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Original Research Article

Genetic diversity and stability analysis based on agro-morphological traits among rice genotypes developed through marker-assisted backcrossing

Jeremiah C. Oginyi[1]*, Samuel C. Chukwu[2], Kelechi U. Paul[2], Kenneth C. Mkpuma[2]

[1]Department of Applied Biology, Ebonyi State University, Abakaliki, Nigeria
[2]Department of Crop Science, Ebonyi State University, Abakaliki, Ebonyi, Nigeria

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***Correspondence:**
Dr. Jeremiah C. Oginyi,
E-mail: oginyichi@yahoomail.com

ABSTRACT

Background: The genetic diversity and stability analysis based on agro-morphological traits among rice genotypes developed through SSR marker-assisted backcrossing was evaluated at college of agricultural science (CAS), Ebonyi State niversity, Abakaliki, Nigeria.

Methods: In this study, 9 rice accessions sourced from the Iinstitute of tropical agriculture and food security (ITAFoS), universiti Putra, Malaysia and Ebonyi, Nigeria; were evaluated for yield stability performance. The experiments were laid out in randomized complete block design (RCBD) with three replications each for two seasons.

Results: Result of the evaluated rice accessions showed highly marked morphological variability based on the mean performance and were grouped into three main clusters. Cluster I had CP, cluster II contained Line4, Line5, Line6, and Line8, and cluster III had Line1, Line7, Line12, and Putra-1. The first, 3 principal components were identified and retained for having the Eigen-value >1. The first PC had an eigenvalue of (6.30) with 52.5% proportion of which plant height accounted most for this variation with (0.359) whereas panicle length contributed the least (-0.13). For stability analysis, CP had highest values for most of the parameters. High heritability value was recorded for all nine traits which range between 71.04% and 95.06%. The highest heritability value (95.06%) was found in Days 50% heading while grain width had the lowest (71.04%).

Conclusions: It could be concluded that CP, Putral-1, and line7 were the most stable in terms of yield across the two seasons of this study; hence, recommended for parental materials for hybridization.

Keywords: Agro-morphological traits, Genetic diversity, Heritability, Nigeria, Rice accessions

INTRODUCTION

Rice (*Oryza sativa* L.) (Asian rice) is a monocotyledonous plant which belongs to the family *poaceae* that has 24 rice specs amongst is *Oryza glabberima* Steud (African rice). *Oryza sativa* is the most commonly cultivated species which is further classified into sub species including, *indica*, *japonica* and *javanica*.[1] Cultivated rice is an annual C3 grass with round jointed culm (stem), flag leaves, terminal panicles and roots. Its growth is made up of different stages namely; vegetative stage, reproductive stage and grain filling and maturation.[2]

According to various forecasts, there will be 9.7 billion population in the world by 2050.[3] Nine countries were projected to have over 50% population growth between now and 2050 of which the majority are located in tropical regions.[4] These countries include India, Nigeria, the Democratic Republic of Congo, Ethiopia, the United

Republic of Tanzania, Indonesia, and Egypt.[3] In these countries, rice is the fastest-growing and preferred stable food, driven by high population growth, rapid urbanization, and changes in eating habits.[5] Nevertheless, rice productivities in the regions are low, and crop yields are often affected by different biotic and abiotic stresses including adverse environmental factors, diseases, and pests.[6,7] Rice cultivation has become pertinent in Nigeria, producing an average of 4.5 million tons of paddy rice and 2 million tons of milled rice.[8] The potential increase in areas for rice production (4.6-4.9 million ha and 1.7 million ha respectively) was reported by.[9] The increase in production as reported by FAO is due to an increase in land under rice cultivation and may not necessarily be due to increase in yield.[8] However, there is a big different between potential yield (4.4-7.2 t/ha has been recorded on research farms) and actual yields in farmer's field around 1.5t/ha).[10]

Utilizing plants' genetic diversity, breeders develop new and improved crop varieties with desirable traits, such as improved yield, tolerance to flood and drought, nutritional and grain quality, resistance to pests and diseases, and in order to tackle worldwide issues related to food security, sustainability, and adaptability to climate change.[11] Understanding the genetic diversity and population structure of rice germplasm available to breeders is very crucial for rice improvement. In accordance with the finding of Khan et al greater genetic variability enhances the probability of identifying elite genotypes within a population.[12] Again, Novoselovi´c et al posted that a limited genetic base is a significant challenge that renders plants more susceptible to biotic and abiotic stress conditions.[13] A successful breeding program will depend on the genetic diversity and stability of a crop for achieving the goals of improving the crop and producing high yield varieties.[14] The evaluation of genetic diversity and stability helps the breeder in selecting appropriate materials for further genetic improvement of rice genetic resources.[15] Evaluation and quantification of genetic diversity is, therefore, an important aspect of plant breeding, and unlocking the genetic diversity for agronomical important traits is vital to providing pre-breeding information upon which selection will act upon.[16,17]

The use of morphological markers has been effective in the studies of diversity in crop plants especially for traits such as yield, maturity, height, grain color, as well as resistance to insect pests and diseases.[18] Genetic diversity among commercial cultivars is on the decrease, making it difficult to get new genes from cultivars for further improvement of grain yield and quality, and sufficient resistance to biotic or abiotic stress, even in rice. Hence, providing motivation for scientists to explore wild and related species, landraces, plant introductions and breeding lines, etc. to find genes to meet these demands.[19] Meanwhile, landraces have built-in genetic variability due to several generations of cultivation and selection by farmers within an environment. They are adapted to the area with some resistance to major pests and diseases prevalent in such areas; thus, sources of genes needed in breeding programmes.[20] Murtadha et al posted that the traits with high heritability estimates, GA and GCV could be good predictors of seed yield in crops.[21] Although, the exclusive reliance on morphological markers has shown to be unreliable because they are limited in number, susceptible to environmental factors, and influenced by the plant growth stages.[22] Hence, a number of rice genotypes have been developed through marker assisted backcrossing (MABC).[23] More so, Chukwu et al also confirmed that molecular markers that are tightly linked with economically important traits have been identified and used for marker assisted backcrossing (MABC) in rice to develop resistance rice lines against bacterial leaf blight and rice blast lines with potential yield, short maturity against bacterial leaf blight and rice blast.[23]

A poor information on the degree of phenotypic and stability of various traits of the newly developed rice genotypes limits the selection of the rice lines for breeding programs to produce high yield varieties; hence, this research aimed to determine the genetic diversity and stability of rice genotypes produced through marker assisted backcrossing through agro-morphological traits.

METHODS

Experimental site: The Experiment was carried out in a screen-house at college of agricultural science (CAS), Ebonyi State University, Abakaliki, Nigeria. Abakaliki is located between latitude 06º4¹N and longitude 08º65¹E at elevation of 71.44 mm above sea level. Its annual rainfall is between 1700-2000 mm which is pseudo-bimodal; starting from April, breaks at August, and finally stops at November. Its relative humidity ranges from 60-80% and temperature from 22-32 ºC.[24]

Experimental design/treatments

The experiment was laid out in RCBD in three blocks. The total number of buckets was eighty-one, three buckets for each genotype, and twenty-seven buckets in each replication. One seedling per hill at 4 cm and three seedlings per bucket at 20 cm spacing. This research was conducted for two seasons: the first season was from April 2020 to July 2020 and the second season was from March 2021 to June 2021. The following agro-morphological traits were evaluated: plant height (cm), flag leaf length (cm), days to heading (days), flag leaf width (cm), flag leaf area (cm^2), days to 50% maturity (days), panicle length (cm), number of tillers per hill (number), grain length (mm), grain width (mm) and number of spikelet, and 1000 grain weight (g).

Sample collection

The plant materials used were nine (9) rice accessions (Line1, Line 4, Line5, Line6, Line7, Line8, Line12, Putra-1, and CP) were collected from the Institute of tropical agriculture and food security (ITAFoS), University, Putra Malaysia and control sourced from Ebonyi, Nigeria as shown in Table 1.

Table 1: Rice genotypes, common name, and source used for this study.

Genotypes	Common name	Source
Line 1	Rice	Putra, Malaysia
Line 4	Rice	Putra, Malaysia
Line 5	Rice	Putra, Malaysia
Line 6	Rice	Putra, Malaysia
Putra-1	Rice	Putra, Malaysia
Line 12	Rice	Putra, Malaysia
Line 7	Rice	Putra, Malaysia
Line 8	Rice	Putra, Malaysia
CP	Rice	Ebonyi, Nigeria

Sample preparation

Following manual from MARDI, the evaluated rice genotypes were put in different petri-dish and exposed to oven at 35°C for four hours for decontamination. It was then soaked and allowed to stand for 4 hours in petri-dish containing tissue paper. The water was drained after 24 hours while the tissue paper provided cool environment. On the second day, the sprouted seeds were dropped on the prepared nursery tray filled with paddy soil and watered daily for 3 weeks before transplanting into the field at 21 days after sowing into the petri-dish.

Statistical analysis

Data collected during the two growing seasons were subjected to clustering using R package version 2.4.3, Dendrogram was constructed using Gowers' similarity coefficient following unweighted pair group mean of arithmetic averages (UPGMA) clustering strategy. Cluster-ordination techniques using principal component analysis (PCA) was applied to confirm the result of cluster analysis. Stability analysis was carried out according to Eberhart and Russell from regression coefficient and mean squares of deviation from regression, Yield-stability statistic was calculated using the program STABLE.[25,26] Heritability was estimated for the former traits, as illustrated by Collins et al and the coefficient of variability values was estimated depending on phenotypic (P.C.V.) and genotypic (G.C.V.) variances according to Yassin.[27,28]

RESULTS

Estimation of the genetic similarities among the rice accessions based on agronomical cluster analysis

Table 2 showed the distribution of nine rice accessions into different clusters for 12 agro-morphological traits, three major clusters were also identified as showed in Figure 1 and 2 and the number of accessions belonging to each cluster varied from 1 to 4. Cluster I was made up of one rice accessions with 11% of total population which consisted of one accession (CP). Cluster II was made up of four accessions which consists of 44% of total population (Line4, Line5, Line6 and Line8). Cluster III was made up of four accessions as well with the proportion 44% of total population of accessions including Line1, Line12, Line7 and Putral-1.

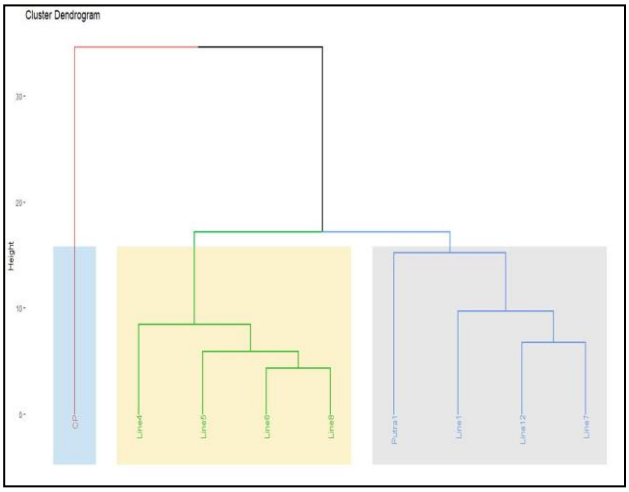

Figure 1: Cluster dendogram.

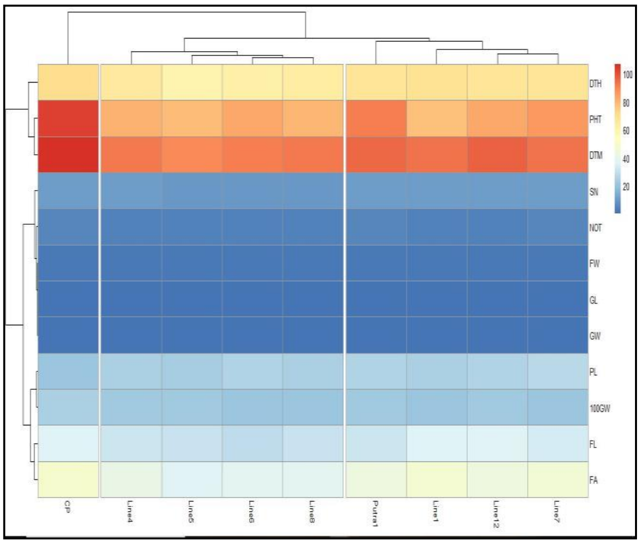

Figure 2: Heatmap cluster.

The divergence in the current materials was also supported by the appreciable amount of variation among cluster mean values for different characters. Each cluster is clearly recognized by their highest mean values for specific target trait and it might be helpful for easy selection of parents with the desired traits for hybridization or selection programs of rice improvement. In general, this clustering study revealed that the nine rice accessions included in this study were moderately divergent. Therefore, variation in agro-morphological traits is an indicator of genetic variation in rice.

Table 2: Clustering pattern of the accessions for the combined season's analysis.

Cluster	No. of accessions	Name of accessions	Characteristics	Proportion (%)
1	1	CP	high PHT, FA, DTH, DTM, 100GW, GL	11
2	4	Line4, Line5, Line6, Line8	LOW PHT, SN, DTM, FW, FL, GW	44
3	4	Line1, Line12, Line7, Putra1	high SN, GW, PL	44

PCA for the traits studied

The principal components analysis (PCA) based on the 12 agro-morphological traits was performed to determine the relative contribution of the different traits to the total variation that existed in the accessions as seen in table 2 and Figure 1 and 2. First, 3 principal components were identified and retained for having the Eigen-value >1 (greater than 1) and accounted for 87.6% of the total variation for the agro-morphological traits as indicated in Table 3. PC1 had Eigen-value of 6.30, explaining 52.5% of the total variation. Traits such as plant height (0.359), number of spikelet (0.133), flag leaf length (0.260), flag leaf width (0.330), flag leaf area (0.333), number of tillers (0.326), days to 50% heading (0.346), days to maturity (0.377), 1000 grain weight (0.308), grain length (0.275) and grain width (0.108) contributed greatly to PC1. PC2 proportion of variance was 23.9% with Eigen-value (2.86) and was associated with panicle length (0.411) and number of spikelet (0.54); while PC3 contributed 11.2% of the total variation with Eigen-value (1.34) and associated with flag leaf length (0.42) and 1000 grain weight (0.21).

Table 3: Eigen values, Cumulative variance and component of the first three principal components using agro-morphological traits.

Variables	PC1	PC2	PC3
PHT	0.359	-0.182	-0.219
PL	-0.130	0.411	-0.288
SN	0.133	0.540	-0.167
FL	0.260	0.278	0.420
FW	0.330	0.252	-0.145
FA	0.333	0.283	0.162
NOT	0.326	-0.226	-0.202
DTH	0.346	0.241	0.118
DTM	0.377	-0.132	0.063
100GW	0.308	-0.279	0.214
GL	0.275	-0.284	-0.152
GW	0.108	0.009	-0.700
Eigenvalue	6.3013	2.8631	1.3444
Proportion (%)	52.5	23.9	11.2
Cumulative (%)	52.5	76.4	87.6

Stability analysis of the rice accessions

Value of regression coefficient (b_i) for each genotype that is closing to unity (b_i=1) ($p<0.01$) together with high trait mean is found to be stable over the seasons. Genotypes are labeled as badly acclimatized to environment when associated with low trait mean performance. Whilst, a b_i higher than unity (b_i>1) indicates that the genotypes are more sensitive to seasonal changes and greater specificity of adaptability to high yielding. The results in Table 4 showed that CP recorded the highest regression slope values (1.56), (1.15), (1.37), (1.67), (1.83), (1.13), and (1.25) for plant height, panicle length, number of spikelet, number of tillers, grain width, grain length, and 1000 grain weight respectively while Putra-1 had the highest values (1.77) for flag leaf area and Line7 (1.08) for days to 50% heading. Meanwhile, the lowest regression slope values (0.03), (0.01), (-0.33), and (0.03) for the number of spikelet, flag leaf area, number of tillers, and days to 50% heading were obtained in Line12 respectively; Line1 had the lowest values (0.31), (0.07), and (0.92) for plant height, grain width, and grain length in that order; Line5 (-1.59) for panicle length; and Line6 (0.24) for 1000 grain weight.

Genetic and phenotypic variances

The result shown in Table 5 revealed that the values of genotypic and phenotypic variation were higher than the values of pooled error for the studied traits; in the exception of genotypic value (3.62) for grain width which was less than the pooled error (3.78). Hence, confirming that the number of replicates utilized in these experiments of these lines for the evaluated parameters were appropriate to confer the best determination for the error variance.

High heritability value was recorded for all nine traits which range between 71.04% and 95.06%. The highest heritability value was found in days 50% heading (95.06%) followed by plant height (87.95%), panicle length (83.46%), and flag leaf area (83.45%); whereas the least heritability value (71.04%) was observed on the 1000 grain weight. More so, values of G.C.V. appeared to be depressed or low for all the traits evaluated as grain length and plant height had the lowest values (13.98 and 19.12 respectively) other than grain width and number of spikelet (48.67 and 48.61 respectively) that were moderate. The values of P.C.V. were also very depressed in grain length and plant height (16.13 and 20.18 respectively); meanwhile, P.C.V. was moderate for grain width (57.38), number of spikelet (55.78), and 1000 grain weight (55.71).

Table 4: Estimation of stability parameters for all study traits of the nine rice lines.

Traits	Plant height			Panicle length			No. spikelet			Flag leaf area			No. of tillers			Days 50% heading			Grain width			Grain length			1000 grain weight		
	Bi	**S^2di**	**R^2**	**Bi**	**S^2di**	**R^2**	**Bi**	**S^2di**	**R^2**	**Bi**	**S^2di**	**R^2**	**bi**	**S^2di**	**R^2**	**bi**	**S^2di**	**R^2**	**Bi**	**S^2di**	**R^2**	**bi**	**S^2di**	**R^2**	**bi**	**S^2di**	**R^2**
CP	1.56	0.91	78.65	1.15	0.38	74.38	1.37	0.37	79.83	1.17	0.32	61.99	1.67	0.43	83.51	1.01	1.35	71.25	1.83	1.14	99.92	1.13	1.12	99.45	1.25	0.35	99.96
Line1	0.31	-0.31	99.52	-0.83	0.05	98.18	0.35	-0.37	95.67	1.07	0.27	88.12	0.05	0.04	95.44	0.52	0.21	99.33	0.07	-0.09	90.98	0.92	0.91	91.33	0.73	0.03	98.23
Line12	0.58	0.46	99.41	-0.08	-1.03	97.83	0.03	-0.17	96.17	0.01	0.08	93.43	-0.33	0.04	95.83	0.03	0.11	97.83	1.09	-1.07	91.93	0.95	0.97	96.56	1.05	0.25	98.25
Line4	0.33	0.21	99.48	-0.49	0.01	97.61	0.07	-0.18	96.83	0.04	0.06	91.38	0.33	0.07	88.34	0.06	0.42	95.67	1.03	0.04	92.27	0.95	0.98	97.61	1.01	0.2	95.2
Line5	0.49	0.22	99.71	-1.59	-1.36	98.88	0.36	0.03	96.5	0.08	0.09	96.92	-0.33	0.06	92.33	0.11	0.08	89.65	1.05	0.08	91.65	0.93	0.93	93.14	1.02	-0.23	98.23
Line6	0.62	0.3	99.35	1.02	0.02	95.14	0.37	0.07	95.67	0.01	-0.24	95.47	-0.33	0.03	91.34	0.07	0.31	88.62	0.77	0.07	90.72	1.02	1.03	95.03	0.24	-0.03	95.24
Line7	0.83	0.36	82.95	1.01	0.38	77.54	1.99	0.24	89.83	1.16	0.14	66.08	0.67	1.03	76.25	1.08	1.11	67.45	1.73	1.13	98.38	1.05	1.07	88.01	1.22	0.21	85.22
Line8	0.47	0.21	99.19	-0.39	-0.31	98.24	0.03	0.07	96.67	0.54	0.22	96.77	0.33	0.04	93.17	0.03	0.53	93.83	1.07	0.07	91.47	0.98	0.97	98.36	0.85	0.05	98.25
Putra1	1.31	0.88	80.85	0.98	0.42	75.05	1.37	0.31	88.5	1.77	0.23	63.2	1.33	0.34	78.67	1.04	1.28	67.65	1.78	1.12	98.72	1.08	1.08	96.99	1.24	0.48	99.36

Table 5: Genotypic (δ2g), phenotypic (δ2ph), error variances (δ2e), heritability (H2) in the broad sense: genotypic (G.C.V.) and phenotypic (P.C.V.) coefficients of variation evaluated for nine traits of rice lines.

Traits	Genotypic variation (δ2 g)	Phenotypic variation (δ2 ph)	Error variation (δ2 e) (pooled error)	Heritability (H2 b%)	G.C.V. (%)	P.C.V (%)
Plant height	6.21	5.73	0.63	87.95	19.12	20.18
Panicle length	6.72	6.31	0.83	83.46	34.12	36.51
No. spikelet	6.78	9.81	2.08	73.69	48.61	55.78
Flag leaf area	3.05	3.76	0.73	83.45	33.42	36.73
No. of tillers	8.31	6.19	1.18	74.11	38.63	43.29
Days 50% heading	3.91	5.05	0.31	95.06	22.13	22.78
Grain width	3.62	4.11	3.78	71.04	48.67	57.38
Grain length	3.63	3.84	0.72	82.34	13.98	16.13
1000 grain weight	5.21	6.78	1.65	71.68	42.56	55.71

Table 6: Correlation heritability (H^2) in the broad sense with genetic parameters.

Variables	Plant height	Panicle length	No. spikelet	Flag leaf area	No. of tillers	Days 50% heading	Grain width	Grain length	1000 grain weight	Genetic trats (h^2)
Plant height	1.00	-	-	-	-	-	-	-	-	-
Panicle length	0.96	1.00	-	-	-	-	-	-	-	-
No. spikelet	0.81	0.94	1.00	-	-	-	-	-	-	-
Flag leaf area	0.96	1.00	0.94	1.00	-	-	-	-	-	-
No. of tillers	0.90	0.98	0.98	0.99	1.00	-	-	-	-	-
Days 50% heading	1.00	0.97	0.82	0.97	0.91	1.00	-	-	-	-
Grain width	0.78	0.92	0.99	0.92	0.97	0.79	1.00	-	-	-
Grain length	1.00	0.95	0.78	0.95	0.88	1.00	0.75	1.00	-	-
1000 grain weight	0.82	0.94	1.00	0.94	0.98	0.83	0.99	0.79	1.00	-
Genetic traits (h^2)	0.95	1.00	0.95	1.00	0.99	0.96	0.93	0.94	0.95	1.00

Correlation of genetic parameters

The result presented in Table 6 showed that genetic trait had strong positive and highly significant correlation with all the parameters studied. This implies that genetic parameters can be transferred and inherited from parent to offspring in a stable way. However, their levels of inheritance vary as the genetic correlations ranged from 0.75 to 1.00 among all the 12 characteristics evaluated in this research.

DISCUSSION

Both cluster and principal component analyses suggested substantial variation in the nine rice accessions which could be exploited in the breeding program to further enhanced yield. Cluster analysis according to Darrock, helps to group individuals on the basis of similarity in their characteristics (traits) such that accessions within clusters are homogeneous and between clusters are heterogeneous. Cluster I containing only the CP had the unique characteristics of high plant height, flag leaf area, days to 50% heading, days to maturity, 1000 grain weight and grain length which are among traits that farmers' and rice breeders look out for in adoption of a variety or hybridization purposes in improvement activities.[29] Therefore, based on the above-mentioned traits, the accessions in cluster I is suggested as the most promising parental materials for best yielding but matures late which calls for improvement. This finding was in conformity with the work of Oketa and Oselebe which observed that the Landrace differed from other hybrid accessions based on its agro-morphological characteristics.[30] Moreover, the clustering pattern revealed highest level of genetic diversity among the landraces compared to the exotic varieties or inbred lines indicating that landraces are indeed good sources of variability and as such should not be allowed to go into extinction.[30] Again, Nayak et al and Zeng et al reported that landraces were diverged across all the clusters showing that the landrace genotypes had highest level of genetic diversity for most of the traits studied.[31,32] This result is also in agreement with the finding of Tang et al which stated that landraces are important genetic resources for genetic improvement of crops because they provide "adaptability genes" for specific environmental conditions.[33] Similar variability was posted by Tamu who studied twelve genotypes of coarse rice to check their yield performance in Kallar tract and reported highly significant variation for different traits.[34]

Cluster III was accessions that exhibited greater number of spikelet, grain width, and panicle length. Cluster II accessions were identified for their average performance and suggested as best source of parental materials for early maturing (lowest days to 50% heading and days to maturity). Cluster III had the highest cluster mean value for panicle length, number of spikelet, and grain width. There were similarities between cluster II and III in this research especially in the days to 50% heading and days to maturity. In accordance with work of Mulualem et al this may be due to the fact that genotypes collected from similar areas belong to the same gene pool or they may have similar ancestral relationships.[35] Conversely, genetic dissimilarity among the rice genotypes studied could arise due to the diverse ancestral origin, high gene flow caused by cross-pollination and possible gene or chromosomal mutation.

PCA explained the genetic variation among the accessions for all agro-morphological traits under study. Factor loadings were considered in each component with Eigen values more than 1, which determines a minimum 10% of the variation.[36] In this current study, principal components that exhibited eigen values of >1 were retained for the agro-morphological traits. The PCA showed cumulative variation of 87.6 %. It indicates that the identified characters within these components showed immense influence on the agro-morphological characteristics of the accessions. PCA explained the diversity of the rice germplasm; it also assesses the importance and the contribution of each coefficient of correct vectors, indicates the degree of contribution of every original character with how each principal component is correlated and that the higher the coefficients, the more effective they will be in discriminating between germplasm, regardless of the positive or negative sign.[37] The result of the PCA in this research was in conformity with that of Oketa and Oselebe which indicated a considerably high level of variations among the studied genotypes; stressed that the landraces produced mainly late heading and maturing, tallest plants, and long panicles; while the exotic genotypes were mostly early and intermediate heading and maturing, short and medium in height.[20]

In this research, variation did exist among nine rice accessions with respect to the traits that were evaluated, for instance, in PC1 (Principal component 1), accounted for 52.5% of variation among the tested materials revealed that major contributors to variation that were observed includes; plant height, flag leaf width, flag leaf area, number of tillers, days to 50% heading, days to maturity and 1000 grain weight were the major discriminating variables. This finding agrees with results of Alemayehu and Becker which stated that the variability among the accessions from diverse origin could be related primarily to their morphological differences and their uses or selection.[38] Divergence studies of morphological and reproductive traits using principal components analyses have been posted by different researchers Jatoi et al who had similar findings to this research.[39]

The levels and patterns of diversity observed among accessions of rice in this study provides the basis to identify desirable parents to create segregating progenies with maximum genetic variability for further selection and conserve genetic resources of the plant.

Regression slope (b_i), deviation from regression (S^2_d) for stability of the newly developed rice genotypes and components of genetic variance based on agro-morphological traits

The value of regression coefficient (b_i) for each genotype, closing to unity ($b_i=1$) ($p<0.01$) together with high trait mean is found to be stable over adverse environments. Genotypes are labelled as badly acclimatized to environments when associated with low trait mean performance. Whilst, a b_i higher than unity ($b_i>1$) indicates that the genotypes are more sensitive to environmental changes and greater specificity of adaptability to high yielding environments. The result of this study revealed that the best rates of the parameter of bi (regression coefficient) were obtained in the rice lines of CP, Putral-1 and Line7, for the nine traits being studied. With respect to the S^2di parameter, the data obtained confirmed that the entry numbers CP, Putral-1 and Line7 recorded the highest values. For the data calculated for the parameter R^2, it could be concluded that the entries CP, Putral-1 and line7 for the studied traits recorded the best results of steadiness. High heritability values were recorded for all nine characters. Days 50% heading followed by plant height and panicle length recorded the highest values for heritability. This result is in complete agreement with Falconer who classified heritability percentage was it into three categorized of; low (0-30%), moderate (30-60%) and high (≥60%).[40] Heritability estimates the inheritance proportion of phenotypic traits or total variance that can be passed from one generation to another. High heritability assists in effective selection for a specific trait. However, it does not always show high genetic gain in next generation. This is because the traits are more controlled by additive genes and the effects of the environment are less for the phenotypic expression of these traits.

Meanwhile, low heritability indicates that the expression of the trait was greatly affected by environmental factors. Selection based on these traits is ineffective since the heritable portion of variation is low. Unfortunately, all traits evaluated in this study recorded low value of heritability, thus signify that direct selection using these traits might be ineffective due to high influences of the environment.

CONCLUSION

In recapitulation, based on the morphological and yield stability analysis, outstanding accessions such as CP, Putral-1 and Line7 were recommended for purification and adoption as varieties with good stable yield to farmers. Further work may also be required at the molecular level using DNA marker technology to ascertain the genome size and variability, as well as the relationship among the nine accessions used in this study to explain the clustering pattern observed in the study. This will further clarify the potential for compatible hybridization within or between the groups of accessions identified in the cluster analysis.

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