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Genetic parameter estimates and diversity studies of upland rice (*Oryza sativa* L.) genotypes using agro-morphological markers

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Abstract

Dearth of well-articulated information on genetic parameter estimates and diversity of upland rice limits the genetic improvement of rice. This study assessed the genetic parameter estimates and genetic diversity among 40 rice accessions using 26 agro-morphological traits. The trial was conducted in 2020 at the Njala University experimental site using 5 × 8 triple lattice design. The agro-morphological traits were analyzed using various multivariate and genetic parameter estimate techniques. Classification based on qualitative and quantitative traits grouped the germplasm into ten and five distinct clusters, respectively. Genotypes Buttercup-ABC, Buttercup-RARC, Jewulay, NERICA L4, Ndomawai, Sewulie and Painipainie produced earliest days to heading (81.8–97.2 days) and maturity (111.2 – 120.7 days). Genotypes Jasmine (3.036 $t.ha^{-1}$), Rok 34 (3.238 $t.ha^{-1}$) and Parmoi (2.663 $t.ha^{-1}$) exhibited the highest grain yields. Principal component analysis (PCA) of qualitative traits exhibited four principal components (PCs) with eigenvalues ≥ 1.0 and cumulative variation of 68.04%, whilst the PCA of quantitative traits had five PCs accounting for 81.73% of the total genetic variation. The findings indicate the presence of enough variability that could be exploited for the genetic improvement of rice varieties and the studied traits can be used for selection. Leaf blade length and width, culm diameter at basal internode, culm length, days to 50% heading, flag leaf girth, panicle number per plant, grain yield, and 100 grain weight had high heritability and genetic advance indicating the presence of additive gene action. Findings are relevant for conservation, management, short term recommendation for release and genetic improvement of rice.

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Introduction

Rice (*Oryza sativa* L.) feeds over 50 percent of the world's population (Rasel *et al*., 2018). The crop is the staple food of Sierra Leone with an annual rice consumption estimated at 530,000 tons (Baggie *et al*., 2018). However, its production and productivity are far below the demand for rice resulting into high government expenditure on importation of about $144,078 annually (GoSL, 2017). The Global Hunger Index (GHI) of Sierra Leone is estimated at 38.3 scores, which falls within the 119 countries with highest GHI ranging from 35.0-49.9 scores (SLNSS, 2017). The low production and productivity of rice in many rice growing areas including Sierra Leone is partly due to the prevalence of low yielding varieties, declining soil fertility, and the influence by climate change involving changes in rainfall and temperature levels that impede its growth and yield (Li *et el*., 2015; Tripathi *et al*., 2016; Bebeley *et al*., 2021). Moreover, the dearth of well-articulated information on genetic parameter estimates and diversity studies of upland rice in Sierra Leone, limits the genetic improvement of the crop. The generation of adaptable varieties largely depends on the availability of desirable genetic variability for important traits (Pratap *et al*., 2014).

Rice germplasm is a rich reservoir of useful genes which researchers can rely on for expanding rice production (Singh *et al*., 2015). Rice contributes a minimum number of the large *ex situ* germplasm accessions in the world (Vanniarajan *et al*., 2012). Local varieties are well known as useful source of genetic diversity that could be utilized for the genetic improvement for yield and other desired traits (Vanniarajan *et al*., 2012; Bidhan, 2013; Singh *et al*., 2015). However, the agronomic performances of these varieties are often influenced by genetic, non-genetic and environmental factors (Rabara *et al*., 2014).

Genetic variability is the basis of plant breeding because crop improvement depends on the amount and direction of genetic association of the traits in the base population (Tuhina-Khatun *et al*., 2015; Aditya and Bhartiya, 2013). Genetic variability provides a wide range of genotypes for selection of parents with desired complimentary traits to develop new varieties (Pandey *et al*., 2009). Useful genetic variability is essential in crop improvement for the efficient utilization of germplasm resources and related crop species (Banumathy *et al*., 2010). Development of elite varieties with desired agronomic traits requires the existence of genetic variability and genetic variability is the key component of breeding programs for broadening the gene pool (North, 2013). Selection is effective when a significant amount of variability exists among the breeding lines (Sumanth *et al*., 2017). The existing genetic variability in genotypes is measured using genotypic and phenotypic coefficient of variation which is used to partition genetic and environmental variances (Onyia *et al*., 2017).

Estimates of the genetic parameters of quantitative traits, such as heritability and genetic advance, are important because they give an indication of the ability of a species to respond to selection and the potential of that species to evolve (Falconer and Mackay, 1996). Development of effective genetic evaluation and improvement programs requires knowledge of the genetic parameters for economic growth and reproduction traits. Heritability is used to assess the amount of genetic improvement that is transmitted to next generation (Dutta *et al*., 2013). Genetic advance denotes the degree of gain obtained in a character under a particular selection pressure (Ogunniyan, and Olakojo, 2014; Norman *et al*., 2021). Both heritability and genetic advance are more powerful in predicting genetic gain than using heritability estimates alone (Ogunbayo *et al*., 2014).

A wide dissimilarity has been reported among and within rice landraces that necessitate future improvement (Singh *et al*., 2015). In Sierra Leone, dearth of knowledge exists on the extent of genetic diversities among upland rice as well as the genetic parameter estimates of relevant traits.

Landraces thrive well in their local environment and are known to harbor valuable genetic traits for rice improvement (Vanniaraja *et al*., 2012). Thus, a good understanding of genetic diversity is important for crop management, crop improvement, selection of parental lines for hybridization or recommendation for short term release, detection of genome structure, and transfer of desirable traits to other plants (Varshney *et al.*, 2008; Sasaki, 2005). The selection decision of the germplasm determines the success of plant breeding program. The objectives of this study were (i) to determine genetic parameter estimates of upland rice genotypes; and (ii) to determine the extent of genetic diversity among rice genotypes using agro-morphological traits in Sierra Leone.

Materials and methods

Experimental site

A field trial was conducted at the experimental site of the School of Agriculture and Food Sciences, Njala campus during the first cropping season (rainy season) of 2020 under rain fed conditions. Njala is situated at an elevation of 54 m above sea level on 8°06′N latitude and 12°06′W longitude. The mean monthly air temperature ranged from 20.4°C to 33.8°C, and the mean monthly relative humidity was 83.9% (SLARI Weather Station, 2020).

Experimental material, layout, design and trial management

A total of 40 upland rice genotypes comprising six improved lines from Rokupr Agricultural Research Centre (RARC) and 34 accessions collected from various Agricultural Business Centers and Farmers fields were evaluated to determine the genetic diversity and genetic parameter estimates among 40 rice accessions using agro-morphological traits (Table 1). The experiment was laid out in a 5 × 8 alpha lattice design with three replications. Trial management was done based on recommended practices in the crop production guidelines for Sierra Leone (MAFFS/NARCC/IAR/RRS, 2005).

Data collection

A total of 26 agro-morphological traits were collected comprising nine qualitative and 17 quantitative traits (Table 2). The traits were collected based on the agro-morphological descriptor of rice described by Bioversity International, IRRI and WARDA (2007).

Table 1. Details of upland rice genotypes used in the study.

Variety	Status	Variety	Code
Kortiwai	Local	Nduuwai	Local
Jewulay	Local	Piralainkay	Local
Yorni	Local	Fillie/Keblei	Local
Gbengbeh	Local	Feant	Local
Kpenyei	Local	Mimie	Local
Jasmine	Improved	Nimisei	Local
Ngukpie	Local	Lokiando	Local
Faro 67	Local	Rok 34	Improved
Nerica L19	Improved	Pindie	Local
Buttikorhun	Local	Rokamp	Local
Bukundie	Local	Sanikui	Local
Mahawa	Local	Parmoi	Local
Faro 66	Local	Ndorgborlukpie	Local
Painipainie	Local	Mbagboi	Local
Ngiyema yakei	Local	Rok 3	Improved
Plakamp	Local	Butter cup (ABC)	Local
Butter cup (RARC)	Local	Gbotima	Local
Sewulie	Local	Nerica L4	Improved
Rice/Lac 23	Local	Rok 16	Improved
Ndomawai	Local	Pissabui.	Local

Table 2. Phenotypic traits measured in 40 rice genotypes.

SN	Trait/Descriptor	Trait acronym	Score code - descriptor state	Sample time/collection
	Qualitative traits			
1	Basal leaf sheath color	BLSC	1= Purple, 2=Light purple, 3=Green with purple lines, and 4=Green.	Late vegetative stage of growth
2	Leaf sheath anthocyanin color	LSAC	0=Absent, 3=Weak, 5=Medium, 7=Strong	Late vegetative stage of growth
3	Leaf blade attitude	LBA	1=Erect, 5=Horizontal, 7=Drooping	Late vegetative stage prior to heading
4	Culm anthocyanin color on nodes	CACN	0=Absent/No visible color, 1=Purple, 2=Light purple, 3=Purple lines	After flowering to near maturity
5	Flag leaf attitude	FLA	1=Erect, 3=Semi-erect, 5=Horizontal,	At anthesis on to time of maturity

SN	Trait/Descriptor	Trait acronym	Score code - descriptor state	Sample time/collection
			7=Descending,	
6	Awn distribution	AD	0=None (awn less), 1=Tip only, 2=Upper quarter only, 3=Upper half only, 4=Upper three-quarters only, 5=Whole length.	Flowering to maturity
7	Panicle attitude of main axis	PAMA	1=Upright, 2=Semi-upright, 3=Slightly drooping, 4=Strongly drooping	Near maturity
8	Panicle attitude of branches	PAB	1=Erect (compact panicle), 3=Semi-erect (semi-compact panicle), 5=Spreading (open panicle), 7=Horizontal, 9=Drooping,	Near maturity
9	Caryopsis/Grain shape	CGS	1=Round, 2=Semi-round, 3=Half spindle-shaped, 4=Spindle-shaped, 5=Long spindle-shaped.	After harvest
	Quantitative traits			
1	Culm diameter at basal internode (mm)	CBDI	direct measurement using veneer caliper	on 5 plants at late vegetative stage
2	Flag leaf length	FLL	direct measurement using meter rule	on 5 plants at late vegetative stage
3	Flag leaf width	FLW	direct measurement using meter rule	on 5 plants at late vegetative stage
4	Leaf length of blade	LLB	direct measurement using meter rule	on 5 plants at late vegetative stage
5	Leaf width of blade	LBW	direct measurement using meter rule	on 5 plants at late vegetative stage
6	Panicle number per plant	PNPP	direct measurement by counting	on 5 plants at late reproductive stage
7	Final Plant height	FPHT	direct measurement using meter rule	on 5 plants at late vegetative stage
8	Tiller number per plant	TNP	direct measurement by counting	on 5 plants at late vegetative stage
9	Awn length (mm)	AL	direct measurement using meter rule	on 5 plants at late reproductive stage
10	Panicle length of main axis	PLMA	direct measurement using meter rule	on 5 plants at late reproductive stage
11	One hundred grain weight	HGWT	direct measurement of 100 grains at 13% moisture content	determined after drying
12	Grain/caryopsis length (mm)	GCL	direct measurement using meter rule	on 5 grains per genotype
13	Seedling height (cm)	SHT	direct measurement using meter rule	on 5 plants at 1 MAP
14	Days to 50% heading (days)	DAYSEH	direct measurement by counting days to 50% heading	plot basis at heading
15	Days to maturity (days)	DAYSM	direct measurement by counting days to maturity	plot basis at maturity
16	Grain yield (t ha^{-1})	GYLD	direct measurement grains weighed at 13% moisture content	determined per plot after drying
17	Culm diameter (mm)	CD	direct measurement using veneer caliper	on 5 plants at late vegetative stage

Source: Bioversity International, IRRI and WARDA 2007.

Data analysis

The data collected were first subjected to a linear mixed model by residual maximum likelihood (REML) procedure (Patterson and Thompson, 1971) to estimate the variance parameters using the GenStat Statistical package version (12th edition, VSN international, Hemel Hempstead). From the variance component analysis different genetic parameters such as broad sense (H^2), genotypic coefficients of variation (GCV), phenotypic coefficient variation (PCV), expected genetic advance (GA) were determined. The GCV and PCV were determined following the formula described in Burton and Devane (1953) as: $\frac{\sqrt{\sigma^2 v}}{\bar{x}} \times 100$ where $\sigma^2 v$ is the respective variance for genetic and phenotypic component for the trait from the final model in REML analysis and $\bar{x}$ is the trait mean value. The GCV and PCV values were categorized using the technique proposed by Deshmukh *et al.* (1986) as follows: values <10% = low, values that are 10–20% = medium and values >20% = high.

Broad sense heritability was determined using a formula by Robinson *et al.* (1949): $H^2 = \frac{\sigma^2 g}{\sigma^2 p} \times 100$ where $\sigma^2 g$, and $\sigma^2 p$ are the total genetic and phenotypic variances, respectively. The H^2 values were considered as low for values that range from 0 – 30%, moderate for values that range from 30 – 60% and high for those >60% as described by Robinson *et al.* (1949).

The expected genetic advance (GA) was estimated based on the equation given by Shukla *et al.* (2006) as: GA = K×H^2×σp, where, K is the selection differential which is 2.06 at 5% intensity, H^2 is heritability due to total genetic effect (broad-sense) and σp is the phenotypic standard deviation. The GA values were classified as low for values <10%, moderate for values ranging from 10–20% and high for values >20% as described by Shukla *et al.* (2006). The 26 agro-morphological data were subjected to principal component (PCA) and hierarchical cluster analysis (HCA). The PCA analysis was done to remove highly correlated traits that provide redundant information in the dataset.

The PCA was performed on correlation matrix option as units of measurement of the individual traits in the dataset differ (Granati *et al.*, 2003). The principal components that had eigenvalue > 1.0 according to the Kaiser criterion (Kaiser, 1960) were retained as sufficient to explain the largest amount of variation possible in the dataset. The significance of trait contribution to the variation accounted by the retained principal component (PC) was based on the absolute eigenvector arbitrary cutoff value of 0.35 disregarding the signs (Richman, 1988).

Results

Genetic parameter estimates

The mean values, ranges and associated genetic parameter estimates for the measured traits are presented in Table 3. There were wide ranges of variability within the measured quantitative traits.

The estimated genetic variances of traits showed that the phenotypic coefficient of variation (PCV) was slightly higher than the genotypic coefficient of variation (GCV) values for all the traits (Table 3). Traits with high PCV were culm diameter at basal internode, flag leaf girth, final plant height, grain yield, one hundred grain weight, leaf blade width, panicle length, panicle number per plant, Seedling height and tiller number.

Traits with high GCV were flag leaf girth, grain yield, one hundred grain weight, leaf blade width, panicle number per plant, and tiller number.

Table 3. Mean, range, genotypic and phenotypic coefficient of variability, heritability and genetic advance of 17 quantitative traits measured in 40 genotypes of rice.

Trait	Mean	Min	Max	GCV (%)	PCV (%)	H_B (%)	GA
Culm diameter (mm)	3.82	2.89	4.64	13.17	18.67	49.73	19.13
Culm diameter at basal internode	6.75	4.87	8.56	16.73	20.71	65.27	27.85
Culm length (cm)	82.26	44.82	102.17	14.69	17.80	68.18	24.99
Days to 50% heading (days)	106.61	81.80	126.20	10.50	11.37	85.21	19.97
Days to maturity (days)	133.47	111.20	149.70	7.61	8.49	80.27	14.04
Flag leaf girth (cm)	1.91	1.27	3.17	21.42	23.93	80.10	39.49
Flag leaf length (cm)	31.27	23.34	38.48	12.80	17.70	52.32	19.08
Final plant height (cm)	86.81	65.14	103.01	13.17	22.08	35.57	16.18
Grain/caryopsis length (mm)	8.80	6.66	10.21	9.86	13.24	55.43	15.12
Grain yield (t ha^{-1})	1.91	1.12	3.24	26.99	29.76	82.24	50.42
Hundred grain weight (g)	5.58	3.40	8.22	20.83	23.66	77.54	37.78
Leaf blade length (cm)	45.89	28.61	59.23	14.40	17.21	69.97	24.81
Leaf blade width (cm)	1.34	0.64	1.80	21.60	25.07	74.22	38.33
Panicle length (cm)	23.61	20.09	31.49	11.70	22.14	27.93	12.74
Panicle number per plant	6.48	4.19	10.26	29.29	36.95	62.82	47.82
Seedling height (cm)	27.37	19.78	36.92	17.19	27.60	38.82	22.07
Tiller number per plant	8.48	4.88	12.74	28.53	38.73	54.28	43.30

Min- minimum, Max- maximum, GCV- genotypic coefficient of variation, PCV- phenotypic coefficient of variation, H_B- broad sense heritability, GA- genetic advance.

The broad sense heritability estimates ranged between 27.93% (panicle length) and 85.21% (days to 50% heading). Traits with high broad sense heritability were culm diameter at basal internode, culm length, days to 50% heading, days to maturity, flag leaf girth, grain yield, hundred grain weight, leaf blade length, leaf blade width and panicle number per plant (Table 3). Genetic advance (GA) ranged from 12.74% (panicle length) and 50.42% (grain yield). High GA values were exhibited for culm diameter at basal internode (27.85%), culm length (24.99%), flag leaf girth (39.49%), grain yield (50.42%), hundred grain weight (37.78%), leaf blade length (24.81%), leaf blade width (38.33%), panicle number per plant (47.82%), seedling height (22.07%) and tiller number (43.30%); whilst the remaining traits had moderate (10.0–20.0%) GA (Table 3). Culm diameter at basal internode, culm length, flag leaf girth, grain yield, hundred grain weight, leaf blade length, leaf blade width, panicle number per plant, seedling height and tiller number combined high braod sense hertibality and GA whilst panicle length combined low braod sense heritability (27.93%) and moderate GA (12.74%).

Genetic diversity using agro-morphological traits

Frequency distribution of accessions according to qualitative traits

Frequency distributions of the qualitative traits are presented in Figs. 1 and 2. Generally, genetic divergence was observed among the 40 rice accessions for nine qualitative traits evaluated. The results revealed that 47.5% of the accessions had erect leaf blade, 42.5% had horizontal leaf blade, 5.0% had drooping and 5.0% had semi-erect leaf blades (Fig. 1a). About 37.5% of the accessions had horizontal flag leaf attitude, 32.5% had semi-erect flag leaves, 25.0% had erect flag leaves and 5.0% had drooping flag leaves (Fig. 1b). The leaf sheath of 65.0% of the accessions exhibited no anthocyanin coloration, while 25.0%, 7.5% and 2.5% of the accessions had weak, medium and strong anthocyanin on their leaf sheaths (Fig. 1c). The basal leaf sheath of 62.5% of the accessions had green with purple lines, 32.5% had green, 2.5% was gold and 2.5% of the accessions had light purple basal leaf sheaths (Fig. 1d). The basal culm anthocyanin color of 42.5% of accessions exhibited light green, 30.0% had thick green, 12.5% light gold, 10.0% green and 5.0% gold (Fig. 1e).

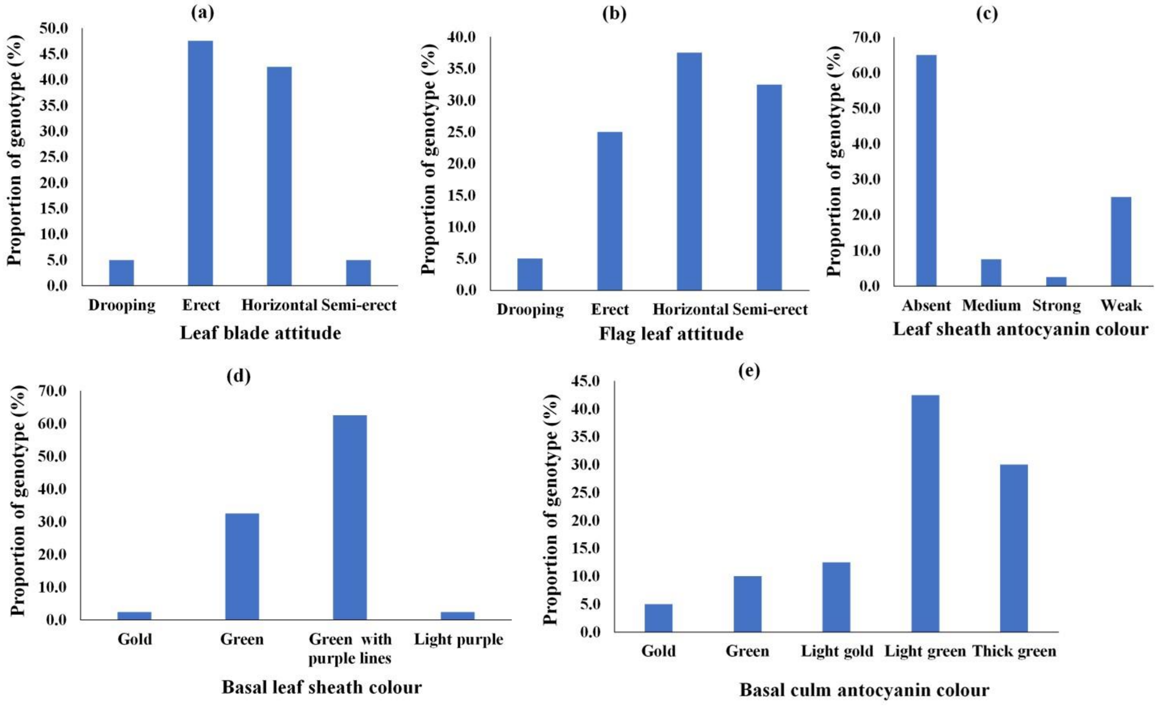

Fig. 1. Percent distribution of a) leaf blade attitude; b) flag leaf attitude; c) leaf sheath anthocyanin color; d) basal leaf sheath color; e) basal culm anthocyanin color among 40 genotypes of upland rice.

About 60.0% of the accessions exhibited drooping panicle attitude of main axis, 30.0% was slightly drooping, 7.5% was semi-upright and 2.5% genotypes had upright panicles of main axis (Fig. 2a).

The panicle attitude of branches of 85.0% of the accessions exhibited drooping type, 7.5% was semi-erect, 5.0% spreading type and 2.5% horizontal (Fig. 2b). About 50.0% of accessions were awnless, 30.0% had tip only, 7.5% had had upper quarter only, 5.0% had upper ¾ only, 5.0% had upper half only and 2.5% had whole length (Fig. 2c).

The caryopsis/grain shape of 47.5% of the accessions exhibited spindle shaped, 22.5% ½ spindle shaped, 10.0% long spindle shaped, 10.0% round shaped, and 10.0% semi-round shaped (Fig. 2d).

Principal component analysis of qualitative traits

The eigenvalues and percentage variations of the principal component analysis are presented in Table 4. Four principal components with eigenvalues $\geq$ 1.0 and total variation of 68.04% among the genotypes were identified. The first PC axis with eigenvalue of 2.583 accounted for 28.7% of the total variation where the second, third and the fourth PC axes with eigenvalues of 1.388, 1.152 and 1.001 accounted for 15.42%, 12.80% and 11.12% of the total variation, respectively. The fifth PC axis with eigenvalue of 0.976 accounted for 10.84% of the total variation. The first principal component with reference to its high factor loadings was associated with basal leaf sheet color, flag leaf attitude, leaf blade attitude, panicle attitude of branches and panicle attitude of main axis (Table 4).

The second PC was associated with awn distribution, leaf characteristics (basal leaf sheet color, panicle attitude of branches and leaf sheath anthocyanin color); the third PC was associated with awn distribution, culm anthocyanin color at node and caryopsis/grain shape; while the fourth PC was associated with traits related to grain characteristics (awn distribution and caryopsis/grain shape) and leaf traits (leaf sheath anthocyanin color and leaf blade attitude).

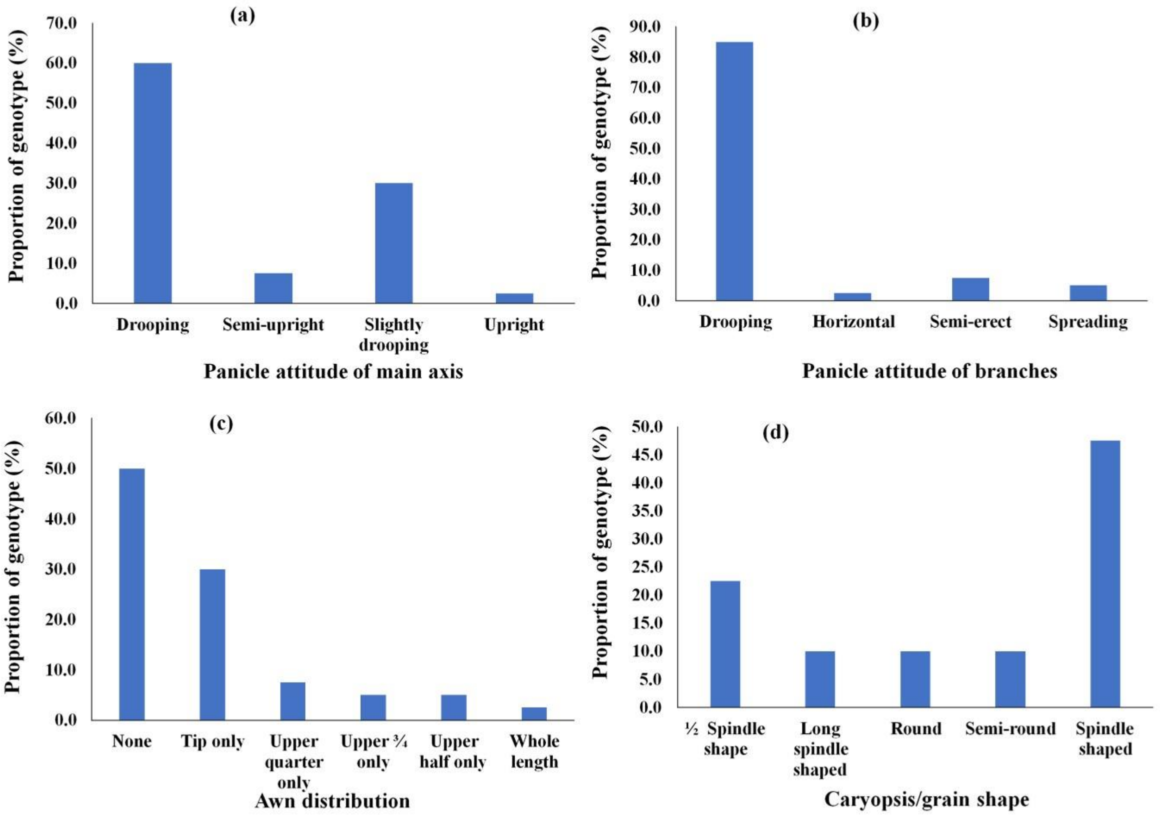

Fig. 2. Percent distribution of a) panicle attitude of main axis; b) panicle attitude of branches; c) awn distribution; d) caryopsis/grain shape among 40 genotypes of upland rice.

Table 4. Principal component analysis, eigenvalues and percentage variation of nine qualitative traits measured in 40 genotypes of rice.

Traits	PC1	PC2	PC3	PC4	PC5
Awn distribution	0.17	-0.41	-0.40	0.56	0.14
Basal leaf sheet color	0.37	0.52	-0.14	0.20	0.23
Culm anthocyanin color at node	-0.11	-0.13	-0.70	-0.26	-0.47
Caryopsis/grain shape	0.27	0.11	-0.46	-0.42	0.57
Flag leaf attitude	-0.41	0.10	-0.29	0.25	0.09
Leaf blade attitude	-0.36	-0.01	-0.01	0.36	0.44
Leaf sheath anthocyanin color	-0.25	-0.52	0.12	-0.40	0.42
Panicle attitude of branches	-0.37	0.49	-0.05	-0.20	0.07
Panicle attitude of main axis	-0.50	0.16	-0.10	0.05	-0.03
Eigenvalue	2.583	1.388	1.152	1.001	0.976
Proportion of variance (%)	28.7	15.42	12.8	11.12	10.84
Cumulative variance (%)	28.7	44.12	56.92	68.04	78.88

Values in bold represent significant traits in the various principal components.

Principal component analysis of quantitative traits

The principal component analysis of quantitative traits had five main principal components with eigenvalues ≥ 1.0 (Table 5). These five PCs accounted for 81.73% of the total variation among the rice genotypes. The first PC axis with eigenvalue of 5.956 accounted for 35.04% of the total variation where the second, third, fourth and the fifth PC axes with eigenvalues of 2.994, 2.569, 1.257 and 1.119 accounted for 17.61%, 15.11%, 7.39% and 6.58% of the total variation, respectively. The fifth PC axis with eigenvalue of 0.976 accounted for 10.84% of the total variation. The variable that significantly correlated with PC axis 1 is culm length (-35%). The variables that were significantly correlated with PC axis 2 are: grain yield (36%) and tiller number (39%). The variables that significantly related to PC axis 3 are: days to 50% heading (- 41%), days to maturity (-44%) and seedling height (37%). The variables that significantly correlated with PC axis 4 are: flag leaf length (53%), grain/caryopsis length (44%), and hundred grain weight (-43%). The variables that significantly related to PC axis 5 are: grain/caryopsis length (-0.65%) and leaf blade length (39%) (Table 5).

Table 5. Principal component analysis, eigenvalues and percentage variation of 17 quantitative traits measured in 40 genotypes of rice.

Traits	PC1	PC2	PC3	PC4	PC5	PC6
Culm diameter	-0.28	-0.25	-0.26	0.04	0.08	-0.16
Culm diameter at basal internode	-0.31	-0.20	-0.27	-0.03	0.02	-0.14
Culm length	-0.35	0.06	0.05	0.01	0.13	-0.07
Days to 50% heading	-0.14	0.32	-0.41	0.15	0.22	-0.01
Days to maturity	-0.09	0.31	-0.44	0.07	0.25	-0.12
Flag leaf girth	-0.24	-0.30	-0.04	0.26	-0.25	0.26
Flag leaf length	-0.18	-0.18	0.29	0.53	0.14	0.13
Final plant height	-0.27	-0.14	0.34	-0.03	0.06	-0.10
Grain/caryopsis length	-0.05	0.04	-0.22	0.44	-0.65	-0.33
Grain yield	-0.22	0.36	0.11	-0.24	-0.16	-0.17
Hundred grain weight	-0.26	-0.09	-0.06	-0.43	-0.31	-0.15
Leaf blade length	-0.30	-0.08	0.02	0.15	0.39	-0.20
Leaf blade width	-0.30	-0.27	-0.04	-0.26	0.04	0.08
Panicle length	-0.29	0.15	-0.09	-0.18	-0.07	0.63
Panicle number per plant	-0.24	0.33	0.01	0.15	-0.24	0.38
Seedling height	-0.23	0.21	0.37	-0.09	-0.10	-0.32
Tiller number	-0.15	0.39	0.29	0.19	0.10	-0.05
Eigenvalue	5.956	2.994	2.569	1.257	1.119	0.708
Proportion of variance (%)	35.04	17.61	15.11	7.39	6.58	4.16
Cumulative variance (%)	35.04	52.65	67.76	75.15	81.73	85.89

Values in bold represent significant traits in the various principal components.

The principal component analysis showed that all the PCs of the qualitative and quantitative trait sets had negative and positive coefficients, implying the differential expressions and contributions of these traits to the genetic variations in the rice accessions. The genetic divergence among the 40 upland rice accessions was accounted for by few eigenvectors with cumulative variance of 68.04% and 81.73%, respectively.

Genetic relationship among 40 rice genotypes using nine qualitative traits

The hierarchical cluster analysis based on nine qualitative traits grouped the 40 rice genotypes into 10 distinct clusters at 0.80 similarities (Fig. 3). The genetic similarity for the nine qualitative traits ranged from 0.4 to 1.0. Cluster 1 comprised of five members with drooping panicle attitude of branches. Cluster 2 consisted of one member (Yorni). Cluster 3 had six members with drooping panicle attitude of main axis and branches, and horizontal leaf blade attitude. Cluster 4 constituted five members with drooping panicle attitude of main axis and branches, and horizontal flag leaf attitude. Cluster 5 exhibited five members with green basal leaf sheath, erect leaf blade and flag leaf attitudes and no anthocyanin on leaf sheath. Cluster 6 comprised of two members with drooping panicle branches, awnless caryopsis, erect and horizontal leaf blade and flag leaf attitudes, respectively. Cluster 7 had eight members with drooping panicle branches and erect leaf blade.

Cluster 8 consisted of two members (Kpenyei and Buttikorhun) with drooping panicle branches, gold basal culm, and horizontal leaf blade and flag leaves. Cluster 9 had two members (Ngukpie and Sanikui) with semi-erect panicle branches, ½ spindle shaped caryopsis, green with purple lines leaf sheath and weak anthocyanin on leaf sheath. Cluster 10 comprised of two members (Ngiyema yakei and Rok 16) with spindle shaped caryopsis, leaf sheath lacking anthocyanin, and erect leaf blade and flag leaf attitudes (Fig. 3).

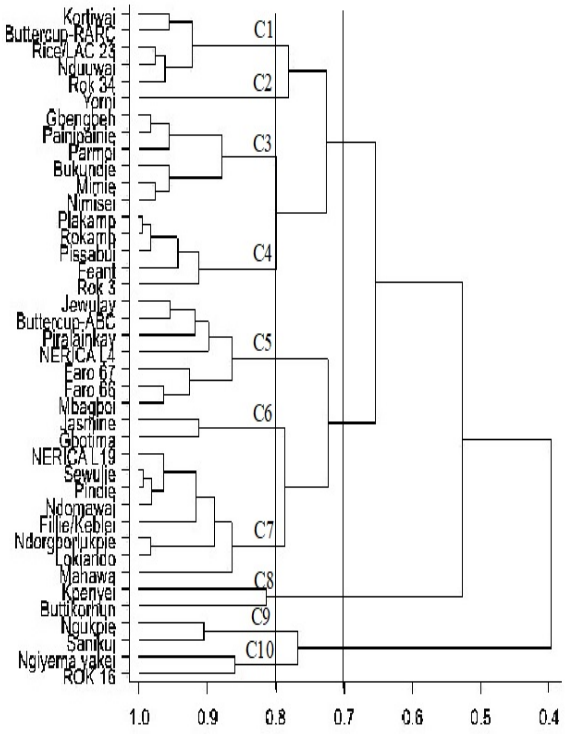

Fig. 3. Dendrogram showing relationships among 40 genotypes of rice classified by UPGMA method using nine qualitative agro-morphological traits.

Genetic relationship among 40 rice genotypes using 17 quantitative traits

Hierarchical cluster analysis of quantitative traits grouped studied genotypes into five clusters almost with the same characteristics as a function of the variables (Fig. 4). The genetic similarity for the 17 quantitative traits ranged from 0.5 to 1.0. At genetic similarity coefficient of 0.8, five clusters were formed. Cluster 1 comprises 14 genotypes, whilst clusters 2, 3, 4 and 5 consist of seven, twelve, two, and five genotypes, respectively.

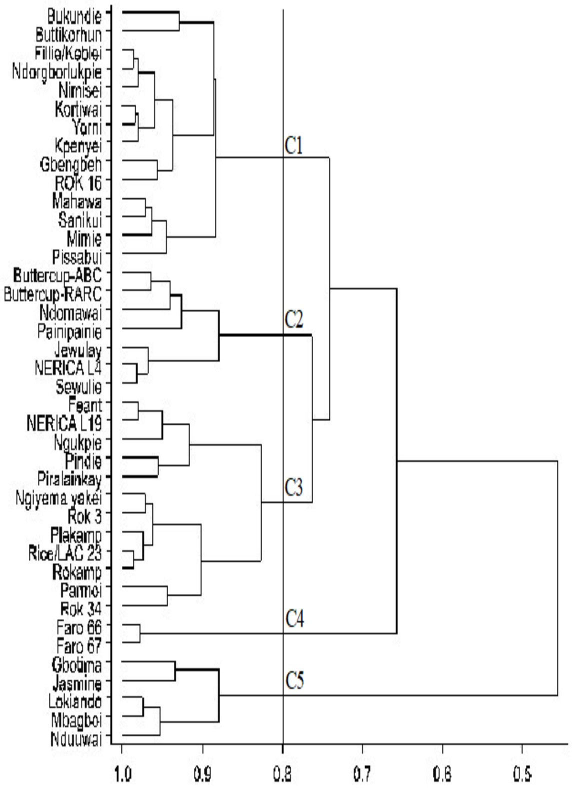

Fig. 4. Dendrogram showing relationships among 40 genotypes of rice classified by UPGMA method using 17 quantitative agro-morphological traits.

Members of cluster 2 (Buttercup-ABC, Buttercup-RARC, Jewulay, NERICA L4, Ndomawai, Sewulie and Painipainie) exhibited the earliest days to heading (81.8 – 97.2 days) and matured earliest (111.2 – 120.7 days) relative to varieties in other clusters. Members of cluster 4 had similar plant height, days to maturity, days to 50% heading, culm diameter, leaf blade length, tiller number, and grain/caryopsis length. Moreover, genotypes Jasmine (3.036 t.ha^{-1}), Rok 34 (3.238 t.ha^{-1}), and Parmoi (2.663 t.ha^{-1}) exhibited the highest grain yields. Rok 34 and Parmoi are members of cluster 3, whilst Jasmine is a member of cluster 5.

Discussion

Knowledge of genetic diversity and genetic parameter estimates is prerequisite for crop improvement program targeted at developing superior recombinants. Our findings showed the presence of useful variation in the rice germplasm that could be exploited through direct selection or population improvement scheme. The slightly higher PCV values relative to the GCV indicate that the traits were less sensitive to environmental effects. In this study, the PCV and GCV values were classified as low (<10.0%), moderate (10.0–20.0%), and high (>20.0%) as suggested by Deshmukh *et al.* (1986). The high broad sense heritability of some of the measured traits are similar with those noted by previous researchers. Pandey *et al.* (2009) noted high broad sense heritability among 40 rice varieties for plant height (99.8%), biological yield (99.6%), harvest index (99%), number of panicles per hills (98.5%), number of spikelets per panicle (98.3%) and grain yield (98.11%).

The variations in some of the traits could be due to the different rice genotypes and /or environmental factors. The traits that had both high heritability and high genetic advance imply that they are under the control of additive genes, whilst those with high heritability and low genetic advance are under the control of non-additive genes. Moreover, traits with high heritability and high genetic advance indicate that they can be improved through direct selection. These findings are partly consistent with Sedeek *et al.* (2009) who found both high heritability and high genetic advance for days to heading, flag leaf area, number of filled grains per panicle, and grain yield per plant. Johnson *et al.* (1955) suggested the relevance of combining heritability with a genetic advance for efficient predictability of response to selection.

The first PC of the quantitative traits was more associated with culm length, PC 2 with tillering and grain yield traits, PC 3 more with heading and maturity traits, whilst PC 4 and PC 5 were more associated with leaf and grain measurement traits. The PCA results also indicated a trend of higher genetic values of some traits with significant strong positive or negative contributions to the observed genetic variability compared to the contributions of those with weak correlation coefficients. Similar patterns of genetic variations in rice have also been reported using principal component analysis. Lasalita-Zapico *et al.* (2010) estimated about 82.7% of cumulative variation among 32 upland rice varieties, of which, PC 1 and PC 2 accounted for 66.9% and 15.87%, respectively. Caldo *et al.* (1996) found the first 10 PCs accounting for 67.0% of cumulative variation. The clustering patterns using UPGMA dendrograms exemplified the genetic relationships among the various upland rice accessions studied. The rice genotypes were grouped based on key agro-morphological traits identified in the principal component analysis. Traits that contributed highest to distinguishing genotypes are among key traits often considered relevant for selection of rice varieties and for the genetic improvement of the crop. Genotypes in the same cluster represent members of one heterotic group. These findings are consistent with Veasey *et al.* (2008) and Ahmadikhah *et al.* (2008), who also found distinct heterotic groups in their rice germplasm characterization studies using agro-morphological traits. Thus, genotypes with distant clusters could be utilized in rice hybridization programs to obtain higher heterotic responses (Latif *et al.*, 2011).

Conclusions

Fourty accessions of upland rice were clustered into ten and five main groups based on qualitative and quantitative traits, respectively. The studied upland rice accessions possessed useful variability and complimentary genes for rice population improvement. Genotypes Jasmine (3.036 $t.ha^{-1}$), Rok 34 (3.238 $t.ha^{-1}$), and Parmoi (2.663 $t.ha^{-1}$) were identified with high grain yields. Traits identified with both high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were flag leaf girth, grain yield, one hundred grain weight, leaf blade width, panicle number per plant, and tiller number. Trait heritability and genetic advance are important genetic parameter estimates useful for identification and selection of elite varieties rice in a rice breeding program. Traits that combined high broad sense hertibality and genetic advance were culm diameter at basal internode, seedling height, leaf blade width, culm length, flag leaf girth, leaf blade length, grain yield, hundred grain weight, panicle number per plant, and tiller number.

The high level of genetic variability and good trait values of the rice accessions would serve as useful resources for the genetic conservation, management, short term recommendation for release and genetic improvement of the crop.

The various groups of the rice accessions can be useful as gene pools that can be adopted for rice breeding involving crosses. The rice accessions possess useful genetic estimates for the measured quantitative traits that could be exploited through direct selection or population improvement scheme. Robust molecular markers such as SNPs, SSRs, etc should be exploited in future studies to further discriminate the diversity in the rice germplasm.

Author contributions

PEN and MG conceived and designed the experiment. AUB, PEN and MG performed the experiment. PEN analyzed and interpreted the data. AUB, PEN and MG wrote the manuscript. All authors reviewed and approved the manuscript.

Declaration of competing interest

The authors declare no conflict of interest.

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