

Variation and Phenotypic Evaluation of Intraspecific *Oryza glaberrima* Lines Resulting from Crossings between Tog5681, Tog5672 and Tog7291

Yves Agnoun¹, E. Ahounou², M. Sié³, S. A. Ogunbayo³, B. Toulou³, K. Futakuchi³ & A. Ahanchédé¹

¹ Faculty of Agricultural Sciences, University of Abomey-Calavi, 01 BP 526, Cotonou, Benin

² Faculty of Science and Technics, University of Abomey-Calavi, 01 BP 526, Cotonou, Benin

³ Africa Rice Center, 01 BP 2031, Cotonou, Benin

Correspondence: Yves Agnoun, Faculty of Agricultural Sciences, University of Abomey-Calavi, 01 BP 526, Cotonou, Benin. Tel: 229-9708-9577. E-mail: yagnoun@yahoo.fr

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Abstract

Rice cultivation in Africa suffers from various biotic and abiotic constraints. The African rice, *Oryza glaberrima*, is a potential source of useful genes for resistance to a range of these stresses. The development of interspecific varieties based on crosses between the high yielding cultivated Asian rice species (*Oryza sativa*) and *O. glaberrima* showed some gaps in the resistance compared to *O. glaberrima*. In order to valorize its genetic potential, intraspecific lines were developed using three *O. glaberrima* lines Tog5681, Tog5672 and Tog7291 as parents. Phenotypic evaluation of the progeny (total of 55 F₆ lines) and checks (*O. glaberrima* and *O. sativa*) using 18 quantitative characters, showed a higher degree of variation in plant height, leaf dimensions, panicle fertility and grain weight. Based on the discriminating characters proposed here for further exploitation, intraspecific lines were grouped into five clusters, two of which (G4 and G5) contained the best lines for vegetative (G4) and productive (G5) characters.

Keywords: *Oryza glaberrima*, intraspecific, evaluation, phenotypic diversity, varietal improvement

1. Introduction

Rice is one of the main stands of global food security and has thus been one of the main focuses of international research for several decades. It is a staple food of about half of the world's population living in Asia and Africa, providing 40 to 70% of their total food calories. In Africa, it is one of the most important food crops and its consumption growth rate is higher than the population growth rate. The estimated annual global rice production was about 688 million tons in 2008 and 689 million tons in 2009 on about 149 million hectares (FAO, 2009). However, despite this strong growth in production, there is a growing demand for rice mainly due to demographic increase, rapid urbanization, increased proportion of rice in the population's diet, especially those of Africans and new end-users (livestock feed, breweries, processors and agri-business farmers etc.). It is expected that this demand will continue to grow. Yet, among the millions of people suffering from chronic hunger throughout the world, over 50% live in areas dependent on rice production. Moreover, about 80% of small-scale rice farmers, generally poor, contribute to the world's rice production primarily to increase their incomes and satisfy their family needs, but also to improve human consumption and his health well-being (FAO, 2004).

In Africa, rice cultivation suffers from a number of constraints, such as weeds competition, salinity, nitrogen nutrition, iron toxicity, pests and diseases, which severely affect rice productivity (Thiémélé et al., 2010; Sahrawat & Sika, 2002; Fofana & Rauber, 2000). To cope with these stresses, interspecific hybridization were used by the Africa Rice Center (AfricaRice) to develop new rice varieties known as NERICA (New Rice for Africa), starting from crossings between the two cultivated rice species *Oryza glaberrima* and *Oryza sativa* (Jones et al., 1997). In general, this interspecific breeding program aimed to combine the positive characteristics of the cultivated African rice *O. glaberrima* resistance genes, and weed competitiveness due to early growth vigor, high tillering ability, large leaf area and droopy leaves with the high yielding ability of the Asian rice *O. sativa*. The high grain productivity of the Asian species is due mainly to its fertile and rich panicles with

secondary branches, erect leaves, without plant lodging or grain shattering. The interspecific breeding program provided AfricaRice scientists an opportunity to improve the agronomic potentialities of *O. sativa*, including its two sub-species japonica and indica. It also provided access to the *O. glaberrima* genome and enabled the introgression of minor oligogenic genes into the Asian varieties, which had hitherto had very limited success (Jones et al., 1997; Ndjioudjop et al., 2008; Agnoun et al., 2012). The current NERICA varieties are inferior to *O. glaberrima* in terms of weed-competitiveness (Rodenburg et al., 2009), resistance to rice insect pests and diseases and are more similar to *O. sativa* than *O. glaberrima* in relation to morphological characteristics at both vegetative and reproductive growth stages.

Recent findings by AfricaRice scientists and their partners, especially breeders, agronomists and nutritionists, have sparked renewed interest in the cultivated African rice species *O. glaberrima* (Sarila, 2005; Joho et al., 2008; Futakuchi & Sié, 2009; Mohapatra, 2010, 2011; Moukoubi et al., 2011). Indeed, *O. glaberrima* has proved to be a rich source of resistance genes for rice production constraints in West and Central Africa (WCA), e.g. resistance to the rice yellow mottle virus (RYMV), cannot be found easily in the variation of *O. sativa*.

Although since several scientific studies have revealed the genetic importance of *O. glaberrima*, AfricaRice is still seeking outstanding *O. glaberrima* genotypes and a good alternative way to better exploit its useful genetic assets. In this regard, two alternative breeding pathways have been suggested: (i) the first possibility for developing NERICA varieties with good introgression of the African rice genome is backcrossing to the *O. glaberrima* parent. However, there is no influence of the *O. glaberrima* parent on the yielding ability of the existing NERICA lines; (ii) the second way, which was adopted in the present study, is to develop intra-specific *O. glaberrima* breeding varieties. According to Futakuchi and Sié (2009), and Sié et al. (2012), the second breeding method is the best way to exploit the unique assets of the cultivated African rice multiple resistances to major WCA constraints, for instance because fixed fertile progeny can be obtained without suffering from a sterility barrier that always crops up in interspecific breeding. Following the overall breeding concept and alternative conventional breeding methods, intra-specific *O. glaberrima* lines were developed starting from three outstanding varieties that are resistant to RYMV: Tog 5681, Tog 5672 and Tog 7291. In this study, we evaluated, through agro-morphological characterization, these intra-specific lines which are adapted to the irrigated lowland cropping system.

2. Materials and Methods

2.1 Plant Materials

The rice germplasm (Table 1) is composed of intra-specific *O. glaberrima* populations derived from crosses between three outstanding *O. glaberrima* lines Tog 5681, Tog 5672 and Tog 7291 which are resistant to rice diseases, especially blast and RYMV (AfricaRice, 2008; Thiémélé et al., 2010; Sié et al., 2002) and lodging (case of Tog7291) reported by (Futakuchi et al., 2008). The plant material evaluated for their agro-morphological traits comprised 55 genotypes, including 11 intra-specific lines of the F₆ generation derived from Tog 5681 × Tog 5672, and 44 F₆ generation lines derived from Tog 5681 × Tog 7291. Five different checks, including three *O. glaberrima* (Tog 5681, Tog 5672 and Tog 7442), and two *O. sativa* (FKR19 and FKR54) were used as checks. Tog5681 and Tog5672 were used as parents and checks because of their good vegetative growth and resistance to different biotic and abiotic West-African constraints such as blast, RYMV, weed-competitiveness, drought, salinity and iron toxicity; Tog7442 possesses good grain productivity and immunity to the African Rice Gall Midge (AfRGM) (Singh et al., 1996). Concerning the two sativa checks, FKR19 is highly adapted to lowland and irrigated ecologies while FKR54 has high yielding potential.

Table 1. Intra-specific lines derived from crosses between *O. glaberrima* varieties (Tog5681, Tog5672 and Tog7291) and checks

No.	Pedigree	Parents	Class	Source	Generation
1	S2-4	Tog 5681/Tog 5672	Class2	AfricaRice	F6
2	S2-5	Tog 5681/Tog 5672	Class2	AfricaRice	F6
3	S2-6	Tog 5681/Tog 5672	Class2	AfricaRice	F6
4	S5-8	Tog 5681/Tog 5672	Class2	AfricaRice	F6
5	S6-9	Tog 5681/Tog 5672	Class2	AfricaRice	F6
6	S7-1	Tog 5681/Tog 5672	Class2	AfricaRice	F6

7	S19-1	Tog 5681/Tog 5672	Class2	AfricaRice	F6
8	S19-3	Tog 5681/Tog 5672	Class2	AfricaRice	F6
9	S19-4	Tog 5681/Tog 5672	Class2	AfricaRice	F6
10	S21-6	Tog 5681/Tog 5672	Class2	AfricaRice	F6
11	S24-9	Tog 5681/Tog 5672	Class2	AfricaRice	F6
12	P1 49-7	Tog 5681/Tog 5672	Class1	AfricaRice	F6
13	PL50-4	Tog 5681/Tog 7291	Class1	AfricaRice	F6
14	PL50-6	Tog 5681/Tog 7291	Class1	AfricaRice	F6
15	PL51-1	Tog 5681/Tog 7291	Class1	AfricaRice	F6
16	PL51-2	Tog 5681/Tog 7291	Class1	AfricaRice	F6
17	PL51-3	Tog 5681/Tog 7291	Class1	AfricaRice	F6
18	PL52-2	Tog 5681/Tog 7291	Class1	AfricaRice	F6
19	PL52-4	Tog 5681/Tog 7291	Class1	AfricaRice	F6
20	PL52-5	Tog 5681/Tog 7291	Class1	AfricaRice	F6
21	PL52-7	Tog 5681/Tog 7291	Class1	AfricaRice	F6
22	PL52-8	Tog 5681/Tog 7291	Class1	AfricaRice	F6
23	PL55-2	Tog 5681/Tog 7291	Class1	AfricaRice	F6
24	PL55-7	Tog 5681/Tog 7291	Class1	AfricaRice	F6
25	PL57-4	Tog 5681/Tog 7291	Class1	AfricaRice	F6
26	PL57-5	Tog 5681/Tog 7291	Class1	AfricaRice	F6
27	PL57-7	Tog 5681/Tog 7291	Class1	AfricaRice	F6
28	PL58-1	Tog 5681/Tog 7291	Class1	AfricaRice	F6
29	PL58-2	Tog 5681/Tog 7291	Class1	AfricaRice	F6
30	PL62-1	Tog 5681/Tog 7291	Class1	AfricaRice	F6
31	PL62-2	Tog 5681/Tog 7291	Class1	AfricaRice	F6
32	PL67-1	Tog 5681/Tog 7291	Class1	AfricaRice	F6
33	PL68-1	Tog 5681/Tog 7291	Class1	AfricaRice	F6
34	PL68-6	Tog 5681/Tog 7291	Class1	AfricaRice	F6
35	PL68-8	Tog 5681/Tog 7291	Class1	AfricaRice	F6
36	PL75-2	Tog 5681/Tog 7291	Class1	AfricaRice	F6
37	PL75-3	Tog 5681/Tog 7291	Class1	AfricaRice	F6
38	PL75-4	Tog 5681/Tog 7291	Class1	AfricaRice	F6
39	PL75-6	Tog 5681/Tog 7291	Class1	AfricaRice	F6
40	PL82-7	Tog 5681/Tog 7291	Class1	AfricaRice	F6
41	PL85-1	Tog 5681/Tog 7291	Class1	AfricaRice	F6
42	PL85-2	Tog 5681/Tog 7291	Class1	AfricaRice	F6
43	PL85-3	Tog 5681/Tog 7291	Class1	AfricaRice	F6
44	PL85-4	Tog 5681/Tog 7291	Class1	AfricaRice	F6
45	PL85-5	Tog 5681/Tog 7291	Class1	AfricaRice	F6
46	PL87-1	Tog 5681/Tog 7291	Class1	AfricaRice	F6
47	PL87-2	Tog 5681/Tog 7291	Class1	AfricaRice	F6
48	PL87-3	Tog 5681/Tog 7291	Class1	AfricaRice	F6

49	PL87-4	Tog 5681/Tog 7291	Class1	AfricaRice	F6
50	PL87-5	Tog 5681/Tog 7291	Class1	AfricaRice	F6
51	PL87-6	Tog 5681/Tog 7291	Class1	AfricaRice	F6
52	PL87-8	Tog 5681/Tog 7291	Class1	AfricaRice	F6
53	PL88-3	Tog 5681/Tog 7291	Class1	AfricaRice	F6
54	PL92-1	Tog 5681/Tog 7291	Class1	AfricaRice	F6
55	PL92-4	Tog 5681/Tog 7291	Class1	AfricaRice	F6
56	Tog 5672 (<i>O. glaberrima</i>)	-	Check 1	AfricaRice	
57	Tog 5681 (<i>O. glaberrima</i>)	-	Check 2	AfricaRice	
58	Tog 7442 (<i>O. glaberrima</i>)	-	Check 3	AfricaRice	
59	FKR 19 (<i>O. sativa</i>)	MASHURI/ IET 1444	Check 4	AfricaRice	
60	FKR 54 (<i>O. sativa</i>)	-	Check 5	AfricaRice	

2.2 Establishment of Experimental Trial

The experiment was established in the 2011 cropping season on the experimental site of AfricaRice located at Ouedeme (6°42'46"N and 1°41'07"E at 21 m altitude), District of Lokossa in Benin (Figure 1). The field was mechanically ploughed, harrowed and leveled, and the trial was laid out using the Augmented Block Design (Federer, 1956). There were five blocks separated by 1 m with 16 genotypes randomized in each block (11 intra-specific *O. glaberrima* lines and 05 checks). After sowing at a spacing of 20 × 20 cm within each plot (5 × 1 m²) comprising five rows for each genotype, seedlings were thinned to one plant per hill in the field. Fertilizers applied included NPK 15-15-15 as basal application at the rate of 100 kg ha⁻¹ during land preparation, and urea applied as top dressing at the rate of 35 at tillering and 65 kg /ha at heading. Hand weeding was carried out at 21 days after sowing (DAS) and at heading just before urea application.

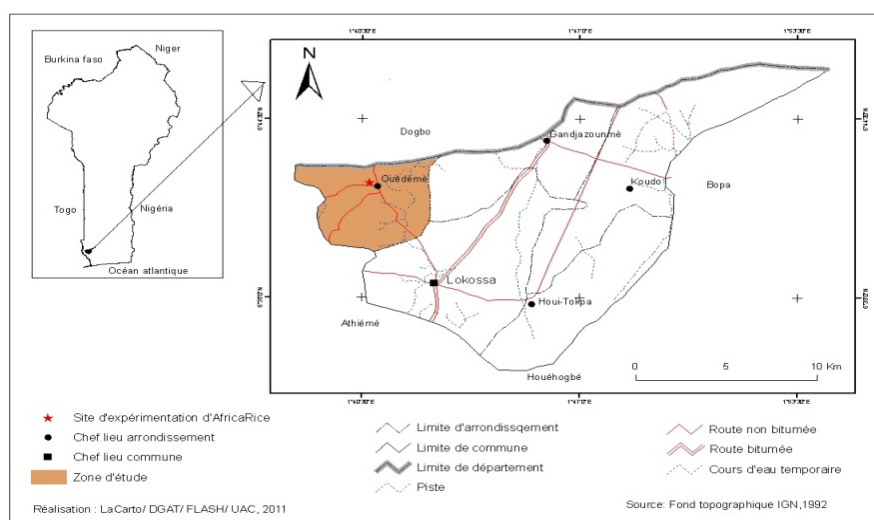


Figure 1. Location of the experimental farm at Ouedeme (Lokossa/Benin)

2.3 Phenotypic Evaluation

Each of the different intra-specific classes was evaluated using 18 agro-morphological quantitative traits. Data were collected from the three middle rows of each plot and average of each quantitative variables were used for the analysis. Plant agro-morphological evaluation was carried out using the Standard Evaluation System (SES) for Rice of the International Rice Research Institute (IRRI, 2002). These variables are presented in Table 2.

Table 2. Quantitative characters measured on the 55 intra-specific *O. glaberrima* lines and checks

S/N.	Characters	Code	S/N.	Characters	Code
1	Days to 50% heading	50% Hdg	10	Panicle length	PnL
2	Tiller number at 60 DAS	Ti 60DAS	11	Primary panicle branches	PPnBr
3	Number of panicles	NPn	12	Secondary panicle branches	SPnBr
4	Plant height at 30 DAS	HT 30DAS	13	Weight of 1000 grains	W1000Gr
5	Plant height at 60 DAS	HT 60DAS	14	Number of full grains	FullGr
6	Plant height at maturity	HT mat	15	Panicle fertility	Pnfert
7	Leaf length	LL	16	Grain length	GrL
8	Leaf width	LW	17	Grain width	GrW
9	Diameter	Diam	18	Days to maturity	Mat

2.4 Statistical Analyses

Average and standard deviation were calculated on each quantitative character. Variation in various measured characters was tabulated and plotted using the Microsoft Excel Program. Comparison was also made between intra-specific crossing groups and checks. Phenotypic associations were assessed between the 55 intra-specific *O. glaberrima* lines and checks using correlation coefficient, principal component analysis (PCA) and cluster analysis. Differences observed between clusters were evaluated through Analysis of Variance (ANOVA). These data analyses were evaluated using Statistica and SPSS software.

3. Results

3.1 Variation within Intra-specific *O. glaberrima* Classes and Checks

The intra-specific *O. glaberrima* evaluated displayed a considerable variation for the measured quantitative characters. There was highly significant variation between the two different classes and checks in plant height at 60 DAS, leaf dimensions, weight of 1000 grains, panicle fertility and grain length (Figures 2-7). Class 1, including the majority (83.63%) of the studied genotypes contains lines characterized by very well developed leaves and a wide range of variation within the measured characters. In opposite, intra-specific lines in from class 2 (16.36%) possess medium to high plant height and relatively long grains, fertile and productive panicles.

The variation observed among the checks showed that *O. glaberrima* varieties, especially Tog5681, have good vegetative growth (expressed by high tillering, plant height and developed leaf area) whereas sativa checks, especially FKR 54, had important yielding characters (panicle fertility, grain length and grain weight). The inheritance of the vegetative characters was observed in class1 because of the rapid vegetative growth of Tog7291 whereas, intra-specific in class2 exhibited good inheritance of productive characters.

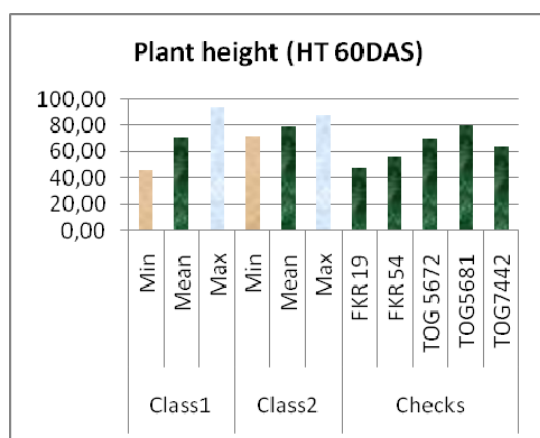


Figure 2. Variation in plant height in intra-specific lines and checks

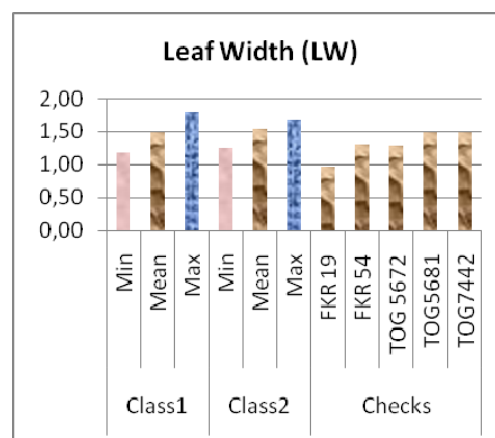


Figure 3. Variation in leaf width for intra-specific and checks

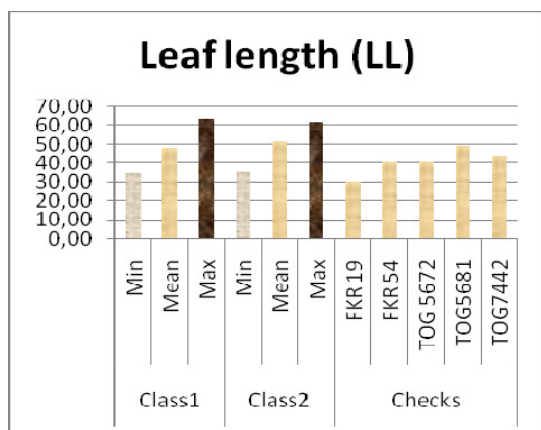


Figure 4. Variation in leaf length for intra-specific lines and checks

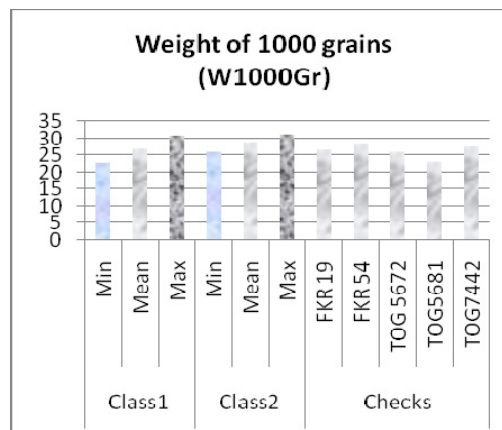


Figure 5. Variation in grain weight for intra-specific lines and checks

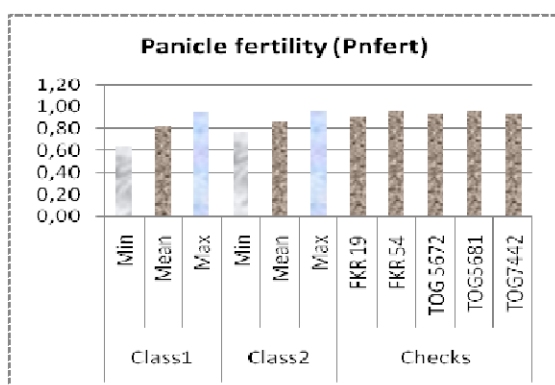


Figure 6. Variation in panicle fertility for intra-specific and checks

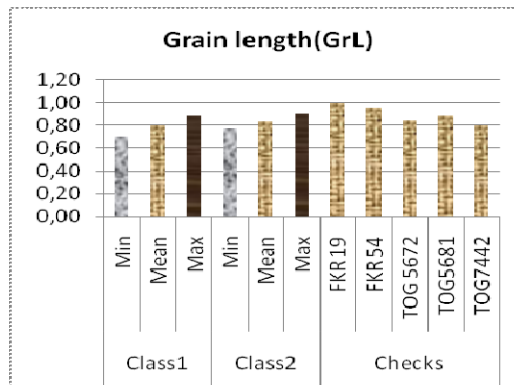


Figure 7. Variation in grain length for intra-specific and checks

3.2 Phenotypic Association and Relationship between Intra-specific *O. glaberrima* Lines

The correlation matrix for all traits is established in Table 3. Irrespective of measuring time, plant height had always a significant and positive correlation with both leaf length and width ($0.56 \leq r \leq 0.57$). Highly significant correlations were also observed between any two of the plant heights measured in different time ($0.63 \leq r \leq 0.89$) and between heading and maturity ($r = 0.92$); leaf length and leaf width ($r = 0.78$); full grain and both primary and secondary panicle branches ($r = 0.54$ and 0.67 , respectively). The PCA performed on the basis of 14 quantitative traits, out of the 18 measured, showed positive correlation with axis 1. The projection of individuals in the two first axes (1 and 2) showed a wide distribution of intra-specific lines (Figure 8 and 9). The relative discriminating power of these axes (Eigen values) was highest for axis 1 (4.77) and lowest for axis 2 (2.04). PC1 (34.08% of the total variation) was mostly correlated with plant height, leaf width, leaf length, panicle length and number of full grains. This axis mainly expressed the plant vegetative growth and grain fertility. The second axis (PC2) was mostly correlated with date of heading, maturity and weight of 1000 grains, i.e. cycle duration and grain productivity. Intra-specific lines located on the positive side of axis 1 (Figure 9) and particularly those joined together in group 1 (especially S19-3, PL55-2, PL51-3 and S6-9) are characterized by raised heights, broad leaves and number of full grains contrary to those located on the opposite side, which include sativa checks, especially FKR19. On the second axis, individuals (e.g. PL87-2 and PL75-2) have longer plant cycle and higher grain productivity contrary to those located on the opposite side (e.g. S21-6 and Tog5672, one of the *O. glaberrima* checks) which are earlier maturing.

The two parents Tog 5681 and Tog 5672 also used as checks exhibited lower vegetative development and grain fertility than intra-specific lines in group1. This low vegetative growth was even more pronounced in both sativa checks (FKR19 and FKR54) and in Tog7442 that are closer to individuals from Group 2.

Table 3. Correlation between the 18 measured quantitative characters

	50% Hdg	Ti 60DAS	NpN	Ht 30DAS	HT 60DAS	matLL	LW	Diam	PnL	PPnBr	SPnBr	W1000Gr	FullGr	Pnfert	GrL	GrW	Mat
50% Hdg	1.00																
Ti 60DAS	-0.05	1.00															
NpN	-0.01	0.50**	1.00														
Ht 30DAS	0.00	0.36**	0.22	1.00													
HT 60DAS	0.01	0.45**	0.30*	0.89**	1.00												
HT mat	0.05	0.44**	0.32*	0.63**	0.65**	1.00											
LL	0.03	0.30*	0.16	0.57**	0.56**	0.42**	1.00										
LW	0.07	0.30*	0.24	0.56**	0.56**	0.54**	0.78**	1.00									
Diam	0.30*	-0.06	0.17	0.24	0.19	0.18	0.36**	0.42**	1.00								
PnL	-0.08	0.17	0.20	0.36**	0.27*	0.30*	0.36**	0.39**	0.26*	1.00							
PPnBr	-0.08	0.31*	0.23	0.25	0.34**	0.38**	0.35**	0.40**	0.25	0.32*	1.00						
SPnBr	-0.05	0.30*	0.08	0.31*	0.27*	0.14	0.29*	0.32*	0.09	0.58**	0.38**	1.00					
W1000Gr	-0.17	-0.08	-0.06	0.22	0.25	0.12	0.03	0.01	0.00	0.24	-0.13	-0.06	1.00				
FullGr	0.08	0.35**	0.10	0.26*	0.26*	0.32*	0.28*	0.38**	0.23	0.59**	0.54**	0.67**	-0.17	1.00			
Pnfert	0.05	0.25	-0.17	0.02	0.01	0.12	-0.14	-0.06	-0.34**	0.19	-0.17	0.29*	0.07	0.39**	1.00		
GrL	-0.12	0.07	-0.24	-0.10	-0.11	-0.20	-0.23	-0.36**	-0.32*	0.03	-0.20	0.12	0.22	-0.04	0.31*	1.00	
GrW	-0.27*	-0.18	-0.09	0.04	0.09	-0.10	0.02	-0.08	-0.19	-0.04	-0.39**	-0.04	0.25	-0.32*	0.00	0.08	1.00
Mat	0.92**	-0.02	-0.11	-0.06	-0.01	0.05	0.06	0.04	0.32*	-0.11	-0.05	-0.07	-0.17	0.12	0.04	-0.12	-0.27* 1.00

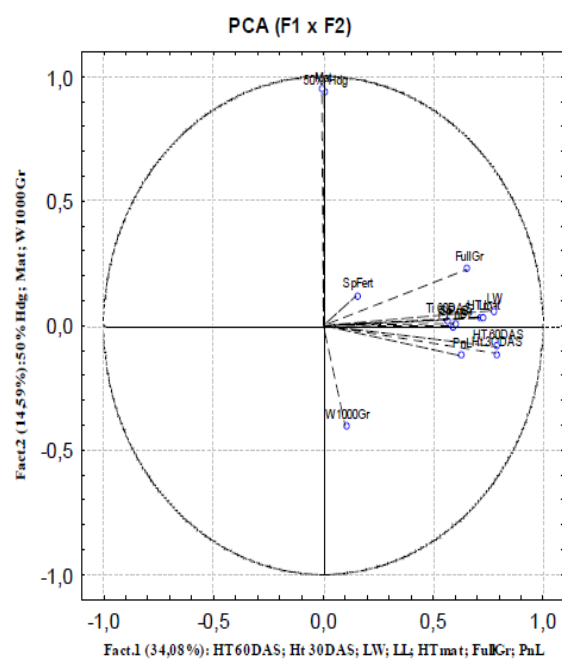
*significant at $P \leq 0.05$ and **significant at $P \leq 0.01$.

Figure 8. Distribution of quantitative traits in axes 1 and 2

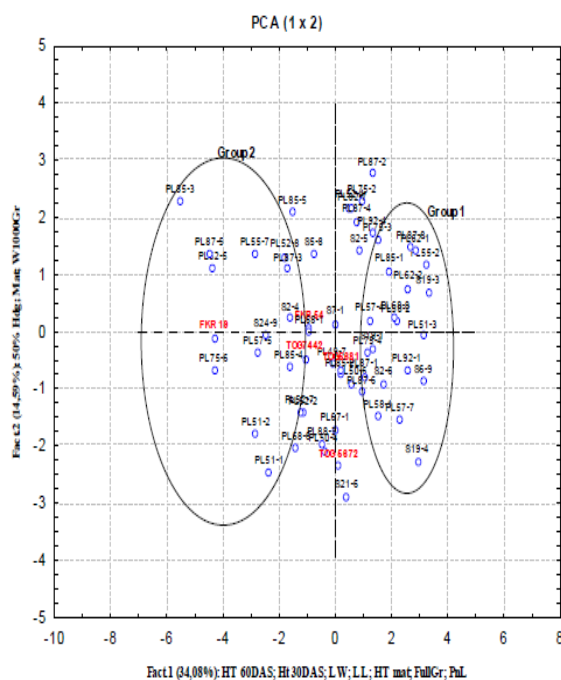


Figure 9. Projection of intra-specific lines and checks in axes 1 and 2

3.3 Evaluation and Grouping of Intra-specific *O. glaberrima* Lines

The dendrogram (Figure 10) established on the basis of the same quantitative traits used for the PCA showed that intra-specific lines were divided into two major groups which were then subdivided into five sub-groups. Genotypes from clusters 1, 2, and 3 possess about 24% of similarity whereas genotypes from clusters 4 and 5 had about 20% of similarity. Analysis of variance performed on these groups (Table 4), showed highly significant differences between all traits except cycle duration characters which were not significant at $P \leq 0.05$. A wide range of variation was exhibited for major characters such as tillering, plant height, leaf length and leaf width, panicle length, primary and secondary panicle branching, grain weight, panicle fertility and number of full grains. These characters are the most important for showing differences between groups. At the vegetative stage, intra-specific lines from group 4 had the best average performance for tillering ability, leaf length (50.52 ± 5.98 cm), leaf width (15.9 ± 1.0 mm) and plant height especially at maturity (139.75 ± 8.13 cm). The best intra-specific lines recorded in this group were PL87-1 and PL85-1 for plant height, PL92-1 for leaf length, PL87-8 for leaf width and PL87-8 for tiller number. This group does not include any of the checks used and its genotypes present higher phenotypic characters than those of most of the checks. Moreover, at the reproductive stage, genotypes belonging to group 5 were the most productive intra-specific *O. glaberrima* lines. This productivity was expressed especially through panicle characteristics such as panicle length (25.27 ± 1.46 cm), primary and secondary panicle branches (14.49 ± 0.20 and 24.53 ± 5.30) respectively, number of full grains (150.21 ± 8.72) and panicle fertility (0.86 ± 0.05). Weight of 1000 grains (28.20 ± 1.70 g) was higher in group 3. There was a close association between checks and intra-specific lines from group 1 (Tog5681 and FKR54) and group 3 (Tog7442 and FKR 19).

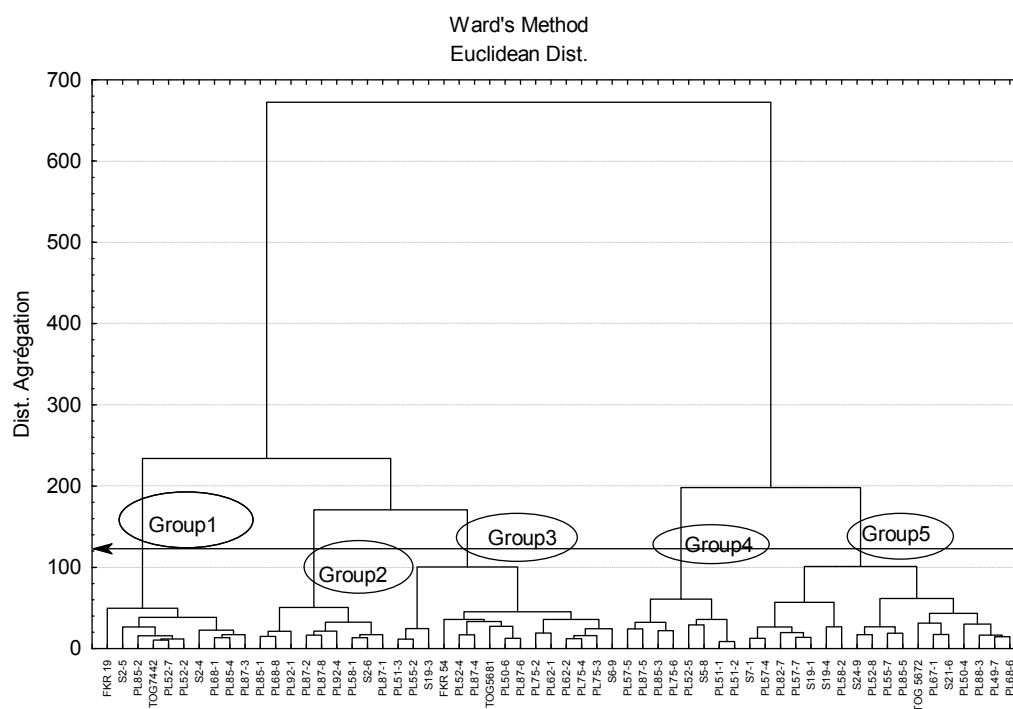


Figure 10. Hierarchical clustering of 55 intra-specific *O. glaberrima* lines and checks based on quantitative characters

4. Discussion

The developed intra-specific populations of *O. glaberrima* present some interesting potentialities for WCA ecosystems. The genotypes tested showed variation with respect to the evaluated traits. Some traits, e.g. total number of tillers, plant height, leaf dimensions, panicle length, number of full grains and panicle ramifications greatly influence the agro-phenotypic performances of the genotypes evaluated. The comparative analysis of the variation between the most distinctive characters within the two intra-specific classes showed that important

discriminating vegetative characters, (e.g. plant height and leaf width and leaf length associated to productive characters especially panicle fertility, grain weight and grain length) were more widely inherited by intra-specific lines in class 2 than those in class 1. The domination of the vegetative characters was also observed more in the *O. glaberrima* checks than in the sativa (FKR19 and FKR54) which were less powerful for these characters but higher for the yielding components. These results confirm the weed-competitiveness of *O. glaberrima* through its high plant vigor, high tillering ability, and large specific leaf areas opening to the plant canopy (WARDA, 1996; Dingkuhn et al., 1999; Rodenburg, 2009; Moukoumbi et al., 2011).

Table 4. ANOVA test and means values performed on the five intraspecific *O. glaberrima* groups resulting from hierarchical clustering

Groups	50% Hdg	Ti 60DAS	HT 30DAS	HT 60DAS	HT mat	LL	LW	PnL	PPnBr	SPnBr	FullGr	Mat	W1000Gr	Pnfert
	106.42	5.68	41.55	65.25	117.55	42.89	1.37	24.01	12.66	16.06	115.92	134.2	27.54	0.87
G1	± 3.88	± 1.52	± 3.84	± 7.77	± 10.55	± 6.05	± 0.14	± 1.34	± 2.10	± 5.07	± 8.56	± 4.93	± 1.43	± 0.07
G2	108.78	3.54	37.73	59.46	109.8	43.02	1.37	22.03	11.30	9.63	75.78	136.89	27.31	0.77
	± 5.14	± 0.92	± 6.79	± 9.88	± 9.17	± 5.77	± 0.15	± 1.65	± 1.76	± 4.01	± 11.15	± 6.43	± 2.32	± 0.08
G3	106.00	6.65	55.26	77.80	129.50	51.77	1.53	23.98	11.80	14.47	91.79	132.85	28.20	0.83
	± 4.55	± 1.32	± 7.42	± 8.17	± 7.55	± 6.71	± 0.07	± 1.88	± 1.56	± 8.24	± 7.17	± 6.66	± 1.70	± 0.07
G4	109.11	7.50	60.44	80.98	139.75	50.52	1.59	24.45	13.28	16.40	123.36	136.67	27.42	0.85
	± 4.28	± 1.49	± 6.28	± 4.40	± 8.13	± 5.98	± 0.10	± 1.11	± 1.12	± 2.70	± 11.04	± 5.20	± 2.03	± 0.07
	107.98	6.44	51.38	74.39	127.61	51.13	1.56	25.27	14.49	24.53	150.21	136.46	26.42	0.86
G5	± 3.62	± 1.60	± 7.01	± 10.10	± 11.44	± 6.85	± 0.14	± 1.46	± 2.00	± 5.30	± 8.72	± 4.42	± 2.12	± 0.05
	107.50	6.04	49.40	71.90	125.00	48.17	1.49	24.11	12.85	17.06	114.93	135.30	27.33	0.84
All Groups	± 4.26	± 1.82	± 9.99	± 11.09	± 13.21	± 7.36	± 0.15	± 1.79	± 2.09	± 7.39	± 27.90	± 5.55	± 1.96	± 0.07
							0.0000			0.00000		0.2959		
P	0.31945 NS	0.0000 ***	0 ***	0.0000 ***	0 ***	0.0005 ***	***	0.0001 ***	0.0003 ***	***	0 ***	NS	0.18678 NS	0.01131 *

PCA and hierarchical clustering generated from similarity or genetic distance matrices provided an overall pattern of variation as well as the degree of relatedness among the genotypes. In addition, the PCA confirmed the contributions of the discriminating traits observed between the two classes when intra-specific lines were plotted on the two axes (1 and 2). The ANOVA test performed after the hierarchical cluster analysis showed many discriminating traits including the first ones identified. The implication of this result is that if selection is to be made between cluster groups for a future breeding exercise, plant height, leaf width, leaf length, panicle fertility, panicle length and panicle ramifications should be given high priorities. Indeed, because *O. glaberrima* is highly adapted to African environments, these intra-specific lines formed the most interesting for morphological (group 4) and agronomic (group 5) performance that have a better capacity for adaptation to the diversity of irrigated and lowland rice systems. Important correlation observed between vegetative characters (plant height and leaf dimensions) and reproductive characters (panicle length, primary and secondary panicles branches) through phenotypic correlation and PCA, highlighted the link between photosynthetic activity and grain productivity. These characters may be exploited hereafter or considered as breeding components to develop good intra-specific varieties.

O. glaberrima showed mostly higher yield than *O. sativa* under unfavorable environments but inferior yields in favorable conditions, (<http://ricecongress.com/previous/pdflink/3936.pdf>). However, the number of spikelets before grain shattering was not lower in *O. glaberrima* than in *O. sativa* at any level of fertilizer input. The inferior yield of *O. glaberrima* in the favorable environments could be due to grain shattering and/or higher incidence of lodging, which may be specific characters of *O. glaberrima*. Yield of 5 - 6 t ha⁻¹ (Futakuchi & Sié, 2009; Sié et al, 2012) were obtained in *O. glaberrima* in the dry season, when plants were shorter, had higher photoperiod sensitivity and avoided lodging. This is true of intra-specific lines in group 1 (e.g. the sativa check FKR19 and the *O. glaberrima* Tog7442 which is resistant to lodging) but which nevertheless present low

yielding ability compare to lines in group 5. In general, grain productivity and grain shattering were improved for the majority of intra-specific lines evaluated. However, seed dormancy is one of the undesirable characters recorded. The use of Tog5681 as a relative female enhanced the development of maternal effect in intra-specific genotypes as it was the case for lowland NERICA varieties (Sie, 2005). If resistance to lodging and grain shattering can be improved through intra-specific breeding, promising *O. glaberrima* varieties may have good yield performance under harsh environments with responsiveness to management inputs. This will open new perspectives for the exploitation of *O. glaberrima* germplasm in crop improvement. In rice, wide crosses have been extensively used to transfer useful traits through interspecific breeding programs (Brar & Khush, 1997). Many advanced lines have been obtained in various genetic backgrounds, but the exact mechanisms of such interspecific transfers remain unknown. Given the recently published work cited above, some of the newly created phenotypic diversity raise the potential for the valorization of the African rice.

5. Conclusions

Intra-specific lines developed present more variation and a good agro-morphological diversity within the two classes of *O. glaberrima* lines. The hierarchical clustering established showed an interesting grouping of lines according to their agro-phenotypic characters. Lines in group4 of the dendrogram present better vegetative performance whereas those in group 5 present better yielding ability than the sativa checks. Such groupings are useful to breeders in identifying possible *O. glaberrima* that may be used as “parents” in breeding for any of the morphological traits that were studied.

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