



Genetic Diversity and Evaluation of Assembled Rice (*Oryza sativa* L.) Germplasm for Breeding Purposes in Northern Ghana

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Article Information

DOI: 10.9734/IJPSS/2022/v34i232573

Open Peer Review History:

This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: <https://www.sdiarticle5.com/review-history/94065>

Original Research Article

Received 20 September 2022

Accepted 29 November 2022

Published 02 December 2022

ABSTRACT

Background of the Study: Rice (*Oryza sativa* L) is an important staple food crop that feed over half of the global population and it has become the cereal that provides a major source of calories for the urban and rural poor in Africa. Rice has is the second most important food staple after maize in Ghana and its consumption keeps increasing as a result of population growth, urbanization and change in consumer habits. Rice yield across Ghana is far below achievable yield. The need for increasing rice yield depends not only on cultural/traditional practices but also on their inbuilt genetic potential to withstand stresses. Adequate diverse rice germplasm is a pre-requisite for breeding varieties to meet local biotic, abiotic and grain quality challenges. Knowledge of germplasm diversity and genetic relationships among breeding materials is valuable information for crop improvement.

Aim: To identify the diversity among assembled rice germplasms for evaluation and possibly exploit its genetic variability for earliness for cultivation in the Guinea and Sudan Savanna ecologies.

Study Design: The experiment was conducted at CSIR-SARI research station, Nyankpala. Using a Randomized Complete Block Design with two replications, and a plot size of 4 m x 3 m was used. Field data taken included 10 qualitative and 11 quantitative traits. The data were statistically analyzed for various descriptive statistics.

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Results: Correlation analysis, Principal Component Analysis (PCA) and Cluster analysis were used to assess genetic variability. Most of the morphological traits showed remarkable differences in their distribution. Five significant principal components were identified accounting for 78.11% of the total variation. Cluster analysis based on the morphological data grouped the germplasm into two distinct clusters suggesting diversity among the assembled rice germplasms.

Conclusions: The rice germplasm used in the present study displayed variability for most of the studied traits with the exception of ligule. Twenty one out of the 100 germplasm were distant from the rest, and were selected to constitute a core collection for further improvement.

Recommendations: Diversity revealed in this study is narrow. It is, therefore, recommended that rice breeding programs in Ghana should include new genetically unrelated genotypes in order to broaden the genetic base of Ghanaian rice germplasm.

Keywords: Rice; germplasm; principal component analysis; correlation; cluster analysis; dendrogram.

1. INTRODUCTION

Rice (*Oryza sativa* L.) is one of the most important food crops grown worldwide. It is the staple food for half of the world's population [1]. On a global basis, it is planted on an area of 159 million hectares with production of 685 million tonnes. China is the leading country in production (193 million tonnes), followed by India (148 million tonnes), Indonesia (60 million tonnes), Bangladesh (47 million tonnes), Vietnam (48 million tonnes) and Thailand (30 million tonnes) [1].

There are two cultivated species: *Oryza glaberrima*, or African rice, and *Oryza sativa*, or Asian rice. Native to sub-Saharan Africa, *O. glaberrima* is thought to have been domesticated from the wild ancestor *Oryza barthii* (formerly known as *Oryza brevilugata*) by people living in the flood plains at the bend of the Niger River some 2,000–3,000 years ago. The two strains of *O. sativa* (*Oryza japonica* and *Oryza indica*) were domesticated independently, both probably in China. It is also possible that Asian rice was domesticated in tropical Asia south of China, but evidence for this possibility is still lacking [2]. Approximately 20 million farmers are engaged in production of rice in sub-Saharan Africa (SSA) and about 100 million people depend on it directly for their livelihoods on the continent [3]. These trends have meant that rice is no longer a luxury food, but has become a major source of calories for the urban poor.

Urban consumption surveys in Burkina Faso, for example, have found that the poorest third of urban households obtain 33% of its cereal-based calories from rice. For that same group, rice purchases represent 45% of its cash expenditures on cereals, a share that is substantially higher than other income classes.

Similar findings have been obtained in several other West African countries, demonstrating that rice availability and rice prices have become a major determinant of the welfare of the poorest segments of West African consumers who are the least food-secure [4].

Rice has become the second most important food staple after maize in Ghana and its consumption keep increasing as a result of population growth, urbanization and change in consumer habits. Between 1996 and 2005, paddy production was in the range of 200,000 and 280,000 tonnes (130,000 to 182,000 tonnes of milled rice) with large annual fluctuation ("NATIONAL RICE DEVELOPMENT STRATEGY (NRDS) - DRAFT," 2009). In Ghana, the three northern regions produce the bulk of rice produced in the country. From 2000 to 2010 there was an evolution of production, area and yield for rice in Ghana, this led to an increase in rice production from 0.09 and 0.16 million hectares while yields fluctuated between 1.7 and 2.7 tonnes per hectare. It however appears that from 2007, rice production has been on the increase with 2010 production levels being more than double 2007 levels (from 185, 300 tonnes in 2007 to 491, 600 tonnes in 2010) with average annual growth of more than 15 percent over the period 2005-2010, despite the production drop experienced in 2007. Reasons for this increase could be attributed to the favorable rain patterns as well as the 2008 fertilizer subsidy programme, the Block Farm programme of 2009 which are also contemplated in the Ghana Rice Strategy [5]. Rice has become the cereal that constitutes a major source of calories for the urban and rural poor rather than the luxury food we use to know. Moreover, it is a nutritional cereal crop, providing 20% of the calories and 15% of proteins consumed by world's population [6]. Increase in rice production is needed if rising population

demand is to be met in Ghana and sub-Saharan Africa as a whole. Rice production in sub-Saharan Africa has been bedevilled with conditions such as environmental degradation due to pesticide usage, excessive water usage, and nutrient contamination, methane emission and ammonia volatilization and these conditions require urgent attention.

The primary consideration to bring about genetic improvement of a crop is the genetic variability. Assessment of variability for any trait is prerequisite for a plant breeder to planning effective breeding programmes to incorporate the trait into other varieties. Heritability is an index of the transmission of characters from parents to their offspring and it plays an important role in the selection process in plant breeding [7]. Characterization of rice germplasm increases its utility in any breeding program. The use of agromorphological traits is the most common approach utilized to estimate relationships between germplasms [8]. Rice yield across Ghana is below achievable yield, necessitating the need to breed for high yielding varieties. A number of factors have been identified to contribute to this yearly gap. The self-sufficiency ratio of rice in Ghana is said to have declined from 38% in 1999 to 24% in 2006 [5]. This has renewed calls from the Food and Agriculture sector, for industry experts to devise new innovative ways to improve the production of rice in the country. This is in accordance with the Ghana's vision to increase productivity and curb the continual importation of rice at higher costs. Characterization of rice germplasm increases its utility in any breeding program. Recent crop genetic improvement programmes may usually have the major objective of increasing yield, to be able to feed the 21st century population. Perhaps, other factors; nutritional content (a requirement for food security), resistance to pests and diseases and several other morpho-agronomic traits which may be species specific, are also considered important in breeding programmes. The global effort to assemble and document the conserved genetic resources is enormous. Characterization of rice germplasm provides the important information about morphological and agronomical aspects of the material that is essential for gene bank management. The estimates of genetic parameters and association of characters are very useful in understanding the nature and magnitude of genetic variability in the breeding material. In the development of high yielding germplasms, knowledge of interrelationship

among these factors is quite necessary; correlation studies in conjunction with coefficient analysis provide information about the cause-and-effect relationship between direct pairs of variables. The available diversity in the germplasms also serves as an insurance against known future needs and conditions, thereby contributing to the stability of farming system at national and global levels. In crop improvement programme, genetic variability for agronomic traits as well as quality tests in almost all the crops is important, since this component is transmitted to the next generation [9]. Study of genetic divergence among the plant materials is a vital tool to the plant breeders for an efficient choice of parents for plant improvement. Genetically diverse parents are likely to contribute desirable alleles to produce high heterotic crosses. This will eventually lead to crop improvement for yield and its related traits.

The objective of the study was to identify the diversity among rice germplasm for evaluation and possibly exploit its genetic variability for earliness for cultivation in the Guinea and Sudan Savanna ecologies.

2. MATERIALS AND METHODS

2.1 Study Area

The trial was conducted from June to October 2018 during the cropping season, at CSIR-SARI research station in Nankpala, in the Northern Region of Ghana. The site is located, 16 kilometers west of Tamale on latitude of 09° 25", longitude of 01° 00" and an altitude of 183 meters above sea level. With one rainy season in the year, the area/site receives about 1000 mm of rainfall annually (SARI, 2013). The mean annual temperature distribution is a minimum of 23.4 degree Celsius and a maximum of 34.5°C with a minimum relative humidity of about 46% and maximum of 76.8%.

2.2 Experimental Design

A Randomized complete block design with two replications was used in a single factor experiment. Plot sizes of 4 m x 4 m with 2 m alley between plots were used for each treatment.

2.3 Experimental Materials

The list below shows the names of the assembled rice germplasms and their sources.

List 1. Names of the assembled rice germplasms and their sources

S/N	Genotype	Source	S/N	Genotype	Source
1	BDR 10	AfricaRice	51	N-13	AfricaRice
2	SBT-1	Cameroon	52	N-14	AfricaRice
3	GR 19	CSIR-SARI	53	N-11	AfricaRice
4	HANGOU 73	China	54	PET 71 BDR	AfricaRice
5	CRI-Amankwatia	CSIR-CRI	55	FORO 64	CSIR-SARI
6	Was 122	AfricaRice	56	N-16	AfricaRice
7	BDR58	Bangladesh	57	FORO 63	CSIR-SARI
8	V27	AfricaRice	58	BINDURI-1	Local
9	Perfume irrigated	Thailand	59	GANU-1	Local
10	DHAN 52	Bangladesh	60	PUSIGA-1	Local
11	SBT 41	Cameroon	61	GANU-2	Local
12	S701	CSIR-SARI	62	BAWKU-1	Local
13	Agra rice	CSIR-SARI	63	BINDURI-2	Local
14	PAC 801	India	64	BINDURI-3	Local
15	SBT 65	Cameroon	65	BINDURI-4	Local
16	CRI-Kantinka	CSIR-CRI	66	PUSIGA-2	Local
17	Katanga	CSIR-SARI	67	GANU-3	Local
18	SBT 281-2	Cameroon	68	GANU-4	Local
19	SBT 48	Cameroon	69	BAWKU-2	Local
20	CRI-Mpomtuo	CSIR-CRI	70	PUSIGA-3	Local
21	Anyofula	CSIR-SARI	71	BINDURI-5	Local
22	CRI-Emopa	CSIR-CRI	72	PUSIGA-4	Local
23	Digang	CSIR-SARI	73	GANU-5	Local
24	OKUMKUM	Local	74	PUSIGA-5	Local
25	PET 45 BDR	AfricaRice	75	GANU-6	Local
26	CRI-Dartey	CSIR-CRI	76	BINDURI-6	Local
27	PAC 83-2	India	77	BINDURI-7	Local
28	WAIQI	China	78	PUSIGA-6	Local
29	Digang-1	CSIR-SARI	79	GANU-7	Local
30	SIKAMO	CSIR-CRI	80	ADABIIMA	Local
31	929	China	81	PUSIGA-7	Local
32	SB7	Cameroon	82	BAWKU-3	Local
33	SBT 87	Cameroon	83	ASAKIBA	Local
34	926	China	84	AJARA Rice	Local
35	PET 82 BDR	AfricaRice	85	ADIZAH	Local
36	Long Grain Ordinary-2	Thailand	86	MUNIRATU	Local
37	GBEWAA Rice	CSIR-SARI	87	ASAANA-1	Local
38	BRI DHC 62	Bangladesh	88	Digang-2	CSIR-SARI
39	GR 18	CSIR-SARI	89	NABOGU	CSIR-SARI
40	WASS 163	AfricaRice	90	Jasmine 85	CSIR-SARI
41	SBT 90	Cameroon	91	Agra rice-1	CSIR-SARI
42	SBT 330	Cameroon	92	80 days	CSIR-SARI
43	SWARNA 2	India	93	Exbaika	CSIR-SARI
44	PRIMAVERA	Cameroon	94	GR 21	CSIR-SARI
45	923	China	95	FARO 15	CSIR-SARI
46	N-17	AfricaRice	96	NERICA 1	CSIR-SARI
47	CRI- Obofo	CSIR-CRI	97	WAS 163	AfricaRice
48	N-12	AfricaRice	98	Amankwatia	CSIR-CRI
49	GIGANTE	AfricaRice	99	Anty Jane	CSIR-CRI
50	N-7	AfricaRice	100	FEITOR-1	Local

2.4 Agronomic Practices

The experimental field was ploughed, the plots were cleared using the hand hoe and then lined and pegged, using the garden line and pegs according to treatment number. Planting was done with a spacing of 20 cm between rows and 40 cm within rows and two plants per hill.

2.5 Data Collection

Data was collected on plants are classified under quantitative and qualitative. Qualitative data collected includes; culm altitude, leaf intensity of green color, basal leaf sheath color, leaf blade pubescence, awns, presence of ligule, ligule shape, ligule color, presence secondary branching and secondary branching. Quantitative data collected includes; tillers count, days to 50% flowering, flag leaf altitude, length of blade, number of panicles per plant, number of filled and unfilled grain per panicle, plant height, 1000 seed weight, time to maturity(days) and panicle length.

2.5.1 Qualitative Characters

Culm altitude: The estimated average angle of inclination of the base of the main culm from vertical. Observed after flowering and scored on erect, semi-erect (intermediate), horizontal, descending.

Leaf intensity of green color: It was observed during late vegetation and scored based on; No green color visible due to anthocyanin, Light, Medium (green), and Dark.

Basal leaf shelf color: Color of the outer surface of the leaf sheath. It was taken at late vegetative and scored green, green with purple lines, light purple and purple.

Flag leaf altitude: Measured near the collar. Angle of attachment between the flag leaf blade and the main panicle axis. record the average of five samples. scored at anthesis on erect, semi-erect (intermediate), horizontal, descending.

Assess both visually and by touch, rubbing fingers over the leaf surface from the tip downwards. Taken at late Stage of vegetation.

Presence of Awns: The presence and distribution of awns along the panicle were observed and scored.

Presence of ligule, ligule shape and ligule color: Plants were physically observed to identify the presence of ligule, its shape and color. Taken at late Stage of vegetation and score on.

Presence secondary branching: The abundance and distribution of spikelet borne on secondary branches of the panicle. Observed near maturity.

2.5.2 Quantitative Characters

Tiller count: Twelve stands of plants were randomly selected per plot within the net plot and tagged for measurement of tillers.

Days to 50% flowering: This was done by counting the number of days from nursing to when half (50%) of the population of rice plant on each plot flowered or started flowering and then recorded.

Leaf width and length of blade: The leaf width was measured from the widest side of the leaf end of each of the randomly selected plants using the measuring tape. Length of blade was also measured transversely from the collar to the tip of the leaf blade.

Number of Panicle per plant: The total number of panicles per plant was counted and recorded at the maturity stage before harvest.

Number of filled and unfilled grain per panicle: Grain from randomly selected panicles were threshed and then counted manually. The mean number of filled and unfilled grain were computed and then recorded.

Plant height: Plant height (cm) was measured from soil surface to tip of the plant at reproductive stage using the measuring tape.

One thousand grain weight: One thousand well developed seeds were randomly selected per replication for each accession. The seeds were obtained from the harvested samples of germplasms after harvest; dried to 13% moisture content and weighed on a balanced precision scale (METTER PM 400) to determine the 1000 grain weight.

Time to maturity: Maturity is the date on which 80% of the grains on the panicles are fully ripened.

Panicle length: Length of main axis of panicle measured from base to the tip. Recorded the average of five representative plants.

2.6 Statistical Analysis

The data were statistically analyzed for various descriptive statistics. Correlation analysis, principal component analysis (PCA) and cluster analysis were used to assess genetic variability.

3. RESULTS

3.1 Qualitative Characters

The results of some qualitative traits assessed among hundred assembled rice germplasm for culm altitude, leaf intensity of green color, basal leaf sheath color, leaf blade pubescence, awns, ligule shape, ligule color and secondary branching are as follows:

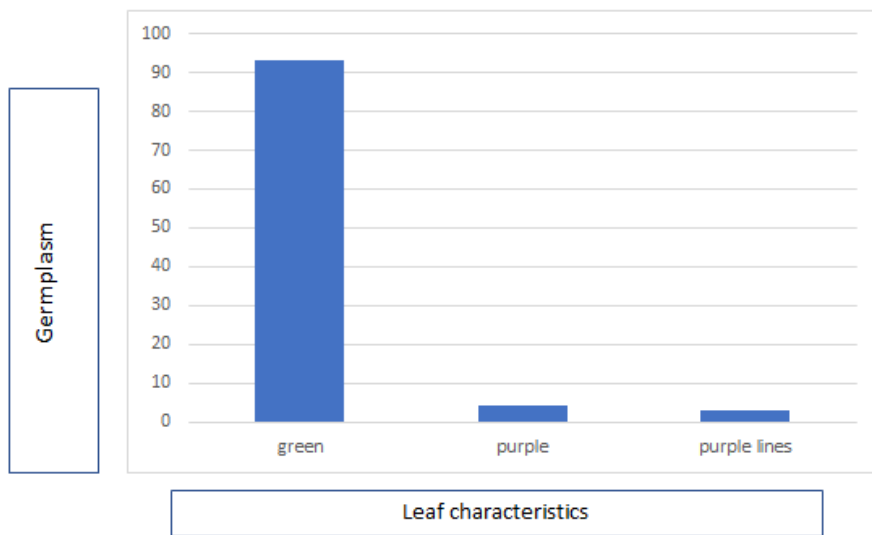


Fig. 1. Distribution of basal leaf-sheath color type for the 100 rice germplasms

Fig. 1 shows the distribution of basal leaf sheath color in the germplasms. There were three types for the 100 rice germplasms, namely; green, purple and purple line. Ninety-three rice germplasms were of the green color type while four and three of the germplasms were of the purple and purple line types respectively.

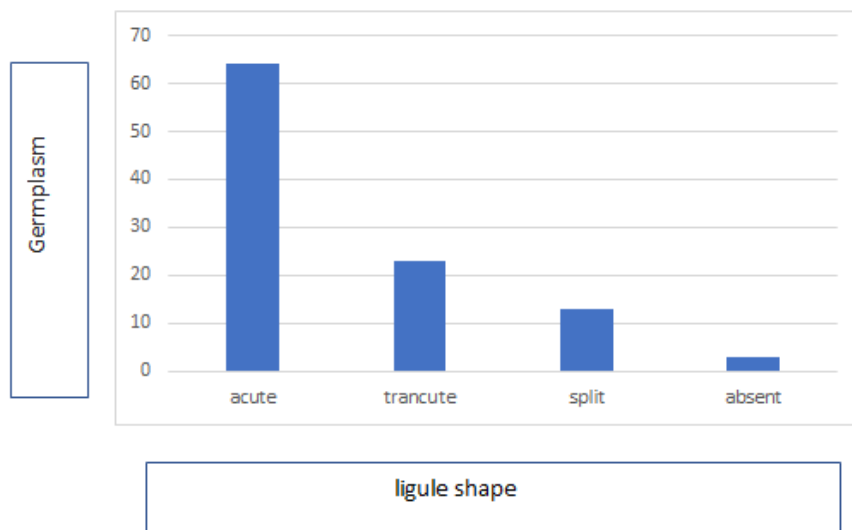


Fig. 2. Distribution of ligule (shape of ligule) type for the 100 germplasms

Distribution of ligule types among all the 100 germplasms. 10 split shaped, 23 truncute shaped, 64 acute shaped leaf ligule and 3 germplasms had no ligule as show in Fig. 2.

The 100 germplasms were classified for three classes of green color intensity namely light green, medium green and dark green. 13 germplasms possess light green, 72 medium green and recorded 15 dark green leaves. Shown in Fig. 3.

Fig. 4 shows that, the 100 germplasms were grouped into 4 classes of leaf blade attitude. 2 germplasms grouped into horizontal, 27

germplasms into semi erect, 56 germplasms into erect type and 15 germplasms into dropping.

Out of 100 germplasms studied, only 23 germplasms exhibited weak and remaining 77 showed strong leaf blade pubescence. Shown in Fig. 5.

Fig. 6 shows that, out of 100 germplasms studied, 7 germplasms had recorded strong, 13 had exhibited clustered while, 70 germplasms had weak secondary branches, 2 germplasms had clustered and 21 germplasms had no secondary branching.

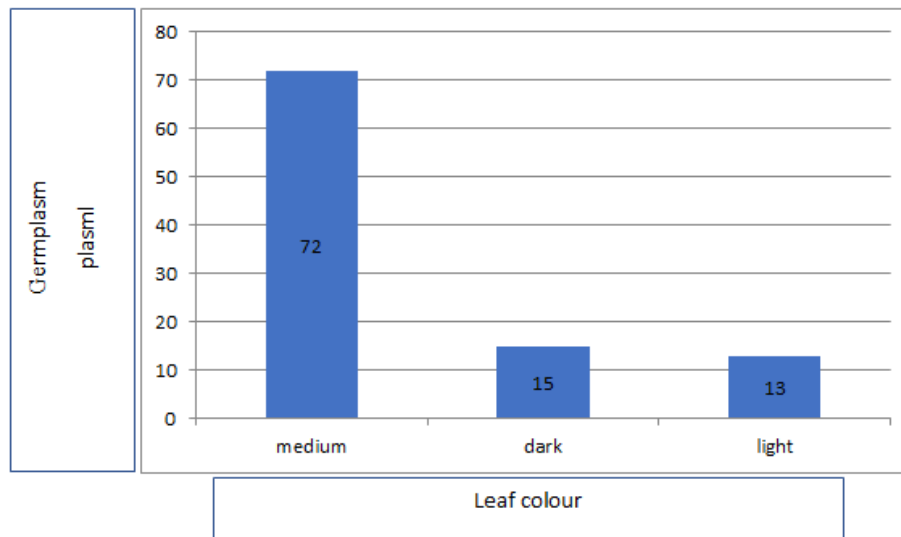


Fig. 3. Distribution of leaf intensity of green color for the 100 rice germplasms

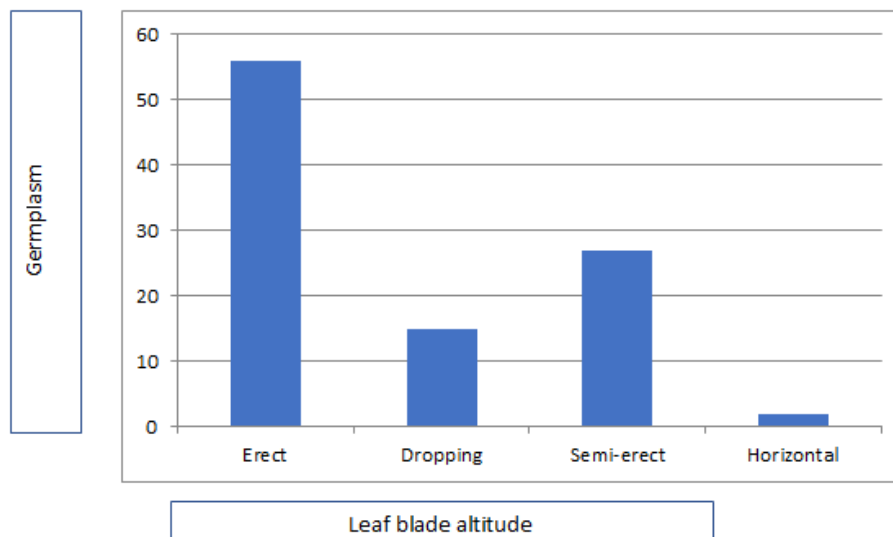


Fig. 4. Distribution of flag Leaf attitude of blade of the 100 rice germplasms

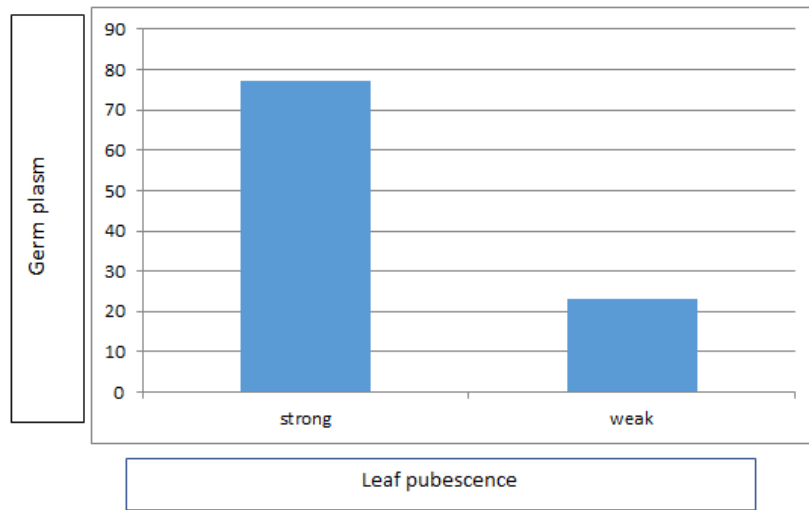


Fig. 5. Distribution of leaf blade pubescence for the 100 rice germplasms

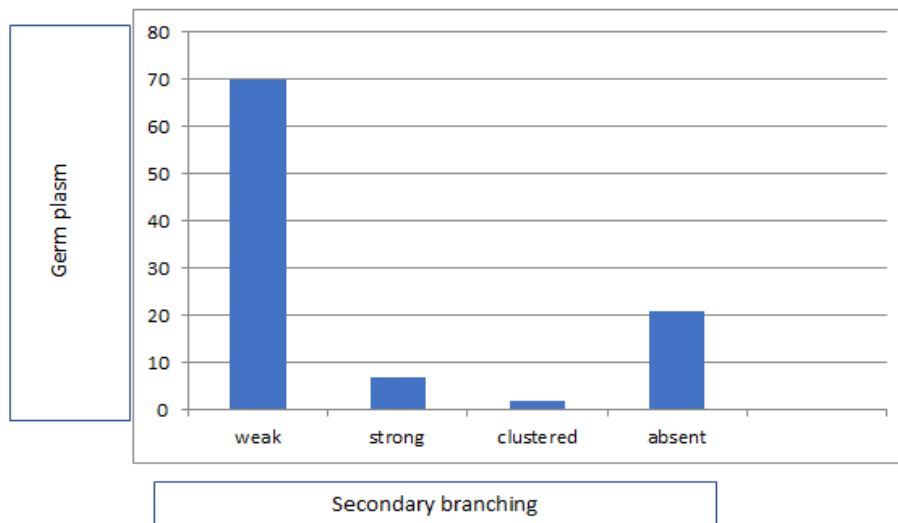


Fig. 6. Distribution of secondary branching types for the 100 rice germplasms

Fig. 7 shows that, the 100 germplasms were grouped into 3 classes of culm attitude. 15 germplasms grouped into spreading, 22 germplasms into semi erect, 63 germplasms into erect type.

Out of 100 germplasms, only 7 germplasms had awn present and 93 germplasms had no awn.

3.2 Quantitative Characters

3.2.1 Pearson correlation among the quantitative traits

This analysis is an important approach in a breeding programme. It gives an idea about relationship among the various characters and

determines the component characters, on which selection can be based for genetic improvement in the grain yield. Degree of association also affects the effectiveness of selection process. The degree of association between independent and dependent variables was suggested by Galton 1888. Correlation studies provide information on nature and extent of association between two pairs of metric characters. However, it could be possible to bring genetic improvement in one character by selection of the other of a pair. Traits that show significant positive correlation in this study could be improved simultaneously. However, traits that exhibit negative relationships could be improved independently in the future.

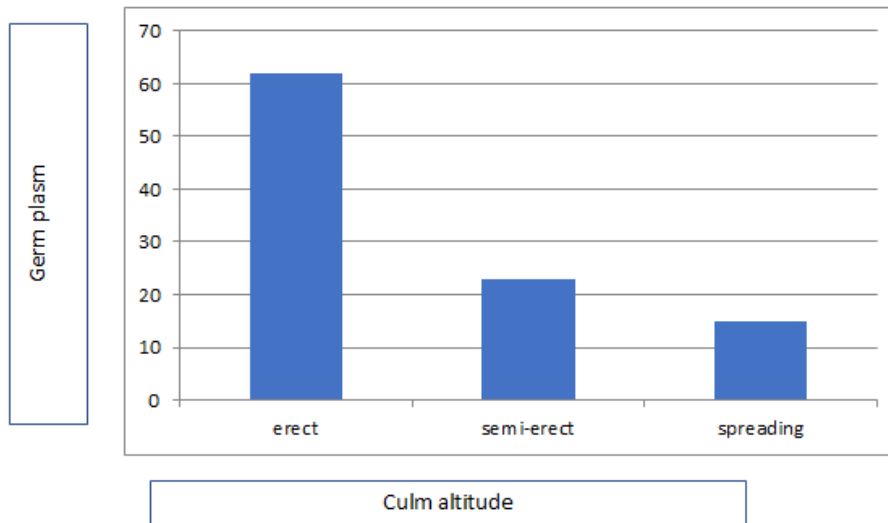


Fig. 7. Distribution of Culm altitude of the 100 rice germplasms

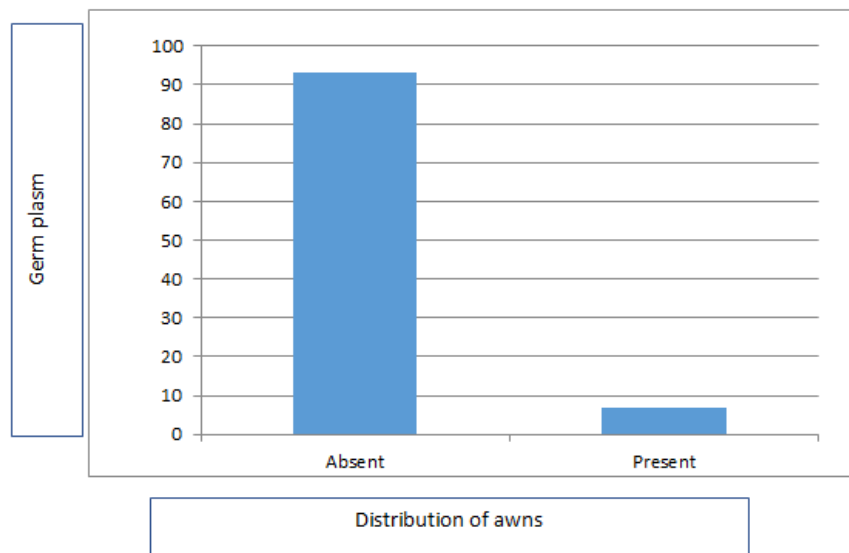


Fig. 8. Distribution of Awns for the 100 rice germplasms

3.3 Principal Component Analysis (PCA)

The principal components analysis based on the 11 quantitative traits was performed individually to determine the relative contribution of the different traits to the total variation in rice. Five significant principal components were identified and accounted for 78.11% of the total variation. PC1 had Eigen-value of 3.538, explaining 32.17% of the total variation (Table 2). Quantitative traits such as Days to 50% flowering (0.43634), Days to maturity (0.43333), Leaf width (0.30372), Panicles per plant (0.43012), Plant height (0.34509) and Tillers per plant (0.42934) contributed greatly to PC1, which accounted the

highest for the total variation. PC2 depicted proportion of variance as 15.45%, PC3 contributed 11.95% to the total variation, PC4 also had a variance of 10.19% and PC5 had 8.35% to the total variation (Table 2). PC2 was associated with Number of filled seed per panicle (0.62821) and Panicle Length (0.65324), also had Eigen value of 1.699. PC3 was associated with Leaf length (0.37549), and No of unfilled seed per panicle (0.56247). The fourth PC had 1.121 as its Eigen-value and it explained 10.19% of the total variation. PC5 PC had 0.918 as its Eigen-value and it explained 8.35% of the total variation.

Table 1. Table below shows Pearson Correlation coefficients among the quantitative traits studied

	%1000 grain weight	Days to 50% flowering	Days to maturity	Leaf length	Leaf width	No of filled seed per panicle	No of unfilled seed per panicle	Panicle length	Panicles per plant	Plant height	Tillers per plant
<i>%1000_grain_weight</i>	*										
<i>Days_to_50%_flowering</i>	0.030	*									
<i>Days to maturity</i>	0.040	0.970	*								
<i>Leaf length</i>	-0.003	0.057	-0.003	*							
<i>Leaf width</i>	-0.097	0.309	0.291	0.047	*						
<i>No of filled seed per panicle</i>	-0.072	0.180	0.207	0.183	0.104	*					
<i>No of unfilled Seed per panicle</i>	-0.108	-0.143	-0.140	0.131	0.0125	-0.082	*				
<i>Panicle length</i>	-0.169	0.088	0.101	0.137	0.0163	0.637	0.078	*			
<i>Panicles per plant</i>	0.094	0.449	0.455	0.147	0.368	0.081	-0.031	0.098	*		
<i>Plant height</i>	-0.002	0.486	0.461	0.069	0.460	-0.010	0.026	0.023	0.367	*	
<i>Tillers per plant</i>	0.048	0.434	0.438	0.155	0.406	0.075	0.007	0.104	0.984	0.373	*

Table 2. Principal component analysis of the quantitative traits

Traits	PC1	PC2	PC3	PC4	PC5
1000 grain weight	0.0148	0.25212	0.13799	0.66114	0.31712
Days to 50% flowering	0.43634	0.04634	0.34726	-0.11899	0.2895
Days to maturity	0.43333	0.03847	0.37012	-0.10944	0.24975
Leaf length	0.08881	-0.25584	-0.37549	0.25998	0.55494
Leaf width	0.30372	0.05645	-0.19438	-0.32879	-0.20656
No of filled seed per panicle	0.13856	-0.62821	0.20009	0.12317	-0.05498
No of unfilled seed per panicle	-0.04485	-0.09928	-0.56247	-0.27249	0.40048
Panicle Length	0.10886	-0.65324	0.0359	0.03574	-0.11694
Panicles per plant	0.43012	0.08698	-0.2829	0.30806	-0.29577
Plant height	0.34509	0.13928	-0.05283	-0.32574	0.20824
Tillers per plant	0.42934	0.07729	-0.32262	0.26333	-0.30773
Eigen values	3.538	1.699	1.314	1.121	0.918
% Variance	32.17	15.45	11.95	10.19	8.35
% Cumulative variance	32.17	47.62	59.57	69.76	78.11

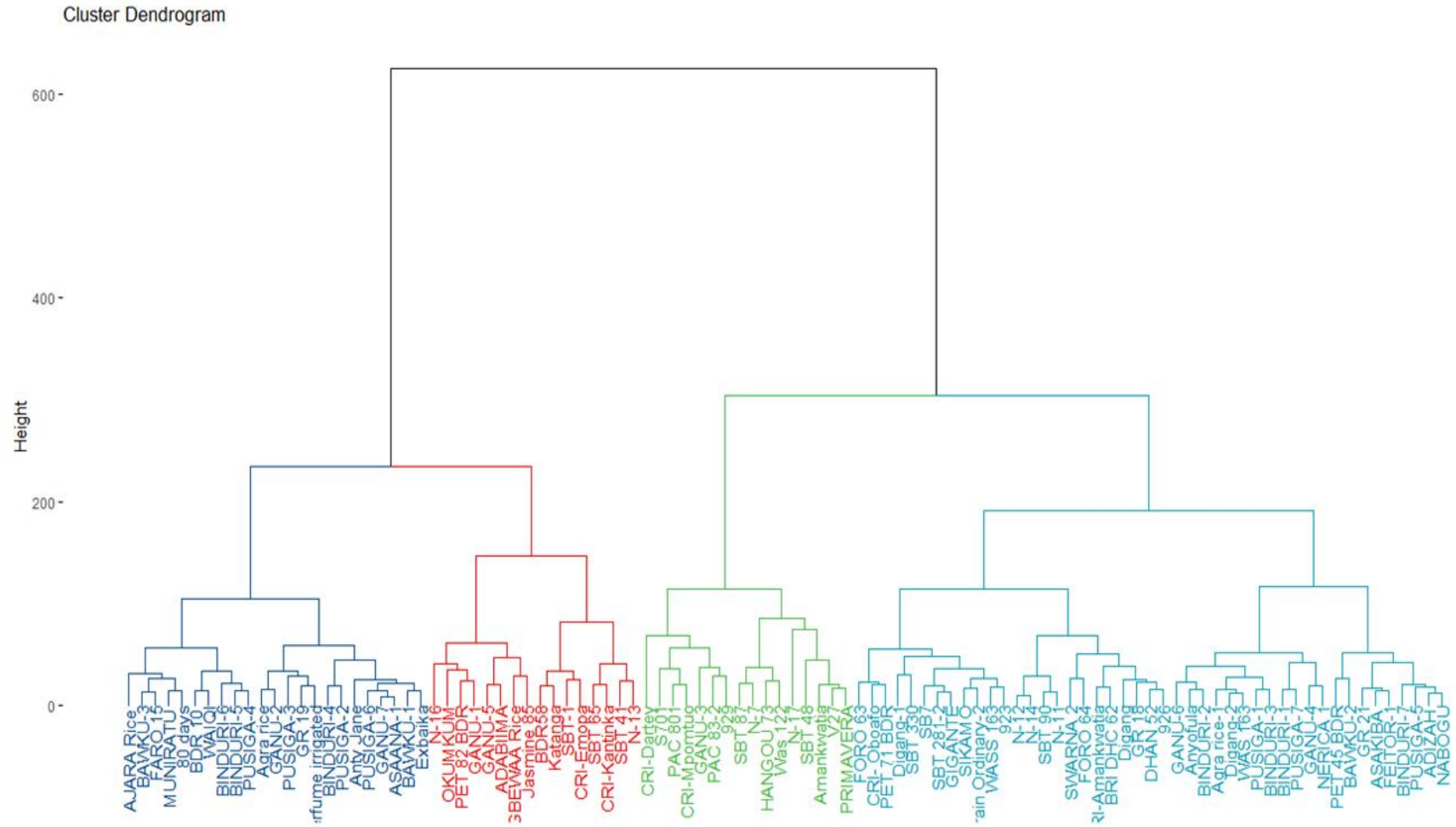


Fig. 9. Cluster dendrogram

3.4 Cluster Analysis

The cluster analysis of rice germplasms generated two main sub divisions that separates majority of the germplasms. Fig. 4 shows at a height of 200 the germplasms clustered into 8 main clusters. Cluster VII was the largest of all the clusters and contained 24 germplasms which are; FORO 63, CRI-OBOAFO, PET 71 BDR, DIGANG-1, SBT 330, SBT 7, GIGANTE, SIKAMO, LONG GRAIN ORDINARY, WASS163, 923, N-12, N-14, SBT 90, N-11, SWARNA-2, FORO 64, CRI-AMANKWATIA, BRI DHC 62, DIGANG, GR 18, SBT 281-2, DHAN 52 and 926 with eleven sub-clusters. Cluster VIII was the second largest cluster with 20 germplasms, namely; GANU-6, BINDURI-2, AGRA RICE-1, DIGANG-2, WASS163, PUSIGA-1, BINDURI-3, BINDURI-1, PUSIGA-7, GANU-4, NERICA-1, PET 45 BDR, BAWKU-2, GR 21, ASAKIBA, FEITOR-1, BINDURI-7, PUSIGA-5, ADIZAH and NABOGU including eight sub-clusters and cluster II had 13 germplasms with four sub-clusters. Cluster I had 10 germplasms with three sub-clusters and next was Cluster VI which had 9 germplasms with three sub-clusters.

Cluster III and IV, had 8 accession each, 3 and 4 sub-clusters respectively. Cluster V had 6 germplasms with three sub-clusters. Germplasms in the same cluster have the same morphological characteristics and sub-clusters indicate that the germplasms have some distinct traits from other members of the clusters. The 100 rice germplasms showed no distinctive morphological characteristics based on geographical origin, as the analysis showed no group of germplasms from either of the geographical locations divergently clustered. Cluster I consist of AJARA Rice, BAWKU-3, FARO 15, MUNIRATU, 80 days, BDR 10, WIAGI, BINDURI-6, BINDURI-5 and PUSIGA-4. Cluster II consist of AGRA Rice, GANU-2, PUSIGA-3, GR 19, PURFUMED IRRIGATED, BINDURI-4, PUSIGA-2, GANU-7, PUSIGA-6, Anty Jane, ASAANA-1, BAWKU-1 and Exbiaka. Cluster III consist of N-16, OKUMKUM, PET 28 BDR, GANU-1, GANU-5, ADABIIMA, GBEWAA Rice and Jasmine Rice. Cluster IV consist of PET 58 BDR, KATANGA, SBT-1, CRI-KANTINKA, SBT-65, CRI-EMOPA, SBT-41 and N-13. Cluster V consist of CRI-DARTEY, SBT 701, PAC 80, CRI-MPUMTUO, GANU-3 and 929. Cluster VI consist of SBT 87, N-7, HANGOU 73, WASS 122, N17, SBT 48, AMANKWATIA, V27 and PRIMAVERA.

4. DISCUSSION

Rice crop is characterized by low productivity due to lack of high yielding varieties adapted to different seasons and agronomic conditions. The presence of genetic variability is also essential pre-requisite for an effective improvement in a crop species [10]. Besides genetic variability, heritability which measures the relationship between phenotypic and genotypic appearance, is important consideration for the success of a breeding programme. It is obvious that selection is usually based on phenotypic observation and the success would naturally depend upon the relationship between phenotype and the genotype [11]. The estimates of heritability are also useful in prediction of genetic improvement following selection and deciding suitable breeding procedure for the improvement of a crop plant [12]. The knowledge about the extent and nature of association of plant characters among themselves and with yield and quality parameters would provide a better understanding in improving seed yield and its quality through selection. Information on genetic diversity and relatedness in crop germplasm is useful for plant breeders because it assists them in planning crosses [10]. Such information could be used to design strategies to improve traits, maintain and manage germplasm in Genetic Resource Centers, or enhance the genetic base of future varieties. Hence, to effectively maintain, evaluate and utilize germplasm, it is important to investigate the extent of available diversity.

4.1 Qualitative Characters

Qualitative traits are important parameters for plant description and evaluation, and are greatly influenced by the consumers' preference [11]. Charts showing distribution for ten qualitative traits are displayed in Fig. 1 to Fig. 8.

For leaf blade intensity of green color, it was observed that 13 germplasms possess light green, 72 medium green and recorded 15 dark green leaves. These trait helps determine the Nitrogen status of the field and also the chlorophyll content in the leaf.

Flag leaf angle is believed to influence the degree of light saturation of the upper leaves of rice crop [13]. Its distribution had 2 germplasms grouped into horizontal, 27 germplasms into semi erect, 56 germplasms into erect type and 15 germplasms into dropping. Mwangi, et al. [14] did observe differences in the flag leaf angle, varying

from erect to semi-erect. It is widely established that erect leaves allow the deeper penetration and more even distribution of light which results in crop photosynthesis [13]. The crop photosynthesis of an erect-leaved canopy is about 20% higher than that of the droopy-leaved canopy when the leaf area index is extremely high [15]. This model assumes that all the leaves are uniformly oriented at angles of 0° or 90° with respect to the horizontal plane. Hence, selection for the ideal ideotype (erect and semi-erect flag leaf) that can intercept light and has the potential for high grain yield will be effective in the collections. Breeders can select such ideotypes for further improvement.

Awning characteristic is another trait recorded among germplasms evaluated. Majority of the germplasms had absented of awns, 7 germplasms out of 100 had awns. Awning is considered a nuisance during milling by many farmers but it has been reported to play a role in preventing birds from sucking the milk-stage rice during grain filling. Breeders may therefore select the short-awned types as a compromise during cultivar development.

Panicles are also important parameters for plant description and evaluation, and are greatly influenced by the consumers' preference, 7 germplasms had recorded strong, 13 had exhibited clustered while, 70 germplasms had weak secondary branches, 2 germplasms had clustered and 21 germplasms had no secondary branching. Mwangi, et al. [14] found panicle exertion a conspicuous character for identification of the rice cultivars.

4.2 Quantitative Characters

Analysis of data revealed plant height mean value of 80.35cm and a wide range of 47.4-120.2cm. Plant height in rice is complex character and the end product of several genetically controlled factors called internodes [16]. Tall plant type is very typical of landrace germplasms which exceed in their capacity to support panicle growth by large stem reserve mobilization. Ali et al. [17] observed relatively greater range in plant height than the other characters. The smallest plant height was recorded for accession BRI DHC 62 and accession BAWKU-2 recorded the highest value. A break-through was realized in plant breeding with speedy development of semi dwarf cultivars with displayed characteristics of lodging resistance and nitrogen responsiveness in erect

leaves pattern. This was why Newmah [18] confirmed the success of the "Green Revolution" to be directly related to intensive use of semi dwarf varieties. This was true because the semi dwarf plant type was extensively utilized in the rice (*Oryza sativa*) cultivars throughout the world. However, depending on the part of the world with improvement in farmers' lives, there is a growing desire to combine desirable characteristics of tall varieties with yielding ability and a new type of architecture intermediate plant height as stated by Zafar et al. [19].

In breeding applications, according to Yu et al. [20], grain size is usually evaluated by the grain weight, which is positively correlated with several characters including grain length, grain width and grain thickness. It is a major determinant of grain weight, one of the three components (number of panicles per plant, number of grain per panicle and grain weight of grain yield). Although the preference for rice grain characteristics varies with consumer groups, long and slender grains are generally preferred and are good valuable attributes that could be exploited to improve the grain characteristics of local rice germplasms [21]. Similar variability was reported by Tamu [21] who studied twelve germplasms of coarse rice to check their yield performance in Kallar tract and reported highly significant variation for different traits. This variation in the grain yield might be due to the environment and genetic constitution of germplasms [22] or the correlation of grain yield per plant with various yield contributing characteristics such as; fertility of soil, flag leaf area, number of grains per panicle and grain weight which showed positive correlations.

The germplasms that produced more productive tillers will contribute to increased yield in a breeding program and could be selected as base germplasms for further improvement.

4.3 Cluster and Principal Component Analysis (PCA)

Cluster analysis based on the morphological data grouped the germplasms into two distinct clusters suggesting diversity among the assembled rice germplasms. The clustering of germplasms from different origin into different clusters suggests diversity of populations within a geographical origin and similarity of populations beyond geographical limits [Gana et al., 2013]. The cluster analysis of rice germplasms generated ten sub divisions that separates

majority of the germplasms. This finding agrees with results of Alemayehu and Becker [23] and Zada et al. [24]. The variability among the germplasms from diverse origin could be related primarily to their morphological differences and their uses or selection.

Divergence studies of morphological and reproductive traits using principal components analyses have been reported by different researchers [14,18,19,24-63]. The levels and patterns of genetic diversity observed among germplasms of rice in this study provides the basis to identify desirable parents to create segregating progenies with maximum genetic variability for further selection, conserve genetic resources of the plant and to introgress desirable genes from diverse germplasm into the available genetic base.

5. CONCLUSIONS AND RECOMMENDATIONS

5.1 Conclusions

The rice germplasm used in the present study displayed variability for most of the studied traits with the exception of ligule. Marked variation was observed for plant height, leaf length, secondary branches panicle, panicle length and days to 50% flowering. There was significant diversity among the rice germplasms evaluated. This should help strengthen the background necessary for the promotion and breeding of improved varieties of rice.

Characterization of crop germplasm through different morphological traits is an important step for assessment of its genetic potential. Our present finding shows great genetic potential of the studied germplasm. The promising germplasms identified during the current study have the potential to be used in future breeding programs for getting productive and quality results. During the current study for most of the qualitative and quantitative traits highly significant and positive differences were found. Among the germplasms studied, 21 out of the 100 were distant from the rest, and were selected to constitute a core collection for further improvement.

The studies also revealed a significant amount of information for breeding programmes interventions. Differences among germplasms were observed for characters such as flag leaf angle, awning, leaf blade pubescence, leaf blade

color, secondary branching type and basal leaf sheath color. These phenotypic traits could be explored for rice improvement. Cluster analysis performed established germplasms with regard on their morpho-agronomic characteristics. Regardless of the germplasm's response to N uptake, there were variations in their grain yield.

5.2 Recommendations

To obtain enough information on the 100 germplasms studied, I recommend that further evaluation of the morphological characterization at multi-locations should be conducted. In comparison with previous studies on landraces, the diversity revealed in this study is narrow. It is, therefore, recommended that rice breeding programs in Ghana should include new genetically unrelated genotypes in order to broaden the genetic base of Ghanaian rice germplasm. Based on the groupings from the cluster dendrogram, germplasms should be selected from each of the groups for molecular studies to gather additional information on their distinctiveness as expressed in the analysis. The germplasms should be analyzed for their phylogenetic relationship and variation based on molecular markers, to complement the morpho-agronomic findings. Future studies should be conducted to obtain complete information on the genetic diversity of the studied germplasms. Also, the studies should employ high number of SSR loci covering all the 12 chromosomes in rice. Biochemical characterization such as mineral and protein analysis should also be included.

ACKNOWLEDGEMENTS

My sincere appreciation goes to the Savanna Agricultural Research Institute for allowing us use their research fields for the study. We would like to thank farmers and research scientist for supporting us in obtaining germplasm for the study.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Muhammad S, Ali Khan S, Khurshid H, Iqbal J, Muhammad A, Saleem N et al.

- Characterization of Rice (*Oryza Sativa* L.) Germplasm Through Various Agro-Morphological Traits; 2015.
2. Linares OF. African rice (*Oryza glaberrima*): history and future potential. Proc Natl Acad Sci U S A. 2002;99(25):16360-5.
 3. Nwanze FK, Mohapatra S, Kormawa P, Keya S, Bruce-Oliver S. Rice development in sub-Saharan African; 2006.
 4. International Rice Research Institute. Rice almanac: source book for one of the most economic activities on Earth; 2013.
 5. MoFA. Analysis of incentives and disincentives for rice in Ghana; 2011.
 6. Oyelola BA. The Nigerian Statistical Association preconference workshop. Universidad Ib. 2012;20-1.
 7. Lingaiah N. Genetic variability, heritability and genetic advance in rice (*Oryza sativa* L.). Asian J Environ Sci. 2015;10(1): 110-2.
 8. Ahmed MSU, Bashir K, Shamsuddin A. Agro-morphological qualitative characterization of Jesso-Balam rice (*Oryza sativa* L.) accessions in Bangladesh. 2016;9.
 9. Singh AN, Singh MP, Singh DN, Mehto J. Cataloging of gora rice germplasm with respect to quantitative traits. Indian J Genet. 1996;56(2):191-5.
 10. Xing Y, Zhang Q. Genetic and molecular bases of rice yield. Annu Rev Plant Biol. 2010;61:421-42.
 11. Zogbo L. Genetic diversity in Liberian and Ghanaian rice (*Oryza sativa* L., *Oryza glaberrima* Steudei) germplasm using morphological and simple sequence repeat (Ssr) marker (master of philosophy). Ghana: Kwame Nkrumah University of Science and Technology; 2016.
 12. Swati J. Agro-morphological and molecular characterization of indigenous aromatic accessions of rice (*Oryza sativa* L.) (masters). Indira Gandhi Krishi Vishwavidyalaya. Raipur; 2017.
 13. Yoshida S. Fundamentals of rice crop science. International Rice Research Institute; 1981.
 14. Mwangi JK, Murage H, Ateka EM, Nyende AB. Agronomic diversity among rice (*Oryza sativa* L.) lines in a germplasm collection from Kenya. Sci Conf. Proc; 2013.
 15. Keulen HV, Goudriaan J, Seligman NG. Plant canopies: their growth, form and function. In: Russell G, Marshall B, Jarvis PG, editors. Modelling the effects of nitrogen on canopy development and crop growth. 1989;83-104.
 16. Cheema AA, Awan MA, Iqbal J. Improvement of plant height architecture in Basmati rice. Pak J Agric Res Pak. 1987.
 17. Ali SS, Jafri SJH, Khan TZ, Mahmood A, Butt MA. Heritability of yield and yield components of rice. Pak J Agric Res. 2008;16:89-91.
 18. Newmah JT. Morpho-agronomic characterization of newly developed upland rice germplasm (*Orzya sativa* L., *Orzya glaberrima* Steudel) from the Africa Rice Center and Ghana [doctoral dissertation]; 2010.
 19. Zafar NA, Aziz S, Masood S. Phenotypic for agro-morphological traits among landrace genotypes of rice (*Oryza sativa* L.) from Pakistan. Int J Agric Biol. 2004;2:335-33.
 20. Yu J, Hu S, Wang J, Wong GK, Li S, Liu B et al. A draft sequence of the rice genome (*Oryza sativa* L. ssp. indica). Science. 2002;296(5565):79-92.
 21. Tamu A. Grain quality characterisation of 87 rice (*Oryza sativa*) accessions in Ghana. KNUST; 2015.
 22. Jamal I, Khalil H, Abdul B, Khan S, Islam Z. Genetic variation for yield and yield components in rice. ARPN J Agric Biol Sci. 2009;4(6):60-4.
 23. Alemayehu N, Becker H. Genotypic diversity and patterns of variation in a germplasm material of Ethiopian mustard (*Brassica carinata* A. Braun). Genet Resour Crop Evol. 2002;49(6):573-82.
 24. Zada M, Zakir N, Rabbani MA, Shinwari ZK. Assessment of genetic variation in Ethiopian mustard (*Brassica carinata* A. Braun) germplasm using multivariate techniques. Int J Agric Biol; 2013.
 25. Africa Rice Center. Nerica: the new rice for Africa-a compendium; 2007.
 26. Ariyo QJ, Odulaja A. Numerical analysis of variation among accessions of Okra [*Abelmoschus esculentus* (L.) Moench], Malvaceae. Ann Bot. 1991;67(6):527-31.
 27. Ashfaq M, Saleem Haider M, Ali A, Ali M, Hanif S, Mubashar U. Screening of diverse germplasms for genetic studies of drought tolerance in rice (*Oryza sativa* L.). Caryologia. 2013.
 28. Bioversity International, IRRI W. Descriptors for wild and cultivated rice (*Oryza* spp.). Rome, Italy: Bioversity International; Los Baños, Philippines: International Rice Research Institute;

- Africa Rice Center, Cotonou, Benin: WARDA; 2007.
29. Calpe C. RICE IN WORLD TRADE, Status of the world rice market-Part II. Thailand; 2002.
 30. Das PK, Charaborty S, Barman B, Sarmah KK. Genetic variation for harvest index, grain yield and yield components in bore rice. 2001;38(3&4):149-50.
 31. De Candolle A. Origin of cultivated plants. London; 1886.
 32. Dzomeku IK, Dogbe W, Agawu ET. Response of NERICA rice varieties to weed interference in the guinea savannah upland. J Agron. 2007:262-9.
 33. Fageria NK, Slaton NA, Balige VC. Nutrient management for improving lowland rice productivity and sustainability; 2003.
 34. Gana AS, Shaba SZ, Tsado EK. Principal component analysis of morphological traits in thirty-nine accessions of rice (*Oryza sativa*) grown in a rainfed lowland ecology of Nigeria. J Plant Breed Crop Sci. 2013;5:120-6.
 35. Global food security response Ghana rice study. Vol. 56; 2009. Micro report.
 36. Gregory PJ, Ingram JS, Kobayash T. Rice production and Global Change. Glob Environ Res. 2000;2:71-7.
 37. Hasib KM. Genetic variability, interrelations and path analysis for panicle characters in scented rice. Crop Res J Hissar. 2005;30(1):37-9.
 38. Jones PG, Sawkins MC, Moass BL, Kerridge PC. GIs and Genetic Diversity-Case Studies in Stylosanthes;1998.
 39. Kehinde AO, Sylvester OO, Christopher JO, Sunday GA, Francis N, Olupomi A et al. Influence of legume/rice sequence and nitrogen on NERICA rice in rainfed upland and lowland ecologies. Global science books; 2013.
 40. Germplasm characterization and evaluation. J Plant Breed Crop Sci. 4:87-93.
 41. Mall AK, abu JDP, Babu GS. Estimation of genetic variability in rice. J Maharashtra agric Univ. 2005;30(2):166-8.
 42. Medhi K, Talukdar P, Barua PK, Baruah I. Extent of genetic variation in indigenous scented rice varieties of Assam. Indian J Plant Genet Resour. 2004;17(1):27-9.
 43. Mishra LK, Sarawgi AK, Mishra RK. Genetic diversity for morphological and quality traits in rice (*Oryza sativa* L.). Adv Plant Sci. 2003;16(1):287-93.
 44. MoFA/IVRDP. SAR j. Production guide; 2005.
 45. Morris ML, Bellon MR. Participatory plant breeding research: opportunities and challenges for the international crop improvement system. Euphytica. 2004; 136(1):21-35.
 46. Nachimuthu VV, Robin S, Sudhaka D, Rajeshwari S, Raveendran S, Subramanian KS et al. Genotypic variation for micronutrient content in traditional and improved rice lines and its role in biofortification programme. Indian J Sci Technol. 2014;7(9):1414-25.
 47. National rice development strategy (NRDS) – draft. 2009;26.
 48. Ng NQ, Chang TT, Vaughan DA, Zuno-Alto VC, 1988. Africa Rice Diversity: Conservation and Prospect for Crop Improvement. Crop Genet Resour. Afr II: 213-227.
 49. Ogunbayo SA, Ojo DK, Guei RG, Oyelakin OO, Sanni KA. Phylogenetic diversity and relationships among 40 rice accessions using morphological and RAPDs techniques. Afr. Crop Sci. J. 2005; 13(2):117-23.
 50. Parikh M, Motiramani N, Rastogi N, Sharma B. Agro-morphological characterization and assessment of variability in aromatic rice germplasm. Bangladesh J Agric Res. 2012;37(1): 1-8.
 51. Parikh M, Rastogi NK, Sarawgi AK. Variability in grain quality traits of aromatic rice (*Oryza sativa* L.). Bangladesh J Agric Res. 2012;37(4):551-8.
 52. Qualset CO, Shands HL. Safeguarding the future of U.S. agriculture: the need to conserve threatened collections of crop diversity worldwide. Genetic conservation program, Univ, California. CA: Davis; 2005.
 53. Roy S, Banerjee A, Senapati BK, Sarkar G. Comparative analysis of agro-morphology, grain quality and aroma traits of traditional and Basmati type genotypes of rice (*Oryza sativa* L.). Plant Breed. 2012;131(4):486-92.
 54. Sasaki T. Rice genomics to understand rice plant as an assembly of genetic codes. Curr Sci. 2002;83:834-9.
 55. Sasaki T. Current status of and future prospects for genome analysis in rice. In:

- Molecular biology of rice. Tokyo: Springer-Verlag Publication; 1999.
56. Sharma MK, Bhuyan J. Genetic variability and divergence studies in ahurices (*Oryza sativa* L.) of Assam. *Adv Plant Sci.* 2004;17(1):323-8.
 57. Singh RK, Singh O. Genetic variation for Yield and quality characters in mutants of aromatic rice. *Ann Agric Res.* 2005; 26(3):406-10.
 58. Singh SP, Singhara GS, Parray CA, Bhat GN. Genetic variability and heritability in rice (*Oryza sativa* L.). *Environ Ecol.* 2005;23(3):549-51.
 59. Sinha SK, Tripathi AK, Bisen UK. Study of genetic variability and correlation coefficient analysis in midland landraces of rice. *Ann Agric Res.* 2004;25(1):1-3.
 60. Sneath H, Peter A, Sokal R, Robert T. Numerical taxonomy: the principles and practice of numerical classification; 1973.
 61. Tsunoda S. A Developmental analysis of yielding ability in field crops (in Japanese, English summary). Tokyo: Maruzen Publishing Co, Nihono-Gskujitdu-Shinkokai; 1964.
 62. Tuhina K, Hanafi MM, Yusop MR, Wong MY, Salleh FM, Ferdous J. Genetic Variation, Heritability, and Diversity Analysis of Upland Rice (*Oryza sativa* L.) Genotypes Based on Quantitative Traits. *BioMed. Res. Int.*;2005.
 63. Tyagi K, Kumar B, Ramesh B, Tomar A. Genetic variability and correlations for some seedlings and mature plant traits in 70 genotypes of rice. *Res Crops.* 2004;1:60-5.

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