Genetic Diversity of Lowland Rice Varieties Evaluated in the Associated Mangrove Swamp of Sierra Leone

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Abstract **– Agro-morphological characterization of germplasm variety is fundamental in order to provide information for plant breeding programs. A clear understanding of genetic diversity is essential for the effective conservation and utilization of rice genetic resources. A study to characterize 30 lowland rice varieties was conducted in the Associated Mangrove Swamp during the 2016 wet cropping season. Results revealed significant genetic differences among the 30 rice varieties for the traits evaluated. The five principal components accounted for 96% of the total variation of which PC1 and PC2 contributed 63% and 15%, respectively. Cluster analysis grouped the 30 genotypes into seven main clusters with cluster II represented the bulk (26.6%) of the total genotypes while cluster VII contributed the least (3.3%) of genotypes. Hybridization between genotypes grouped in clusters IV and VI would not be effective as their genetic make-up is almost similar while crossing between genotypes in clusters III and V will be effective, as genotypes in these clusters were identified as being most divergent.**

Keywords **– Diversity, Genetics, Characterization, Conservation and Utilization.**

I. INTRODUCTION

Rice is a major food crop, ranking second to wheat among the most cultivated cereals in the world [1], as over half of the world's population depends on rice as their diet. In Sierra Leone, rice (*Oryza sativa* L.) is the main staple food as it is eaten on a daily basis by almost every household in the country [2]. Rice is grown mainly by small scale farmers on both the upland and diverse lowland ecologies including inland valley swamp, mangrove swamp, boliland and riverine grassland [3].

The conservation and characterization of genetic resources is a necessity not only for posterity, but also for utilization in different improvement programs such as breeding for improved yield and tolerance to various stresses [21]. Rice genetic resources are key components to breeding programs, and farmers have played important roles in contributing to rice diversity by developing and nurturing thousands of rice varieties for several years [4]. Rice germplasm including landraces and traditional varieties is a good source of important alleles and serve as the foundation of any rice breeding program because they are the source of important traits necessary for improving and developing new breeds of rice varieties [5]. The use of agro-morphological traits is the most common approach utilized to estimate relationships between genotypes [6].

Several workers reported the use of agro-morphological markers in the characterization of rice diversity.

Meanwhile [7] examined the genetic diversity in 132 genotypes of rice and placed cluster analysis in 10 different categories. Reference [8] used 25 genotypes to investigate the genetic diversity of rice and divided into 5 clusters according to yield performance. Furthermore [9] used Cluster analysis based on Ward's method to investigate genetic diversity of 24 genotypes of modified rice according to qualitative and quantitative traits; genotypes were divided in three main clusters. Reference [10] characterized 34 landraces of rice in Bankura District of West Bengal, based on 12 quantitative agro-morphological characters. Their results grouped genotypes into five cluster groups and PCA showed the contribution of each character to the classification of the rice landraces into different cluster groups. The first three principal components explained about 86.9% of the total variation among the 12 characters. The results of PCA suggested that characters such as leaf length, leaf width, panicle length and grain size (100 grain weight, length and width of grain and kernel) were the principal discriminatory characteristics of landraces of rice.

It is important to assess the diversity of rice germplasm materials to provide insights in the diversity and increase utilization of these materials. However, scares information does exist on the genetic diversity of lowland rice germplasm in Sierra Leone. The objective of this study, therefore, is to determine the genetic diversity of 30 lowland rice varieties evaluated in the Associated Mangrove Swamp.

II. MATERIALS AND METHODS

A. *Description of Experimental Site*

The experiment was conducted at the Mawirr crop site of the Rokupr Agricultural Research Centre (RARC), Rokupr (8° 40'N and 12° 23'W) at an altitude of 80m above sea level during 2016 wet season. Rokupr is in the Magbema Chiefdom, Kambia District, Northern Province of Sierra Leone. Rokupr had an average rainfall of 0.6mm and temperature of 33°C during the time of experimentation. The crop was grown on an associated mangrove swamp soil with some characteristics of Entisols poorly drained swamps or lagoons that are waterlogged throughout the year.

B. *Experimental Materials, Trial Design, Crop Management Practices and Data Collection*

Trial consisted of thirty diverse lowland rice varieties including one check obtained from the Crop Improvement Program (CIP) and Farm Management Unit (FMU) (Table

1). The land was brushed manually and debris was cleared. The land was ploughed and puddle using a power tiller machine. Long handle native hoes were then used to level the plot in order to facilitate uniform distribution of water.

Seedlings were raised on 1m x 7m dry seed beds prepared on the upland. The rice varieties were sown on drilled rows 20cm apart using short handle drilling hoes. The seeds were covered with soil to prevent damage by birds and rodents. Each variety was sown in five rows, leaving a space of 40 cm between plots to avoid mixtures.

Twenty-one-day old seedlings were transplanted in five rows per plot in 1m x 5m plots at 1 seedling per hill, spaced 20cm within and between rows and 40 cm between plots. Trial was laid out in randomize complete block design with three replications.

Table 1. List of rice varieties and seed source

Entry number	Variety	Source
1	ARICA 6	CIP
2	ARICA 9	CIP
3	CCA	CIP
4	CK 90-1	CIP
5	Hitomebore	FMU
6	NERICA-L-4	CIP
7	NERICA-L-8	CIP
8	NERICA-L-16	CIP
9	NERICA-L-19	CIP
10	NERICA-L-20	CIP
11	NERICA-L-21	CIP
12	NERICA-L-29	CIP
13	NERICA-L-32	CIP
14	NERICA-L-34	CIP
15	NERICA-L-36	CIP
16	NERICA-L-38	CIP
17	NERICA-L-43	CIP
18	NERICA-L-45	CIP
19	NERICA-L-48	CIP
20	NERICA-L-49	CIP
21	NERICA-L-50	CIP
22	NERICA-L-53	CIP
23	NERICA-L-60	CIP
24	OM3242	CIP
25	ROK 11	CIP
26	ROK 14	CIP
27	ROK24	CIP
28	ROK 30	CIP
29	ROK34 (Check)	CIP
30	TGR 19	CIP

NPK 15:15:15 fertilizer was applied at the rate of 67.5 kgha^{-1} at transplanting. This was followed by the application of 55.2 kgha^{-1} N in the form of urea in two equal splits at 21 days and 42 days after transplanting. Hand weeding was done prior to fertilizer application at 21 days and 42 days after transplanting.

At physiological maturity, the rice crop in each plot was harvested separately, cutting the tillers at the height of 15 cm above ground level by using a harvesting knife. The harvested rice was threshed, sun dried, winnowed and put in separate delva cloth bags.

The following data was collected according to the stand-ard evaluation system for rice [11]:

Tiller Number Per Plant:
Average number of tillers per plant was counted and recorded on five individual plants.

Panicle Number Per Plant:
Average number of tillers per plant bearing panicles was counted and recorded on five plants.

Days to 50% Heading:
Observation was made on plot basis on the time when 50% of the plants produced heading.

Days to Maturity:
Observation was recorded on plot basis from seeding to the time when 85% of grains on panicle became mature and ripe.

Plant Height:
Average height of five plants on plot basis measured from the soil surface to the tip of the tallest panicle.

Culm Diameter:
The diameter of culm of five plants was measured on plot basis using Vernier caliper.

Grain Yield:
The dried grains obtained from each plot were weighed and moisture content recorded. The grain weight was then adjusted to 14% according to the following formula:

$$\text{Adjusted grain weight} = \frac{\text{Grain weight x (100 - Moisture content)}}{(100 - 14)}$$

C. *Statistical Analysis*
Data collected for the 30 lowland rice varieties were subjected to principal component and cluster analyses to determine genetic diversity of agro-morphological traits. The Statistical Tool for Agricultural Research [12], version 2.0.1 was used for the analyses.

III. RESULTS

A. *Principal Component Analysis*
Table 2 shows the principal component analysis of traits for 30 rice varieties of main crop.

Results explained the genetic diversity of the 30 rice varieties and showed that, the five principal components (PC1, PC2, PC3, PC4, and PC5) accounted for 96% of the total variation. PC1 and PC2 had the Eigen values greater than one, while PC3 showed Eigen value close to one. PC1 contributed 63% of the total variation whereas PC2, PC3, PC4, PC5 contributed 15%, 11%, 4% and 3%, respectively to the total variation. Traits such as number of tillers per hill and effective tillers per hill contributed more positively to the first principal component (PC1) whereas number of hills harvested and plant height contributed more positively to PC2. The large variation detected in PC3 was contributed by culm diameter. The traits which contributed more positively to PC4 and PC 5 are plant height and grain yield; and culm diameter, effective tillers per hill, number of tillers per hill and plant height, respectively.

Figure 1 shows the Dendogram of Euclidean distance measure using Ward's clustering method. Result revealed

that, there were seven main cluster groups, each group contains different number of genotypes. Cluster I consists of six genotypes, cluster II eight, cluster III four, cluster IV six, cluster V two, cluster VI three and cluster VII one.

Results also showed different number of sub-clusters in the main groups. Each of the main clusters consisted of two sub-clusters, except clusters I and VII which consisted of four sub-clusters and one sub-cluster, respectively.

Table 2: Principal component analysis of traits for 30 rice varieties of main crop evaluated at Rokupr, 2017.

| Statistics	PC1	PC2	PC3	PC4	PC5
Standard deviation	2.25	1.11	0.96	0.60	0.49
Proportion of Variance	0.63	0.15	0.11	0.04	0.03
Cumulative Proportion	0.63	0.78	0.89	0.93	0.96
Eigen values	5.04	1.22	0.91	0.36	0.24
Eigen vectors					
Variables	PC1	PC2	PC3	PC4	PC5
Number of hills harvested	-0.09	0.63	-0.69	-0.32	-0.11
Number of tillers per hill	0.38	-0.25	-0.39	0.02	0.28
Plant height	-0.38	0.23	0.01	0.47	0.27
Days to 50% flowering	-0.37	-0.44	-0.21	-0.22	-0.17
Days to maturity	-0.37	-0.44	-0.22	-0.19	-0.28
Culm diameter	-0.39	0.00	0.13	-0.46	0.76
Effective tiller per hill	0.37	-0.30	-0.37	0.11	0.38
Grain yield	-0.37	-0.09	-0.33	0.60	0.08
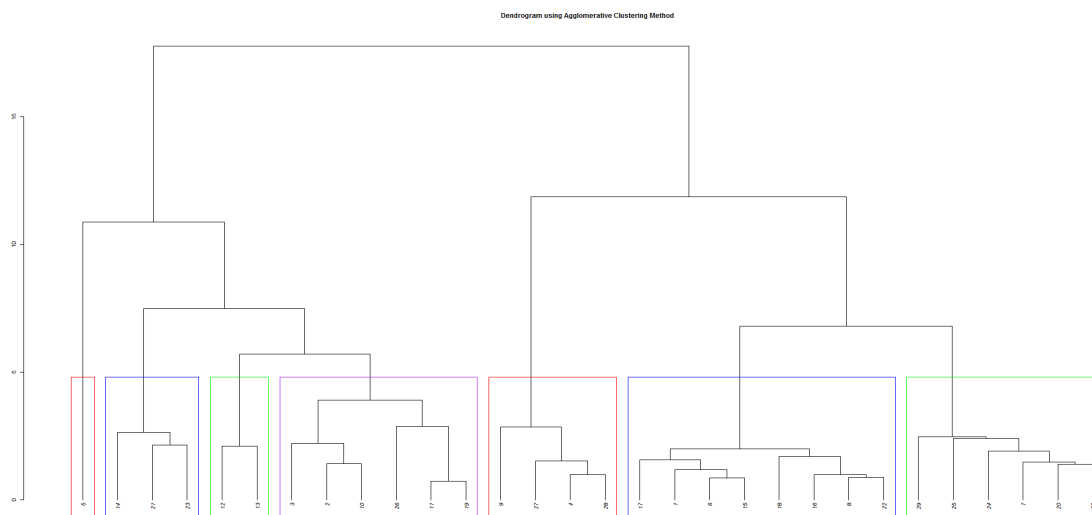
Fig. 1. Dendogram of Euclidean distance measure using Ward's clustering method.

B. *Cluster means of Traits of main Crop*

Table 3 presents cluster means of traits for 30 rice varieties of main crop. Results showed that genotypes included in the second cluster contributed to the bulk (26.6%) of the total genotypes. In this cluster, genotypes were grouped based on their number of tillers per hill which showed high number of tillers per hill. Genotypes in the first and fourth cluster contributed 20% each of the total genotypes. Genotypes in the first cluster had moderate number of hills harvested, medium days to maturity and large culm diameter whereas in cluster four highest number of tillers per hill were observed, least plant height, very early days to 50% flowering, very early maturity, least culm diameter and highest effective tillers per hill was recorded. Genotypes in cluster three had 13.3% of total genotypes expressing higher number of

harvested hills, moderate number of tillers per hill, highest plant height, longest duration to 50% flowering and maturity and largest culm diameter but lower effective tillers per hill and highest grain yield. In cluster five, 6.6% of genotypes expressed higher number of hills harvested, lowest number of tillers, higher plant height, longer days to 50% flowering, medium culm diameter and higher grain yield. Genotypes in cluster six showed 10%, expressed higher number of tillers per hill, lower plant height, early to 50% flowering and higher effective tillers per hill. Cluster seven contributed 3.3% of the total genotypes and the least among all the clusters, it showed higher number of days to 50% flowering and number of days to maturity, medium culm diameter and moderate effective tillers per hill.

Table 3. Cluster means of traits for 30 rice varieties of main crop evaluated at Rokupr, 2017.

Cluster	Number of hills harvested	Number of tillers per hill	Plant height	Days to 50% flowering	Days to maturity	Culm diameter	Effective tiller per hill	Grain yield
I	119.08	7.4	104.15	99.96	130.04	0.44	5.42	2006.41
II	118.45	9.02	107.34	98.89	129.61	0.38	6.63	2064.55
III	121	7.08	138.72	111.17	140.17	0.47	5.38	3092
IV	118.67	12.6	60.87	74.67	104.67	0.21	9.27	732.7
V	120	5.99	133.3	100	129.56	0.43	4.58	2314
VI	112.17	10.57	78.5	94.5	125	0.29	8	1465
VII	95.22	7.98	102.89	103.89	132.67	0.42	6.09	2162.77

IV. DISCUSSION

Evaluation and characterization of rice genotypes is important due to increasing needs of varietal improvemen--t. Assessment of genetic diversity is very important in rice breeding from the standpoint of selection, conservation of different genotypes of rice and proper utilization [13]. Agro-morphological characterization of germplasm variety is fundamental in order to provide information for plant breeding programs [14].

Results of the principal component analysis confirmed wide spectrum of genetic diversity among the 30 rice varieties. This is in line with [15] who found considerable morphological variation among rice landraces in China. The five principal components accounted for 97% of the total variation of which PC1 and PC2 contributed 63% and 15%, respectively. This result corroborates with the findings of [16] observed that the first two principal components accounted for 95.2% of the total variation with PC1 and PC2 contributed 84.6% and 10.6%, respectively. Meanwhile, [17] reported that the first four principle components of 22 traits of 43 rice genotypes accounted for about 72% of the total variation and indicated a wide variation among the genotypes. The traits which contributed more positively to the variation of PC1 are number of tillers per hill and effective tillers per hill whereas number of hills harvested and plant height contributed more positively to the variation of PC2.

The distribution pattern of genotypes into various clusters indicated the presence of considerable genetic divergence among the genotypes for the traits evaluated. The 30 genotypes were clustered into seven main groups of which genotypes in the second cluster represented the bulk (26.6%) of the total genotypes followed by genotypes in clusters one and four with 20% each. Cluster seven contributed the least (3.3%) of genotypes. In their studies of correlation and cluster analysis of some yield and yield related traits in 20 rice genotypes, [18] reported that the cluster analysis grouped genotypes into six main clusters. Reference [17] reported cluster analysis based on 22 traits grouped 43 rice genotypes into five clusters. Moreover, [19] reported genetic diversity among 84 landraces by grouping them into five major clusters. Also [9] used Cluster analysis based on Ward's method to investigate genetic diversity of 24 genotypes of modified rice according to qualitative and quantitative traits; genotypes were divided in three main clusters. In this study, genotypes were grouped in each cluster based on their unique characteristics expressed. For instance, genotypes in cluster I were grouped based on their moderate number of hills harvested, medium days to maturity and large culm diameter. The unique characteristic which characterized genotypes in cluster II was high number of tillers per hill. In cluster III, genotypes were characterized by higher number of hills, moderate number of tillers per hill, highest plant height, longest days to 50% flowering and maturity, largest culm diameter, highest grain yield and lower effective tillers per hill. Genotypes in cluster IV had highest number of tillers per hill and effective tillers per hill, least plant height, very early days to 50% flowering and maturity, and least culm diameter. Higher number of hills, plant height and grain yield; longer days to 50% flowering, medium culm diameter, and lowest number of tillers were the peculiar characteristics of genotypes in cluster V. Genotypes in cluster VI expressed higher number of tillers per hill and effective tillers per hill, shorter plant height and early days to 50% flowering. Genotypes in cluster VII had longer days to 50% flowering and maturity, medium culm diameter and effective tillers per hill.

For the selection of parents, genetic diversity is one of the important decisive factors [20]. This study highlighted that genotypes grouped in clusters IV and VI were the most similar clusters in terms of lowest grain yield, suggesting that hybridization between these clusters will not be effective, as their genetic make-up is almost similar. However, crossing between genotypes in clusters III and V will be effective, as genotypes in these clusters were identified as being most divergent. This could result in heterotic expression and a large variability in the segregating generation [17].

V. CONCLUSION

The five principal components accounted for 96% of the total variation of which PC1 and PC2 contributed 63% and 15%, respectively. Number of tillers per hill and effective tillers per hill contributed more positively to the variation

of PC1 while number of hills harvested and plant height contributed more positively to the variation of PC2. Cluster analysis grouped the 30 genotypes into seven main clusters with cluster II represented the bulk (26.6%) of the total genotypes while cluster VII contributed the least (3.3%) of genotypes. Hybridization between genotypes grouped in clusters IV and VI would not be effective as their genetic make-up is almost similar while crossing between genotypes in clusters III and V will be effective, as genotypes in these clusters were identified as being most divergent.

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