Original Research Article

Genetic Diversity of Selected Upland Rice Genotypes (*Oryza sativa* L.) for Grain Yield and Related Traits.

ABSTRACT

Seventy-seven upland rice genotypes including popular cultivars in Nigeria and introduced varieties selected from across rice-growing regions of the world were evaluated under optimal upland ecology. These genotypes were characterised for 10 traits and the quantitative data subjected to Pearson correlation matrix, Principal Component Analysis and cluster analysis to determine the level of diversity and degree of association existing between grain yield and its related component traits. Yield and most related component traits exhibited higher PCV compared to growth parameters. The yield had the highest PCV (41.72%) while all other parameters had low to moderate GCV. Genetic Advance (GA) ranged from 9.88% for plant height at maturity to 41.08% for yield. High heritability estimates were recorded for 1000 grain weight (88.71%), days to 50% flowering (86.67%) and days to 85% maturity (71.98%). Furthermore, grain yield showed significant positive correlation with days to 50% flowering and number of panicles m^{-2}. Three cluster groups were obtained based on the UPGMA and the first three principal components explained about 64.55% of the total variation among the 10 characters. The PCA results suggests that characters such as grain yield, days to flowering, leaf area and plant height at maturity were the principal discriminatory traits for this rice germplasm indicating that selection in favour of these traits might be effective in this population and environment.

Keywords: Cluster analysis; Germplasm; Heritability; secondary traits; UPGMA

1. INTRODUCTION

Rice (*Oryza sativa* L.) is an important cereal grown and consumed the world over to meet the daily calorie needs of ever increasing world population mainly in Asia and Sub-Saharan Africa. This important cereal is cultivated and consumed across Nigeria but its production is characterized by poor yields resulting from use of low farm inputs and cultivation of unimproved cultivars with poor yield potentials. Germplasm characterization and evaluation is a basic pre-requisite for a successful breeding programme and can lead to the identification of traits with high heritability and appreciable association with yield [1,2]. Agro-morphological characterization of germplasm is fundamental to provide the preliminary information for planning and initiating a breeding programme [3]. The amount of genetic variability present in a germplasm is also essential to crop improvement and can be exploited by plant breeders for yield improvement [4]. Until germplasm collections have been properly evaluated and their attributes known to breeders, they have little practical use in crop genetic improvement. Thus, understanding the genetic variability among genotypes in a germplasm collection serves as a guide for parental selection aimed at hybridization to introgress desired traits into new cultivars [5]. For selection to be effective there must be ample heritable genetic variability within the gene pool under evaluation.

Traditional rice genotypes that still exist in the Nigeria upland rice ecosystems can provide the genetic diversity needed to develop improved high yielding rice varieties having farmers' preferred traits. Challenges involved with the improvement of upland rice landraces can be mitigated via the introduction of new genes from other rice genotypes, thereby creating wide genetic variation for selection of promising progenies with good adaptation and agronomic traits. Indirect selection for yield based on yield components is possible if the traits associated with yield are highly heritable and positively correlated with yield. Heritability, either in the broad sense (H^2) or narrow sense (h^2), of a trait is important in determining its response to selection. This helps to estimate the degree of transmissibility of selected traits of interest to progenies during a breeding programme [6]. Genetic advance has a direct relationship between heritability and response to selection. High genetic advance with high heritability estimates offer the most effective conditions for breeders to quickly select and advance desired traits in a population [7]. Rice plant is known to exhibit great morphological variation, particularly in vegetative and reproductive traits such as plant height, leaf length, days to flowering, yield and associated yield components [8]. The current study assessed the level of diversity and degree of association existing between grain yield and its related component traits to identify potential suitable traits that might contribute to future upland rice genetic improvement programmes.

2. MATERIALS AND METHODS

2.1 Genetic materials and planting

The plant materials included 77 genotypes from diverse genetic backgrounds and origins (Table 1). The experiment was carried out at AfricaRice Centre, Ibadan, Nigeria during 2015 planting season. Prior to sowing, seeds were incubated in the oven at 37 °C for 12 h to break seed dormancy. Three seeds per hill were sown directly and thinned to two seedlings 21 days after sowing (DAS) at a spacing of 0.2 m within and between rows. The design was 11 x 7 alpha lattice with four replications with plot area of 1 m^2 having 25 stands per plot. A pre-drilling base application of 200 kg ha^{-1} of NPK (15-15-15) was made, followed by a total of 100 kg ha^{-1} of urea in two applications of 35 kg ha^{-1} at 21 days after seeding and 65 kg ha^{-1} at the panicle initiation. Two manual weeding were carried out.

[Table 1 near here]

2.2 Data Collection and Statistical Analyses

Twelve uniform plants excluding the border rows in each plot were measured for plant height at maturity, number of panicles per plant, tiller number at 60 days after sowing, average leaf area and number of panicles per meter square. Each plot was recorded for heading date when 50% of the plants in the plot were headed and days to 85% maturity according to the IRRI standard evaluation system (SES). Grain yield per plot was sampled by cutting the matured plants from the bottom (right above the soil surface). Plants sampled from each plot were put into a paper bag and air dried inside the glass house for 5-7days. The dried samples were then threshed and measured for total grain yield per plot and 1000 grain weight.

The data collected were subjected to statistical analysis using [9] and R statistical packages. The plot means for each character were subjected to analysis of variance using the method of [10]. Yield and its components were used to estimate the genotypic and phenotypic variances according to [11]. The variance components were used to compute the genotypic coefficient of variation (GCV), the phenotypic coefficient of variation (PCV), broad sense heritability and expected a genetic advance.

The genotypic variance (Vg), environmental variance (Ve), genotypic (GCV) and phenotypic (PCV) coefficient of variation components were computed using the formulae suggested by Burton (1952) as follows:

Genotypic variance: $Vg = \frac{\mathrm{MSG - MSE}}{r}$

Where MSG is the mean square of accessions, MSE is mean square of error, and *r* is number of replications.

Phenotypic variance: $Vp = Vg + Ve$

where Vg is the genotypic variance and Ve is the mean squares of error.

Genotypic coefficient of variation (GCV): GCV % = $\frac{\sqrt{Vg}}{\bar{x}}$ x 100

Phenotypic coefficient of variation (PCV): PCV % = $\frac{\sqrt{Vp}}{\bar{x}}$ x 100

Where, GCV% = Genotypic coefficient of variation; Vg = Genotypic variance; PCV % = Phenotypic Coefficient of variation; Vp = Genotypic variance;

Heritability (Broad sense): $H_b^2 = \frac{Vg}{Vp}$

Expected genetic advance (GA): GA% = K x Vp x h^2_B x 100

Where, K = 2.06 at 5% selection intensity for trait; Vp = Phenotypic variance for trait; h^2_B = Broad Sense heritability of the trait; Genetic advance as %age of mean is calculated as,

GA% = K x $\frac{\sqrt{Vp}}{\bar{x}}$ x h^2_B x 100

Pearson's correlation coefficients were computed to evaluate the relationship among the observed variables and the data analyzed using Unweighted Paired Group Method based Centroids (UPGMC). Genetic relationships were also calculated and a dendrogram derived to show the morphological relatedness of the upland rice cultivars under study. Principal component analysis was employed to reveal the underlying sources of morphological variability within the germplasm.

3. RESULTS AND DISCUSSION

3.1 PCV, GCV, Genetic Advance and Heritability of Estimated Traits

The mean performance of 77 upland rice genotypes based on 10 yield related traits indicated significant variability among the rice germplasm evaluated with respect to most of the measured characters (Table 2). Yield and most of its component traits exhibited higher phenotypic coefficient of variation (PCV) compared to growth parameters such as plant height and leaf area.

Low to moderate PCV was recorded for most of the traits except for yield (Table 2). Yield had the highest PCV (41.72%) while number of panicles per plant had the lowest PCV. Most of the characters in this experiment had low to moderate genotypic coefficient of variation (GCV). The GCV ranged from 6.19% for days to maturity to 28.85% for yield. Phenotypic coefficient of variation was higher than the GCV for all the observed parameters. The high phenotypic and genotypic coefficient of variation observed for grain yield indicates the existence of sufficient variation among the genotypes for potential yield improvement through selection. This observation is consistent with [17,18] but contradicts [19] who reported low PCV and GCV for grain yield among 15 rice genotypes evaluated in eastern Nigeria. The extent of environmental influence on a particular trait is determined by the magnitude of the difference between PCV and GCV. Slight differences indicate minimum influence of environmental effects and a higher role of genetic effects in the expression of the given trait under consideration. The predominant role of the environment in the expression of this trait might be attributed to the wide differences observed between PCV and GCV. Moderate to low phenotypic and genotypic variances were also exhibited for days to 50% flowering, 1000 seed weight and days to 85% maturity. These results contradict [17] who reported high phenotypic and genotypic variances for 50% flowering and 1000 seed weight. Minimum differences were recorded between GCV and PCV values for 1000 grain weight, days to flowering and number of panicles, indicating insignificant influence of the environment. This is in accordance with [20,19] that reported the genetic control of days to flowering and number of panicles in rice. Heritability estimates defined as the proportion of observed variation that can be attributed to genetic variances are known to be unique to the given population under study and the growing environment [12]. The highest level of heritability (88.71%) was seen for 1000 grain weight while lowest heritability estimates were observed for number of tillers at 60 DAS (15.16%). High heritability in the broad sense recorded for 1000 seed weight, days to 50% flowering (86.67%), days to 85% maturity (71.98%), and number of panicles (63.89%) shows that these traits can be easily selected phenotypically in the field during a breeding programme. Genetic Advance (GA) ranged from 9.88% for plant height at maturity to 41.08% for yield. The average of GA values in growth traits was lower than the average of GA values for yield and yield components (Table 2). Previous studies [8] had reported high heritability and genetic advance for yield, days to flowering, and flag leaf length-to-width ratio in rice. Moderate to high estimates of heritability, GA and GCV observed for some of the traits such as yield, 1000 seed weight and number of panicles could be explained by additive gene action. This suggests that genetic improvement of these traits can be achieved through mass selection [21]. Traits such as plant height at maturity, tiller number at 60 DAS, number of filled grains and number of panicles, which exhibited low heritability estimates, are likely to be more influenced by the environment and selection must be based on progeny tests or in later generations of selfing. High heritability and genetic advance for grain yield had earlier been reported [13,14,15]. Previous studies [16] suggested that high broad sense heritability; PCV and GCV for yield and yield related traits are good predictors for high grain yield in crops.

[Table 2 near here]

3.2 Genetic similarity among evaluated rice genotypes.

The hierarchical cluster analysis based on 10 agronomic characters is presented in Fig. 1. Three major groups were observed among 77 upland rice genotypes based on multivariate analysis. Cluster 1 contained 28 genotypes or 36.36% of all the genotypes. Cluster 3 was made up of 26 genotypes (33.77%) while cluster 2, having 23 genotypes, was the smallest cluster. As previous study had reported [24], clustering of the genotypes showed minimum relationship between geographic regions and diversity. Selecting parental materials from the diverse clustered groups identified in this study for hybridization might result in segregants with best combinations of superior alleles for various traits such as high yield potential, increased number of panicles and earliness. For instance, high yielding varieties such as IR 68704-145-1-1-B, CIRAD 3941 (cluster 1) and ITA 301 (cluster 2) could be deployed to significantly improve the grain yield of low yielding cultivars like Ebonyi local, Igbemo Red, Igbemo White, Ofada 3 and Ofada 1 grouped in clusters 1 and 3. Since number of panicles per meter square positively associated with grain yield, ITA 315 and ITA 117 from cluster 3 with the highest mean for this trait might be a suitable parents for breeding programs aimed at increasing yield through indirect selection for increased number of panicles.

[Figure 1 near here]

3.3 Association between Traits

The relationships existing between 10 quantitative traits represented as correlation coefficients are presented in Table 3. Grain yield was positively correlated with days to 50% flowering (r= 0.22), days to maturity (r= 0.21), number of panicles m^{-2} (r= 0.25) and number of tillers at 60 DAS (r= 0.13). Positive associations were also observed between days to maturity, leaf area (r=0.18), and filled grain (r= 0.17), while plant height showed positive significant correlation with 1000SW (r= 0.22) and filled grain (r= 0.27). Thousand grain weight (1000GW) also exhibited negative association with number of days to flowering (r= -0.26) and number of panicle m^{-2} (r= -0.25) and had no association with plant yield (Table 3). The degree of association among traits is an important factor when dealing with a complex character such as yield that is controlled by many genes and highly influenced by the environment [10]. The positive significant phenotypic correlations between yield and some of the traits are indications that selection in favour of these traits can lead to positive indirect selection for high grain yield [17]. The negative correlation observed between yield and some traits in this experiment suggests that indirect selection of these traits for improved grain yield might not be successful. Positive but low correlations between yield per meter square and days to flowering, days to 85% maturity and number of panicles per meter square shows that selection in favour of these parameters might lead to improved grain yield. Previous studies [19] reported high positive correlations between grain yield and all the quantitative characters studied except for days to booting, days to 50% heading and unproductive tiller numbers among 15 rice genotypes in Nigeria. Also, high positive correlations were reported for days to 50% flowering and plant height at maturity; number of grains per panicle and 1000 grain weight among 123 accessions of *Oryza glaberrima* and *O. sativa* [23].

[Table 3 near here]

3.4 Principle Components and Scatter Plot of Genotypes

The principal components analysis (PCA) partly confirmed the results from cluster analysis. The first three PCA accounted for 64.6% of total variation for which PC1 showed 27.6% of the variation, PC2 and PC3 explained 24.93% and 12.02% of total variation, respectively (Table 3). Grain yield, days to flowering and days to maturity had significant contributions to PC1 with days to maturity having the highest weight. Leaf area, plant height at maturity and number of panicles were also among the highest contributors to the observed variation based on PC2 while number of tillers at 45 days after sowing was the source of highest variations in PC3. Principal component analysis measures the contribution of each component or independent impact of a particular character to the total variance observed in a given population in relation to the traits of interest to the breeder. PCA has been used to determine the optimum number of clusters [25], to complement cluster analysis [26], and to investigate patterns of genetic diversity [27]. Principal component analysis was used to reduce the complexity of the data set and to partition the observed variation within traits based on their degree of importance [28]. Days to 50% flowering, days to 85% maturity and yield were the main principal discriminatory characteristics of the studied germplasm. This indicates that resources and time can be saved by concentrating on these characters during selection and advancement in this population. The results of this study are not in agreement with earlier reports [29] that leaf width, number of grains, and panicle length contributed more to the variation among 39 lowland rice varieties evaluated in Nigeria. This might be due the different rice ecologies (lowland and upland) under which these two studies were conducted. Using PCA, the numbers of traits controlling the observed phenotypic variation within the germplasm collection were identified and this might be useful during selection in a breeding programme.

[Table 4 near here]

Distribution of traits and genotypes based on the biplot analysis is presented in Figure 2. Genotypes 03 and 57 had the highest yield but also exhibited late flowering and maturity. The output from the biplot confirms the results obtained in the correlation analysis. Positive correlation was observed between yield, days to flowering, and days to maturity with stronger association exiting between yield and days to flowering than days to maturity (Figure 2). Weaker but positive correlation was seen between grain yield and number of filled grain.

[Figure 2 near here]

4. Conclusions

The results revealed significant diversity among 77 upland rice genotypes evaluated for morphological variability. Majority of the traits had high heritability and genetic advance. The

77 lines were clustered into three main groups with days to 85% maturity and yield as the main discriminatory traits of the studied germplasm. The study showed that number of days to 50% flowering and number of panicles m^{-2} are the principal secondary traits that could be exploited by breeders for indirect selection to achieve higher genetic gain in grain yield within this germplasm.

References

1. Habib SH, Bashar MK, Khalequzzaman M, Ahmed MS, Rashid ESMH. Genetic analysis and morpho-physiological selection criteria for traditional biroin Bangla desh rice germplasm. Journal of Bioogical Science. 2005;5:315–318.

2. Yang W, Peng S, Laza RC, Visperas RM, Dionisio-Sese ML. Grain yield and yield attributes of new plant type and hybrid rice. Crop Science. 2007; 47: 1393-1400.

3. Lin MS. Genetic base of Japonica rice varieties released in Taiwan. Euphytica 1991; 56: 43-46.

4. Idahosa DO, Alika JE, Omoregie AU. Genetic variability, heritability and expected genetic advance as indices for yield and yield components selection in Cowpea (*Vigna ungiculata* (L.) Walp. Acade-mia Arena. 2010; 5: 22-26.

5. Nayak AR, Chaudhury D, Reddy JN. Genetic divergence in scented rice. Oryza. 2004; 41:79-82.

6. Sabesan T, Suresh R, Saravanan K. Genetic variability and correlation for yield and grain quality characters of rice grown in coastal saline lowland of Tamiluadu. Electrical Journal of Plant Breeding. 2009;1: 56-59.

7. Larik AS, Malik SI, Kakar AA, Naz MA. Assesment of heritability and genetic advance for yield and yield components in *Gossypium hirsutum L.* Scientific Khyber. 2000; 13: 39-44.

8. Sohrabi M, Rafii MY, Hanafi MM, Siti Nor Akmar A, Latif MA. Genetic diversity of upland rice germplasm in Malaysia based on quantitative traits. The Scientific World Journal. 2012.

9. Breeding Management System. 2015.

10. Steel RGB, Torrie JH. Principles and Proceedrers of Statistics. 1980.

11. Prasad SR, Prakash R, Sharma CM, Haque MF, Genotypic and phenotypic variability in quantitative characters in oat. Indian Journal of Agricultural Sciences (India). 1981.

12. Fischer KS, Fukai SI, Kumar A, Leung H, Jongdee B. Field phenotyping strategies and breeding for adaptation of rice to drought. Frontiers Physiology. 2012;3: 282.

13. Li W, Song TM. Estimates of genetic parameters for 13 quantitative traits in a recombined high oil maize population of IHO [(80) x Alexo (C23)]. Acta Agronomica Sinica. 1991;17:470-475.

14. Jha PB, Ghosh J. Genetic variability in fodder maize Journal of Research, Birsa Agricultural University. 1998;10:139-143.

15. Singh JM, Dash B. Analysis of genetic variability and character association in maize. African Crop Science Journal. 2000; 5: 1-8.

16. Murtadha S, Ariyo OJ, Kehinde OB. Character association of seed yield and its components in okra [Abelmoschus esculentus (L.) Moench]. Ogun Journal of Agricultural Science. 2004;3: 222-233.

17. Ahmadikhah A. Study on selection effect, genetic advance and genetic parameters in rice. Annals of Biological Research. 2010;4: 45-51.

18. Dutta P, Partha ND, Borua PK. Morphological Traits as Selection Indices in Rice: A Statistical View Universal Journal of Agricultural Research. 2013;3: 85-96.

19. Ukaoma AA, Iwunor OP, Ijeoma OR, (Heritability and character correlation among some rice genotypes for yield and yield components. Journal of Plant Breeding and Genetics. 2013; 2: 73-84.

20. Sedeek SEM, Hammoud SA, Ammar MH, Metwally TF. Genetic variability, heritability, genetic advance and cluster analysis for some physiological traits and grain yield and its components in rice (*Oryza sativa* L.). Journal of Agricultural Science. 2009; 35: 858-878.

21. Ibrahim MM, Hussein RM, Variability, heritability and genetic advance in some genotypes of roselle (Hibiscus sabdariffa L.) World Journal of Agricultural Science. 2006;2: 340-345.

22. Sinha AK, Mishra PK. Morphology based multivariate analysis of phenotypic diversity of landraces of rice (Oryza sativa L.) of Bankura district of West Bengal. Journal of Crop and Weed. 2013;9: 115-121.

23. Maji TA, Shaibu AA. Application of principal component analysis for rice germplasm characterization and evaluation. Journal of Plant Breeding and Crop Science 2012;4 :87-93.

24. Banumathy S, Manimaran R, Sheeba A, Manivannan N, Ramya B, Kumar D, Ramasubramanian GV. Genetic diversity analysis of rice germplasm lines for yield attributing traits. Electronic Journal of Plant Breeding. 2010;1: 500-504.

25. Thompson JA, Nelson RL, Vodkin LO Identification of diverse soybean germplasm using RAPD markers. Crop Science. 1998;38: 1348-1355.

26. Lombard V, Baril CP, Dubreuil P, Blouet F, Zhang D. Genetic relationships and fingerprinting of rapeseed cultivars by AFLP: consequences for varietal registration. Crop Science. 2000;40: 1417-1425.

27. Mohammadi SA, Prasanna BM Analysis of genetic diversity in crop plants—salient statistical tools and considerations. Crop Science. 2003;43: 1235-1248.

28. Ringnér M. What is principal component analysis?. Nature biotechnology. 2008; 26: 303-304.

29. Gana AS, Shaba SZ, Tsado EK, Principal component analysis of morphological traits in thirty-nine accessions of rice (Oryza sativa L.) grown in a rainfed lowland ecology of Nigeria. Journal of Plant Breeding and Crop Science. 2013; 4: 120-126.

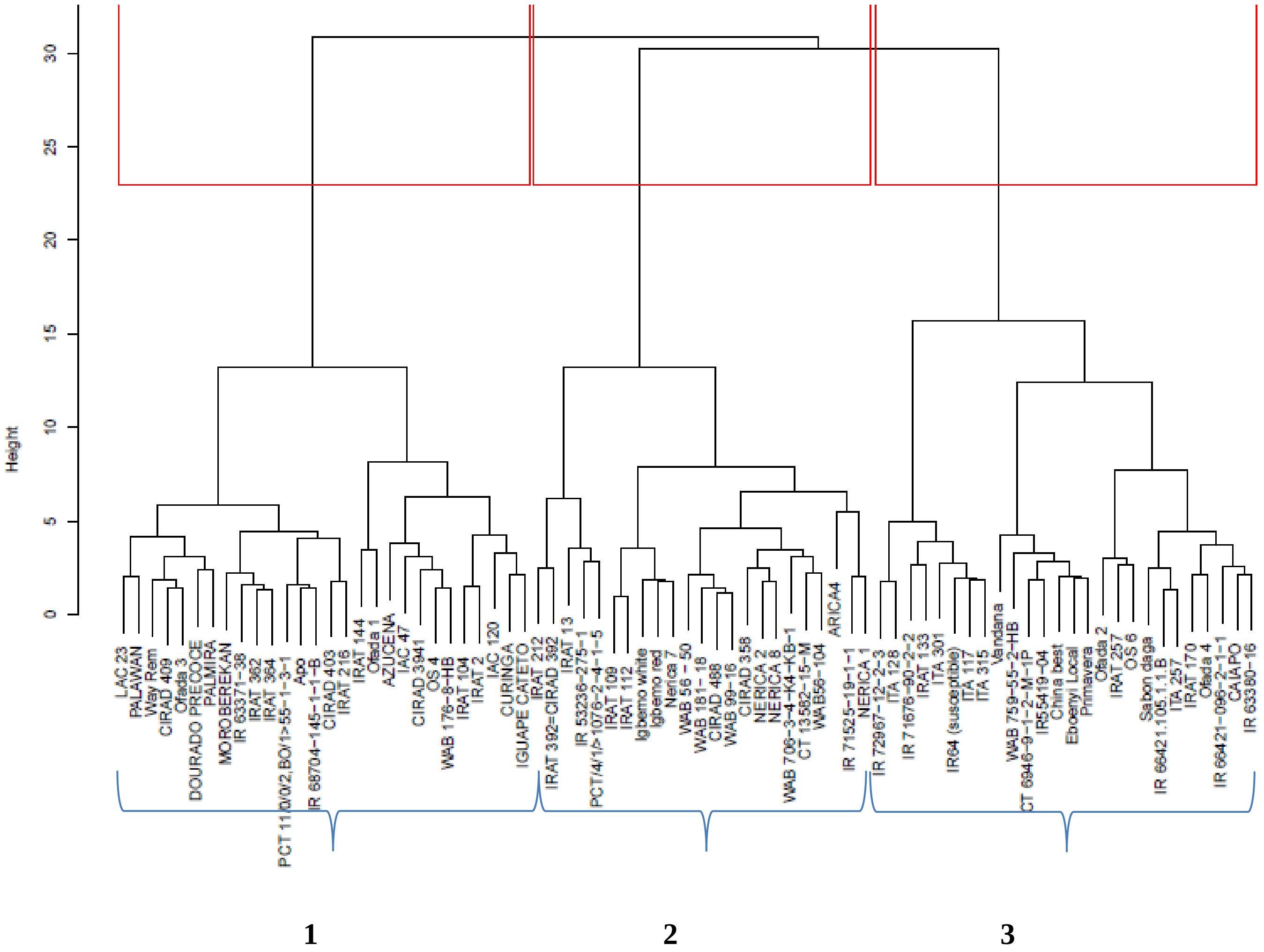

Fig 1 Dendrogram of 77 upland rice genotypes based on 10 morphological traits

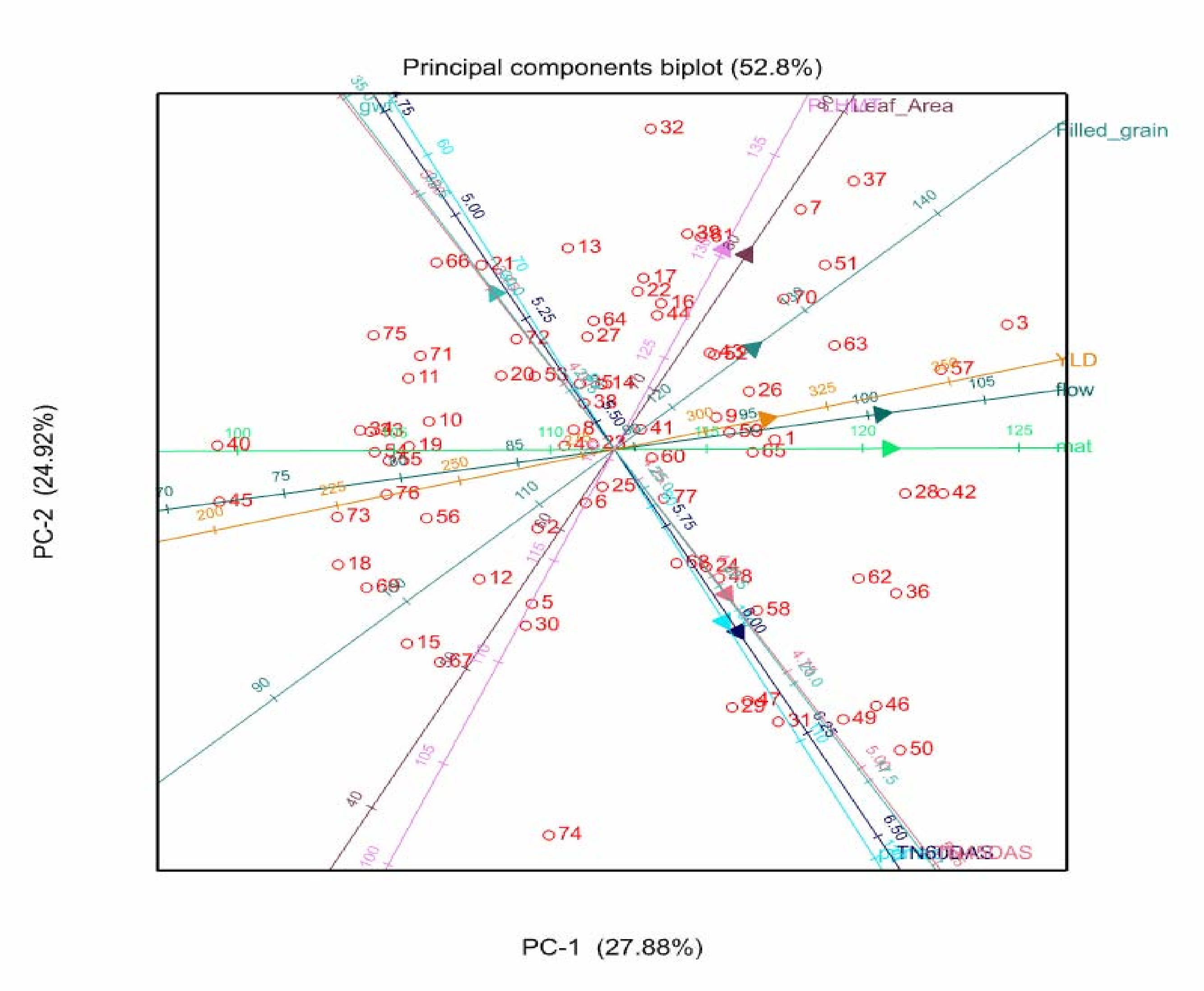

Fig 2 Biplot graphical display of the measured traits in 77 upland rice genotypes.

Table 1 List of rice germplasm and source

S.No	Germplasm	Origin/Source	S.No	Germplasm	Origin/Source
1	AZUCENA	Philippines	40	MOROBEREKAN	Cote d'Ivoire
2	CAIAPO	Brazil	41	OS 4	Nigeria
3	CIRAD 358	Cote d'Ivoire	42	OS 6	Nigeria
4	CIRAD 394	Madagascar	43	PALAWAN	Phillipines
5	CIRAD 403	Brazil	44	PALMIRA	Costa Rica
6	CIRAD 409	Columbia	45	PCT 11/0/0/2,BO/1>55-1-3-1	Columbia
7	CIRAD 488	Madagascar	46	PCT/4/1/>1076-2-4-1-5	Columbia
8	CT 13582-15-M	CIAT	47	WAB 176-8-HB	AfricaRice

9	CT 6946-9-1-2-M-1P	CIAT	48	WAB 706-3-4-K4-KB-1	AfricaRice
10	CURINGA	Brazil	49	WAB 99-16	AfricaRice
11	DOURADO PRECOCE	Cote d'Ivoire	50	Primavera	Brazil
12	IAC 120	Brazil	51	WAB 759-55-2-HB	AfricaRice
13	IAC 47	Brazil	52	NERICA 7	AfricaRice
14	WAB 181- 18	AfricaRice	53	IRAT 109	Cote d'Ivoire
15	IGUAPE CATETO	Brazil	54	ARICA4	AfricaRice
16	IR 53236-275-1	IRRI	55	Way Rem	Indonesia
17	IR 63371-38	IRRI	56	Vandana	India
18	IR 63380-16	IRRI	57	Apo	Philippines
19	WAB 56 – 50	AfricaRice	58	WAB56-104	AfricaRice
20	IR 66421.105.1.1.B	IRRI	59	IR64	IRRI
21	IR 66421-096-2-1-1	IRRI	60	Sabon Daga	Nigeria
22	IR 68704-145-1-1-B	IRRI	61	ITA 117	IITA
23	IR 71525-19-1-1	IRRI	62	ITA 128	IITA
24	IR 71676-90-2-2	IRRI	63	ITA 257	IITA
25	IR 72967-12-2-3	IRRI	64	ITA 301	IITA
26	IRAT 104	Cote d'Ivoire	65	ITA 315	IITA
27	IRAT 112	Cote d'Ivoire	66	Ofada 1	Nigeria_landrace
28	IRAT 13	Cote d'Ivoire	67	Ofada 2	Nigeria_ landrace
29	IRAT 144	Cote d'Ivoire	68	Ofada 3	Nigeria_ landrace
30	IRAT 170	Cote d'Ivoire	69	Ofada 4	Nigeria_ landrace
31	IRAT 2	Senegal	70	Igbemo White	Nigeria_ landrace
32	IRAT 212	Cote d'Ivoire	71	Igbemo Red	Nigeria_ landrace
33	IRAT 216	Cote d'Ivoire	72	China Best	China
34	IRAT 257	Brazil	73	Ebonyi Local	Nigeria_ landrace
35	IRAT 362	Nicaragua	74	NERICA 1	AfricaRice
36	IRAT 364	Nicaragua	75	NERICA 2	AfricaRice
37	IRAT 392=CIRAD 392	Madagascar	76	NERICA 8	AfricaRice
38	LAC 23	Liberia	77	IR55419-04	IRRI
39	IRAT 133	Cote d'Ivoire			

Table 2 Genetic variance of 10 morphological characteristics

Traits	Minimum	Mean	Maximum	V_p	V_g	V_e	PCV (%)	GCV (%)	h^2_B (%)	GA (%)	Std. Dev
GY	96.92	281.63	434.2	13807	6599.8	6870.4	41.72	28.85	47.80	41.08	81.24
TGW	19.22	25.99	37.4	26.3	23.33	2.97	19.73	18.58	88.71	36.06	4.83
DTF	70.23	89.15	105	94.81	82.17	11.89	10.92	10.16	86.67	19.50	9.06
DM	99.43	112.06	125.6	66.8	48.09	18.46	7.29	6.19	71.98	10.82	6.94
PHT	101.99	120.48	139.7	364.46	110.36	250.56	15.86	8.72	30.28	9.88	10.51
NP	4.99	6.29	7.7	3.63	0.85	2.21	30.29	14.66	23.41	14.61	0.92
TN60DAS	4.47	5.45	6.3	2.41	0.37	1.94	28.48	11.16	15.16	8.89	0.60
LA	41.25	65.74	102.4	377.3	159.63	133.75	29.55	19.22	42.31	25.75	12.63
NPM	38.73	85.13	134	445.09	284.38	139.83	24.78	19.81	63.89	32.62	16.86
FG	86.28	115.66	184	1467.00	480.2	966.90	33.12	18.94	32.73	22.33	21.91

GY=Yield per meter square, TGW= 1000grain weight, DTF= Days to 50% flowering, DM= Days to 85% maturity, PHT = Plant height at maturity, PN= Number of panicles per plant, TN60DAS=Tiller number at 60days after sowing, LA=Average leaf area, NPM= Number of panicles per meter square, FG= Number filled grains.

Replications = 4, n =77

Table 3 Correlation coefficients among 10 quantitative traits of 77 upland rice cultivars

	TGW	DTF	DM	PHT	TN45DAS	TN60DAS	LA	NPM	FG
GY	0	0.22**	0.21**	0.07	0.12*	0.13*	0.09	0.25**	0.05
TGW		-0.26**	-0.26**	0.22**	-0.07	-0.20**	0.15*	-0.25**	-0.08
DTF			0.82**	0.17*	0.02	0.12*	0.26**	0.07	0.14*
DM				0.18*	0.05	0.16*	0.18*	0.16*	0.17*
PHT					-0.15*	-0.20**	0.33**	-0.18*	0.27**
TN45DAS						0.61**	0.06	0.05	-0.16*
TN60DAS							-0.08	0.18*	-0.09
LA								-0.20**	0.12*
NPM									0.01

GY=Yield per meter square, TGW= 1000grain weight, DTF= Days to 50% flowering, DM= Days to 85% maturity, PHT = Plant height at maturity, PN= Number of panicles per plant, TN45DAS=Tiller number at 45days after sowing, TN60DAS=Tiller number at 60days after sowing, LA=Average leaf area, NPM= Number of panicles per meter square, Number filled grains.

*, ** = Significant at 5 and 1% probability levels, respectively

Table 4 Principal component analysis of 10 agro-morphological characters for 77 upland rice cultivars.

Variable	**PC1**	**PC2**	**PC3**
LA	0.29	0.41	0.20
PHT	0.23	0.45	0.24
TN45DAS	0.10	-0.30	0.60
TN60DAS	0.21	-0.43	0.30
GY	0.32	-0.01	0.34
DTF	0.52	0.03	-0.33
TGW	-0.20	0.37	0.33
DM	0.53	-0.05	-0.30
NPM	0.18	-0.41	0.07
FG	0.29	0.20	0.13
Eigenvalue	2.76	2.49	1.20
Variation (%)	27.60	24.93	12.02
Cumulative (%)	27.60	52.53	64.55

GY=Yield per meter square, TGW= 1000grain weight, DTF= Days to 50% flowering, DM= Days to 85% maturity, PHT = Plant height at maturity, PN= Number of panicles per plant, TN45DAS=Tiller number at 45days after sowing, TN60DAS=Tiller number at 60days after sowing, LA=Average leaf area, NPM= Number of panicles per meter square, FG= Number filled grains.