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Research Article
Genetic Diversity Study on Upland Rice (*Oryza sativa* L.) Genotypes Based on Morphological Traits in Southwestern Ethiopia

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Abstract

Background and Objective: Understanding the extent of genetic diversity among genotypes and organizing individuals into groups whose members are similar in some ways have an immense importance in plant breeding program. The objective of this study was to estimate the genetic diversity of 36 upland rice genotypes based on quantitative morphological traits. **Materials and Methods:** The field experiment was conducted using 6×6 simple lattice design in to two locations of southwestern Ethiopia (viz., Gojeb and Guraferda) during the 2016 main cropping season. Cluster analysis, distance analysis and principal component analysis were done using the SAS software version 9.3. **Results:** The analysis of variance over the two locations revealed significance differences ($p \leq 0.05$) among genotypes for plant height, panicle length, culm length, filled grains per panicle, number of primary branches per panicle, days to maturity, days to heading, harvest index and grain yield. Cluster analysis indicated that 36 genotypes were grouped into 6 clusters and divergences between all pairs were significant ($p \leq 0.01$). The inter-cluster distance was maximum between cluster five and six ($D^2 = 997$) followed by cluster four and six ($D^2 = 811$). The first six principal components (PCs) with eigenvalues greater than one explained 75.2% of the total variation among genotypes. The first and second PCs were responsible for about 19.3 and 14.5% of the total variation, respectively. In the first principal component character such as plant height (16.8%), panicle length (18.6) and culm length (18.3%) accounted high contribution effect of the total variation. **Conclusion:** This study confirmed the presence of variability among genotypes for most of the studied traits, which will create an opportunity for breeders to improve the yield of rice and other traits.

Key words: Cluster analysis, genetic diversity, southwestern Ethiopia, trait correlations, plant breeding program, upland rice

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Data Availability: All relevant data are within the paper and its supporting information files.

INTRODUCTION

Rice accounts for more than one-fifth of the calories consumed by human beings globally[1] and it is one of the most important sources of daily dietary intake of large population of Asian and sub-sahara African countries. In Asia, rice accounts for 60-70% of energy intake for over two billion people[1]. It was reported that, rice grain contains 75-80% starch, 12% water and 7% protein[2]. It is also an important source of vitamins, like thiamine, riboflavin and niacin and minerals like magnesium, phosphorus and calcium. In Ethiopia, rice is used for various traditional foods like Injera, bread and local beverage[3].

It is believed that, rice was introduced to Ethiopia in the 1970s and has since been cultivated in relatively few parts of the country[4]. The three-main rice producing regions of the country: namely, Amhara, Oromia and SNNPR have 76, 14.9 and 5.2% of the country's rice production, respectively. In terms of areas of production, rice production shows a growing importance in the country, which is reflected in the increase in the area of production from 24,434 ha in the year 2000 to 46,832 ha in 2016, which is almost doubled during this period[5,6]. The average rice productivity in Ethiopia is estimated[6] at 2.8 t ha^{-1}, which is much lower than the world's average[7] of 4.4 t ha^{-1}.

The limited production of rice, which is mainly attributed to lack of improved varieties with better productivity and adaptability can be improved through developing high yielding varieties, which largely depends on the existence of sufficient genetic diversity in rice germplasm[8]. This is because, plant genetic improvement in breeding programs, mainly depends on the amount of genetic diversity present in the population[9].

In Ethiopia different researchers conducted genetic variability studies on upland rice, such as Seyoum *et al.*[10] reported the presence of significant variation among genotypes for most of the studied traits (viz., days to 50% flowering, days to 85% maturity, plant height, panicle length and 1000-grain weight), Fentie *et al.*[11] and Mulugeta[12] reported significant variation among genotypes for most of the studied traits. The materials used in this study are different from the previously used materials by other researchers.

Upland rice is a unique rice ecotype that can be grown on upland fields under rainfed conditions without surface water accumulation[13] and large amount of upland rice germplasm suited for production are imported every year from African rice, African based International Rice Research Center, for adaptability and performance evaluation in the country. However, there is little information on the genetic diversity of these genotypes in the study areas and hence the objective of this study was to determine the extent of genetic diversity among upland rice genotypes using multivariate statistical techniques.

MATERIALS AND METHODS

Description of the study areas: The field experiment was carried out during the main cropping season of 2016 in two locations of Gojeb and Guraferda districts in southern Nations, Nationalities and Peoples Regional State of Ethiopia. The two locations represented two different major rice producing agro-ecologies of the region (Table 1).

Experimental materials: The materials used in this experiment consisted of 36 upland rice genotypes which were obtained from Fogera and Bonga Agricultural Research Centers (Table 2).

Data collection: Data collection was done according to the Standard Evaluation System for Rice (SES)[14]. Data were collected on plant basis (average of 10 randomly taken plants) and plot basis from the central five rows of size (4×1.25 m = 5 m^2). Plant height (PH, cm), panicle length (PL, cm), culm length (CL, cm), number of filled grains per panicle (FGPP), number of unfilled grains per panicle (UFGPP), number of fertile tillers per plant (FTTP), total number of tillers per plant (TNTPP), number of non-fertile tillers per plant (NFTPP), number of primary branches per panicle (NPBPP) were measured from 10 randomly selected sample plants in the middle five rows of each plot. Days to 50% heading

Table 1: Details description of the study area

Zones	Experimental site	Altitude (m)	Longitude (°E)	Latitude (°N)		Temperature (°C)	Mean annual rainfall (mm)
				Minimum	Maximum		
Kaffa	Gojeb	1235	036°0' 0"	07°15' 0"	16.7	24	1710
Benchi-maji	Guraferda	1138	035°17' 16"	06°50' 368"'	25	39	1332

Table2: Description of experimental materials (upland rice genotypes)

Genotypes	Status	Origin	Genotypes	Status	Origin
ARCCU16Bar-22-1-1-2-B-1	URNVT, 2015	IRRI	IR 78937-B-20-B-B-4	URNVT, 2015	IRRI
ARCCU16Bar-9-2-10-4-B-1	URNVT, 2015	IRRI	WAB880SG14	URNVT, 2015	IRRI
ARCCU 16Bar-13-15-18-1-B-1	URNVT, 2015	IRRI	ARCCU16 Bar-9-20-6-1-1-1	URNVT, 2015	IRRI
ARCCU 16 Bar-15-5-1-26-B-1	URNVT, 2015	IRRI	IR 83750-B-B-131-1	URNVT, 2015	IRRI
ARCCU 16 Br-12-12-33-3-B-1	URNVT, 2015	IRRI	WAB415-B-11A1-2	URNVT, 2015	IRRI
ARCCU 16 Bar-12-17-3-4-B-1	URNVT, 2015	IRRI	ARCCU16 Bar-4-14-2-4-B-B	URNVT, 2015	IRRI
ARCCU 16 Bar-9-9-24-4-B-1	URNVT, 2015	IRRI	ARCCU16 Bar9-13-1-2-1	URNVT, 2015	IRRI
ARCCU 16 Bar9-26-29-1-B-1	URNVT, 2015	IRRI	IR 82616-B-B-64-3	URNVT, 2015	IRRI
SUPERICA-1	Released	WARDA	NERICA-13	Released	WARDA
NERICA-4	Released	WARDA	ARCCU16Bar-5-10-12-2-B-B	URNVT, 2015	WARDA
ARCCU15Bar-7-16-30-2-B-B	URNVT, 2015	IRRI	ARCCU16Bar-12-13-14-2-B-B	URNVT, 2015	IRRI
WAB-450-IB-P-18-HB	URNVT, 2015	IRRI	WAB-550-IB-P-9/1	URNVT, 2015	WARDA
IR82635-B-B-47-2	URNVT, 2015	IRRI	ARCCU16Bar-12-12-16-3-B-B	URNVT, 2015	WARDA
ARCCU16 Bar-9-21-4-1-1-1	URNVT, 2015	IRRI	Tana	Released	IRRI
ARCCU16 Bar-11-8-5-2-B-1,	URNVT, 2015	IRRI	Kokit	Released	IRRI
IR 82635-B-B-25-4	URNVT, 2015	WARDA	ARCCU16Bar-4-14--2-2-B-1,	URNVT, 2015	IRRI
IR 82635-B-B-59-2	URNVT, 2015	IRRI	Andassa	Released	IRRI
ARCCU16 Bar-29-13-3-B-1	URNVT, 2015	IRRI	ARCCU16Bar-13-2-16-2-1-1	URNVT, 2015	WARDA

URNVT: Upland Rice National Variety Trial, IRRI: International Rice Research Institute, WARDA: West Africa Rice Development Association

(HD, days) and days to 85% maturity (MD, days) were also collected on a plot basis. At harvest maturity, an area of (0.5 m×0.5 m) 0.25 m^2 within each plot were harvested, grain and straw were separated and oven-dried for 72 h at 70°C and weighed, then biological yield per hectare was determined. Thousand grain weight, harvest index in percentage and grain yield also determined after harvest maturity.

Statistical analysis: Homogeneity of error variance was tested using F-max test method of Hartley[15], with the equation:

$$F-max = \frac{\text{Largest MSE}}{\text{Smallest MSE}}$$

Pooled ANOVA over location was done using SAS software[16]. Clustering of genotypes was performed by average linkage method using the SAS software version 9.1. Points where local peaks of the pseudo F-statistic join with small values of the pseudo t^2 statistic followed by a larger pseudo t^2 for the next cluster fusion were examined to decide the number of clusters. Mahalanobis's D^2 statistics was used to examine the genetic distance between populations[17]. The significance level of genetic distance between clusters was tested both at 1 and 5% level of probability using chi-square test. The D^2 values obtained for pairs of cluster were considered as the calculated values of chi-square (χ^2) and tested for P degree of freedom, where P is the number of characters considered[18].

Principal Component Analysis (PCA): Principal component analysis was performed using the SAS software. The contribution of observation i to component l is, denoted by and obtained using the formula suggested by Saporta and Niang[19]:

$$Ctr_{i,l} = \frac{f_{i,l}^2}{\lambda_l} \times 100$$

where, $f_{i,l}^2$ squared factor scores of each observation, λ_l is the eigenvalue of the l-th component.

RESULTS

Analysis of variance: The combined analysis of variance over the two locations revealed significant differences ($p \leq 0.05$ or ≤ 0.01) among genotypes for most of the studied traits, except for total number of tillers per plant, number of fertile tillers per plant, number of non-fertile tillers per plant,1000-grain weight, number of unfilled grains per panicle, days to maturity and biological yield (Table 3).

Cluster analysis: Cluster analysis using average linkage methods, on the basis of their similarity through quantitative traits, grouped 36 upland rice genotypes into six cluster groups (Table 4). The first (C_I, n = 11) and the sixth cluster (C_{VI}, n = 1) had the largest and smallest number of genotypes with 30.5 and 2.7% proportion from the studied genotypes, respectively.

The sixth cluster contained only one genotypes. Pair-wise generalized square distance (D^2) between six clusters was persented in Table 5. The pooled mean value of each quantitative trait in each cluster was presented in Table 6. The

Table 3: Mean squares for different sources of variation and the corresponding CV in percentage for the 15 traits over two locations

Traits	MSL(1)	MSG (35)	MSGXL (35)	MSE (60)	CV (%)	R^2
PH	778.80**	70.60**	56.4*	38.3	7.5	0.7
PL	295.20**	2.97**	1.7^{ns}	1.6	5.1	0.8
CL	0.070^{ns}	67.90**	40.7^{ns}	39.5	10.1	0.6
TTPP	169.80**	5.6^{0ns}	8.3**	4.2	21.01	0.7
FTPP	16.08*	2.26^{ns}	4.5^{ns}	4.2	31.4	0.6
NFTPP	177.20**	1.86^{ns}	1.2^{ns}	1.5	12.1	0.8
FGPP	903.80**	858.70**	57.5^{ns}	195.7	19.3	0.7
UFGPP	239.70^{ns}	53.90^{ns}	64.3^{ns}	81.7	14.0	0.6
TGW	354.70**	6.20^{ns}	4.6^{ns}	6.0	9.7	0.8
NBPP	76.85**	5.30*	4.5^{ns}	3.3	21.5	0.7
DM	7656.00**	32.00^{ns}	150.0**	23.7	4.7	0.9
HD	67.00**	125.50**	48.2*	26.1	8.4	0.8
BY	2349.40**	373.40^{ns}	255.5^{ns}	253.0	25.3	0.7
HI	0.0469**	0.010**	0.0043^{ns}	0.0032	15.8	0.8
GY	2267.80**	79.80*	68.3*	47.24	28.5	0.8

*/**Significant and highly significant at 0.05 and 0.01 probability levels, respectively, ns: Non significant, figures in parenthesis indicate degrees of freedom, MSG: Mean squares of genotypes, MSE: Mean squares of error, CV: Coefficient of variation, R^2: Coefficient of determination, PH: Plant height, PL: Panicle length, CL: Culm length, TTPP: Total number of tillers per plant, FTPP: Number of fertile tillers per plant, DH: Days to 50% heading, NFTPP: Number of non-fertile tillers per plant, DM: Days to maturity, FGPP: Number of filled grains per panicle, BY: Biological yield, TGW: Thousand grain weight, UFGPP: Number of unfilled grains per panicle, NPBPP: Number of primary branches per panicle, HI: Harvest index, GY: Grain yield

Table 4: Clusters of 36 upland rice genotypes on the basis of quantitative characters

Clusters	No. of genotypes	Proportion (%)	Genotypes
CI	11	30.5	ARCCU16 Bar-9-21-4-1-1-1, ARCCU16 Bar-11-8-5-2-B-1, IR 82635-B-B-25-4, IR 82635-B-B-59-2, ARCCU 16 Br-12-12-33-3-B-1, Andassa, ARCCU16Bar-4-14--2-2-B-1, NERICA-13, IR 83750-B-B-131-1, WAB880SG14, IR 78937-B-20-B-B-4
CII	9	25	ARCCU 16Bar-13-15-18-1-B-1, ARCCU 16 Bar-12-17-3-4-B-1, ARCCU 16 Bar9-26-29-1-B-1, SUPERICA-1, ARCCU15Bar-7-16-30-2-B-B, ARCCU16 Bar9-13-1-2-1, IR 82616-B-B-64-3, NERICA-4, ARCCU16Bar-12-13-14-2-B-B
CIII	7	19.4	ARCCU16Bar-9-2-10-4-B-1, ARCCU 16 Bar-15-5-1-26-B-1, ARCCU 16 Bar-9-9-24-4-B-1, IR82635-B-B-47-2, ARCCU16 Bar-9-20-6-1-1-1, ARCCU16 Bar-4-14-2-4-B-B and WAB-550-IB-P-9/1
CIV	4	11.1	ARCCU16 Bar-29-13-3-B-1, WAB415-B-11A1-2, ARCCU16Bar-5-10-12-2-B-B and Kokit
CV	4	11.1	ARCCU16Bar-22-1-1-2-B-1, ARCCU16Bar-12-12-16-3-B-B, Tana and WAB-450-IB-P-18-HB
CVI	1	2.7	ARCCU16Bar-13-2-16-2-1-1

Table 5: Pair-wise generalized square distance (D^2) between six clusters constructed from 36 upland rice genotypes evaluated over two locations

Clusters	I	II	III	IV	V	VI
I		28.1*	43.6**	151.6**	256.0**	277.2**
II			123.8**	64.8**	137.2**	454.2**
III				331.8**	471.8**	123.1**
IV					27.4*	810.9**
V						997.0**
VI						

*/**Significant at 0.05 and highly significant at 0.01 probability levels, respectively

existence of considerable variation among the different clusters for individual traits was showed by cluster mean performance. Cluster I, consisted of eleven genotypes which were characterized by the highest cluster mean for plant height and panicle length. Cluster II, which contained nine genotypes showed highest cluster mean for culm length, panicle length and grain yield and the second highest mean for number of unfilled grains per panicle, days to maturity and days to 50% heading. Cluster III, consisted of seven genotypes and relatively had highest cluster mean for number of filled grains per panicle and the second lowest cluster mean for number of non-fertile tillers per plant. Cluster IV, consisted of only four genotypes, which were characterized by highest mean for panicle length, days to maturity and grain yield. Cluster V, with four genotypes gave highest cluster mean for plant height, panicle length, number of primary branches per panicle, thousand grain weight, days to 50% heading and biological yield.

Principal componenet analysis: The PCA showed that the first six principal components with eigenvalues greater than one explained 75.2% of the total variation among 36 upland rice genotypes evaluated for 15 quantitative character in two locations (Table 7). The six principal components PC1-PC6

Table 6: Cluster mean and mean differences for the 15 quantitative traits of 36 upland rice genotypes over two locations

Characters	C1	Cluster mean diff.	C2	Cluster mean diff.	C3	Cluster mean diff.	C4	Cluster mean diff.	C5	Cluster mean diff.	C6	Cluster mean diff.	Grand mean
PH	83.6**	1.0	82.9	0.3	83.3	0.7	82.3	-0.3	83.6**	1.0	79.7*	-2.9	82.6
PL	21.8**	0.3	21.8**	0.3	21.4	-0.1	21.8**	0.3	21.3**	-0.2	21.0*	-0.5	21.5
CL	62.8	1.2	64.6**	3.0	62.0	0.4	62.2	0.6	62.6	1.0	55.6*	-6.0	61.6
TTPP	10.1	0.2	10.0	0.1	9.7	-0.2	9.0*	-0.9	9.2	-0.7	11.6**	1.7	9.9
FTPP	8.1	0.1	8.1	0.1	8.0	0.0	7.4*	-0.6	7.5	-0.5	8.8**	0.8	8.0
NFTPP	2.0	0.0	1.9	-0.1	1.7	-0.3	1.6*	-0.4	1.8	-0.2	2.9*	0.9	2.0
FGPP	77.0	4.5	74.5	2.0	83.0**	10.5	75.5	3.0	75.8	3.3	49.4*	-23.1	72.5
UFGPP	21.6	1.3	22.2	1.9	18.4	-1.9	17.4*	-2.9	19.6	-0.7	22.7**	2.4	20.3
TGW	24.6	-0.5	25.1	0.0	25.5	0.4	25.2	0.1	25.6**	0.5	24.5*	-0.6	25.1
NPBPP	8.0	-0.3	8.3	0.0	8.1	-0.2	8.8	0.5	9.7**	1.4	6.8*	-1.5	8.3
DM	101.8	-1.2	104.7	1.7	103.2	0.2	104.8**	1.8	103.3	0.3	100.0*	-3.0	103.0
HD	58.5	-1.6	62.6	2.5	60.6	0.5	58.6	-1.5	63.4**	3.3	57.0*	-3.1	60.1
BY	62.8	-0.2	63.0	0.0	62.0	-1.0	62.2	-0.8	70.0**	7.0	55.6*	-7.4	63.0
HI	0.3*	-0.1	0.4	0.0	0.4	0.0	0.4	0.0	0.4	0.0	0.3*	-0.1	0.4
GY	22.2*	-1.7	26.6**	1.6	25.5	0.5	26.6**	1.6	25.7	0.7	22.2*	-2.8	25.0

*The lowest cluster mean, **Highest cluster mean, PH: Plant height, PL: Panicle length, CL: Culm length, TTPP: Total number of tillers per plant, FTPP: Fertile tillers per plant, DH: Days to 50% heading, NFTPP: Non-fertile tillers per plant, DM: Days to 85% maturity, FGPP: Number of filled grains per panicle, BY: Biological yield, TGW: Thousand grain weight, UFGPP: Number of unfilled grains per panicle, NPBPP: Number of primary branches per panicle, HI: Harvest index, GY: Grain yield

Table 7: Relative contributions of characters to the total divergence in upland rice genotypes

Characters	PC1	Ctri, l (%)	PC2	Ctri, l (%)	PC3	Ctri, l (%)	PC4	Ctri, l (%)	PC5	Ctri, l (%)	PC6	Ctri, l (%)
PH	0.70	16.88	0.22	2.29	0.53	13.70	0.03	0.05	-0.05	0.19	-0.27	6.8
PL	0.74	18.86	-0.11	0.56	0.43	9.22	-0.04	0.11	0.09	0.72	0.04	0.2
CL	0.73	18.25	0.37	6.33	0.35	6.12	-0.11	0.71	-0.14	1.50	-0.07	0.5
TTPP	0.56	10.84	-0.23	2.35	-0.29	4.22	0.30	5.11	-0.17	2.39	0.60	32.6
FTPP	0.43	6.47	0.52	12.34	-0.34	5.86	-0.28	4.30	0.06	0.31	0.41	15.3
NFTPP	0.32	3.53	-0.60	16.78	0.02	0.01	0.46	11.59	-0.26	5.28	0.13	1.5
FGPP	0.06	0.12	0.30	4.27	-0.25	3.00	0.56	17.13	-0.37	10.99	-0.24	5.3
UFGPP	-0.15	0.74	-0.34	5.21	0.48	11.32	-0.06	0.17	0.58	26.68	0.05	0.3
TGW	0.11	0.44	0.56	14.37	-0.44	9.64	-0.20	2.14	0.36	10.62	0.10	0.9
NBPP	-0.08	0.22	0.03	0.04	0.25	3.22	0.79	34.78	0.40	12.88	0.14	1.9
MD	-0.49	8.21	0.19	1.68	0.46	10.66	-0.12	0.84	-0.49	19.42	0.37	12.6
HD	-0.55	10.44	0.19	1.59	0.55	14.74	-0.17	1.65	-0.19	3.00	0.28	7.0
BY	-0.03	0.03	0.52	12.68	0.34	5.73	0.29	4.82	0.22	3.87	0.31	8.6
HI	-0.37	4.72	0.31	4.52	-0.19	1.70	0.48	12.73	0.11	0.93	0.00	0.0
GY	-0.09	0.25	0.58	15.42	0.15	1.11	0.29	4.69	-0.14	1.58	-0.28	7.0
Eigenvalue	2.9		2.17		2.02		1.8		1.2		1.1	
Proportion (%)	19.3		14.5		13.5		12.1		8.3		7.4	
Cumulative (%)	19.3		33.8		47.3		59.4		67.7		75.2	

Ctri, l: The contribution of observation i to component l, PH: Plant height, PL: Panicle length, CL: Culm length, TTPP: Total number of tillers per plant, FTPP: Fertile tillers per plant, DH: Days to 50% heading, NFTPP: Number of non-fertile tillers per plant, DM: Days to maturity, FGPP: Number of filled grains per panicle, BY: Biological yield, TGW: Thousand grain weight, UFGPP: Number unfilled grains per panicle, NPBPP: Number of primary branches per panicle, HI: Harvest index, GY: Grain yield

had eigenvalues of 2.9, 2.2, 2.0, 1.8, 1.2 and 1.1, respectively. The first and second principal components were responsible for about 19.3 and 14.5% of the total variation, respectively. The percentage contribution of each observation per component was determined by the ratio of the squared factor score of this observation by the eigenvalue associated with that component. Accordingly, character such as plant height (16.88%), panicle length (18.86%) and culm length (18.25%), accounted high contribution effect for the first principal component. The second principal component accounted for 14.5% of the total variation in the population, of which grain yield (15.42%) and biological yield (12.68%) were highly and positively contributed to the total variation, while non- fertile tillers per plant (16.78%) had large negative weight in this principal component. The third principal component accounted for 13.5% of the total variation and it was highly contributed by days to 50% heading (14.74%), plant height (13.70%) and days to maturity (10.66%). The fourth principal component accounted for 12.1% of the total variation and was indicated with high contribution of number of primary branches per panicle (34.78%), number of filled grains per panicle (17.13%) and harvest index (12.73%). The fifth principal component accounted 8.3% of the variation in the population and was more contributed by number of unfilled

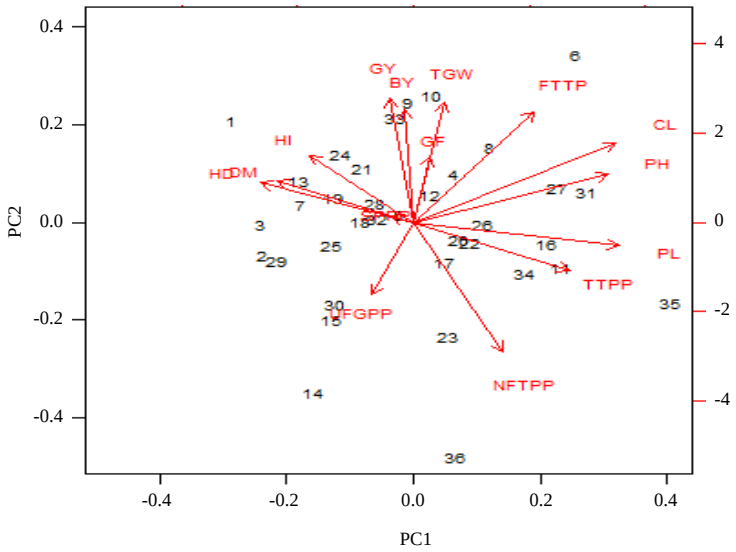

Fig. 1: Plot of the first two PCAs showing the contributions of various rice traits to the total variation
For explanation of character symbols, see section material and methods

grains per panicle (26.68%) and days to maturity (19.42%). The last principal component also accounted for 7.4% of the total variation and chief contributors of this component were total number of tillers per plant (32.6%) and number of fertile tillers per plant (15.3%). The first two principal component loading correction plot using variables from the two location trail revealed that plant height, panicle length and culm length loaded more heavily on the first component than others (Fig. 1).

DISCUSSION

The presence of significant differences among the tested genotypes might be due to the existence of dissimilarity in the genetic composition among them. Besides, environmental influences might be the possible causes of their significant differences or both. The highly significant differences observed among genotypes for some of the studied characters revealed the presence of substantial variability among genotypes.

Some of these cluster grouping were depends on geographical locations from which genotypes were obtained and some of them did not rely on geographical locations (Table 4). For instance, in cluster five a total of four genotypes were included, of which three genotypes (ARCCU16Bar-22-1-1-2-B-1, WAB-450-IB-P-18-HB and Tana) and one genotype (ARCCU16Bar-12-12-16-3-B-B) was from the IRRI and WARDA, respectively. This indicated, the importance of genetic divergences for grouping these genotypes in different cluster rather than locations from which genotypes were obtained. Besides, it might be due to selection pressure for certain common important traits and/or free exchange of genetic material from different nations. Sharma *et al.*[20] stated that, the pattern of genotype distribution within the various cluster was independent of geographical isolation. In line with the current results, Jain *et al.*[21] and Singh *et al.*[22] also grouped genotypes obtained from different sources of origin in the same cluster.

The standardized Mahalanobis D^2 statistics showed the existence of accepted difference between all clusters and the genetic divergences between all pairs were highly significant ($p \leq 0.01$) except between cluster one and two, between cluster four and five. This finding is in line with the result of Tesfaye *et al.*[23]. Regarding the inter-cluster distance, maximum distance was found between cluster five and cluster six ($D^2 = 997$), followed by cluster four and cluster six ($D^2 = 811$). The minimum distance was obtained between cluster four and five ($D^2 = 27$) followed by the genetic distance between cluster one and two with $D^2 = 28.1$ (Table 5). In this study, upland rice genotypes with highest mean performance for grain yield and panicle length were grouped into cluster two and four but cluster six showed relatively low yielding genotypes with smallest panicle length (Table 6). This indicated, the maximum contribution of grain yield and panicle length, towards the divergence of genotypes grouped in the last cluster from genotypes found in cluster two and four. In line with this result, Zia-ul-Qamar *et al.*[24] reported the significant contribution of these two traits for the divergence between clusters in rice genotypes.

The higher inter-cluster distance values in this study might be largely due to the inclusion of genotypes which have

wider genetic diversity. Parents for exploiting hybrid vigor and higher genetic recombination during hybridization could be selected on the basis of large inter-cluster distance. In this study, a cross which involves genotypes from cluster five and cluster six might be rewarding for the improvement of upland rice through heterosis breeding. According to Khodadadi *et al.*[25] and Rahim *et al.*[26] the cross between genotypes with maximum genetic distance would bring maximum heterosis.

In the first principal component character such as plant height (16.88%), panicle length (18.86) and culm length (18.25%) accounted high contribution effect of the total variation. Similarly, the high contribution of plant height and panicle length for separating genotypes in the first principal component was reported by Worede *et al.*[27] and Tuhina-Khatun *et al.*[28]. The greater eigenvectors percentage proportions of traits in the first and/or second principal components indicated that, these traits had higher contribution to the total distinction of the populations into clusters. Selection efforts based on these traits may be more effective in rice improvement program. Generally, PC analysis showed the high level of diversity among the studied genotypes as the entire variation cannot be explained by few principal components (Table 7).

The first two principal components which contributed to 33.8% of the variance were plotted to observe relationships between the measured characters of upland rice (Fig. 1). According to Dehghani *et al.*[29], the correlation between any two characters is approximated by the cosine of the angle between their vectors. The most prominent relationships shown in Fig. 1 are a strong positive association between grain yield and biological yield; plant height and fertile tillers per plant; as indicated by the small obtuse angle between their vectors ($r = \cos 0 = +1$). The proximate perpendicular vectors ($r = \cos 90 = 0$) between harvest index and number of unfilled grains per panicle were shown near zero correlation between respective characters. The loading plot of the first and second component revealed that plant height, panicle length and culm length loaded more heavily on the first component than others.

CONCLUSION

The multivariate analysis indicated that genotypes used in this study are not closely related and could serve as a genetic source for multiple attributes. Therefore, to exploit heterosis at F1 generation, it will be better to use parents from cluster five and six with selection efforts based on traits, plant height, panicle length, culm length, 1000-grain weight, fertile tillers per plant and grain yield.

SIGNIFICANCE STATEMENT

This study results showed the existence of variability among the newly introduced genotypes of the region, on which so far in the study areas, little were know about the genetic diversity of those materials. Thereby, the current results will create an opportunity for breeders to improve rice yield and other desirable traits.

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