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Evaluation of Korea Rice Germplasm for Yield and Yield Components Adaptable to Nigeria Environmental Conditions

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Abstract: In this current century, West Africa will continue facing major problem of food shortage. This implies increase in the rice cultivation and productivity as rice is one of their major staple crops. This study was carried out at Africa Rice Center, International Institute of Tropical Agriculture (IITA) Ibadan, Nigeria, and evaluated 30 accessions (anther culture derived) from South Korea with 10 adapted genotypes form Nigeria for their performance. The experiment was conducted in dry season using Alpha lattice design with eight blocks each planted in five entries, replicated three times. Analysis of variance revealed highly significant differences *($P \leq 0.05$)* among the genotypes of the studied traits. Thus, suggest the presence of wide genetic variability, which is of important, as it gives large spectrum of selection to the breeders for hybridization. Based on their means, genotypes such as FARO 67, UPN 287, FARO 66, UPN 315 and UPIA1 showed maximum tillering ability per plant, while, UPN 349, UPN 335, UPN 271, UPN 324 and UPN 300 showed the highest number of spikelets per panicle. The genotypes such as UPIA 1, SAHEL 21, UPN 301, UPN 266 and FARO 57 proved to be better for 1000_grain weight, while UPIA 1, UPN 266, UPN 349, UPN 300 and FARO 67 were better for grain yield per plant. Cluster analysis grouped the 40 genotypes into five clusters. Dendogram showed maximum genetic distance between group A and group E indicating genetic diversity among these groups. Minimum genetic diversity was observed between group B and group E. FARO 67, UPN 287, UPN 349, UPIA 1, UPN 266 and UPN 300 shown to be the most promising genotypes that could be used for rice hybridization, genetic improvement and rice hybrid programme.

Keywords: Oryza, Yield Components, Genotypes, PCA, Cluster

1. Introduction

Rice plant is of grass species belongs to the family Poaceae and subfamily Oryzoidae. The Centre of origin of rice is believed to be South-East Asia (for *Oryza sativa*) and Africa (for *O. glaberrima*) and some of the rice producing countries being China, Burma, India, Indonesia, Japan, United States, Spain, Italy and Brazil Oko et al., 2012 [1]. The potential for rice development in West Africa is determined by the agro-ecological conditions in which rice can be produced and the type of technology potentially available to enhance rice yields Lançon and Erenstein, 2002 [2]. This important cereal is cultivated and consumed across West Africa including Nigeria but its production is characterized by poor yields due to the use of low farm inputs and cultivation of unimproved cultivars with poor yield potentials. *Oryza sativa* L., the most widely grown rice, is the staple food for an estimated 3.5 billion people

worldwide IRRI, 2013 [3]. In sub-Saharan Africa, rice consumption among urban dwellers has steadily grown, with a per capita consumption that has doubled since 1970 IRRI, 2013 [3]. Two types of rice have been mainly cultivated in West Africa: the African rice (*Oryza glaberrima*) and the Asian rice (*Oryza sativa*). In recent times, new rice varieties have been introduced by the West African Rice Development Association (WARDA) named NERICA (New Rice for Africa), it is an interspecific hybrid between the African and Asian rice Kumar *et al*. 2017 [4] The tremendous growth of the human population worldwide has increased the demand for rice production, demanding a production of about 50% by the year 2025 Kumar *et al*. 2017 [4]. Rice consumption is on the increase in West Africa, and so its production. However, over the last decade, rice production was insufficient to meet consumption rate, resulting to the increase in rice importation to close the consumption gap. This raises number of issues, as the burden of increase in rice importation is unlikely to be sustainable. Improving rice productivity through identification of the best performing genotypes and genotypes that can be used as parents in future crosses are two principal objectives of most rice breeding programs Fasahat et al., 2016 [5]. Germplasm characterization and evaluation is a basic prerequisite for a successful breeding programme and could lead to the identification of traits with high heritability and appreciable association with yield Habib *et al.*, 2005 [6] and Yang *et al.*, 2007 [7]. Agro-morphological characterization of germplasm is fundamental to provide the preliminary information for planning and initiating of a breeding programme Lin, 1991 [8] cited by Anyaoha *et al.*, 2018. [9] 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 Idahosa *et al.*, 2010. [10]. Hence, a successful breeding programme depends on identifying useful parents for achieving the goals of improving crop and producing high yielding varieties. Grain yield in cereals is one of the most important and complex traits in plant breeding experiments. Continue improvement of grain yield remains the top priority in most of the breeding programmes Yan et al., 2002 [11] In rice, grain yield depends on various growth and yield component traits such as the panicle number per plant, the filled grain number per panicle, and the weight per grain Yoshida, 1983 [12] cited by Efisue *et al.*, 2014. [13]

The objective of this study is to evaluate the morphological and agronomic traits of 30 accessions (anther culture derived) of rice from Korea for their adaptability and productivity to the environmental conditions in Nigeria.

2. Materials and Methods

2.1. Plant Materials

Thirty (30) accessions of rice (anther culture derived) from South Korea, of *O. sativa* L. species, lowland and high yield were evaluated and ten (10) adapted lowland/ irrigated and drought tolerance rice genotypes of Nigeria used as control. (Table 1).

Table 1. *Materials used for the study.*

ENTRY_NO	DESIGNATION	SOURCES
1	UPN324	UPN19DS-02:100
2	UPN337	UPN19DS-02:113
3	UPN333	UPN19DS-02:171
4	UPN309	UPN19DS-02:85
5	UPN313	UPN19DS-02:89
6	UPN284	UPN19DS-02:220
7	UPN287	UPN19DS-02:173
8	UPN295	UPN19DS-02:71
9	UPN297	UPN19DS-02:73
10	UPN289	UPN19DS-02:65
11	UPN246	UPN19DS-02:151
12	UPN301	UPN19DS-02:77
13	UPN268	UPN19DS-02:260
14	UPN262	UPN19DS-02:167
15	UPN315	UPN19DS-02:257
16	UPN349	UPN19DS-02:153
17	UPN300	UPN19DS-02:76
18	UPN275	UPN19DS-02:51
19	UPN235	UPN19DS-02:191
20	UPN265	UPN19DS-02:41
21	UPN266	UPN19DS-02:42
22	UPN335	UPN19DS-02:219
23	UPN271	UPN19DS-02:47
24	UPN290	UPN19DS-02:66
25	UPN346	UPN19DS-02:255
26	UPN307	UPN19DS-02:83
27	UPN247	UPN19DS-02:30
28	UPN341	UPN19DS-02:258
29	UPN241	UPN19DS-02:16
30	UPN296	UPN19DS-02:72
31	ARICA 3	Nigeria
32	UPIA 1	Nigeria
33	UPIA 2	Nigeria
34	UPIA 3	Nigeria
35	FARO 66	Nigeria
36	FARO 67	Nigeria
37	FARO 57	Nigeria
38	FARO 44	Nigeria
39	SAHEL 210	Nigeria
40	SAHEL 134	Nigeria

2.2. Design and Planting

The experimental layout was Alpha lattice design with eight blocks and each block planted in five entries and replicated three times. The experiment was carried out in an irrigated field and nursery bed established in wet condition. The field was cleared, ploughed, leveled and well irrigated to facilitate the establishment of the seedlings. The seedlings were transplanted after three weeks into a well puddled rice field. Each genotype was grown in two rows with row length of 3 m and a distance of 20 cm between plants and between rows. NPK (15:15:15) was applied as a basal application of 200 kg ha-1 (N_2, P_2O_5 and K_2O).

All essential cultural practices like weeding, pesticides and irrigation were applied equally to all the experimental plots. Three weeks after transplanting, Urea was applied at the rate of 65kg/ha and the second rate of 35kg/ha was applied at the beginning of booting stage.

2.3. Data Collection

Data was collected at appropriate stage of the crop

development. The agronomic characters were measured at weekly intervals. The 'Standard Evaluation System (SES) for Rice' reference manual IRRI, 2002 [14] was used for all trait measurements except where stated otherwise.

Randomly sampled plants per plot were used for data recording. Days to 50% flowering was recorded for all genotypes from seeding date to the day when 50% flowered. Three randomly sampled panicles per genotype were used for data recording for panicle traits at maturity such as panicle length, number of seed (spikelet) per panicle, panicle weight and spikelet fertility this was calculated by dividing the filled seed by total seed per panicle and then converted into percentage. Day to maturity was calculated from the seeding day to the day when appropriately 85% of the total seed grains on the panicles got fully matured. Grain yield was recorded in kilograms after threshing all the two rows of individual plot by counting and weighting three different 1000 grain and taken their mean and then the data was converted into kg ha-1. Plant height was measured by a meter ruler from the base of the plant to the apex.

2.4. Statistical Analysis

The data were evaluated using Analysis of Variance technique with the help of Statistical Analysis System SAS, version 9.4 2013. [15] Differences were declared statistically significant when *($P \leq 0.05$)*. Where significant differences were detected, the means were separated by the least significant difference (LSD) at 5% probability level. Genotypic (GCV) and phenotypic (PCV) coefficients of variation were computed for all traits according to Singh and Chaudhary 2004 [16] using the equations:

$$GCV\ (\%) = \{(\sqrt{\sigma^2 g})/x\} \times 100$$

$$PCV\ (\%) = \{(\sqrt{\sigma^2 p})/x\} \times 100$$

where $\sigma^2 g$ = genotypic variance, $\sigma^2 p$ = phenotypic variance and x = grand mean for the trait.

The GCV and PCV were considered low if the value less than 10%, moderate if value is 10 to 20% and high when greater than 20% as explained by Deshmukh et al. 1986 [17] cited by Abe and Adelegan 2019 [18].

2.5. Cluster Analysis

R-- software (version 3.5.2) was used to run cluster and principal components analysis (PCA).

On the traits evaluated to characterize the genotypes and determine their relationships. In the cluster analysis procedure, the Euclidean distance was calculated using standardized morphological data and Ward's method was used to construct the dendrogram using the standardized values for the 40 rice genotypes. The traits and the genotypes were respectively analyzed as variables and individuals in PCA and the criterion of Raji 2002 [19] was used to determine the cut-off limit for the coefficients of the proper vectors. The correlation coefficients between the traits were derived from the PCA and tested for significant.

3. Result

3.1. Agronomic Trait Evaluation of the Genotypes

Analysis of variance (ANOVA) results revealed significant differences among genotypes and block within replication for all traits under consideration except number of spikelets per panicle (SSP), panicle length (PLT) and panicle weight (PANWT), which were non-significant for the Block (rep) (Table 2). The variance among genotypes was very highly and at significant level ($P \leq 0.001$). A high significant mean square ($P \leq 0.001$) for number of panicles per plant (PAN), number of tillers per plant (TILL) and day to 50% flowering (DFLW) which revealed the block within replication effect on the genotypes. Also, significant mean squares ($P \leq 0.01$) were observed for some traits, but the block within replication variance for some traits such as number of spikelets per panicle (SPP), panicle length (PLT), and panicle weight (PANWT) were non-significant (Table 2).

Table 2. *ANOVA (mean square) for different traits measured.*

SV	DF	GV	HT	PAN	TILL	DFLW	DM
REP	2.00	3.63^{NS}	30.81^{NS}	2.29*	1.61^{NS}	18.31**	33.95***
BLOCK (REP)	21.00	2.58*	39.23*	2.36***	2.94***	8.01***	9.55*
Genotype	39.00	2.92**	160.38***	1.73***	1.87**	76.88***	13.58**
Error	57.00	1.26	21.05	0.69	0.97	2.70	4.44
Mean		3.27	95.31	7.53	8.25	89.33	120.30
CV (%)		34.37	4.81	11.05	11.93	1.84	1.75

Table 2. *Continued.*

SV	SPP	PLT	PANWT	SpFert	Yield	TGW
REP	1676.13^{NS}	1.07^{NS}	0.71^{NS}	26.95^{NS}	16372792.34***	13.30***
BLOCK (REP)	1090.40^{NS}	2.14^{NS}	0.66^{NS}	63.30*	771950.73**	2.91**
Genotype	2186.43***	8.37***	1.28***	82.19***	934954.10***	9.54***
Error	676.66	2.96	0.42	31.36	298648.40	1.21
Mean	139.71	25.68	3.42	83.39	2797.89	24.03
CV (%)	18.62	6.70	18.97	6.72	19.53	4.58

*, **, *** indicate significances at the 0.05, 0.01 and 0.001 levels respectively. Rep: Replication; DF: Degree of freedom; SV: Source of Variance; GV: Growth Vigor; HT: plant height, PAN: Number of Panicle per Plant PLT: Panicle Length, DFLW: Day to 50% flowering; DM: Day to Maturity; SPP: Number of Spikelets per Panicle; PANWT: Panicle Weight; SpFert: Spikelets Fertility; TGW: 1000-grains weight, TILL: Number of Tillers per plant; Yield: grain yield.

Twenty genotypes exhibited high performance above the overall mean for plant height 95.31cm (Table 3). Number of panicles per plant (PAN) ranged from 5 to 9 with nineteen genotypes above the overall mean and the genotype with the highest was FARO 67 (9) while UPN335 the lowest number of panicle (5). Panicle is an important yield component as it determines the numbers of spikelets. High number of panicles is the result of high number of productive tillers which impact positively for high yield in FARO 67 (9), UPN 266 (8) and UPN 349 (9). (Table 3).

Table 3. *Mean performance of agronomic traits of the studied genotypes.*

Genotypes	Plant Height	No. of panicle/plant	No. of Tiller/ plant	Day of flowering	Day to maturity
ARICA 3	101.55	9	9	88	118
FARO 44	87.47	8	9	85	119
FARO 57	94.27	8	8	91	120
FARO 66	95.17	9	10	84	119
FARO 67	113.46	9	10	91	118
SAHEL 13	83.13	8	9	81	116
SAHEL 21	92.29	7	9	93	119
UPIA 1	101.64	9	9	92	120
UPIA 2	97.27	8	9	88	118
UPIA 3	97.19	7	9	82	115
UPN235	84.97	7	8	83	114
UPN241	88.71	7	7	89	119
UPN246	93.2	8	8	94	120
UPN247	98	7	8	101	126
UPN262	88.24	6	7	85	116
UPN265	79.87	7	8	87	118
UPN266	104.47	8	8	94	124
UPN268	94.84	7	8	89	117
UPN271	101.74	7	7	96	120
UPN275	97.18	7	8	90	119
UPN284	101.16	7	7	93	121
UPN287	95.58	9	10	95	122
UPN289	103.98	8	8	93	119
UPN290	106.11	7	8	93	121
UPN295	92.51	8	9	83	118
UPN296	87.95	7	8	75	107
UPN297	82.18	7	7	88	121
UPN300	100.13	8	7	96	121
UPN301	99.39	8	9	89	118
UPN307	91.04	7	8	91	119
UPN309	95.64	7	8	95	119
UPN313	82.89	7	8	80	110
UPN315	91.54	9	9	88	122
UPN324	97.82	8	9	79	112
UPN333	99.58	7	8	96	123
UPN335	119.1	5	6	92	120
UPN337	94.3	8	8	95	121
UPN341	84.65	7	8	86	119
UPN346	90.7	7	7	86	118
UPN349	101.66	9	9	95	121
Means	95.31	8	8	89	119
CV (%)	4.81	11	12	2	7
LSD (0.05)	7.50***	1.36***	1.61***	2.69***	3.43***

The phenotypic observation of those genotypes revealed high tillering ability (6-10 tillers per plant) with thick stems, dark green and erect leaves and showing vigorous root system. Tillering ability of the genotypes also showed highly significance difference among the genotypes tested (Table 3) with three genotypes FARO 67, UPN287 and FAR 66 having the higher number of tillers (10) and UPN335 having lowest tillers (6). The flowering data (days to 50%) showed a range from 75 days to 101 days. The longest days was observed in genotype UPN247 (101) while UPN296 had the lowest day (75). Similarly, a range of 107 days to 126 days were obtained as days to maturity. The early matured genotype was UPN296 (107) and the late matured genotype was UPN247 (126) (Table 3).

In Table 4, the highest number of spikelets per panicle were exhibited by the genotypes UPN349 (197 spikelets) and FARO 66 (81 spikelets) the lowest. Therefore, a range of 81 to 197 spikelets confirming the highly significance difference among the genotypes. The genotype UPN290 with 28.3 cm displayed long panicle length and UPN297 was the shortest with 21.8 cm. The panicle length ranged between 21.8 to 28.3 and 22 genotypes were above the overall means (25.68cm) of the panicle length. High significance difference among the genotypes for grain yield was observed and it

ranges from 1279.75 kg/ha to 4158.66 kg/ha. The genotypes UPIA 1, UPN 266 and UPN 349 had the highest yield (4158.66 kg/ha, 3901.01kg/ha and 3856.18kg/ha), respectively. The grain weight showed highly significance difference among the genotypes tested. (Table 4).

Table 4. *Mean performance of agronomic traits of the studied genotypes.*

Genotypes	No. Spickelet/ Panicle	Panicle length (cm)	Yield (kg/ha)	1000 Grain Weight
ARICA 3	106	27.22	2806.19	24.12
FARO 44	109	26.65	2791.32	24.59
FARO 57	141	26.94	2989.19	25.74
FARO 66	81	26.83	1829.79	25.29
FARO 67	133	27.85	3503.43	24.46
SAHEL 13	110	22.04	2184.25	23.74
SAHEL 21	149	25.09	3228.05	29.12
UPIA 1	109	26.95	4158.66	30.55
UPIA 2	126	28.3	3180.81	23.93
UPIA 3	98	25.68	2051.74	23
UPN235	124	24.31	2724.09	24.56
UPN241	167	24.54	2209.93	23.95
UPN246	154	26.58	3069.12	25.04
UPN247	169	25.51	2900.36	22.24
UPN262	104	26.75	2185.66	23.21
UPN265	138	26.01	2390.14	23.17
UPN266	127	27.16	3901.01	26.83
UPN268	146	25.5	3480.57	24.03
UPN271	185	24.66	3292.96	21.72
UPN275	126	24.35	2296.89	23.33
UPN284	138	24.53	2944.07	23.69
UPN287	182	21.98	3339.29	25.17
UPN289	162	27.69	3117.44	22.69
UPN290	164	28.3	3353.97	22.97
UPN295	106	21.92	1279.75	22.22
UPN296	137	26.9	2123.07	24.64
UPN297	123	21.8	2736.16	23.87
UPN300	182	26.67	3524.38	24.01
UPN301	137	28.15	3091.11	28.18
UPN307	125	25.17	2359.25	22.1
UPN309	115	26.88	2720.68	22.57
UPN313	77	27.06	1958.39	24.9
UPN315	150	23.49	3040.38	23.25
UPN324	183	23.75	1961.24	22.68
UPN333	126	26.6	2936.22	23.09
UPN335	196	27.9	1918.03	24.07
UPN337	178	24.16	3402.36	24.06
UPN341	165	24.66	2620.13	21.88
UPN346	140	24.88	2459.43	19.87
UPN349	197	25.93	3856.18	22.48
Means	140	25.68	2797.89	24.03
CV (%)	19	6.7	19.53	4.58
LSD (0.05)	42.53**	1.36***	893.51***	1.80***

The study revealed highest genotypic variance far all the traits measured more than phenotypic variance (Table 5). The PCV estimates were higher in all traits than the corresponding GCV. The GCV and PCV were higher for GV, GCV and PCV were low for DFLW although they were moderate high for PAN and TILL. Low PCV was recorded for PLT, SpFert and TGW whereas GCV showed moderately high value for the same traits. High GCV was observed for PANWT, FLGR, UNFLGR, SPP and grain yield (Table 5).

Table 5. *Genetic variability estimates and genotypic and phenotypic coefficient of variation.*

Trait	Mean	σ2g	σ2p	GCV	PCV
GV	3.266667	2.916837	6.183504	52.28188	76.1224
HT	95.31425	160.3808	255.695	13.28674	16.77657
DFLW	89.33333	76.87592	166.2092	9.814804	14.43159
PAN	7.5325	1.732096	9.264596	17.47217	40.40863
PLT	25.6835	8.371299	34.0548	11.26529	22.72139

Trait	Mean	σ2g	σ2p	GCV	PCV
PANWT	3.4225	1.275458	4.697958	32.99816	63.33024
FLGR	116.7555	1772.002	1888.758	36.05411	37.22295
UNFLGR	22.92508	234.4665	257.3916	66.79279	69.982
TILL	8.24525	1.868913	10.11416	16.58024	38.57102
SPP	139.708	2186.426	2326.134	33.46926	34.52201
SpFert	83.39492	82.19458	165.5895	10.87131	15.43039
Yield	2797.893	934954.1	937752	34.55923	34.6109
TGW	24.025	9.544287	33.56929	12.85903	24.11613

σ2g = genotypic variance; σ2p = phenotypic variance; GCV = genotypic coefficient of variation; PCV = phenotypic coefficient of variation; GV: Growth Vigor; HT: plant height, PAN: Number of Panicle per Plant PLT: Panicle Length, DFLW: Day to 50% flowering; FLGR: Filled grain; UNFLGR: Unfilled grain; SPP: Number of Spikelets per Panicle; PANWT: Panicle Weight; SpFert: Spikelets Fertility; TGW: 1000-grains weight, TILL: Number of Tillers per plant; Yield: grain yield.

3.2. Correlation and Cluster Analysis of the Genotypes

The correlation analysis done on the studied genotypes using R-software version 3.5.2 (Figure 1), revealed that days to 50% flowering exhibited positive and highly significant correlation with days to maturity and positive significant correlation with plant height, panicle weight, number of spikelets, spikelet fertility and yield. Days to maturity was significant positively correlated with panicle weight. Plant height showed significant correlation with the panicle weight. Number of panicles was highly significant positively correlated with number of tillers per plant with which it was and highly significant negatively correlated with the phenotypic acceptability (Figure 1).

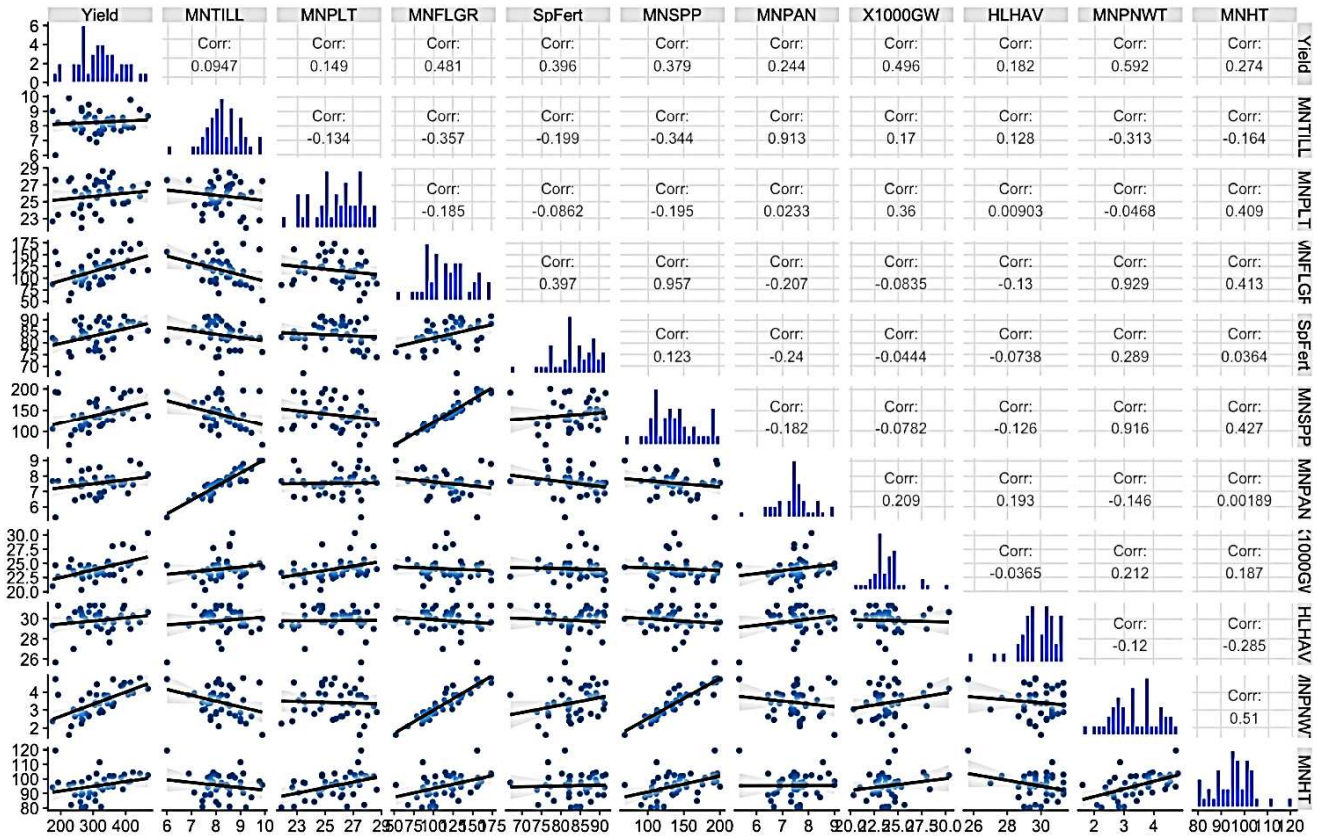

Figure 1. *The Correlation coefficient between rice yield and its yield components.*

MNTILL (number of tiller per plant), MNPLT (Panicle length), MNFLGR (Number of filled grain), SpFert (Spikelet fertility), MNSPP (Number of spikelet per panicle), M NPAN (Number of panicle per plant) X1000GW (1000 grain weight), MNPNWT (Panicle weight), MNHT (Plant height)

Highly significant positive correlation with unfilled grain per panicle and number of spikelet per panicle while non-significant positive correlation with filled grain per panicle and spikelet fertility and non-significant negative correlation with panicle length.

Yield showed significant positive correlation with 1000_grain weight, significant positive correlation with day to 50% flowering. Significant positive correlation with

panicle weight and unfilled grain per panicle. The 1000_grain yield showed significant positive correlation with yield. (Figure 1).

3.3. Cluster and Principal Components Analysis of Rice Genotypes Evaluated

Hierarchical cluster analysis of some agronomic traits and yield are presented in the Figure 2. Five main groups (A, B, C, D and E) were identified at 0.9% coefficient of similarity index. The dendrogram revealed that each group containing 9, 7, 11, 8 and 5 genotypes for A, B, C, D and E, respectively. At 1% coefficient of similarity index majority of the genotypes assumed individual identity. Dendrogram showed that maximum genetic distance is present between group A and group E indicating wide diversity of genetic material. Within the group C, FARO 44 and UPN 290 had most distance of diversity. Minimum genetic diversity is present between group B and group E. Group E includes cultivars which had better characters such as grain yield, number of panicle per plant and grain weight while group B and C includes the cultivars which were superior for total tillers per plant, panicle length, plant height and number of productive tillers. The group D was mixture of important traits such number of tillers, yield, number of panicle, day to maturity and was composed of SAHEL 21, UPN301, UPN284, UPN289, UPN246, UPN337, and UPN300. (Figure 2)

Principal component analysis indicates that the first four components accounted for 75.42% of total variation (Table 6). It also revealed that the first principal component accounted for 32.37% of total variance. The second component accounted for 19.57% of the total variance with variables such as numbers of tiller per plant (0.41), number of panicles (0.48), Yield (0.32) and thousand grain weight (0.30) contributing most positively. The third principal component accounted for 13.32% and the variables contributing positively were number of spikelet per panicle (0.32), panicle length (0.11) and panicle weight (0.15) while spikelet fertility contributed negatively. The fourth principal component accounted for 10.16% of the total variance. The variables that contributed positively are panicle length (0.64) and thousand grain yield (0.36) while the number of spikelet per panicle and spikelet fertility contributed negatively. The principal component 5, 6, 7, 8, 9, and 10 explained the remaining variation among the studied genotypes. (Table 6).

Agronomic parameters projection in the PCA plots showed the phenotypic variation among the populations this indicated how they widely dispersed along each principal component (Figure 3). The genotypes UPIA 1, UNP287 and UPN349 on the top right part of the principal component showed high yielding in either axis of principal component 1 and 2 while the genotypes UPN335 is low yielding in either axis of the principal component 1. The distribution across the principal component revealed that the genotypes near the center of the axis such as UPN275, UPN284, UPN301, and UPN324 are intermediate (not high and not low) yielding (Figure 3). The PC grouped the accessions into groups over the four quadrants based on the quantitative traits and the accessions remained scattered in all the four quadrants (Figure 3).

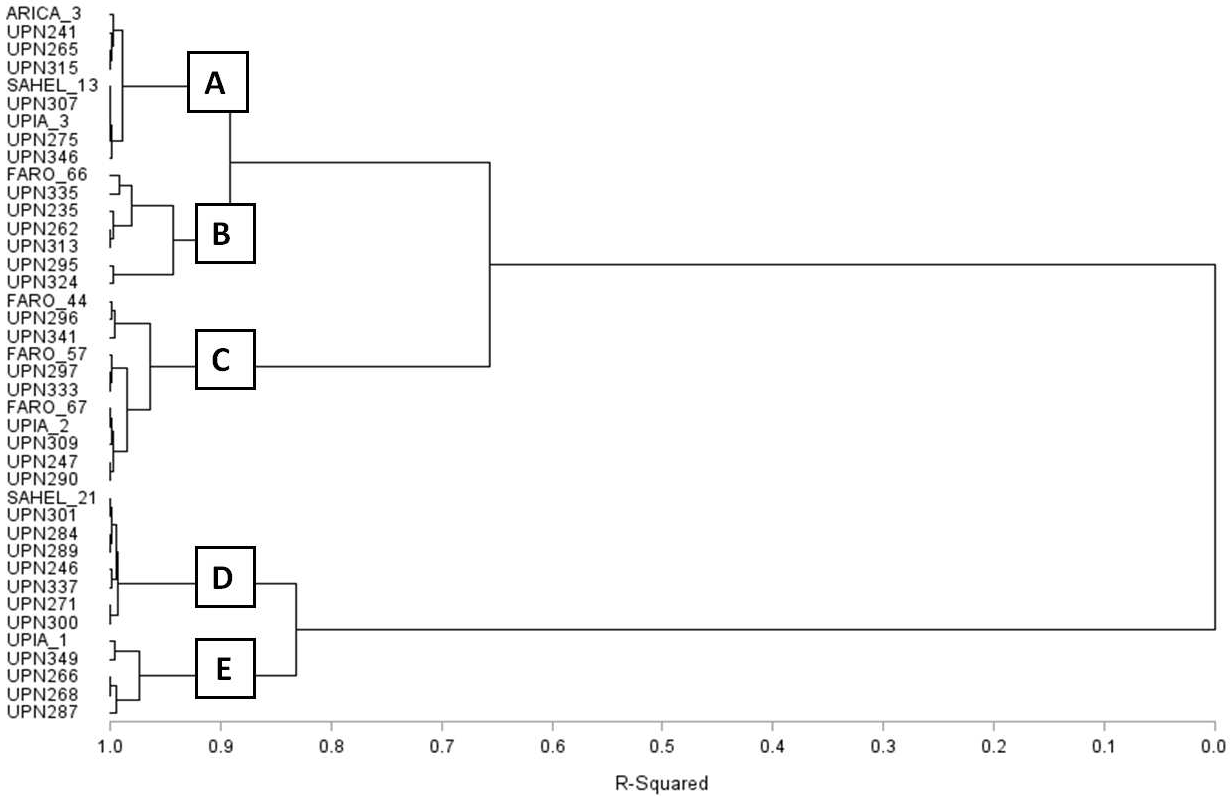

Figure 2. *Dendrogram showing genetic diversity of the genotypes.*

Table 6. *Principal Component Analysis of studied genotypes.*

Variables	PC1	PC2	PC3	PC4
Eigenvalue	5.179	3.131	2.131	1.625
Proportion (%)	0.324	0.196	0.133	0.102
Cumulative (%)	0.324	0.519	0.653	0.754
Eigen Vectors				
TILL	-.193107	0.409909	-.050614	-.194287
PAN	-.120521	0.479303	0.000893	-.128705
YIELD	0.273273	0.320556	-.189394	-.035145
TGW	0.050789	0.298995	-.096412	0.369621
SPP	0.371498	-.002137	0.315742	-.174090
PLT	0.025678	0.115188	-.153901	0.638785
PANWT	0.403574	0.081949	0.154820	-.078076
SpFert	0.196869	-.091496	-.522149	-.262824

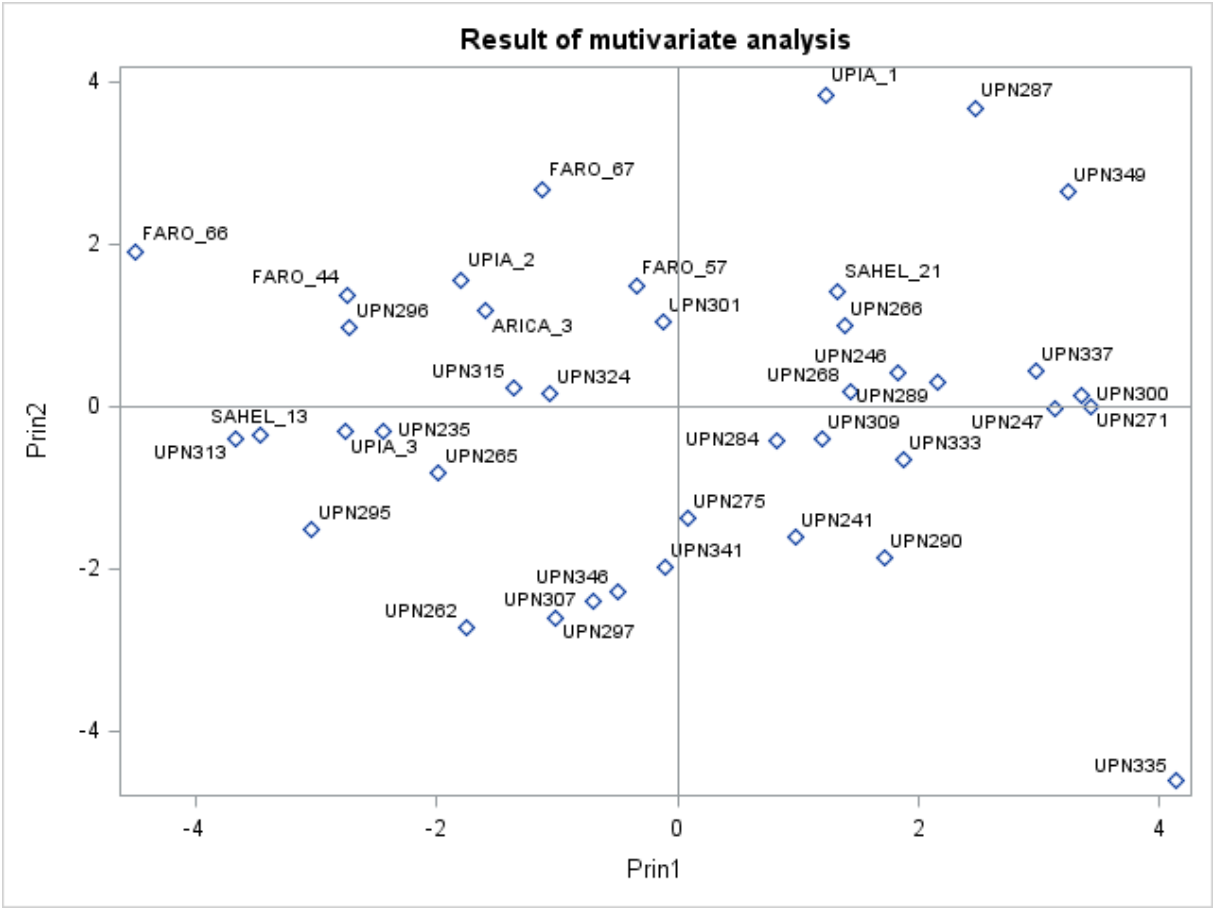

Figure 3. *Special distributions of genotypes across the principal component 1&2 axis for yield.*

4. Discussion

4.1. Performance of Agronomic Trait of the Genotypes

Breeding programs oriented to crop improvement need heritable variation for the main agronomic traits of the crop. The magnitude of genetic variability for yield and yield components traits in the breeding materials is key for efficient selection. The high diversity observed in this study indicates the necessity to group the genotypes into clusters to know the divergent groups. This agree with Bharadwaj *et al.* 2001 [20] and Kotaiah *et al.* 1986 [21] observed significant differences among the rice genotypes thus necessitated in grouping them into clusters to identify the divergent groups. In addition, this wide range of diversity indicated a sufficient variability in all the traits among the genotypes, which is beneficial to breeders for selection in a breeding programme. Plant height is one of the predominant factors determining the nitrogen response and lodging behaviour of rice plant Efisue *et al.*, 2014 [13]. The plant height shown significance difference among the genotypes tested, in addition, tall plants facilitates light penetration Chandrasekaran *et al.*, 2007 [22] which may increase photosynthetic activities of plant. Aside, the negative effect of these good agronomic traits is that tall plants easily lodge and this affects negatively the yield production. Thus,

recommend that a balance should be with strong culm (stem) that will resist lodging and fertilizer responsive that may translate to high yield, when breeders develop varieties, such as UPIA 1 (101.6), UPN 349 (101.6) and UPN 266 (104.5) genotypes. The high numbers of panicle observed in some genotypes such as in FARO 67 (9), UPN 266 (8) and UPN 349 (9) are good materials for the breeder for yield improvement as high panicle numbers determine the numbers of spikelets in the crop plant. As an important agronomy trait for grain production, Olubukola *et al.*, 2017 [23] and Efisue *and Igoma* 2019 [24] observed that tillering ability is one of the most important yield components of rice, which determines grain yield. Too few tillers result in too few panicles, but excess tillers caused high tiller mortality, small panicles, poor grain filling and consequent reduction in grain yield Peng *et al.*, 1994. [25] Thus, genotypes exhibiting high productive tillering could have the above mentioned characters such as FARO 67 (10), UPN 287 (10), FARO 66 (10), UPN315 (9) and UPIA1 (9).

The significant differences of panicle length among genotypes may be explained by genetic variability. This in accordance with Jaballa 1995 [26] that reported the difference in the panicle length trait among studied varieties.

4.2. Genetic Variability Estimates Studies

Information about the variability using parameters like genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) is of utmost importance for effective breeding programme. The observed higher values of PCV over GCV in this study for some traits could be due to the fact that variation at the phenotypic level was due to the effect of genotypes and influence of environment as reported by Singh 1999. [27] The observed high value differences between PCV and GCV for most of the traits indicates low effect of environmental influence on the expression of these traits. The observed higher vales PCV over GCV for GV, PAN, SPP, 1000_grain yield, PLT, PANWT and TILL in this study indicated that the expressions of these traits may not be significantly influenced by environment, thus, guarantees selection progress and improvement for these traits. Dursum 200 [28] who tested the variability, heritability and co-relation studies of 40 common bean genotypes. However, Tyagi and Khan 2010 [29] reported that, high GCV estimates are an indicative of less amenability of these traits to environmental fluctuations and hence, greater emphasis should be given to these characters, while breeding cultivars from the present material. Salehi *et al.*, 2008 [30] who reported narrow differences between PCV and GCV on the study of interrelationship between different traits in common bean. Osman *et al.*, 2012 [31] Hossain *et al.*, 2015 [32] and Tuhina-Khatun *et al.*, 2015 [33] reported that the environmental effect on any trait is indicated by the magnitude of the differences between the genotypic and phenotypic coefficients of variation, thus, adaptability of these material might be agro-specific to Nigeria conditions.

4.3. Correlation Analysis of Genotypes

Selection based on the detailed knowledge of magnitude and direction of association between yield and its attributes is very important in identifying the key characters, which can be exploited for crop improvement through suitable breeding programme Babu *et al.*, 2012. [34] The correlation analysis in this study and comparison with earlier studies showed the effect of genetic variation and environmental factors on grain yield and related components. The significance association of some traits was expected. These are in agreement with Nadan *et al*. 2010 [35] who found positive correlation between days to heading and days to maturity. As important parameters, these traits determine the output of rice plant performance in terms of yield. The positive and significant association of these traits such as 1000_grain weight, day to 50% flowering, panicle weight and unfilled grain per panicle will provide plant breeders an understanding of the phenotypic traits and their degree of association to be able to plan breeding schemes and managements of plant germplasm. These results are in agreement with the finding of Efisue *et al.*, 2014 [13]. Borbora *et al.* 2005 [36] found that 1000-grain weight were highly associated with rice grain yield. Al-Salim *et al.*, 2016 [37] Surek and Beser 2003 [38] reported grain yield significantly correlated with its component characters like the number of productive tillers and the number of filled grains per panicle, which is not in agreement with our findings.

4.4. Cluster Analysis of the Genotypes

Hierarchical cluster analysis of some agronomic traits and yield revealed five main groups (A, B, C, D and E) were identified at 0.9% coefficient of similarity index. Basically, crossing of genotypes of the same cluster may not to give superior hybrids or segregants, because of the little divergence that will be observed among them. However a larger divergence will generate high amount of heterosis in F1 and subsequent generations. Minimum genetic diversity present between group B and group E indicates their close relationship. The observations from cluster analysis indicate that genotypes from group A in association with those from Group E could be good candidate in breeding programme as they have maximum genetic distance and characterized by important traits, this observation corroborate the studies Agrama *et al.*, 2007; [39] Khan *et al.*, 2008. [40] Principal component analysis indicated that the first four components accounted for 75.42% of total variation giving a clear idea of the structure underlying the variables of the genotypes under studied. This is in support of many studies which have used more than three principal components to study genetic diversity in rice germplasm Nachimuthu *et al.*, 2014 [41], Mahendran *et al.*, 2015, [42] Varthini *et al.*, 2017 [43] and showed that more than three principal components are often the most important in reflecting the variation patterns among genotypes, and the characters associated with these components are more useful in differentiating the genotypes. The results from agronomic parameters projection in the PCA plots are confirmation of early finding and indicated

that those genotypes are good candidate and can be considered in breeding programme for yield improvement. The scattered aspect of the accessions in all four quadrants confirmed large genetic variability for the traits studied.

5. Conclusion

Results revealed that for a breeding programme, plant breeders should pay more attention on high associated traits with grain yield, especially grain weight, day to 50% flowering, panicle weight, number of unfilled grain. Significant and positive correlation observed between the unfilled grain and yield indicated that genotypes with high spikelets infertility could negatively affect the yield improvement. Breeders should take this into consideration when setting a breeding programme for yield improvement. The presence of wide genetic variability is of important use as it gives a large spectrum of selection to the breeders for hybridization. These genotypes, FARO 67, UPN287, FARO 66, UPN315 and UPIA1 showed high productive tillers per plant, while UPN349, UPN335, UPN271, UPN324 and UPN300 showed high number of spikelets per panicle. The first four components of PCA accounted for 75.42% of total variation giving a clear idea of the structure underlying the variables of the genotypes under studied. The maximum genetic distance was observed between group A and group E indicating that the genotypes are genetically diverse while group B and group E had minimum genetic diversity, which could be used for rice hybridization and improvement programme for rice hybrid development.

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