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Research Article Open Access

Multivariate Analyses of Grain Yield and Its Agronomic Traits in Lowland Rice (*Oryza sativa L.*) Genotypes

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Abstract

The study was conducted at Pawe Agricultural Research Center and Fogera National Rice Research and Training Center during 2015cropping season to estimate the genetic diversity and principal component analyses in rain fed lowland rice. The study was conducted using 6x6 simple lattice design with two replicates. The analysis of variance revealed 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. Clustering of genotypes were not associated with their geographical origin instead of the genotypes were mainly grouped based on morphological significances. The Mahalanobis D2 statistics showed 36 genotypes were grouped into five distinct clusters and the chi-square test for the five clusters showed the presence of highly significant difference (p<0.01) among the clusters, which confirming that the studied genotypes were highly divergent. Principal component (pc) analyses showed the first four PCs having eigen values greater than one accounted about 79.23% of the total variation. Moreover, 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.

Key words: Diversity; PCA; Rice; Path Coefficient Analyses

Introduction

Rice (*Oryza sativa* L.) is a self-pollinated cereal crop belonging to the family Gramineae having chromosome number 2n=24. Rice belongs to the genus *Oryza,* the family Gramineae, and is a widely cultivated crop. It is become a commodity of strategic significance and the fastest-growing food source in Africa, such that its availability and price are now a major determinant of the welfare of the poorest people, who are the least food secure consumers in Africa [1]. In developing countries, approximately 60 % of total calories consumed are derived directly from cereals with values exceeding 80% in the poorest countries. Among the cereals, rice is the most important source of calories for humans. While per capita consumption is declining in parts of Asia, the demand for rice has increased considerably in Sub-Saharan Africa since 1995 and is growing more rapidly there than in any other continent. Rice production in Sub Saharan Africa though rising from 8.6 million tonnes of paddy rice in 1980 to 12.6 million tonnes in 2005, has not kept pace with demand [2]. As a result, the quantity imported yearly by the region increased from 2.5 million tonnes in 1980 to 7.2 million tonnes in 2005. SSA spends more than US$1.5 billion in foreign exchange every year for its rice imports. Yield is a complex trait and controlled by combined effect of various traits. It is controlled by many genes [3]. So selection of parents only on the basis of yield is not trustable. An efficient selection strategy required knowledge about relationship between yield and its contributing characters. Genetic divergence is the statistical distance between genotypes [4]. It is determined by using cluster analysis into different groups. 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. According to Vivekananda and Subramanian (1993) genetic divergence is an efficacious tool for an effective choice of parents for hybridization and breeding program [5]. Genetic diversity of rice plays an important role in sustainable development and food security as it allows the cultivation of crops in the presence of various biotic and abiotic stresses [6]. It is also important for the selection of parents that can be used in plant breeding programs. 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. Moreover, diversity in plant genetic resources provides opportunity for plant breeders to develop new and improved cultivars with desirable characteristics which include both farmer preferred traits and breeders preferred traits. Study has 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. Study 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 [7]. 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, reported that the first four PCs accounted for about 72% of the total variation among 43 upland rice genotypes tested. 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. According to Ogunbodede, it states that the identification of 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 and enables multi-dimensional relationship to be plotted on two or three principal axes. PCA chooses independent or orthogonal axes, which are minimally correlated and represents linear combination of the original characters. In view of the importance of the crop in Ethiopia, researchers must

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Received December 07, 2020; **Accepted** December 21, 2020; **Published** December 28, 2020

Citation: Abebe T (2020) Multivariate Analyses of Grain Yield and Its Agronomic Traits in Lowland Rice (*Oryza sativa L.*) Genotypes. J Rice Res 8: 227.

be utilizing available genetic resources to reconstruct the ideotype of the plant in order to meet the ever increasing requirements of the population through improvement in yield, other desirable agronomic and phenological traits as well as quality of rice.

Materials and methods

The field experimentwas conducted during 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 Regional states, respectively. Fogera National Rice Research and Training Center is located 607km from Addis Ababa 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 1810 m above sea level. Based on ten years' average meteorological data, the annual rainfall, and mean annual minimum and maximum temperatures are 1300 mm, 11.5°C and 27.9°C, respectively. The soil type is black with pH of 5.90. Pawe Agricultural Research Center is located 578 km 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.

Experimental materials

Thirty four rice genotypes along with two checks were used (Table 1). Among the tested materialsseventeen genotypes were from the medium maturing group whilenineteen were from the early maturing group. All rice genotypes were obtained from Fogera National Rice Research and Training Center and were introduced from Africa Rice Center.

Experimental Design and Management

In each location**,** the experiment is arranged in 6x6 simple lattice designs with two replications. At two sites, the entries were hand-drilled in six row plots, 5m long each with 0.2m spacing between rows and 1.0m and 0.3m between blocks and plots spacing was used across

Table1: 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.

locations. For data collection, the middle four rows only were used for determination of grain yield and yield related traits. 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.

Data Collected

The data collected were such as days to 50 % heading, days to 85 % maturity, grain yield per plot (g), thousand grains weight (g), above ground biomass yield (gram per plot), harvest index (%), plant height (cm), panicle length (cm),culm length (cm), flag leaf length (cm), fertile tillers per plant, number of filled grains per panicle, number of total spikelet's per panicle and number of unfilled grains per panicle according to the rice descriptors (IRRI, 2002) and Bioversity International (2007).

Cluster Analysis

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 dendrograms. 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.

Divergence Analysis

The generalized genetic distance between clusters was calculated using the generalized Mahalanobis' 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.

Principal Component Analysis

Principal components based on correlation matrix were calculated by following PRINCOMP procedureof SAS version 9.2 (SAS, 2008) to examine 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 (Table 1).

Results and Discussion

Divergence Analysis

Genetic divergence quantifies the genetic distance between 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. Inter-cluster distances among the clusters generated are given in Table 2. 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 sergeants for grain yield and other agronomic traits of rice. 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. 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 program for obtaining a wider range of variability to generate sergeants for grain yield and other important agronomic traits. Parental lines selected from these four clusters may be used in a hybridization program, since hybridization between divergent parents is likely to produce variability and transgressive segregations with high heterotic effects. 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 2) which indicates lower genetic distance 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

Table 2: 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.

desirable sergeants and high vigor at F1 generation. Population from geographically separated areas and having complex environment are normally expected to accumulate enormous genetic diversity. However, 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. Moreover, it might be also due to germplasm exchange. Some genotypes from same origin were found to distribute 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 instance, genotypes originated from IRRI are distributed in different clusters. 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 example, 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. Therefore, 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, in which they grouped 81 sesame genotypes into seven clusters and observed the lack of relationship between geographic and genetic diversity. Studies reported that the clustering analysis done on Persian wheat (*Triticumturgidum* ssp. *carthlicum*) accessions using EST-SSR markers suggested that most of the accessions with adjacent geographic origins had the tendency to cluster together. Similarly, reported absence of significant relationship between genetic and geographical diversity among 81 sesame landraces of Ethiopia (Table 2).

Clustering of genotypes

The thirty-six genotypes under study were grouped into five distinct clusters using Mahalanobis (D^2) analysis (Table 3 and Figure 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 in 21 rice varieties using 13 morphological traits, 14 physiological traits grouped the varieties into five clusters. Study reported by tested 113 genotypes was formed 10 clusters based on D^2 cluster analysis. These 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, it has been 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).

Cluster mean analysis

The mean value of all the 14 traits in each cluster is presented (Table 4). 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 grain 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 grains 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 grains 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 grains weight (25.37 g/plot), moderate grain yield 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 grains 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 grains 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

Table 3. 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

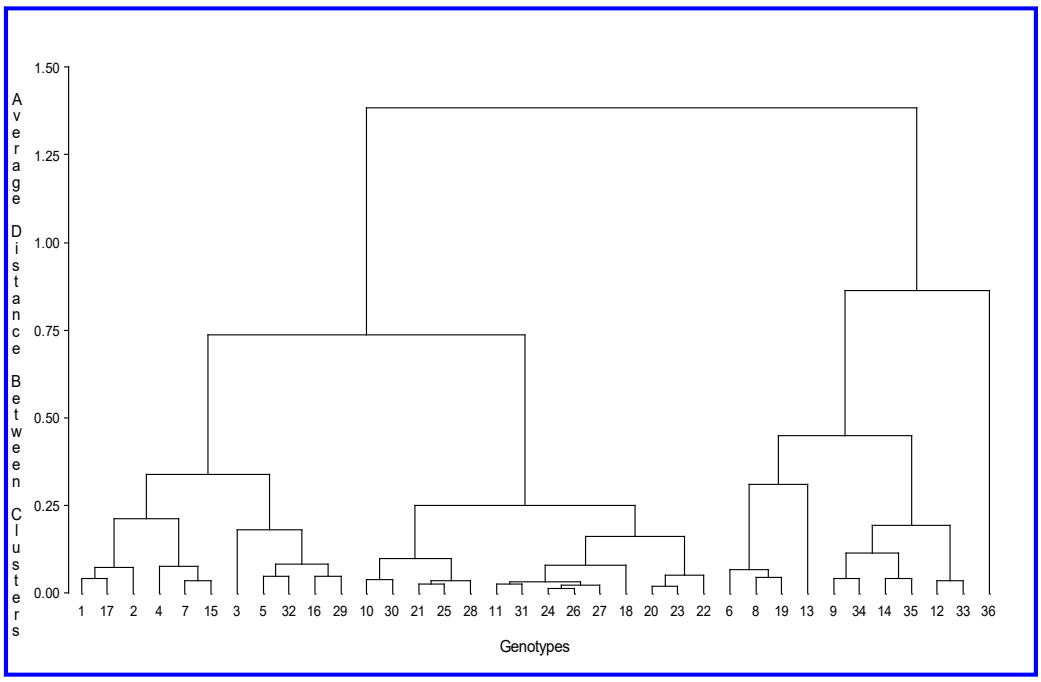

Figure 1: Dendogram of 36 genotypes for 14 characters with average linkage clustering strategy.

Table 4: 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 spikeletsper panicle

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 grains weight (22.87 g/plot), the lowest paddy yield potential (2886.3 kg/ha) and had the lowest harvest index (0.17).

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 5). Therefore, variation for these four PCs was given an emphasis for further explanation. According to Gue*iet al.* (2005) the first three principal components are often the most important in reflecting the

Table 5: 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 Grains Weight, USPP= Unfilled spikeletsper panicle

variation patterns among accessions, and the characters associated with these, are more useful in differentiating accessions. According to 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. Studies 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 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, studies also reported the first four PCs having eigen values greater than one accounted for 84.78% of the total variation.

Conclusion

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 explained28.43%, 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 intercluster 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.

Conflict of Interests

The author(s) have not declared any conflict of interests.

Acknowledgments

We would like to express our heartfelt gratitude to Fogera National Rice Research and Training Center and Pawe Agricultural Research Center staffs for hosting the trials and collecting the data. We also extend our thanks to Tepi National Spices Research Center to facilitate financial for this research and the Ethiopian Institute of Agricultural Research for their financial support.

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