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Introgression progress for phenotypic traits and parent-progeny diversity at advanced segregation population from *Oryza barthii* and *O. glaberrima/O. sativa* crosses

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Abstract

Oryza barthii has candidature for some significant economic traits but its utilization in rice breeding is rare. This study traced introgression of heritable traits in the offspring of *O. barthii* with an Africa-Asian progenitor to F_8 and assessed diversity between the parents and the F_8 population. Significant ($P<0.05$) genotypic variation existed for some traits. Grains per panicle and days to 50% flowering had respective least (3.34%) and highest (96.32%) broad sense heritability. Genotypic coefficient of variation (GCV) was lower than phenotypic coefficient of variation (PCV) in all traits. Grains per panicle and tiller number had respective least (5.28% and 8.05%) and highest (90.8% and 98.1%) GCV and PCV. Progenies significantly differ in panicles and grains sizes, shapes, colours, presence or absence of awns. Five principal components explained 80.1% of the total variance. Plant height at maturity was the only trait with significant ($p \leq 0.01$) correlation and regression between F_6 and F_7. Progenies resemblance to P_1 retrogressively declined while offspring similarity to P_2 progressively increased from F_6 to F_8. The present diversity study discovered three heterotic groups: the *O. barthii* (11%), *O. sativa* (67%) and the intermediate group (22%). This research has added to rice genetic resources, making investigation of the nutritional status of the different progenies interesting research for further studies.

Keywords: advanced population; gene introgression; inter-generation diversity; *Oryza barthii*; parent-progeny correlation; segregation

Introduction

Rice is a global staple which is cultivated on every continent except Antarctica. It is adaptable to numerous climates, soil, altitudes, terrains etc. It is cultivated in more than 115 countries and feeds over 50% of the world population (Liu *et al.*, 2015). Rice is a prince among the cereals, producing the highest calories per

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unit of land (Gujja and Thiyagarajan, 2009). It is the backbone of India's economy, providing direct employment to about 70% (Vanniarajan and Ramalingam, 2011). It is dignified as relished culinary in different cultures and languages; and comes first among the important commercial food crops of the world (IRRI, 2005). The unattainment of four hundred and eighty-one million tones projected for 2020 (Mohanty, 2009) must have been subject to COVID 19 pandemic among other factors.

The cultivated rice, genus *Oryza* whose chromosome number is 12 (Matsuo *et al*., 1997) has over 20 species. Only two species, Africa rice - *Oryza glaberrima* (Steud.) and Asian rice - *Oryza sativa* (Linn.) are the cultivated species. *O. sativa* originated from South-East Asia, particularly India and Indochina, where its richest diversity exists (Sampath, 1973). The species is well distributed throughout the tropics and parts of the temperate regions of the world (Oka, 1988). The primary and secondary centres of diversity for *O. glaberrima* is the swampy basin of the upper river Niger and the south-west area near the Guinean coast (Maclean *et al.,* 2002). The cultivation of *O. glaberrima* is confined to West Africa.

Crop wild relatives harbor extremely valuable genetic resources for crop breeding. Their incorporation in crop improvement through introgression can lead to considerable proportion of alleles sharing (Jin *et al*., 2018). *O. barthii* is the progenitor of *O. glaberrima* (Linares, 2002; Sarla and Swamy 2005). It has long been recognised as a wild species of rice (Li *et al*., 2011) with interesting features, such as long flag leaf, presence of awns, long panicles and diverse grain sizes and weight (Africa Rice, 2012).) The flag leaf shields the panicles from the sight of flying birds while the long awns prevent insects from accessing the grains (Africa Rice, 2012). Other very useful traits for which *O. barthii* is notable include: tolerance to drought, high vigor, high weed competitiveness, early maturing, and production of many tillers (National Research Council, 1996; Africa Rice, 2012).

Crosses followed by selfing leads to the generation of segregating populations which allows homozygous gene expression for particular traits (Govintharaj *et al*., 2017). Parent-offspring correlation and regression between two generations according to Vanniarajan and Ramalingam (2011) are usually undertaken to estimate the genetic proportion of gene transferred from one generation to the other. It is noteworthy that parent-progeny correlation and regression values are less influenced by the environment, and it is a very useful guide to selection in segregating population (Govintharaj *et al*., 2017). While available rice genetic resources need to be sustainably conserved, continuous generation of variation remains a strong course of pursuit in pre-breeding program, for it will enhance and address improved productivity, food security and alleviate poverty amidst climatic challenges.

In the present study, our choice of the male and the female parent following Lin *et al*. (2020) was based on the identification of genetic variation between them. Notably, the unique adaptive features in *O. barthii* may have enhanced its survival for over 3,500 years (AfricaRice, 2012). The same wild species holds significant features and wide diversity, notwithstanding it has been greatly underutilized in rice breeding programs. The present investigation seeks to identify the possible introgression of heritable traits in the offspring of the wild species (*O. barthii*) with an Africa-Asian rice and to access significant phenotypic diversity between the parents and the F_8 population. Moreover, the study seeks to evaluate the level of diversity in the 8^{th} segregating populations derived from the cross.

Materials and Methods

Crosses were made between IRGC 104084 (*Oryza barthii*) and TGS 25 [(*Oryza glaberrima x Oryza sativa*) *x Oryza sativa*] to generate F1 hybrids. Through a three-year (2014-2016), selfing program involving seven cycles, 27 progenies were viable at F6 out of the 55 F1 generated. Table 1 has the list, pedigree and descriptive feature (absence or presence of awn) of the 29 genotypes involved in this study. Single seed descent

breeding method was employed for the first four cycles while the last three cycles were done using single plant selection. The 27 progenies and the two parents were evaluated on the field. The experiment was laid out in an Augmented Randomized Complete Block Design at the Africa Rice regional station, International Institute of Tropical Agriculture (IITA), Ibadan (Latitude 7° 30'N and Longitude 3°45'E), Nigeria. Each of the test entries including the two parents were evaluated in single plots of 5 rows of 5 metre. The seeds were hand-dibbled at even depth and uniform spacing of 20 x 20cm apart. NPK 15-15-15 fertilizer was applied at the rate of 200 Kg/ha as basal application immediately after planting. Subsequently, 100 Kg/ha urea (46% N) was applied in two equal split doses at tillering and panicle initiation stages. Weeding was timely carried out. The 27 progenies and the two parents were evaluated for various phenotypic traits using Standard Evaluation System for Rice (SES, 2002). Studied traits include: days to 50% flowering, days to 85% maturity, plant height at maturity, panicle length, fertility percentage, lodging and shattering score, phenotypic acceptability, panicle exsertion, a thousand (1000) grain weight, number of panicles per plant, number of spikelets per panicle and grain yield per plot from which yield per hectare was estimated.

Table 1. Pedigree of the F8 genotypes with or without the presence of awn

Codes	Pedigree	Presence of awn
P1	IRGC104084	†1
P2	TGS 25	‡0
G1	ART31-1-1-1-1-1-1-B	0
G2	ART31-1-2-1-1-1-1-B	0
G3	ART31-1-3-1-1-1-1-B	1
G4	ART31-38-2-1-1-1-3-B	0
G5	ART31-5-2-1-1-1-1-B	1
G6	ART31-6-2-1-1-1-1-B	1
G7	ART31-7-2-1-1-1-1-B	1
G8	ART31-38-2-1-1-1-5-B	0
G9	ART31-13-1-1-1-1-1-B	0
G10	ART31-17-2-1-1-1-1-B	0
G11	ART31-17-3-1-1-1-1-B	0
G12	ART31-19-1-1-1-1-1-B	1
G13	ART31-19-2-1-1-1-1-B	1
G14	ART31-38-2-1-1-1-7-B	0
G15	ART31-23-1-1-1-1-1-B	0
G16	ART31-23-2-1-1-1-1-B	0
G17	ART31-26-3-1-1-1-1-B	0
G18	ART31-27-1-1-1-1-1-B	0
G19	ART31-27-2-1-1-1-1-B	1
G20	ART31-28-3-1-1-1-1-B	1
G21	ART31-29-1-1-1-1-1-B	1
G22	ART31-29-2-1-1-1-1-B	0
G23	ART31-30-1-1-1-1-1-B	0
G24	ART31-32-1-1-1-1-1-B	0
G25	ART31-36-2-1-1-1-1-B	0
G26	ART31-40-2-1-1-1-1-B	1
G27	ART31-41-1-1-1-1-1-B	0

†1-Awn present, ‡0 -Awn absent

Analysis of variance was carried out on the quantitative and transformed scored data, following the procedure of Scott and Milliken (1993). A SAS program (version 9.4 (SAS, 2011) model Augmented Randomized Complete Block Designs was used. The linear model is as shown below:

$Y_{ij} = \mu + b_j + c_i + X_i\ (C_i) + \Sigma_{ij}$

Where: Y_{ij} is the treatment, μ is the mean, b_j denotes the block effect, *ci* is the check effect and $X_i\ (C_i)$ denotes the entry effect.

Gower genetic distance was carried out using the 29 × 15 matrix mean values of genotypes and phenotypic traits. The similarity paired distance obtained was subjected to principal component and clustering analysis. Parent-progeny correlation and regression analysis between F6 with F7 and F7 with F8 was carried out on the significant quantitative traits, following the procedure of Govintharaj *et al*. (2017) and Aananthi (2018). To further identify the introgression trend for each genotype for the combined 15 phenotypic traits, similarity of each genotype to each of parent was performed for F_6, F_7 and F_8 data using Gower genetic distance in SAS (version 9.4 (SAS, 2011). Moreover, within the Statistical Tool for Agricultural Research (STAR, 2014) software, genotype by trait interaction was conducted and presented as a two-dimensional biplot graph.

Results and Discussion

Continuous selfing of the earlier generation of progeny to advanced generations is aimed at obtaining higher homozygotic status. The main objective of single seed descent method is to rapidly advance the generation of crosses which at the end a random sampling, homozygous genotypes are obtained (Janwan *et al*., 2013). *O. barthii* derivatives are useful sources of positive alleles, especially for 1000 grain weight, high number of grains per panicle, high tillering ability, early flowering and high milling yield (Maricel, 2010). These traits have significant contribution to economic productivity in rice.

Table 2 presents descriptive and variance statistics and genetic estimates of the 15 phenotypic data used in the evaluation of the two parents and the 27 F_8 progenies from IRGC 104084 × TGS 25 crosses.

Table 2. Descriptive, genetic and variance statistical estimates of 15 phenotypic variables

Variables	Mean±SE	Range	MS Genotypes	MS GxE	MS Error	R^2	Hb (%)	GCV (%)	PCV (%)
† Plhtmat	99.27±2.37	58.0-231.9	1146.17**‡	240.33ns	72.34	0.99	81.25	54.56	62.94
Tilno	12.91±0.34	6.6-30.9	11.72ns	8.99ns	26.23	0.91	39.80	90.78	98.09
PAM	255.47±0.99	144.4-522.5	4012.18ns	3612.82ns	1119.74	0.99	50.16	70.50	80.78
Panpl	16.31±0.83	5.7-47.2	11.52*	9.55*	1.44	0.99	53.43	70.61	82.14
Panlt	19.72±0.82	6.2-28.7	4.72**	3.31**	0.21	0.99	58.27	23.96	41.13
Fert	82.41±1.53	20.1-98.4	127.23***	123.91***	1.87	0.99	50.54	54.37	60.47
Grnpan	87.74±3.12	29.0-171.8	4.63ns	1.35ns	398.08	0.98	3.34	5.28	8.05
Shatt	1.10±0.04	0.7-2.1	0.47***	0.10**	0.004	0.99	82.45	43.20	52.40
PA	1.48±0.02	0.69-2.0	0.12**	0.03*	0.004	0.99	78.71	8.52	10.82
PE	1.07±0.04	0.69-1.7	0.45***	0.08***	0.01	0.99	84.84	42.44	50.03
Log	0.75±0.15	0-4.5	6.27***	0.64**	0.04	0.99	90.47	82.56	91.87
Flw	78.98±1.35	55-102	534.36***	19.24ns	3.55	0.99	96.32	67.50	70.36
Mat	110.92±1.15	86-126	395.11**	23.11ns	10.38	0.99	93.70	35.19	38.14
GRNWT	3.17±0.03	2.5-4.3	0.25ns	0.05ns	0.07	0.97	74.61	7.91	10.60
YLD	311.73±16.12	27-861	44116.05*	10555.18ns	10048.55	0.98	76.03	51.67	61.06

† Plhtmat- Plant height at maturity, Tilno- Tiller number, PAM- Panicle per meter square, Panpl- Panicle per plant, Panlt- Panicle length, Fert- Fertility %, Grnpan- Grain per panicle, Log- lodging Score, Flw- Days to 50% Flowering, Mat- Days to 85% maturity, GRNWT- 1000 grain weight, Shatt- Shattering score, PA- Phenotypic Acceptability, PE- Panicle exsertion, YLD- Yield g/m^2

‡ *, **, *** - significance at $p \leq 0.05$, 0.01 and 0.001

Among the 29 genotypes, significant (P<0.05) genotypic variation existed for all the traits except tiller number, panicle/metre squared, grains/panicle and 1000 grain weight. Moreover, tiller number had the least (0.91) R^2 and grains/panicle had the least (3.34%) broad sense heritability (Table 2). The observed variation among the genotypes in this study agrees with the known axiom that landraces / accessions / genotypes / cultivars / varieties, etc. differ from one another, based on specific characterization scheme (morphology, biochemical or genomic). Morphologically, the black panicle of *O. barthii* had awn but the colour of the awnless panicle of *O. sativa* was straw. Very clear variations were observed in the different progenies, especially panicle and grain sizes, shapes, colours, presence or absence of awns etc. Significantly, some of the progenies combined the features in the two parents in various proportion (Figure 1).

Furthermore, in Table 2, the lower genotypic coefficient of variation (GCV) to the higher phenotypic coefficient of variation (PCV) observed in all the traits agreed with norms. This is due to the disparity in the proportion of both genotypic and the phenotypic variances. PCV is always larger because its component includes the genotypic and the residual variance. Generally, in this study, the least (5.28% and 8.05%) GCV and PCV were from grains/panicle while tiller number had the highest (90.8% and 98.1%) for the two estimates (Table 2). Heritability is a very important genetic estimate (Prajapati *et al.,* 2011) with immense utility in trait-based genotype selection. High heritability estimate was observed in plant height at maturity, fertility percent, panicle length, shattering score, phenotypic acceptability, panicle exsertion, days to 50% flowering and days to 85% maturity (Table 2); corroborating the findings of Ogunbayo *et al.* (2014). High heritability and GCV in traits indicate that the influence on the phenotype is more dependent on the genetic rather than the environmental component.

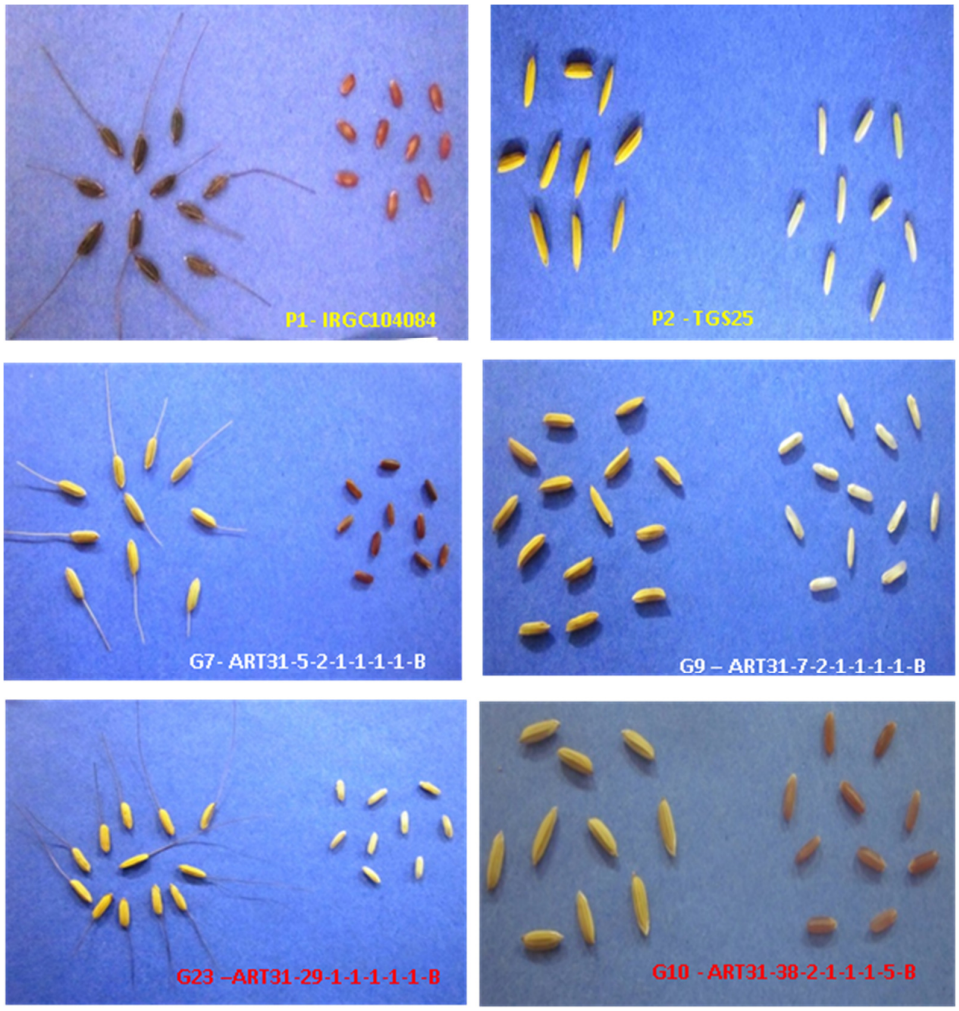

Figure 1. Phenotypic variations in panicles and grains of the parents and some of the F_8 rice progenies

Each of the five principal component axes in Table 3 had approximately 1.0 eigenvalues and above. The highest eigenvalue and correspondence variance proportion to the total variance was recorded in PC1. Eigenvalues and contributions to the total variance consistently decrease from PC1 to PC5 (Table 3). The total variance explained by the first five PC axes was 80.1% (Table 3).

Table 3. Proportions of variances and eigenvector loadings of each of the fifteen traits within principal component axes one to five

Variance components	PC1	PC2	PC3	PC4	PC5
Eigenvalues	5.028	2.820	2.202	1.036	0.928
Proportional variance	0.335	0.188	0.147	0.069	0.062
Cumulative variance (%)	33.5	52.3	67.0	73.9	80.1
	Eigenvectors				
Variables	PC1	PC2	PC3	PC4	PC5
†Plhtmat	0.107	-0.158	-0.544	-0.287	0.093
Tilno	0.341	0.215	0.053	0.091	-0.073
PAM	0.367	0.086	0.287	-0.062	-0.092
Panpl	0.300	0.137	0.218	-0.080	-0.460

Panlt	0.182	-0.222	0.225	-0.115	0.640
Fert	0.274	-0.191	0.007	0.421	-0.217
Grnpan	0.106	-0.445	-0.227	0.234	-0.148
Shatt	-0.171	0.256	-0.381	0.031	-0.173
PA	-0.070	0.431	0.146	0.309	0.188
PE	-0.290	0.239	0.316	-0.089	0.008
Log	0.253	0.275	-0.189	-0.097	0.386
Flw	-0.367	-0.224	0.116	0.125	0.058
Mat	-0.330	-0.239	0.217	0.250	0.008
GRNWT	0.053	0.220	-0.258	0.664	0.218
YLD	0.316	-0.282	0.199	0.148	0.147

† Plhtmat- Plant height at maturity, Tilno- Tiller number, PAM- Panicle per meter square, Panpl- Panicle per plant, Panlt- Panicle length, Fert- Fertility %, Grnpan- Grain per panicle, Log- lodging Score, Flw- Days to 50% Flowering, Mat- Days to 85% maturity, GRNWT- 1000 grain weight, Shatt- Shattering score, PA- Phenotypic Acceptability, PE- Panicle exsertion, YLD- Yield g/m

Tiller number, panicle/metre square, panicle/plant, fertility percentage, panicle exsertion, lodging scoring, days to 50% flowering, days to 85% maturity and yield were prominent in their contribution to the variance proportion in PC1; panicle length, grain/panicle, shattering score, phenotypic acceptability and 1000 grain weight were prominent in PC2 while, plant height at maturity had the highest eigenvector loading in PC3 (Table 3). The eigenvector loadings of the listed variables (for each PC, above) were ≥ 0.3 (Table 3), revealing that all morphological traits do not contribute to total variance equally. Furthermore, variance proportion by each trait is not static. The genetic materials involved in a study and the environment of the experiment (in time or space) are the specific determinants of the variance proportions of phenotypic traits. Genomic diversity is not influenced by either factor, hence, its generous recommendation (Mohammadi and Prasanna, 2003).

At the 0.10 points of inflection in Figure 2, four clusters were visible. P1 stood alone in cluster I, cluster III (with only two genotypes) was closest to it with Gower genetic similarity of 0.95 (Table not shown) and both clusters (I and III) joined at 0.125 similarity point (Figure 2). Cluster II had the highest (20) population of genotypes with P2 as one of its members. The similarity among the 20 genotypes in cluster II was 0.78 (Table not shown). Clustering analysis is based on similarities (depending on the employed phenotypic traits) which informed that the 19 progenies in cluster II were very similar to P2 (TGS 25). Within cluster II, two sub-clusters with population of 11 and 9 were prominent, each with sub-cluster similarities of 0.79 and 0.80 (Table not shown). Cluster IV contained six genotypes. The Gower genetic similarities of the six genotypes were 0.79 (Table not shown). The six formed an independent population with differing significant features of both *O. barthii* and *O. sativa.* Based on plant types, three groups were visible in this study, they are: the *O. barthii* group (11%), *O. sativa* group (67%) and the intermediate plant type group (22%). This informs that the present research has led to the increase in genetic diversity of rice germplasm, thus adding more to the genetic resources with promising potentials for rice improvement program. Moreover, the origination of a new group stemmed from the hybridization program of elite alleles into the wild relative (*O. barthii*) species/populations. Meanwhile, according to Jin *et al.* (2018) the introgression procedure has changed the genetic structure of the progenies due to genetic recombination. Continuous creation of variation is a primary duty in plant breeding because abundance of genetic diversity and rational population structure of germplasm is a great resource in crop breeding (Liu *et al*., 2015). The inter-cluster variations observed in this study revealed four heterotic grouping of genotypes and within each there are specific notable traits of prominence for which every member share high similarity. The present status provides access to meaningful selection based on phenotypic performances of each group and individual genotypes.

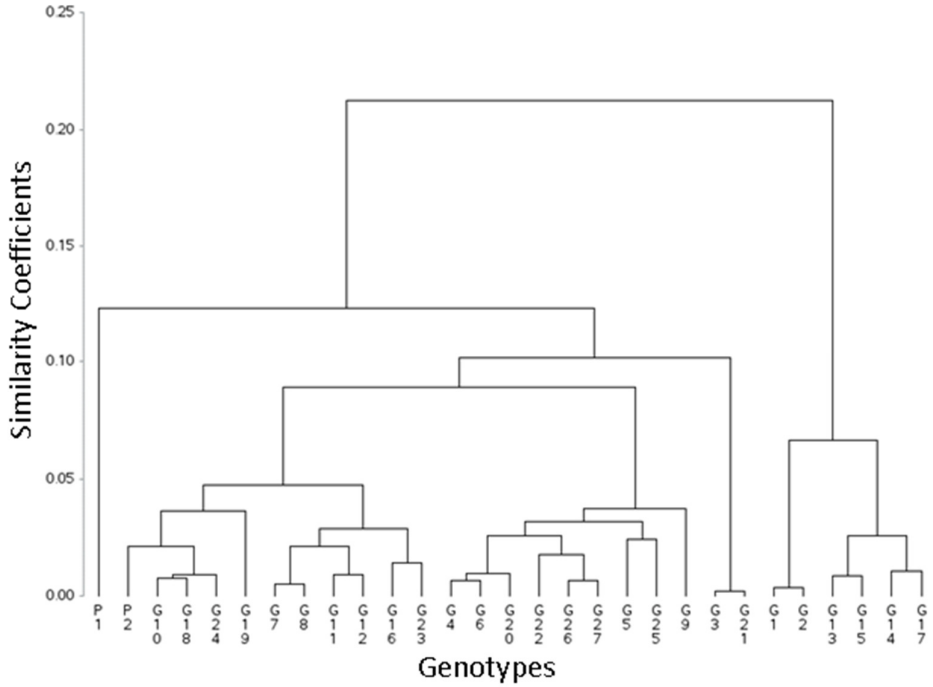

Figure 2. Grouping relationship among the two parents and the 27 F_8 genotypes derived from the cross between IRGC 104084/TGS 25

Mean performances of the different groups of genotypes in the various clusters were further investigated. P1 (IRGC 104084) which solely appeared in cluster I had the least value for plant height at maturity, panicle length, grain/panicle, and yield. However, the same genotype had the highest value for tiller number, shattering score, phenotypic acceptability, panicle exsertion and 1000 grain weight, thereby approving the initial assertion of AfricaRice (2012) on *O. barthii*. The twenty genotypes in cluster II had the least mean for 1000 grain weight meanwhile, mean value from this group of genotypes was next to the best for final grain yield. G3 and G21 which were the only two members in cluster III had the highest mean for plant height, PAM, panicle length, panicles/plant, fertility percentage, grains/panicle, lodging score and the highest grain yield. Moreover, the genotypes in the cluster had the lowest value for shattering score, PA, PE, days to 50% flowering and days to 85% maturity. Genotypes in cluster IV were distinguished for the lowest tiller number, PAM, panicle length, fertility percentage and zero lodging but flowered and matured latest.

The total variance which captured the display of genotype by trait interaction in Figure 3 by the first two PC axes was 52.3%. The interactions featured in the four quadrants. P1 and P2 were separately located at quadrants one and three respectively (Figure 3). Panicle exsertion, phenotypic acceptability and shattering scores were the prominent traits in the first quadrant and P1, G1, G12 and G14 were the genotypes with corresponding highest values for them (Figure 3). In quadrant two, G3, G9, G20, G21, G22, G25, G26 and G27 had significant higher performances for 1000 grain weight, logging score, tiller number, panicle length and panicle/metre square (Figure 3). Prominent traits which associated with the nine genotypes in quadrant III were: fertility percent, height at maturity, panicle length, grains/panicle and yield. Days to 50% flowering and days to 85% maturity were significantly correlated in quadrant IV and genotypes with significant association with them include: G11, G12, G13, G15, G16, G17 and G23 (Figure 3). Genotype by Trait analysis, according to Yan and Kang (2003) unveils individual genotype performances for specific trait(s) as well as the associations among different traits for specific genotypes, thus providing vivid guide to trait-based selection.

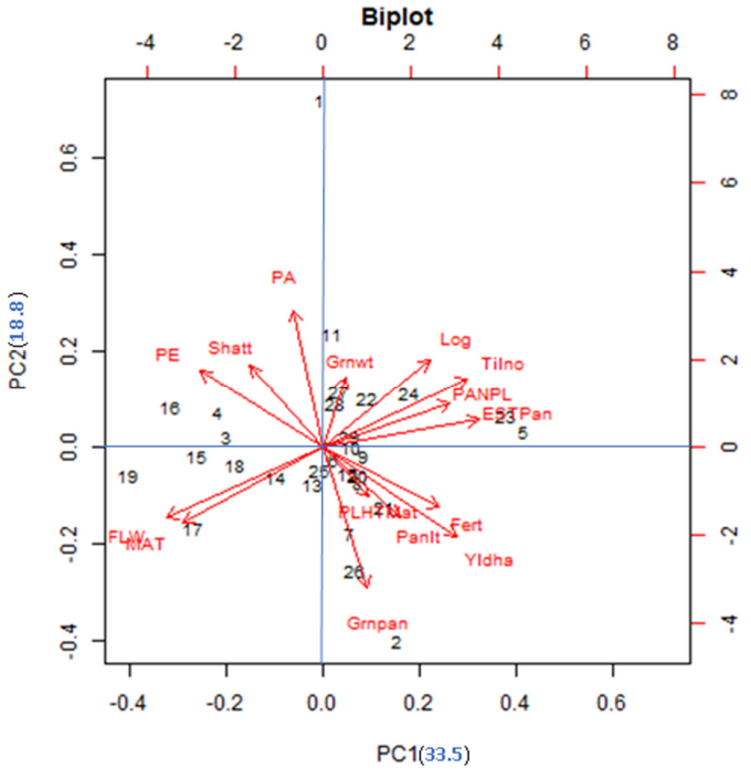

Figure 3. Twenty-nine genotypes by fifteen traits interaction displayed within the first two principal components

* Plhtmat- Plant height at maturity, Tilno- Tiller number, PAM- Panicle per meter square, Panpl- Panicle per plant, Panlt- Panicle length, Fert- Fertility %, Grnpan- Grain per panicle, Log- lodging Score, Flw- Days to 50% Flowering, Mat- Days to 85% maturity, GRNWT- 1000 grain weight, Shatt- Shattering score, PA- Phenotypic Acceptability, PE- Panicle exsertion, YLD- Yield g/m2

**1 - P1, 2 - P2, 3 - G1, 4 - G2, 5 - G3, 6 - G4, 7 - G5, 8 - G6, 9 - G7, 10 - G8, 11 - G9, 12 - G10, 13 - G11, 14 - G12, 15 - G13, 16 - G14, 17 - G15, 18 - G16, 19 - G17, 20 - G18, 21 - G19, 22 - G20, 23 - G21, 24 - G22, 25 - G23, 26 - G24, 27 - G25, 28 - G26, 29 - G27

Proportional similarities of each of the 27 progenies to P1 and P2 is presented in Table 4. Generally, similarity of the 27 progenies to P1 declined linearly from F6 to F8 while the similarity of the same 27 progenies to the P2 rose from F6 to F8 in a positive linear trend (Table 4). Individual similarity of the 27 progenies to the two parents differed with the identification of four notable trend responses. These include: positive linear, negative linear, positive quadratic and negative quadratic. None of the progenies exhibited positive linearity with P1, however, 40.8% exhibited negative linearity, 37% exhibited positive quadratic and 22.2% exhibited negative quadratic trend with P1 from F6 to F8 (Table 4). The cytoplasmic inheritance role of P1 (IRGC 104084) according to Wolf and Wade (2009) on the progenies in the introgression process was very low. However, in the same Table, the respective percentage response of the similarity of the 27 progenies with P2 were 14.8% (positive linear), 14.8% (negative linear), 40.8% (positive quadratic) and 29.6% (negative quadratic).

Table 4. Proportional similarities of each of the 27 progenies to the two parents at F6, F7 and F8

Genotypes	Similarities with P1				Similarities with P2			
	F6	F7	F8	Remarks	F6	F7	F8	Remarks
G1	43.16	48.42	46.52	-ve Quadratic	73.84	83.22	64.34	-ve Quadratic
G2	60.38	32.38	46.97	+ve Quadratic	49.39	86.46	57.69	-ve Quadratic
G3	43.06	37.89	56.31	+ve Quadratic	65.41	92.51	69.56	-ve Quadratic
G4	59.28	65.59	55.53	-ve Quadratic	62.88	57.62	78.82	+ve Quadratic
G5	65.29	60.47	45.92	-ve Linear	91.33	76.19	83.67	+ve Quadratic
G6	65.68	48.60	46.92	-ve Linear	72.32	64.38	87.87	+ve Quadratic
G7	60.05	38.10	49.05	+ve Quadratic	78.47	91.08	76.74	-ve Quadratic
G8	59.28	50.58	43.20	-ve Linear	62.88	66.18	80.63	+ve Linear
G9	56.51	56.28	64.41	+ve Quadratic	72.07	61.63	71.73	+ve Quadratic
G10	76.49	64.70	56.51	-ve Linear	61.94	64.74	81.17	+ve Linear
G11	73.55	66.79	44.40	-ve Linear	73.63	59.96	78.63	+ve Quadratic
G12	73.18	51.69	47.95	-ve Linear	54.52	81.01	74.17	-ve Quadratic
G13	65.14	81.60	51.40	-ve Quadratic	76.68	52.85	60.18	+ve Quadratic
G14	59.28	69.51	55.13	-ve Quadratic	62.88	58.95	54.38	-ve Linear
G15	66.51	51.43	31.07	-ve Linear	83.50	80.22	57.84	-ve Linear
G16	67.83	42.48	46.19	-ve Quadratic	82.50	91.26	74.26	-ve Quadratic
G17	83.44	51.92	42.68	-ve Linear	70.96	70.96	55.44	-ve Linear
G18	69.28	59.65	49.49	-ve Linear	73.01	71.17	84.41	+ve Quadratic
G19	70.11	50.97	48.21	-ve Linear	87.34	60.42	72.27	+ve Quadratic
G20	55.24	52.07	65.96	-ve Quadratic	73.67	48.62	73.65	+ve Quadratic
G21	53.97	43.50	54.92	+ve Quadratic	77.00	73.27	69.71	-ve Linear
G22	66.81	37.28	62.54	+ve Quadratic	67.25	88.20	64.86	-ve Quadratic
G23	58.70	36.03	41.65	+ve Quadratic	71.79	78.04	83.36	+ve Linear
G24	78.78	50.84	40.72	-ve Linear	73.81	71.52	86.98	+ve Quadratic
G25	62.54	48.73	56.33	+ve Quadratic	54.87	80.63	68.73	-ve Quadratic
G26	77.12	44.75	59.59	+ve Quadratic	78.73	70.39	78.77	+ve Quadratic
G27	70.21	48.28	52.44	+ve Quadratic	68.51	85.99	87.76	+ve Linear
Mean	**64.48**	**51.50**	**50.44**	**-ve Linear**	**71.15**	**72.87**	**73.24**	**+ve Linear**

Table 5. Parent-offspring correlation and regression for some traits in IRGC 104084/TGS 25 cross

Traits	Correlation (r)		Regression (b)	
	F_6-F_7	F_7-F_8	F_6-F_7	F_7-F_8
Days to 50% flowering	0.096ns	-0.013ns	0.108ns	-0.014ns
Days to 85% maturity	0.111ns	-0.077ns	0.146ns	-0.086ns
Plant height at maturity	0.479**	-0.019ns	0.576**	-0.021ns
Tiller numbers	-0.181ns	-0.093ns	-0.236ns	-0.535ns
Panicle exsertion	0.079ns	0.185ns	0.147ns	0.478ns
Shattering score	-0.043ns	0.326ns	-0.119ns	0.866ns
Phenotypic acceptability	0.009ns	-0.127ns	0.011ns	-1.151ns
Fertility percentage	0.033ns	-0.087ns	0.003ns	-0.187ns

Among the eight phenotypic traits measured for the three generations (F_6, F_7 and F_8) in Table 5, only plant height at maturity had significant ($p \leq 0.01$) correlation and regression between F_6 and F_7. F_6-F_7 and F_7-F_8 seemed to be too advanced a stage for effective selection of majority of the measured phenotypic traits in this study except plant height at maturity. Selection response of traits differs just as the most effective generation to make selection for each trait based on correlation and regression analyses outcome equally differs. In respect of segregation generations, many authors (Vanniarajan and Ramalingam, 2011; Govintharaj *et al*., 2017; Aananthi, 2018) have hinted that selection at earlier generations are most effective for many traits. Majority (88%) of our measured traits seem to conform to the above since our single plant selection program commenced at F_6. However, there are some traits whose effective selection would be most appropriate at the advanced generations (Aananthi, 2018). Our study identified plant height at maturity as one of such phenotypic traits whose most effective selection can be achieved at F_6-F_7 intergeneration and indicating F_6 as a good indicator for F_7 performances for the trait in the studied rice genotypes. Selection of traits and identification of superior genotypes is most effectively reliable at the generation when the correlation and regression analyses are both significant.

Conclusions

This study identified three subsisting germplasm; those similar to Oryza barthii (IRGC 104084 - P1), *Oryza glaberrima* x *Oryza sativa*) x *Oryza sativa* (TGS 25 - P2) and the intermediate. Parent-progenies diversity were elucidated and level of genetic diversity with respect to plant types within the genus *Oryza* were equally unveiled. Among all the traits, only plant height at maturity could be 244 delayed to an advanced introgression scheme of F_6 for reliable selection. The generated and distinct recombinants (hybrids) produced in this study was added to the genetic resources of rice. Moreover, investigation of nutritional status of the different progenies in this study would be interesting for further selection, research and utilization.

Authors' Contributions

PBO and COI - Conceptualization; PBO - Data curation; ABD and PBO - Formal analysis; PBO, ABD, OCJ and BMO - Investigation; PBO, COI and ABD - Methodology; PBO - Resources; COI and BMO - Supervision; PBO - original draft; ABD, CJO and BMO - review and editing.

All authors read and approved the final manuscript.

Ethical approval (for researches involving animals or humans)

Not applicable.

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Conflict of Interests

The authors declare that there are no conflicts of interest related to this article.

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