2. Growth related traits

Minimum and maximum plant height ranged from 62.60 cm to 110.05 cm recorded for IR 81047-B-106-2-4 and IR 75518-84-1-1-B genotypes respectively, with a mean value of 83.77 cm (Table 4). According to IRRI (2002) low land rice plant height is classified as semi-dwarf (less than 110cm), intermediate (110-130 cm) and tall (more than 130 cm). Based on this classification, in the present study 94.4% of the tested genotypes group under the semi-dwarf class whereas the remaining 5.6 % (IR 75518-84-1-1-B and CHOMRONG) genotypes fall within the tall statured class (Appendix Table 3). This indicated that the tested genotypes had inherent variability in stature to develop lodging resistant varieties (semi-dwarf) that will have higher response to nitrogen application. Mitiku (2011); Shahriar (2014) and Kamara (2015) also reported variation in plant height in the rice genotypes they evaluated. Number of fertile tillers per plant ranged from 5.85 to 9.4 for the genotypes ARCCU16Bar-13-2-16-2-1-1) and (IR76999-52-1-3-2), respectively. However, a value of 5.95 number of fertile tillers per plant was recorded by the standard check variety and a value of 6.45 number of fertile tillers per plant was recorded by the local check, which indicated the local check having a better tillering

ability than the standard check, but had lower tillering ability than the remaining tested genotypes except ARCCU16Bar-13-2-16-2-1-1. Hence, the local check should be considered along with IR76999-52-1-3-2 for having higher tillering ability with most of the tillers being fertile when parental sources for better number of fertile tillers per plant will be needed in low land rice breeding programme.

The mean value of panicle length recorded was 19.16 cm with maximum value of 22.4 cm and minimum of 16.35cm for IR 75518-18-1-2-B and the standard check (Ediget), respectively. According to Bioversity International (2007), panicle length is classified as very short (<11 cm), short (~15 cm), medium (~25 cm), long (~35 cm) and very long (>40 cm). Thus, based on this argument, the present finding showed that there is enough medium variability for panicle length between the tested genotypes important for improving panicle architecture and grain yield due to high association of this trait that determines the number of grains it can hold and consequently rice yield in future conventional rice breeding programme. The grand mean of culm length recorded was 66.02cm with the maximum and minimum value of 91.40 and 46.05cm respectively. On the other hand, the maximum and minimum values recorded for flag leaf length were 30.95 and 16.15 cm, respectively with a mean value of 21.34 cm.

4.2.3. Paddy yield and yield related traits

Paddy yield is the primary interest in most breeding programs. Wide range of variations (2886.0 to 6759.0kg/ha) observed among the genotypes across locations with a mean value of 5370.0 kg/ha. Genotypes significantly varied in paddy grain yield and about eighty percent (80.5%) of the genotypes had higher grain yield than the standard check (Ediget) and 97.2% of them produced higher grain yield than the local check (X-Jigna). Among the genotypes, IR 83383-B-B-141-2, IR 83372-B-B-115-4, IR 83372-B-B-115-3, IR 83383-B-B-141-1 and IR80463-B-39-3 were the top yielders with corresponding grain yield of 6.759, 6.688, 6.685, 6.520 and 6.507 ton/ha, respectively (Appendix Table 3). The local check(X-Jigna) was the lowest yielder with mean grain yield of 2886.3 Kg/ha. Therefore, the presence of such range of variations of the traits indicated that the existence of large amount of genetic variation among the genotypes or populations which is the source of variable genetic materials.

Thousand grains weight ranged from 20.21 to 28.35 g/plot for the genotype IR80420-B-22-2 and IR 75518-18-1-2-B, respectively. Karim *et al*. (2007) reported mean values ranged from 5.9 to 30.72 g for 1000 grain weight. Mean values for harvest index varied from 17% for local check variety (X-Jigna) to 36% for IR76999-52-1-3-2 which indicating variability among the tested genotypes in their efficiency in partitioning assimilate into grain yield. Moreover, the genotypes IR76999-52-1-3-2 (36%), YUNJING 23 (32%), IR 81047-B-106-2-4 (32%) and WAB880-1-32-1-2-P1-HB (31%) were the most efficient than the standard check which had harvest index of 24.5%. The maximum and minimum above ground biomass yields were harvested from WAB376-B-10-H3 (11.15 kg $plot^{-1}$) and IR 83222-F11-167 (5.28 kg $plot^{-1}$). Based on these results, 50% or 18 genotypes exceeded the overall mean (8.17 kg $plot^{-1}$) of the tested genotypes while genotypes exceeded 72.2% and 75% of the standard check and local check, respectively (Appendix Table 3).

The number of filled spikelets per panicle is one of the most important components of yield and probably this trait will be helpful in breaking the yield plateau. The mean filled spikelets per panicle registered was 92.93 with the maximum and minimum values of 109.5 for IR 83222-F11-66 and 74.8 for CHOMRONG. Seventy-seven percent of the genotypes showed higher values for this trait than the standard check and 80.5% of the genotypes showed higher values than the local check variety indicating the existence of sufficient variability among the tested genotypes in their filled spikelets per panicle potential (Appendix Table 3). Therefore, those genotypes can be considered as source breeding materials when improvement of this character is required. However, the maximum and minimum number of unfilled spikelets per panicle recorded was 4.95 for WAB880-1-38-20-17-P1-HB and 1.0 for CHOMRONG with a mean value of 2.84 number of unfilled spikelets per panicle. Including the checks 55.6% of the tested genotypes gave above the grand mean for unfilled spikelets per panicle. On the other hand, the number of spikelets per panicle varied from 78.95 to 114.35 with mean value of 97.33. The maximum and minimum mean recorded for number of total spikelets per panicle was 114.35 and 78.95 in IR 83222-F11-66 and CHOMRONG, respectively (Appendix Table 3). Kamara, (2015) reported number of total spikelets per panicle ranging from 61 to 298.

Table 4. Estimation of mean, standard error, range, variances, coefficients of variations, broad sense heritability (H^2b), genetic advance and genetic advance as percent of mean in 14 quantitative traits of 36 lowland rice genotypes evaluated across locations in 2015/2016 cropping seasons.

Traits	Mean±SE	Range		Variances		Coefficient of Variation (%)		H^2b (%)	GA	GAM
		Min	Max	σ^2p	σ^2g	GCV	PCV			
DH	98.07±6.90	82.50	110.00	277.21	136.69	11.92	16.98	49.31	11.89	12.13
DM	133.38±7.68	116.50	145.50	199.88	87.07	7.00	10.60	43.56	8.37	6.28
PH	83.77±14.37	62.60	110.05	706.98	566.27	28.41	31.74	80.10	39.26	46.87
PL	19.16±1.44	16.35	22.40	6.77	4.44	10.99	13.58	65.50	2.84	14.83
CL	66.02±13.91	46.05	91.40	670.62	544.15	35.33	39.23	81.14	38.99	59.06
FLL	21.34±3.31	16.15	30.95	32.95	9.36	14.34	26.90	28.41	1.79	8.39
FSPP	92.93±7.63	74.80	109.50	173.59	62.92	8.54	14.18	36.25	5.92	6.37
USPP	2.84±0.79	1.00	4.95	2.20	0.84	32.32	52.41	38.03	0.72	25.32
FTP	7.29±0.93	5.85	9.40	3.46	0.63	10.92	25.57	18.24	0.30	4.10
NTSPP	97.33±7.80	78.95	114.35	183.82	58.33	7.85	13.93	31.73	4.99	5.13
BY	8.17±1.56	5.28	11.15	17.55	5.31	28.85	33.67	73.41	3.56	43.63
TGW	24.42±2.26	20.21	28.35	7.55	5.54	9.44	17.31	30.00	1.41	5.78
PY	5370.00±1065.0	2886.00	6759.00	3.27	1.77	24.80	33.65	54.35	1.49	27.77
HI	0.27±0.04	0.17	0.36	0.005	0.001	12.87	25.25	25.97	0.02	6.89

Phenotypic variance(σ^2p) genotypic variance (σ^2g), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability (h^2b) and genetic advance (GA), genetic advance as percent of mean (GAM) ,Min=Minimum and Max=Maximum, SD=standard deviation. BY= Biomass Yield, DH= Days to Heading, CL= Culm Length, DM= Days to Maturity, FSPP = Filled Spikelets per panicle, FLL= Flag Leaf Length, FTP= Fertile Tiller per plant, PY= Paddy Yield kg ha^{-1} , HI= harvest Index , NTSPP= Number of Total Spikelets Per Panicle , PH= Plant Height, PL= Panicle Length, TGW= Thousand Grain Weight, UGY= Unfilled spikelets per panicle.

4.3. Estimates of Variance Components and Coefficients of Variation

4.3.1. Estimates of heritability (H^2b)

Heritability estimates of the 14 quantitative traits ranged from 18.24% for fertile tillers per plant to 81.14 % for culm length across locations (Table 4). Heritability was classified as low (below 30%), medium (30-60%) and high (above 60%) as suggested by Johnson *et al.* (1955). Considering this delineation, high heritability values were observed for culm length (81.14%) followed by plant height (80.10%), biomass yield (73.41%) and panicle length (65.50%). High heritability in broad sense values indicate that the characters under study are less influenced by environment in their expression. Therefore, the rice breeders may make superior genotypes selection on the basis of phenotypic performance for these traits.

Days to heading (49.31%), days to maturity (43.56%), number of filled spikelets per panicle (36.25%), number of unfilled spikelets per panicle (38.03%), number of total pikelets per panicle (31.73%) and paddy yield (54.35%) had medium heritability indicating that improvement can be made by simple selection. These findings were mostly supported by the reports made earlier in rice by (Krupakar *et al*., 2012 and Pandey *et al*., 2012) for days to heading, plant height, panicle length and biomass yield per plot in rice.

In contrast, flag leaf length (28.41%), number of fertile tiller per plant (18.24%), 1000 grain weight (29.73%) and harvest index (25.97%) had low heritability which indicates greater role of environment on the expression of the traits. Thus, direct selection for these traits will be ineffective. Similar results were also reported by other investigators (Akinwale *et al*., 2011; Hoque., 2013; Fentie *et al*., 2014) for number of fertile tillers per plant (Akinwale *et al*., 2011) reported low heritability for 1000 grain weight. In contrary, Fentie *et al*. (2014) and Osman *et al*. (2012) reported high broad sense heritability for 1000 grain weight. Dutta *et al*. (2013) and Rai (2014) also observed high broad sense heritability finding for number of fertile tillers per plant and harvest index. On the contrary, Rai (2014) and Yadav *et al*. (2010) reported high broad sense heritability for flag leaf length and harvest index. Shahriar *et al*. (2014) registered high heritability for 1000 grain weight.

Heritability alone provides no indication of the amount of genetic improvement that would result from selection of individual genotypes. Hence knowledge about heritability coupled with genetic advance and genotypic coefficient of variations are most useful. Thus, in the present study, high to medium heritability coupled with high genotypic coefficients of variation (GCV) and high genetic advance as percentage of mean were recorded by plant height followed by culm length ,biomass yield , paddy yield and number of unfilled spikelets per panicle, which indicated that the traits were simply inherited in nature and controlled by few major genes or possessed additive gene effects. This indicates that simple selection could be effective for improving the characters. Similar result were reported by Osman *et al*.(2012) who tested thirteen upland rice genotypes. Rai *et al*. (2014) also by evaluated 40 rice genotypes and observed similar results for biological yield.

4.3.2. Phenotypic and genotypic coefficients of variation

The genotypic coefficients of variation (GCV) ranged from 7.0 % for days to maturity to 35.33% for culm length (Table 4). However, phenotypic coefficients of variation (PCV) ranged from 10.60 % for days to maturity to 39.23 % for culm length (Table 4). Phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) were categorized as low (0-10%), moderate (10-20%) and high (>20%) as indicated by Sivasubramanian and Madhavamenon (1973). High PCV and GCV values were recorded for plant height, culm length, number of unfilled spikelets per panicle, paddy yield and biomass yield, which suggests the possibility of improving this trait through selection. Similar results were also reported by Satheeshkumar and Saravanan *et al*. (2012); Hoque. (2013) and Devi *et al*. (2013) for plant height and similarly Pratap *et al*. (2012) for biomass yield and plant height. On the other hand, the estimates of GCV and PCV were low in the present study for days to maturity (7.00%, 10.60%) (Table 4). Similar findings were reported by Pandey *et al*. (2012).

The magnitude of phenotypic coefficient of variation (PCV) estimates in the present study was found to be slightly higher than their respective genotypic coefficient of variations (GCV) for all the studied characters which might be the result of influence of environment on the development of characters period. Similar report noticed earlier by many researchers (Idris *et*

al., 2012; Singh *et al.*, 2012; Ogunbayo *et al.*, 2014) in rice. However, the narrow magnitude of difference between phenotypic and genotypic coefficients of variations were recorded for characters such as days to maturity, plant height , biomass yield ,culm length and panicle length indicating limited influence of environment in the expression of these characters. The result is in agreement with Idris and Mohamed (2013) who reported small differences between genotypic and phenotypic coefficients of variations for plant height and panicle length. Thus, selection based on phenotypic performance of these characters would be effective to bring about considerable genetic improvement. But, there was considerable difference between the phenotypic and genotypic coefficient of variations for the rest traits which, indicates greater effects of environmental factors in the phenotypic expression of these characters. Thus, selection based on phenotypic performance of these characters would be ineffective to bring about considerable genetic improvement of these traits in the genotypes considered in the current study.

4.3.3. Genetic advance and genetic advance as percent of mean

Heritability in conjunction with genetic advance would give a more reliable selection value (Johnson *et al.*, 1955). In the present finding the genetic advance as percent of mean was ranged from 4.10 % for number of fertile tillers per plant to 59.06% for culm length across locations. According to Johson *et al*. (1955) genetic advance as percent of mean classified as low (<10%), moderate (10-20%) and high (>20%). Based on this argument, in the present study, traits such as plant height (46.87 %), culm length (59.06 %), biomass yield (43.63%) , paddy yield (27.77%) and number of unfilled spikelets per panicle (25.32%) gave high genetic advance as percent of mean while moderate genetic advance as percent of mean was computed for days to heading (12.13%) and panicle length (14.83%). These traits also had high and moderate heritability. Therefore, selection based on the above traits with high and moderate genetic advance as percent of mean, result in the improvement of the genotypes for the traits. The present finding is in corresponding to the work of Rahman *et al. (*2014) and Shrivastava *et al*. (2014) for number of unfilled spikelets per panicle. Shrivastava *et al*. (2015) noticed similar result for culm length, number of unfilled spikelets per panicle, biomass yield and paddy yield. The finding is supported also by Mulugeta (2015) for biomass yield and number of unfilled spikelets per panicle.

Low estimates of genetic advance as per cent mean was also noticed for days to maturity (6.28%), flag leaf length (8.39 %), number of fertile tiller per plant (4.10%), number of filled spikelets per panicle (6.37 %), number of total spikelets per panicle (5.13 %), 1000 grain weight (5.78 %) and harvest index (6.89 %), respectively (Table 4). This indicates the characters governed by non-additive gene action and heterosis breeding will be useful. Similar results were reported by Hoque (2013) for number of fertile tillers per panicle.

4.4. Characters Association

4.4.1. Correlation of paddy yield with other traits

Grain yield, which is the major economic character in rice, depends on several component traits which are mutually related. Phenotypic (r_p) and genotypic (r_g) correlation estimates between the various characters are presented in Table 5.

Very close values of genotypic and phenotypic correlations were observed between some character combinations, such as days to heading with plant height, plant height with panicle length, culm length and biomass yield per plot, panicle length with flag leaf length, culm length with number of filled spikelets per panicle, biomass yield per plot with harvest index which might be due to reduction in error (environmental) variance to minor proportions as reported by Dewey and Lu (1959).

Paddy yield (kg/ha) exhibited positive and highly significant (P <0.01) genotypic correlation with traits like days to heading (r_g=0.678**), days to maturity (r_g=0.803**), number of filled spikelets per panicle (r_g=0.523**), number of fertile tillers per plant (r_g=0.702**), harvest index (r_g=0.668**), number of total spikelets per panicle (r_g=0.501**) and biomass yield per plot (r_g = 0.730**), respectively, which indicates that improving these traits may result in the improvement of grain yield as the results of positive and strong correlation (Table 5). Moreover, this also is indicating the importance of these traits for yield improvement in rice. Thus, the indirect selection for higher yield based on these characters would be reliable.

Similarly, Iftekharuddaula *et al*. (2002) reported the positive correlation of grain yield with panicle length and harvest index. In addition, days to heading (r_g= 0.532**), days to maturity

(rg=0.471**), number of fertile tillers per plant (r_g=0.314*), number of total spikelets per panicle (r_p=0.382*), biomass yield (r_p=0.654**) and harvest index (r_p=0.430**) respectively, showed positive and significant association with grain yield at phenotypic level.

Similar finding reported by Nandan *et al*. (2010) for days to heading. Similar results were also reported by Karim *et al*. (2014) who observed positive association between harvest index and grain yield. Indris *et al.* (2013); Ekka *et al*. (2011) and Kishore *et al*. (2015) reported positive association of number of filled grains per panicle with grain yield. Laza *et al*. (2004) also reported similar argument for number of spikelets per panicle with grain yield in rice. Corresponding finding was noticed by Naseem *et al*. (2014) for days to maturity and number of spikelets per panicle. Fentie *et al*. (2014) also confirmed positive correlation of biomass yield with grain yield. On the other hand, paddy yield had non-significant but positive phenotypic correlation with number of unfilled spikelets per panicle (r_p=0.246), number of filled spikelets per panicle (r_p=0.417) and panicle length (r_p=0.278) suggesting that selection for these traits would not improve grain yield.

Moreover, paddy yield showed positive and highly significant phenotypic association with days to heading (r_p = 0.532**), number of total spikelets per panicle (r_p=0.382*), number of fertile tillers per plant (r_p = 0.314*), biomass yield per plot (r_p = 0.654**) and harvest index (r_p=0.430**). Traits such as days to heading (r_g=0.678**, r_p=0.532**), days to maturity (rg=0.803**, r_p=0.471**), number of total spikelets per panicle (r_g=0.501**, r_p=0.382*), biomass yield per plot (r_g=0.730**, r_p=0.654**), number of fertile tillers per plant (r_g=0.702**, r_p=0.314*) and harvest index (r_g=0.381*, r_p=0.430**) showed positive and significant correlation at both genotypic and phenotypic levels with grain yield. This indicate that selection for higher days to heading, days to maturity, number of spikelets per panicle, biomass yield per plot, number of fertile tillers per plant and harvest index are important for improvement of grain yield in low land rice ecology.

Table 5. Estimates of genotypic (r_g) above diagonal and phenotypic (r_p) correlation coefficients below diagonal for 14 traits of 36 genotypes studied at Pawe and Fogera during the 2015/2016 main season.

Traits	DH	DM	PH	PL	CL	FLL	FSPP	USPP	FT	NTSPP	BY	TGW	HI	PY
DH	**1**	0.930**	-0.098	0.509**	-0.138	0.195	0.614**	0.396*	0.281	0.588**	0.731**	-0.305	-0.083	0.678**
DM	0.747**	**1**	-0.075	0.446**	-0.116	0.186	0.459**	0.154	-0.001	0.431**	0.756**	-0.099	0.067	0.803**
PH	-0.089	-0.063	**1**	0.450**	0.997**	0.783**	0.076	-0.402*	-0.311	0.053	0.337*	0.680**	-0.702**	-0.145^{ns}
PL	0.356*	0.277	0.403*	**1**	0.369*	0.511**	0.503**	0.500**	0.292	0.524**	0.729**	-0.061	-0.439**	0.415*
CL	-0.127	-0.095	0.995**	0.333*	**1**	0.756**	0.043	-0.453**	-0.362*	0.019	0.300	0.685**	-0.695**	-0.178^{ns}
FLL	0.115	0.104	0.687**	0.539**	0.656**	**1**	0.319	-0.029	-0.347*	0.309	0.411*	0.497**	-0.667**	-0.046^{ns}
FSPP	0.457**	0.296	0.104	0.426**	0.068	0.235	**1**	0.659**	0.005	1.000**	0.580**	-0.237	-0.084	0.523**
USPP	0.149	0.112	-0.181	0.218	-0.212	0.007	0.283	**1**	1.000**	0.600**	0.373*	-0.27	0.352*	0.615**
FT	0.177	0.13	-0.131	0.106	-0.155	-0.185	0.222	0.151	**1**	-0.042	0.378*	-0.434**	0.633**	0.702**
NTSPP	0.427**	0.278	0.092	0.387*	0.063	0.153	0.951**	0.334*	0.288	**1**	0.531**	-0.151	-0.04	0.501**
BY	0.648**	0.565**	0.337*	0.539**	0.292	0.32	0.466**	0.251	0.252	0.418*	**1**	0.035	-0.356*	0.730**
TGW	-0.209	-0.031	0.464**	0.084	0.482**	0.368*	-0.122	-0.187	-0.034	-0.095	-0.013	**1**	-0.456**	-0.298^{ns}
HI	-0.058	-0.057	-0.566**	-0.281	-0.559**	-0.520**	-0.003	0.077	0.095	0.001	-0.332*	-0.231	**1**	0.381*
PY	0.532**	0.471**	-0.091^{ns}	0.278^{ns}	-0.125^{ns}	-0.082^{ns}	0.417^{ns}	0.246^{ns}	0.314*	0.382*	0.654**	-0.184^{ns}	0.430**	**1**

"**" significant at 1% and "*" significant at 5% respectively. BY= Biomass Yield, DH= Days to Heading, CL= Culm Length, DM= Days to Maturity, FSPP = Filled Spikelets per panicle, FLL= Flag Leaf Length, FTP= Fertile Tiller per plant, PY= Paddy Yield kg ha^{-1} , HI= harvest Index , NTSPP= Number of Total Spikelets Per Panicle, PH= Plant Height, PL= Panicle Length, TGW= Thousand Grain Weight, USPP= Unfilled spikelets per panicle

4.4.2. Correlation among the component traits

4.4.2.1. Phenotypic correlation

Correlations among yield components and other quantitative traits help in understanding the interdependence of the traits. Days to heading had positive and significant ($p<0.01$) phenotypic association with days to maturity ($r_p=0.747^{**}$), panicle length ($r_p=0.356^{*}$), number of filled spikelets per panicle ($r_p=0.457^{**}$), biomass yield per plot ($r_p=0.648^{**}$) and number of total spikelets per panicle ($r_p=0.427^{**}$). Days to maturity showed significant correlation at ($p<0.01$) with biomass yield ($r_p=0.565^{**}$) whereas on-significant for the rest of the traits.

Plant height showed positive and significant association with panicle length ($r_p=0.403^{*}$), culm length ($r_p=0.995^{**}$), flag leaf length ($r_p=0.687^{**}$), biomass yield ($r_p=0.337^{*}$) and 1000 grain weight ($r_p=0.464^{**}$) and negative and significant correlation with harvest index ($r_p=-0.566^{**}$). It, however, had non-significant association with number of filled spikelets per panicle, number of unfilled spikelets per panicle, number of fertile tillers per plant and number of total spikelets per panicle. The finding is in conformity with Ghosal *et al. (*2010) and Kishore *et al. (*2015) for panicle length. Moreover, panicle length showed significant and positive association with culm length ($r_p=0.333^{*}$), flag leaf length ($r_p=0.539^{**}$), number of filled spikelets per panicle ($r_p=0.426^{**}$), number of total spikelets per panicle ($r_p=0.387^{*}$) and biomass yield ($r_p=0.539^{**}$) but non-significant association with number of unfilled spikelets per panicle (rp=0.218), number of fertile tillers per plant ($r_p=0.106$), 1000 grain weight ($r_p=0.084$) and harvest index ($r_p=-0.281$).

Culm length had significant and positive association with the traits such as flag leaf length ($r_p=0.656^{**}$) and 1000 grain weight ($r_p=0.482^{**}$) whereas it had negatively associated with harvest index ($r_p=-0.559^{**}$) but non-significant association with the rest of the traits. Flag leaf length manifested positive and significant association with 1000 grain weight ($r_p=0.368^{*}$) and had negative association with harvest index ($r_p=-0.520^{**}$) whereas non-significant association with the rest of the traits. Number of filled spikelets per panicle showed a positive strong to moderate correlation with number of total spikelets per panicle ($r_p=0.951^{**}$) and biomass

yield (r_p=0.466**), respectively. It had non-significant correlation with the rest of the traits. However, in contrary to the observation of Karim *et al*. (2014) who reported highly significant negative correlation between 1000 grain weight and number of filled grain per panicle. According to Adams and Grafius (1971) the negative correlations arise primarily from competition for a common possibility, such as nutrient supply. If one component gets advantage over the other, a negative correlation may arise. The genetic reasons for this type of negative association may be linkage or pleiotropy. Number of unfilled spikelets per panicle showed significant and positive correlation with number of total spikelets per panicle (r_p=0.334*) but it had non-significant correlation with the rest of the traits. Number of total spikelets per panicle revealed positive correlation with biomass yield (r_p=0.418*) and non-significant with 1000 grain weight (r_p=-0.095) and harvest index (r_p=0.001), respectively. Biomass yield per plot had significant and negative association with harvest index (r_p=-0.332*).

4.4.2.2. Genotypic correlation coefficient

The genotypic correlation coefficients for some of the traits were higher than their corresponding phenotypic correlation coefficient values (Table 5), indicating a fair strong inherent relationship among the traits due to suppressing effect of the environment, which modified the phenotypic expression of these traits by reducing phenotypic coefficient values at the period of characters' development or elimination of environmental effects led to strengthen genetic association. Similar findings were reported by Zahid *et al*. (2006) and prasad *et al*. (2001). The yield components exhibited various trends of association among themselves. For instance, days to heading showed significant and positive correlation at ($p<0.01$) with days to maturity (r_g=0.930**) followed by biomass yield (r_g=0.731**), number of filled spikelets per panicle (r_g=0.614**), number of total spikelets per panicle (r_g=0.588**), panicle length (r_g=0.509**) and number of unfilled spikelets per panicle (r_g=0.396*) whereas it had non-significant genotypic correlation with the rest of the traits. Moreover, days to maturity manifested significant and positive correlation ($p<0.01$) with panicle length (r_g=0.446**), number of filled spikelets per panicle (r_g=0.459**), number of total spikelets per panicle (r_g=0.431**) and biomass yield per plot (r_g=0.756**) however, non-significant with the rest of the traits.

Plant height had significant and positive genotypic correlation with traits such as panicle length (r_g=0.450**), culm length (rg=0.997**), flag leaf length (r_g=0.783**) and biomass yield per plot (r_g=0.337*) but it had negative and significant correlation with number of unfilled spikelets per panicle (r_g=-0.402*) and harvest index (r_g=-0.702**) and non-significant correlation with the rest of the traits. Likewise, Iftekhalruddaaula *et al*. (2001) reported highily significant and positive correlation of plant height with panicle length and negative correlation for harvest index. Similarly, Ghosal *et al. (*2010); Babu *et al. (*2012) and Kishore *et al*. (2015) reported positive correlation of plant height with panicle length. Panicle length was positively and significantly correlated with culm length (r_g=0.369*), flag leaf length (r_g=0.511**), number of filled spikelets per panicle (r_g=0.503**), 1000 grain weight (r_g=0.405*), number of unfilled spikelets per panicle (r_g=0.500**), number of total spikelets per panicle (r_g=0.524**) and biomass yield per plot (r_g=0.729**). Harvest index had a negative and significant correlation with panicle length (rg=-0.439**) culm length (-0.695**) ,flag leaf length (-0.667**) , biomass yield (-0.356*) and 1000 grain weight (-0.456**) while positive significant association with number of infilled spikelets per panicle(0.352*) and non-significant for the rest traits. In contrast, Kishore *et al*. (2015) noticed non-significant association with number of filled spikelets per panicle and 1000 grain weight.

Number of filled spikelets per panicle had strong positive association total spikelets per panicle (1.000**) followed by number of unfilled spikelets per panicle (0.659**) and biomass yield (0.580**) whereas the rest traits were indicated non- significant association. Number of unfilled spikelets per panicle showed positive association at genotypic level with number of unfilled spikelets per panicle (1.000**), number of total spikelets per panicle (0.600**), biomass yield (0.373*) and harvest index (0.352*). However, it had non -significant with the rest of the traits. Number of fertile tillers per plant displayed significant positive association with biomass yield per plot (0.378*) and harvest index (0.633**) while it showed significant and negative correlation with 1000 grain weight (-0.434**). Similarly, Rokonuzzaman *et al*. (2008) reported significant negative correlation for 1000 grain weight. Number of total spikelets per panicle was indicated significant association with biomass yield (0.531**) but no significant association with 1000 grain weight and harvest index.

On contrary, Iftekhalruddaaula *et al*. (2001) observed significantly negative association with harvest index and 1000 grain weight. Biomass yield per plot manifested negative and significant association with harvest index (-0.356*). Culm length revealed positive and significant correlation with flag leaf length (0.756**) and 1000 grain weight (0.685**) whereas it had negative and significant association with unfilled spikelets per panicle (-0.453**), number of fertile tillers per plant (-0.362*) and harvest index (-0.695**). Similarly, flag leaf length exhibited positive and significant correlation with 1000 grain weight (0.497**) and biomass yield per plot (0.411*). However, harvest index (-0.667**) and number of fertile tillers per plant (-0.347*) showed significant and negative correlation.

4.5. Path Coefficient Analysis

Paddy yield, being the complex outcome of various traits was considered to be the dependent character. In the present study, 13 characters were selected as casual variables to estimate the contribution of these individual characters to grain yield (Table 6).

4.5.1. Direct effect of various traits on grain yield

A perusal result of genotypic path analysis revealed that biomass yield (1.052) followed by harvest index (0.722), number of total spikelets per panicle (0.643) and plant height (0.459) had the highest direct effect on paddy yield with significant and positive genotypic association across locations, which indicates the correlation explains the true association with paddy yield and a direct selection through these traits will be effective. Hence, selection of genotypes with more number of total spikelets per panicle, harvest index, biomass yield and plant height on which an emphasis should be given during simultaneous selection to prove effectively in increasing yield potential of rice (Table 6). These characters have also been identified as major direct contributors towards paddy (grain) yield by Srek and Beper (2002) and Pratap *et al*. (2012) for biomass yield and harvest index for rice, respectively. Similarly, Khare *et al. (*2014) reported the highest positive direct effect of the number of spikelets per panicle on grain yield in earlier study. Sravan *et al*. (2012) reported a maximum direct effect of biological yield on grain yield, followed by harvest index, spikelets per panicle in upland rice. Mulugeta (2015) reported biomass yield per plot and plant height as the major contributors to

grain yield and had direct effect on grain yield in upland rice. Karim *et al*. (2014) and Kishore *et al*. (2015) reported that plant height had high direct positive effect on grain yield.

On the other hand, days to heading (-0.020), days to maturity (-0.068), panicle length (-0.062), culm length (-0.580), number of unfilled spikelets per panicle (-0.257), number of filled spikelets per panicle (-0.503) and 1000 grain weight (-0.049) had negative direct loading on paddy yield except on culm length, panicle length, and 1000 grain weight but exhibited positive and significant genotypic correlation with paddy yield. The negative direct effect indicates that the direct selection through these traits would not prove to be useful for the improvement of grain yield. Similar results reported earlier by Mulugeta *et al*. (2012) for days to maturity and Kiani and Nematzadeh (2012) also noticed negative direct effect of panicle length on grain yield. In the contrary, Kiani and Nematzadeh (2012) reported the positive direct effect of number of filled grains per panicle on grain yield.

4.5.2. Indirect effect of various traits on paddy yield

The highest and positive indirect effect on grain yield was exhibited by days to maturity through biomass yield per plot (0.796) , days to heading via biomass yield per plot (0.769), panicle length through biomass yield per plot (0.767), number of filled spikelets per panicle through number of total spikelets per panicle (0.648) , number of filled spikelets per panicle by biomass yield per plot (0.611), number of total spikelets per panicle by biomass yield per plot (0.559), number of fertile tillers per panicle through harvest index (0.457) and culm length via plant height (0.457). Hence, indirect selection based on these characters should be considered simultaneously as indirect selection criteria for paddy yield improvement. In the contrast, Karim *et al*. (2014) reported negative indirect effect of panicle length on paddy yield. The perusal of path analysis result indicated that plant height exhibited high negative indirect effect on grain yield through culm length (-0.578) and harvest index (-0.506), number of total spikelets per panicle through number of spikelets yield per panicle (-0.507) and culm length via harvest index (-0.502). The indirect effect of days to heading through culm length (0.080), flag leaf length (0.030), number fertile tiller per plant (0.037) number of total spikelets per panicle (0.378), biomass yield (0.769) and 1000 grain weight (0.015) counter

balanced the negative direct effect of number of days to heading on grain yield (-0.020) and reduced the correlation coefficient to +0.678.

Correspondingly, the indirect effect of days to maturity through culm length (0.067), flag leaf length (0.029), number of fertile tillers per plant (0.0001) number of total spikelets per panicle (0.277), biomass yield per plot (0.796), 1000 grain weight (0.005) and harvest index (0.049) counter balanced the negative direct effect of days to maturity on paddy yield (-0.068) and reduced the correlation coefficient to +0.803. Moreover, the indirect effect of panicle length through plant height (0.206), flag leaf length (0.079), number of fertile tillers per plant (0.038), number of total spikelets per panicle (0.337), biomass yield (0.767) and 1000 grain weight (0.003) counter balanced the negative direct effect of number panicle length on paddy yield (-0.062) and reduced the correlation coefficient to +0.415 (Table 6). The negative direct effect of culm length on grain yield per hectare (-0.580) was counter balanced mainly by its positive indirect effects through plant height (0.457) and reduced its genotypic correlation to -0.178. Similarly, the indirect effect of number of filled spikelets per panicle mainly counter balanced through number of total spikelets per panicle (0.648) and biomass yield per plot (0.611) reduced its genotypic correlation to +0.523.

The residual effect determines how best the causal factors account for the variability of the dependent factor. In this case, the dependent factor was grain yield. The residual effect was (0.118) indicated that the characters which are included in the genotypic path analysis explained 88.2% of the total variation on grain yield that was contributed by 13 characters studied. The residual 11.8% indicated that there are some more traits that were not included in the study but could contribute to paddy yield. Generally, characters like biomass yield, harvest index, number of total spikelets per panicle and plant height has the highest direct effect on paddy yield with significant and positive genotypic association. This indicates that the correlation revealed that the true relationship and direct selection through these characters will be effective.

Table 6. Estimates of direct (bold diagonal and underlined) and indirect effect (off diagonal) at genotypic level of 13 traits on grain yield in 36 rice genotypes tested at Pawe and Fogera in 2015/2016 cropping seasons

Traits	DH	DM	PH	PL	CL	FLL	FSPP	USPP	FTP	STPP	BY	TSW	HI	r_g
DH	**-0.02**	-0.063	-0.045	-0.032	0.08	0.03	-0.309	-0.102	0.037	0.378	0.769	0.015	-0.06	0.678
DM	-0.019	**-0.068**	-0.034	-0.028	0.067	0.029	-0.231	-0.04	0.000	0.277	0.796	0.005	0.049	0.803
PH	0.002	0.005	**0.459**	-0.028	-0.578	0.122	-0.038	0.104	-0.041	0.034	0.355	-0.033	-0.506	-0.145
PL	-0.01	-0.03	0.206	**-0.062**	-0.214	0.079	-0.253	-0.129	0.038	0.337	0.767	0.003	-0.317	0.415
CL	0.003	0.008	0.457	-0.023	**-0.58**	0.117	-0.022	0.117	-0.047	0.012	0.315	-0.034	-0.502	-0.178
FLL	-0.004	-0.013	0.359	-0.032	-0.438	**0.155**	-0.161	0.007	-0.045	0.199	0.432	-0.024	-0.482	-0.046
FSPP	-0.012	-0.031	0.035	-0.031	-0.025	0.05	**-0.503**	-0.169	0.001	0.648	0.611	0.012	-0.06	0.523
USPP	-0.008	-0.01	-0.185	-0.031	0.263	-0.005	-0.331	**-0.257**	0.134	0.386	0.393	0.013	0.254	0.615
FTP	-0.006	0	-0.142	-0.018	0.21	-0.054	-0.003	-0.264	**0.131**	-0.027	0.397	0.021	0.457	0.702
NTSPP	-0.012	-0.029	0.024	-0.033	-0.011	0.048	-0.507	-0.154	-0.005	**0.643**	0.559	0.007	-0.029	0.501
BY	-0.015	-0.051	0.155	-0.045	-0.174	0.064	-0.292	-0.096	0.049	0.342	**1.052**	-0.002	-0.257	0.73
TGW	0.006	0.007	0.312	0.004	-0.397	0.077	0.119	0.069	-0.057	-0.097	0.037	**-0.049**	-0.329	-0.298
HI	0.002	-0.005	-0.322	0.027	0.403	-0.104	0.042	-0.091	0.083	-0.026	-0.374	0.022	**0.722**	0.381

Residual Effect=0.118, BY= Biomass Yield, DH= Days to Heading, CL= Culm Length, DM= Days to Maturity, FSPP = Filled Spikelets per panicle, FLL= Flag Leaf Length, FTP= Fertile Tiller per plant, HI= harvest Index , NTSPP= Number of Total Spikelets Per Panicle, PH= Plant Height, PL= Panicle Length, TGW= Thousand Grain Weight, USPP= Unfilled spikelets per panicle

4.6. Genetic Divergence Analysis

Genetic divergence quantifies the genetic distance among the selected genotypes and reflects the relative contribution of specific traits towards the total divergence. Clustering of genotypes into similar groups was performed using the average linkage based on D^2 statistic developed by Mahalanobis (1936) to classify the divergent genotypes into different groups.

4.6.1. Estimates of genetic distance (D^2)

Inter-cluster distances among the clusters generated are given in Table 7. The x^2 (chi-square) test for the five clusters indicated that there was statistically highly significant difference ($p<0.01$) among the five different clusters. The maximum average inter cluster distances were found between clusters I and IV (D^2=2968.92) followed by between clusters II and IV (D^2=2558.64) and I and V (D^2=2167.19) which showed that the genotypes contained in these clusters are genetically more divergent than any other groups. Based on the inter cluster distances, hybridization between the genotypes of cluster I with cluster IV, cluster II with cluster IV and cluster I with cluster V is expected to generate promising segregants for grain yield and other agronomic traits. Increasing parental distance implies a great number of contrasting alleles at the desired loci and then to the extent that these loci recombine in the F2 and F3 generation following a cross of distantly related parents, the greater will be the opportunities for the effective selection for yield factors (Ghaderi *et al*.,1984). Therefore, in present study, hybridization between the genotypes of cluster I with cluster IV, cluster II with cluster IV and cluster I with cluster V which, suggested that the genotypes belonging to the distant clusters could be used in hybridization programme for obtaining a wider range of variability to generate segregants for grain yield and other important agronomic traits. Parental lines selected from these four clusters may be used in a hybridization programme, since hybridization between divergent parents is likely to produce variability and transgressive segregations with high heterotic effects (Rama, 1992).

The more inter cluster distances, the more variability among the genotypes between the cluster and vice-versa. Hence, superior hybrids vigor or recombinants can be realized by mating between the genotypes of these clusters in a definite fashion. Generally, the present

study confirmed the presence of acceptable genetic diversity between any pair of clusters which could be exploited through hybridization. However, lowest inter cluster distance was recorded between clusters I and II (D^2=411.45) (Table 7), which indicates lower genetic distance (presence of genetic relationship) among genotypes contained in these two clusters and a limited genetic diversity among them. Crossing between genotypes from this two clusters might not be expected to generate high yielding desirable segregants and high vigor at F1 generation.

Population from geographically separated areas and having complex environment are normally expected to accumulate enormous genetic diversity (Chandel and Joshi, 1983). Nevertheless, the distribution of genotypes in different clusters did not follow definite pattern with regards to geographical origins in the present study. Some genotypes from different areas were found to be closely related regardless of their geographic origins. And the rugged nature of the topography which could have favored isolation among the genotypes and hence, distinct lines of evolution in each region. This could be realized from the overlapping in clustering pattern among genotypes from different countries. Several possible reasons could be given for the genetic similarity among genotypes from different regions. There could also be a tendency, particularly among resources poor farmers in marginal areas, of selecting for the same traits of interest like yield stability, resistance to diseases, insects and biotic calamities and low dependence on the external inputs (de boef *et al*.,1996). Moreover, it might be also due to germplasm exchange. Some genotypes from same origin were found to distributed over different clusters while others were limited to two or three clusters, indicating that genetic diversity in rain fed lowland rice is not uniformly distributed over the regions.

In most cases, genotypes from the same place of origin fell into the different clusters and from different places of origins also fell into same clusters. For as witnessed, genotypes originated from IRRI are distributed in different clusters. For instance, the results showed that 57.14% of the genotypes are under cluster I, 9.52% in cluster II, 19.04% in cluster III and 14.28% distributed in cluster IV, respectively. Genotypes that also originated from Africa rice center distributed into different clusters. For instance, 10% of the genotypes under cluster I, 30% in cluster II, 50% in cluster III and 10% in cluster IV were scattered, respectively. This indicates

that genotypes from different regions might have similar genetic background and the genotypes might be of the same origin. Hence, the geographic diversity should not necessarily be used as an index of genetic diversity and parental selection should be based on a systematic study of genetic diversity in a specific population. The current finding is in line with the reports of Dawud and Mekbib (2015), in which they grouped 81 sesame genotypes into seven clusters and observed the lack of relationship between geographic and genetic diversity. Zhuang *et al*. (2011) reported that the clustering analysis done on Persian wheat (*Triticum turgidum* ssp. *carthlicum*) accessions using EST-SSR markers suggested that most of the accessions with adjacent geographic origins had the tendency to cluster together. Similarly, Gidey *et al*. (2012) reported absence of significant relationship between genetic and geographical diversity among 81 sesame landraces of Ethiopia.

Table **7**. Inter cluster D^2 values among five clusters in low land evaluated at Pawe and Fogera in the 2015/2016 cropping seasons

Cluster	**I**	**II**	**III**	**IV**	**V**
I	**—**	411.45**	1229.21**	2968.92**	2167.19**
II		**—**	818.92**	2558.64**	1756.80**
III			**—**	1739.80**	938.02**
IV				**—**	801.90**
V					**—**

x^2= 22.36 at 5% and x^2 = 27.69 at 1%, respectively.

4.6.2. Clustering of genotypes

The thirty-six genotypes under study were grouped into five distinct clusters using Mahalanobis (D^2) analysis (Table 8 and Fig.1) which makes them divergent. The number of genotypes in each cluster varied cluster to cluster. The genotypes distributed in such a way that 14 genotypes (38.89 %) grouped into cluster I, 11 genotypes (30.56%) into cluster III, 6 genotypes (16.67%) grouped into cluster II, 4 genotypes (11.11%) grouped into cluster IV and 1 genotype (2.78 %) were grouped into cluster V as a solitary cluster, respectively. Similar study conducted by Rahman *et al*. (2011) in 21 rice varieties using 13 morphological traits, 14 physiological traits grouped the varieties into five clusters. Islam *et al*. (2016) reported by tested 113 genotypes was formed 10 clusters based on D^2 cluster analysis. They indicated also selection of parents from the clusters of V and X followed by hybridization would possibly result in desirable heterosis for the development of heterotic rice hybrids. Similarly, Kumbhar *et al. (*2015) evaluated 50 rice genotypes that comprising landraces, local selections and improved varieties were characterized by using binary data of polymorphic markers, grouped the genotypes into five clusters.

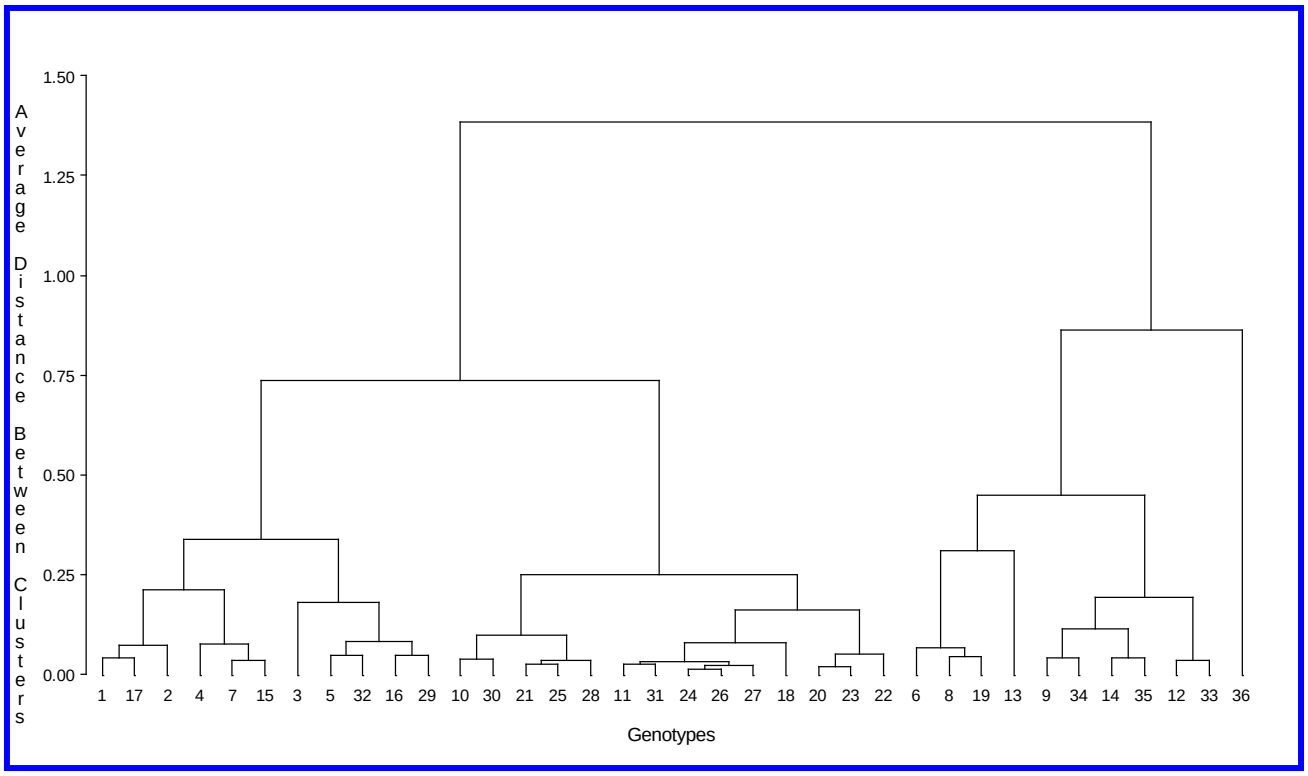

Figure 1: Dendogram of 36 genotypes for 14 characters with average linkage clustering strategy

Table 8. Clustering of 36 low land rice genotypes based on D^2 statistics

Cluster No	No of genotypes	Proportion (%)	List of genotypes
I	14	38.89	IR 83383-B-B-141-1, IR80463-B-39-3, IR 83372-B-B-115-4, IR 83372-B-B-115-3, IR 72768-8-1-1, IR76999-52-1-3-2, IR 81047-B-106-2-4, IR 83377-B-B-93-3, IR80420-B-22-2, IR 75518-18-1-2-B, IR 83222-F11-66, YUNLU N0.33, IR 83383-B-B-141-2, WAS 161-B-6-B-B-1-B (NERICA-L-38)
II	6	16.67	IR 83249-F9-29, ARCCU16Bar-21-5-12-3-1-2-1, IR 83222-F11-209, ARCCU16Bar-13-2-16-2-1-1, CHOMRONG, and EDIGET
III	11	30.56	IR 83222-F11-18, WAB880-1-38-20-17-P1-HB, IR74052-184-3-3, IRAT112, WAB880-1-32-1-2-P1-HB, IR 75518-84-1-1-B, WAB376-B-10-H3,WAS161-B-6-B-1 (NERICA-L-36), YUNJING 23, PSBRC44, WAB502-8-5-1
IV	4	11.11	IR 83222-F11-200, WAB 326-B-B-7-H1, IR 83222-F11-167, STEJAREE 45
V	1	2.78	X-Jigna

4.6.3. Cluster mean analysis

The mean value of all the 14 traits in each cluster is presented in (Table 9). Cluster I comprised a maximum of 14 genotypes that had its own unique characteristics of semi dwarf in height (80.6), the shortest culm length (62.45 cm), the highest paddy yielding ability (6429.14 kg/ha), the highest harvest index (0.29), late maturing period (138.91 days), late 50% heading period (102.68 days), highest grain filling ability (96.51), high biomass yield (9.14 kg/plot), high tillering ability (7.65), the highest number of total spikelets per panicle (100.98), intermediate heavy 1000 grain weight (23.69 g/plot), high number of unfilled spikelets per panicle (3.01), relatively tall panicle length (19.6 cm) and had the shortest flag leaf length (20.66 cm) of all clusters in present investigation.

Cluster II contained 6 genotypes, which comprised early heading period (89.83 days), relatively late maturity (127.08 days), the tallest plant height (88.7 cm), tall culm length (70.76 cm), medium panicle length (18.78 cm), short flag leaf length (21.02 cm), the heaviest 1000 grain weight (25.37 g/plot), moderate paddy ability (4386.68 kg/ha), moderate number of filled spikelets per panicle, moderate number of total spikelets per panicle (93.99) the lowest number of unfilled spikelets per panicle (2.28) and moderate harvest index (0.26) of the mean values.

Cluster III consisted of 11 genotypes followed by cluster I and had the following feature: late maturity period (133.18), relatively short in plant height (85.96 cm), relatively tall culm length (68.31cm), the highest number of unfilled spikelets per panicle (3.09), higher tillering ability (6.88), relatively high number of filled spikelets per panicle (93), high biomass yield (8.48 kg) and high paddy yielding ability (5371.04 kg/ha), heavy 1000 grain weight (24.78g/plot), high number of total spikelets per panicle (97.51), relatively late heading period and high harvest index (0.27).

The rest cluster IV had four genotypes with possessing of genotypes with early heading period (93.63 days), relatively early maturing period (126.44 days), moderate number of total spikelets per panicle (91.1), moderate tillering ability (6.66), the lowest biomass yield (6.04 kg/plot), substantial heavy 1000 grain weight (24.97 g/plot), moderate harvest index (0.26), short stature in plant height (78.01cm), panicle length (17.98 cm), flag leaf length (21.51cm) and culm length (61.7cm). On the other hand, cluster V had only one genotype and had a characteristic of early in maturing period (123.75 days), the tallest plant height (97.4 cm), the tallest panicle length (19.65cm), the tallest culm length (79.55 cm), the tallest flag leaf length (23.55cm), the lowest number of filled spikelets per panicle (85.85), moderate tillering ability (6.45) , the lowest number of total spikelets per panicle (89.05) , moderate biomass yield (6.9 kg/plot), relatively moderate days to heading (95.5 days), the lowest 1000 grain weight (22.87 g/plot), the lowest paddy yield potential (2886.3 kg/ha) and had the lowest harvest index (0.17).

Table 9. Cluster mean for 14 quantitative traits among 36 low land rice genotypes evaluated at Pawe and Fogera in 2015/2016

Traits	I	II	III	IV	V
DH	102.68**	89.83*	98.55	93.63	95.5
DM	138.91**	127.08	133.18	126.44	123.75*
PH	80.6	88.7	85.96	78.01*	97.4**
PL	19.6	18.78	19.2	17.98*	19.65**
CL	62.45	70.76	68.31	61.7*	79.55**
FLL	20.66*	21.02	22.11	21.51	23.55**
FSPP	96.51**	89.97	93	86.45	85.85*
USPP	3.01	2.28*	3.09**	2.51	2.3
FTP	7.65**	6.88	7.36**	6.66	6.45
NTSPP	100.98**	93.99	97.51	91.1	89.05*
BY	9.14**	6.95	8.48	6.04*	6.9
TGW	23.69	25.37**	24.78	24.97	22.87*
PY	6429.14**	4386.68	5371.04	3759.5	2886.30*
HI	0.29**	0.26	0.27	0.26	0.17*

"**" and "*" indicates the highest values and the lowest values, respectively. BY= Biomass Yield, DH= Days to Heading, CL= Culm Length, DM= Days to Maturity, FSPP = Filled Spikelets per panicle, FLL= Flag Leaf Length, FTP= Fertile Tiller per plant, PY= Paddy Yield kg ha^{-1} , HI= harvest Index , NTSPP= Number of Total Spikelets Per Panicle, PH= Plant Height, PL= Panicle Length, TGW= Thousand Grain Weight, USPP= Unfilled spikelets per panicle

4.6.4. Principal component analysis (PCA)

Principal component analysis is a data matrix extracts the dominant patterns in the matrix in terms of a complementary set of scores and loading plots. In this study, the data matrix of 14*36 was used for principal component analysis, and 14 principal components (pcs) generated out of these, the first four principal components that revealed eigen values greater than one were found to be significant. The remaining ten PCs explained non-significant amount of variation and were not worth interpreting. The eigen values are used to determine how many factors to retain. The sum of eigen values is usually equal to the number of variables. The principal component analysis showed in this experiment that four principal components across the two locations PC-1, PC-2, PC-3 and PC-4 exhibited more than one eigen value with the eigen values of 4.768, 3.981, 1.268 and 1.076, respectively, and explained about 79.23% of the total variation for all the characters with high correlation among the traits analyzed (Table 10).

Therefore, variation for these four PCs was given an emphasis for further explanation. According to Guei *et al.* (2005) the first three principal components are often the most important in reflecting the variation patterns among accessions, and the characters associated with these, are more useful in differentiating accessions. According chahal and gosal (2002) characters with larges absolute values closer to unity within the first principal component influence the clustering more than those with lower absolute values closer to zero. Raji (2002) chosen to determine the cutoff limit for the coefficients of the proper vectors; this criterion treated coefficients greater than 0.3 as having a large enough effect to be considered important, while traits having a coefficient less than 0.3 were considered not to have important effects on the overall variation.

Accordingly, in the present study, the first principal component (PC-1) which accounted for 34.06% of the total morphological variability among genotypes were attributed to discriminatory traits, namely, biomass yield (0.400), days to heading (0.373) followed by number of total spikelet per panicle (0.362), number of filled spikelets per panicle (0.361), panicle length (0.332) and paddy yield per ha (0.331 kg/ha) suggesting that these components reflected the yield potential of each genotype through some yield component aspects and they

were the ones that more differentiated the clusters. Likewise, 28.43 % of total morphological variability among the tested genotypes accounted for the second PCA originated from variation due to culm length (0.464), followed by plant height (0.462), flag leaf length (0.380) and 1000 grain weight (0.328) suggesting that these components reflected the yield potential of each genotype. Similarly, the third PCA which accounted for 9.06 % of the total variation contributed from number of unfilled grain yield per panicle (0.423), number of total spikelets per panicle (0.423) and number of filled spikelets per panicle (0.399). Furthermore, the fourth PCA accounted for 7.68 % of total variance and number of fertile tillers per plant (0.716), 1000 grain weight (0.332) were the main loading factors.

Therefore, the present study confirmed that rain fed low land rice genotypes showed adequate amount of variations for the character studied and it also suggested that ample opportunities for genetic improvement of low land rice genotypes and conservation of the materials for future utilization. In line with the finding of Adebisial *et al.* (2012) that employed PCA for detecting variation in 24 low land rice genotypes in which the first three PCs were adequate in determining more than 86% of total variation. Similarly, Wijayawardhana *et al. (*2015) also reported the first four PCs having eigen values greater than 1 accounted for 84.78% of the total variation.

Table 10. Eigen values total variance, percent of cumulative variance and eigen vectors for 14 characters studied in 36 rice genotypes

Characters	PC-1	PC-2	PC-3	PC-4
DH	0.373*	-0.108	-0.281	-0.218
DM	0.316*	-0.087	-0.514*	-0.169
PH	0.099	0.462*	0.018	0.16
PL	0.332*	0.155	0.079	0.068
CL	0.074	0.464*	0.012	0.15
FLL	0.184	0.380*	0.094	-0.08
FSPP	0.361*	-0.039	0.399*	-0.227
USPP	0.208	-0.184	0.423*	0.191
FTP	0.139	-0.185	0.059	0.716*
NTSPP	0.362*	-0.056	0.423*	-0.181
BY	0.400*	0.07	-0.238	0.137
TGY	-0.049	0.328*	-0.075	0.332*
PY	0.331*	-0.221	-0.234	0.251
Eigen value	4.768	3.981	1.268	1.076
percent of variance	34.06	28.43	9.06	7.68
Cumulative variance	34.06	62.49	71.54	79.23

"*" Indicating loading value greater than 0.3, BY= Biomass Yield, DH= Days to Heading, CL= Culm Length, DM= Days to Maturity, FSPP = Filled Spikelets per panicle, FLL= Flag Leaf Length, FTP= Fertile Tiller per plant, PY= Paddy Yield kg ha^{-1} , HI= harvest Index , NTSPP= Number of Total Spikelets Per Panicle, PH= Plant Height, PL= Panicle Length, TGW= Thousand Grain Weight, USPP= Unfilled spikelets per panicle

5. SUMMARY AND CONCLUSION

The advancement of crop improvement programme depends on the choice of materials, the extent of variability present and the knowledge of quantitative traits association with grain yield. The current study comprised of 36 rice genotypes that were evaluated at two locations, namely Fogera and Pawe to estimate the extent of genetic variability and trait association of rain fed low land rice genotypes for yield and yield related traits.

The combined analysis of variance (ANOVA) revealed statistically significant variations among the 36 lowland rice genotypes for 14 traits studied. Moreover, there were significant (P<0.01) genotype × location (G × L) interaction for days to maturity, plant height, panicle length, culm length, flag leaf length, number of filled spikelets per panicle and number of total spikelets per panicle and while significant ($P < 0.05$) for days to heading, biomass yield, paddy yield and harvest index indicating the different responses of genotypes for these traits under the two locations.

Paddy yield ranged from 6759.00 kg/ha for IR 83383-B-B-141-2 to 2886.00 kg/ha for the local check (X-jigna). Among the genotypes evaluated IR 83383-B-B-141-2, IR 83372-B-B-115- 4, IR 83372-B-B-115- 3, IR 83383-B-B-141-1 and IR80463-B-39-3 were the five top yielders with corresponding mean paddy yield of 6759.0, 6687.7, 6684.8,6520.4 and 6507.0 Kg/ha.

PCV were consistently greater than GCV for all the fourteen traits indicating that they all interacted with the environment to some extent. High PCV and GCV values were recorded for plant height, culm length, number of unfilled spikelets per panicle, paddy yield and biomass yield, which suggests the possibility of improving this trait through selection. However, the estimates of GCV and PCV were low in the present study for days to maturity (7.00%, 10.60).

High broad sense heritability was recorded; and ranges from 18.24 to 81.14 percent. The characters that had highest heritability was for culm length (81.14%) followed by plant height (80.10%), biomass yield (73.41%) and panicle length (65.50%). In contrast, flag leaf length (28.41%), number of fertile tiller per plant (18.24%), 1000 grain weight (29.73%) and harvest

index (25.97%) had low heritability, which indicates greater role of environment on the expression of the traits. Heritability alone does not provide indication of the amount of genetic improvement that would result from selection of individual genotypes. Hence knowledge about the heritability coupled with genetic advance and genotypic coefficient of variations (GCV) are most beneficial. The positive combination of genotypic coefficient of variation (GCV), heritability and genetic advance as percent of mean were recorded for plant height followed by culm length ,biomass yield , paddy yield and number of unfilled spikelets per panicle, which indicated that the traits were possessed additive gene effects.

Genetic advance as percent of mean ranged from 4.10 % for number of fertile tillers per plant to 59.06% for culm length. plant height (46.87 %), culm length (59.06 %), biomass yield (43.63%) , paddy yield (27.77%) and number of unfilled spikelets per panicle (25.32%) gave high genetic advance as percent of mean. Therefore, direct selection on the basis for these characters will be advantageous. However, low estimates of genetic advance as percent mean were recorded for days to maturity (6.28%), flag leaf length (8.39 %), number of fertile tiller per plant (4.10%), number of filled spikelets per panicle (6.37 %), number of total spikelets per panicle (5.13 %), 1000 grain weight (5.78 %) and harvest index (6.89 %), respectively. This indicates the characters governed by non-additive gene action.

Paddy yield exhibited positive and highly significant ($P < 0.01$) genotypic correlation with traits like days to heading, days to maturity, number of filled spikelets per panicle, number of fertile tillers per plant, harvest index, number of total spikelets per panicle and biomass yield per plot, respectively. This indicates the importance of these traits for yield improvement in rice. Thus, the indirect selection for higher yield based on these characters would be reliable.

Path coefficient analysis revealed that biomass yield, harvest index and number of total spikelets per panicle had the highest direct effect on paddy yield with significant and positive genotypic association, which indicates the correlation explains the true association with paddy yield and direct selection though these traits will be effective. Thus, selection of genotypes with more number of total spikelets per panicle, harvest index, biomass yield and plant height are important to develop high yielder varieties and an emphasis should be given for these traits in future breeding efforts.

Principle component analysis of the genotypes across the two locations revealed that the first four PCs having eigen values greater than one explained 79.23% of the total variation. This suggested a strong correlation among the characters examined. PCA-1 accounted about 34.06 %, PCA-2 explained 28.43 %, PCA-3 for 9.06% and PCA-4 7.68 % of the total morphological variability was assigned for the variation, respectively.

Clustering of genotypes was not related with their geographical distribution instead genotypes were mainly grouped based on morphological differences. All of the 36 rice genotypes were grouped into five distinct clusters. The highest inter cluster divergence was observed between clusters I and IV (D^2=2968.92), followed by between clusters II and IV (D^2=2558.64) and I and V (D^2=2167.19) which showed that genotypes contained in these clusters were genetically more divergent from each other than genotypes contained in any other clusters. Based on the inter cluster distances, hybridization between the genotypes of cluster I with cluster IV, cluster II with cluster IV and cluster I with cluster V would generate promising segregating populations that could be used as source materials for improvement of grain yield through selection.

In conclusion, the present study identified the presence of moderate inherent genetic variability and genetic divergence among 36 tested genotypes. The study also identified desirable genotypes that could be promoted for further evaluation and/or recommended for release for possible commercialization.

Biomass yield, harvest index and number of total spikelets per panicle showing positive and significant correlation and positive direct effect combined over the two locations, these will be a useful trait for indirect selection to increase paddy yield.

This study was carried out for one season and at two locations. Therefore, it is advisable to repeat the study at least more than one season considering major rice growing areas by including additional materials to make sound recommendations. Moreover, it is recommended that future rice research explore molecular means to further confirm the outcome of this study findings.

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7. APPENDICES

Appendix Table 1. Analysis of variance for mean square of the 14 characters of 36 genotypes tested at Pawe 2015/2016

Source of variation	Mean squares					R	CV	Relative efficiency to RCBD
	Rep	Blocks within rep	Genotypes (Adj)	Intera block error	RCBD			
Degree of freedom	**1**	**10**	**35**	**25**	**35**			
DH	43.556	9.306	59.62**	14.176	12.784	0.900	3.900	90.180
DM	98.000	51.417	172.38**	53.673	53.029	0.890	5.100	98.800
PH	44.400	44.400	628.88**	23.532	29.494	0.980	5.110	110.500
PL	0.067	1.495	5.13**	1.671	1.620	0.890	5.610	96.990
CL	32.267	37.038	580.55**	22.492	26.648	0.980	6.270	106.520
FLL	0.109	6.610	44.89**	7.448	7.208	0.920	10.700	96.780
FSPP	171.120	30.215	92.46*	47.830	42.797	0.800	6.570	9.480
USPP	7.094	2.529	1.71^{NS}	1.350	1.687	0.750	23.200	110.260
FTP	8.681	1.040	3.36*	1.623	1.457	0.790	15.080	89.730
NTSPP	108.540	36.793	109.09*	52.852	48.264	0.810	6.670	91.320
TGW	0.605	3.659	4.28**	4.211	4.053	0.910	8.000	116.160
BY	23.805	2.076	20.42**	0.944	1.267	0.920	11.350	96.250
HI	0.027	0.001	0.002*	0.001	0.001	0.840	13.560	86.910
PY	657.390	1040117.000	2.48**	833290.000	892384.000	0.880	15.880	101.330

"*"= Significant at 5% probability level and "**"= Highly significant at 1% probability level and NS= Non- Significant. BY= Biomass Yield, DH= Days to Heading, CL= Culm Length, DM= Days to Maturity, FSPP = Filled Spikelets per panicle, FLL= Flag Leaf Length, FTP= Fertile Tiller per plant, PY= Paddy Yield kg ha^{-1} , HI= harvest Index , NTSPP= Number of Total Spikelets Per Panicle , PH= Plant Height, PL= Panicle Length, TGW= Thousand Grain Weight, UGY= Unfilled spikelets per panicle.

Appendix Table 2. Analysis of variance for mean square of the 14 characters of 36 genotypes tested at Fogera (2015/2016)

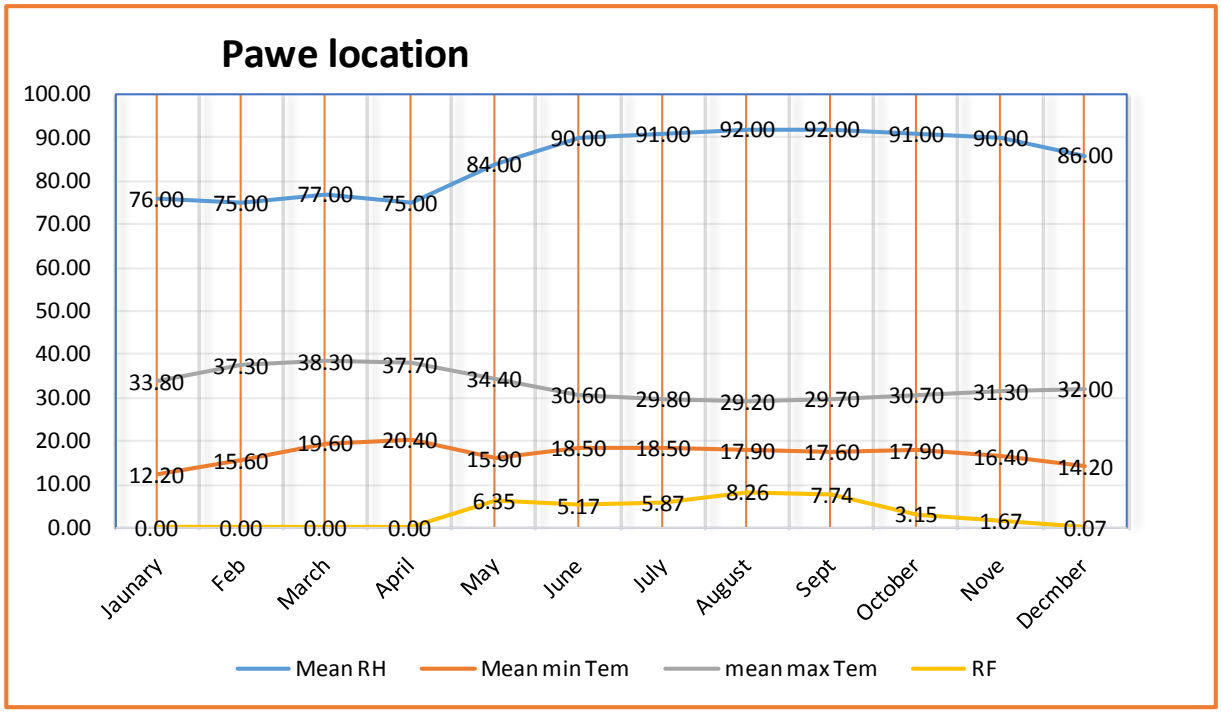
Source of Variation	Mean squares					R	CV	Relative efficiency to RCBD
	Rep	Blocks within rep	Genotypes (Adj)	Intera block error	RCBD			
Degree of freedom	**1**	**10**	**35**	**25**	**35**			
DH	1.680	1.560	94.42**	2.167	1.995	0.99	1.27	92.05
DM	55.125	60.725	156.95**	51.725	54.296	0.84	5.16	100.71
PH	34.169	7.566	178.09**	5.292	5.942	0.98	3.29	103.4
PL	0.001	0.579	3.56**	1.041	0.909	0.86	5.55	87.3
CL	6.361	4.187	173.98**	6.261	5.668	0.98	4.01	90.53
FLL	0.467	2.842	11.13**	4.055	3.708	0.87	10.2	91.45
FSPP	125.350	45.303	189.70**	32.227	35.963	0.93	6.34	103.09
USPP	13.005	0.454	1.88*	0.734	0.654	0.85	26.5	89.11
FTP	34.169	4.685	2.43**	1.209	2.202	0.87	16.5	150.29
NTSPP	290.400	64.021	202.32**	34.664	43.052	0.93	6.14	109.81
TGW	62.329	6.843	12.67^{NS}	12.049	10.562	0.69	12.6	106.59
BY	0.451	0.914	4.83**	0.554	0.657	0.93	9.88	87.66
HI	0.003	0.002	0.005**	0.001	0.001	0.89	12	110.02
PY	211829.000	464106.000	2.001**	288724.000	338833	0.92	10.6	105.92

"*"= Significant at 5% probability level and "**"= highly significant at 1% probability level and NS= Non- Significant. BY= Biomass Yield, DH= Days to Heading, CL= Culm Length, DM= Days to Maturity, FSPP = Filled Spikelets per panicle, FLL= Flag Leaf Length, FTP= Fertile Tiller per plant, PY= Paddy Yield kg ha^{-1} , HI= harvest Index , NTSPP= Number of Total Spikelets Per Panicle , PH= Plant Height, PL= Panicle Length, TGW= Thousand Grain Weight, UGY= Unfilled spikelets per panicle.

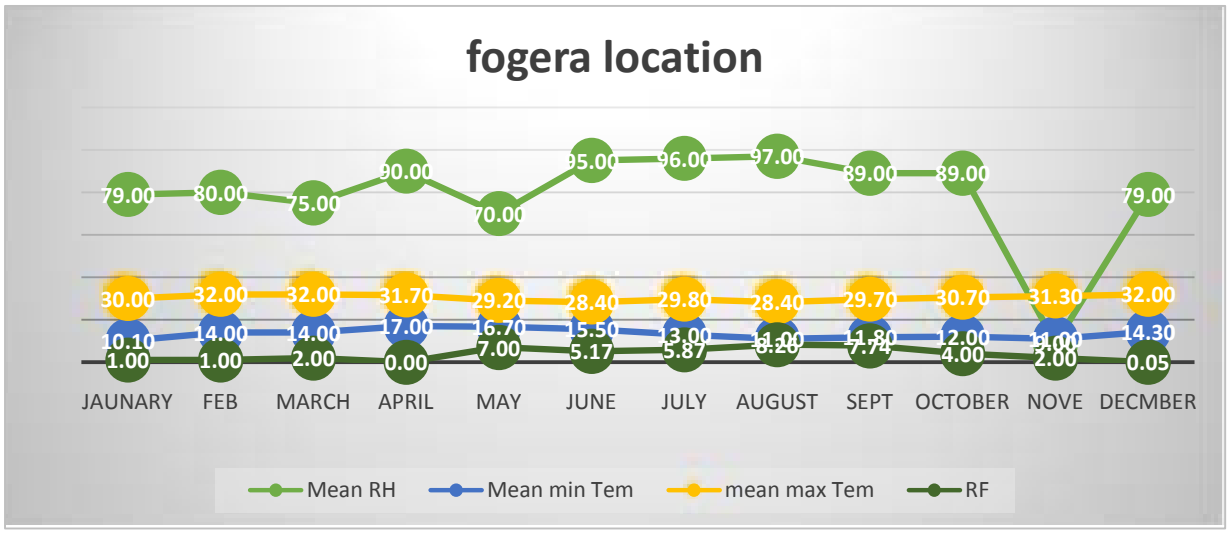
Appendix Table 3. The combined mean values of the studied 36 genotypes evaluated at Pawe and Fogera in 2015 cropping season

GENOTYPES	DH	DM	PH	PL	CL	FLL	FGY
IR74052-184-3-3	103.5	140.5	71.7	20.25	53	20.15	93.9
YUNJING 23	94.75	135	74.1	16.5	58.5	20.75	81.65
WAB502-8-5-1	98.5	129.75	103.25	19.3	85.9	24.9	89.65
PSBRC44	110	132.5	85.75	19.75	68.5	19.3	98.5
WAB376-B-10-H3	99.25	129.75	108.65	20.9	89.45	25.3	97.3
IR 83222-F11-167	97.5	125.25	66.9	18.2	51.4	20.15	94.45
IR 83222-F11-18	95	135.25	68.65	17.7	52.3	20.95	92.2
IR 83222-F11-200	88.75	123.75	68.9	16.4	53.95	18.3	85.65
IR 83222-F11-209	92.5	125	70.65	17	53.9	16.15	93.3
IR 83222-F11-66	102.5	142.75	105.35	18.7	88.1	24.35	109.5
IR76999-52-1-3-2	105	136.75	69.45	19.55	50.6	18.15	93.05
IR 83249-F9-29	87.25	121.5	74.85	19.55	56.5	21.95	103.15
STEJAREE 45	87.5	126	85.1	17.3	69.9	16.65	75.9
CHOMRONG	82.5	116.5	110.05	19.45	91.4	21.25	74.8
WAB880-1-38-20-17-P1-HB	89.5	125.25	90.6	19	72.85	21.35	92.9
WAB880-1-32-1-2-P1-HB	88	121	83.45	18.35	66.85	20.55	90.95
IRAT112	92	126.75	83.3	18.4	66.45	20.2	94.2
WAS 161-B-6-B-B-1-B (NERICA-L-38)	104	143.25	70.9	20.9	51.4	18.9	93.15
WAB 326-B-B-7-H1	100.75	130.75	91.15	20	71.55	30.95	89.8
IR 83372-B-B-115-4	96.5	142.25	74.6	19.75	56.35	20.2	85.95
IR 83377-B-B-93-3	105.75	139	72.65	18.45	55.25	18.35	102.7
IR 83383-B-B-141-2	105	138.5	76.1	19.4	58.55	19.2	97.2
IR 83372-B-B-115-3	100.25	128.25	74.6	20.8	55.6	20.9	104.2
IR 83383-B-B-141-1	103.75	138.75	74.3	19.8	56.45	18.65	90.75
IR80420-B-22-2	100.5	135	76	19.25	56.85	20.6	95.4
IR80463-B-39-3	102.25	136.75	73.15	19.5	54.6	20.1	98.55
IR 72768-8-1-1	104.75	140.5	91.15	18.65	74.4	22.65	97.35
IR 75518-18-1-2-B	103.75	140.5	105.3	22.4	85.75	24.95	105.1
IR 75518-84-1-1-B	107.75	145.5	110.05	22.3	89.25	30.65	99.7
YUNLU N0.33	102	142.75	102.2	19.3	84.4	25	96.2
IR 81047-B-106-2-4	101.5	139.75	62.6	17.95	46.05	17.25	82
WAS 161-B-6-B-1 (NERICA-L-36)	105.75	143.75	66.05	18.8	48.4	19.1	92.1
ARCCU16Bar-21-5-12-3-1-2-1	94	134	89.45	20.2	71.55	22.5	91.6
ARCCU16Bar-13-2-16-2-1-1	94.5	135.75	98	20.15	78.1	22.95	90.9
Ediget	88.25	129.75	89.2	16.35	73.1	21.3	86.05
X-jigna	95.5	123.75	97.4	19.65	79.55	23.55	85.85
Mean	98.07	133.38	83.77	19.16	66.02	21.34	92.93
LSD (5%)	3.92	10.76	5.58	1.49	5.23	3.13	8.51
CV (%)	2.82	5.7	4.71	5.52	5.6	10.37	6.48

GENOTYPES	UGY	FT	NST	BY	TSW	GY	HI
IR74052-184-3-3	3.2	7.95	98.4	7.88	23.11	5307.1	0.28
YUNJING 23	1.7	6.05	85.1	6.73	24.5	5382.5	0.32
WAB502-8-5-1	3.45	8.25	94.55	10.4	25.99	5835.4	0.23
PSBRC44	2.15	6.85	102.35	8.93	20.7	5078.3	0.23
WAB376-B-10-H3	3.35	8.2	101.4	11.15	24.79	5647.6	0.21
IR 83222-F11-167	3.1	6.3	99.4	5.28	22.8	3934.6	0.3
IR 83222-F11-18	2.6	7.35	96.05	7.03	24.78	4949.3	0.29
IR 83222-F11-200	2.55	6.65	90.35	5.7	20.92	3815.8	0.28
IR 83222-F11-209	2	6.85	97.35	5.88	23.02	4354.5	0.3
IR 83222-F11-66	2.15	8.55	114.35	9.5	27.34	6094.4	0.26
IR76999-52-1-3-2	4	9.4	99.65	7.25	23.24	6457.8	0.36
IR 83249-F9-29	2.8	7.55	107.9	6.03	22.96	4548.8	0.31
STEJAREE 45	1.4	6.75	80	5.38	27.81	3413.3	0.25
CHOMRONG	1	8.8	78.95	6.33	26.79	4185.7	0.27
WAB880-1-38-20-17-P1-HB	4.95	7.15	98.55	7.23	26.09	4990.8	0.28
WAB880-1-32-1-2-P1-HB	3	7.4	95.65	7.75	25.7	5539.8	0.31
IRAT112	3.75	6.9	99.35	7.15	27.78	5249.6	0.3
WAS 161-B-6-B-B-1-B (NERICA-L-38)	3.55	8.15	99	8.98	24.63	6379.6	0.29
WAB 326-B-B-7-H1	3	6.95	94.65	7.78	28.35	3874.3	0.2
IR 83372-B-B-115-4	2.8	7.15	89.85	9.13	21.47	6687.7	0.3
IR 83377-B-B-93-3	3.35	8.55	106.95	9.65	23.08	6251.2	0.26
IR 83383-B-B-141-2	3.45	8.45	102.3	10.53	24.57	6759	0.26
IR 83372-B-B-115-3	3.6	7.4	108.45	9.08	21.01	6684.8	0.3
IR 83383-B-B-141-1	3.15	7.3	95.55	9.53	22.3	6520.4	0.28
IR80420-B-22-2	3.4	7.7	99.75	8.45	20.21	6286.4	0.3
IR80463-B-39-3	3.35	8.35	102.55	8.85	22.98	6507	0.3
IR 72768-8-1-1	2.7	6.3	101.4	8.75	23.05	6499.6	0.3
IR 75518-18-1-2-B	2.2	6.1	108.5	10.73	27.97	6246.4	0.23
IR 75518-84-1-1-B	2.6	6.95	104.5	9.75	25.64	5489.6	0.23
YUNLU N0.33	2.25	5.85	99.65	9.33	25.06	6146.2	0.27
IR 81047-B-106-2-4	2.25	7.8	85.75	8.25	24.7	6487.4	0.32
WAS 161-B-6-B-1 (NERICA-L-36)	3.2	7.9	96.75	9.23	23.45	5611.4	0.25
ARCCU16Bar-21-5-12-3-1-2-1	3.6	6.25	96.5	8.23	24.92	4590.7	0.23
ARCCU16Bar-13-2-16-2-1-1	2.5	5.85	93.9	8.2	26.62	4401	0.22
Ediget	1.8	5.95	89.35	7.03	27.9	4239.4	0.25
X-jigna	2.3	6.45	89.05	6.9	22.87	2886.3	0.17
Mean	2.84	7.29	97.33	8.17	24.42	5370	0.27
LSD (5%)	1.57	1.64	9.09	1.30	4.03	1060.5	0.05
CV (%)	22.32	15.99	6.61	11.28	11.66	13.96	12.52



Appendix Figure 1. Pawe location environmental descriptions.



Appendix Figure 2. Fogera location environmental descriptions