



Research Article

Genetic Study on Inheritance of Agro-Morphological Traits in Rice (*Oryza glaberrima* Steud.) Germplasm

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Abstract

Oryza glaberrima survives in the African harsh environment with low human interference. It had developed characters that permits adaptation to environment and presents a lot of useful traits to overcome biotic and abiotic stresses. F₃ segregation populations of *O. glaberrima* were evaluated at National Cereals Research Institute, Badeggi in 2016 cropping season. The objective of the study was to assess the inheritance pattern of some morphological traits that are of interest to the plant breeders for improvement. The F₃ lines were evaluated in a Randomized Complete Block Design with three replications. Plot size of 5m x 3m and plant spacing was 20cm inter and intra row. Data were collected on culm habit, leaf blade colour, basal leaf sheath colour, grain colour, plant height, number of tillers per plant, panicle length, number of days to 50 % flowering, number of panicles per plant, number of grains per panicle, 1000 grain weight and grain yield per plant. Genetic analysis showed a significant chi square ratio on basal leaf sheath from crosses between Tog5384 and Tog7236 with the segregation ratio of 9:7 (green: purple). Green pigmentation of Tog5384 was dominant over the purple coloration of Tog7236. Monogenic gene action was observed from the population derived from cross between Tog5384 x Tog7236. Grain yield with segregation ratio of 3:1, have dominance parent Tog5384 over the recessive parent Tog7236. Use of Tog5384 *Oryza glaberrima* rice line in breeding program should be more advantageous on grain yield

Keywords: Genetic, Inheritance, *O. glaberrima*, Rice, Population

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Introduction

Rice is one of the principal crops targeted for global food security and has thus been major focus of national and international research for several decades. It is a staple food for about half of the world's population living in Asia and Africa, providing 40% to 70% of their total food calories (FAO, 2009). In Africa, it is one of the most important food crops and its consumption growth rate is higher than the population growth rate (FAO, 2009).

Oryza glaberrima has many important traits which are unique, such as weed competitiveness, drought tolerance and ability to respond to low input conditions. It is resistant to pests and

diseases, and is a good source of variation for important abiotic stresses. It has the ability to grow in a wide range of difficult ecosystems such as rainfed hilly areas, deep-water floating conditions and in coastal mangrove areas. The weed competitive ability of *O. glaberrima* is due to the early vigour, low extinction coefficient, high sunlight use efficiency, and high specific leaf area leading to high canopy growth for given amount of assimilates. It has droopy leaves which prevent sunshine from reaching the soil surface. Further, its high root biomass accumulation and thin roots with better soil penetration ability help it to compete effectively with weeds for nutrients. Rice breeders are interested in developing cultivars with improved yield and other desirable

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agronomic characters. Genetic variability for agronomic traits is the key component of breeding programmes for broadening the gene pool of rice. The study of genetic inheritance of quantitative and qualitative traits of the *O. Glaberrima* accessions for the selection of appropriate breeding procedure will facilitate the development of superior yielding varieties for farmers. The aim of this study was to evaluate the genetic and inheritance of some morphological characters in (*O. glaberima*) rice accessions.

Materials and Methods

Crossing materials were *Oryza glabberima* lines, two high yielding male parents (Tog7236, and Binta Kouroure) and one low yielding female parent (Tog5384). These were collected from rice breeding unit of AfricanRice Centre, located in IITA Ibadan, Oyo state, Nigeria. The field experiment was conducted in 2015/2016 at National Cereals Research Institute, Badeggi, Nigeria. The experimental materials comprised of two populations, population I (124 accessions) generated from the crosses between Tog5384 x Tog7236, while population II (120 accessions) generated from crosses between Tog5384 x Binta Kouroure in total of 244 *O. glabrrima* rice lines with three parents (Tog5384, Tog7236 and Binta Kouroure) as checks. Experiment was laid out in a randomized complete block design with 3 replications, plot size of 5m x 3m and 20cm inter and intra row spacing in an irrigated condition. Standard agronomic practices were followed to maintain the crop health. Birds were controlled using bird net from reproductive stage untill harvesting time. Five plants in the middle plot were selected to eliminate the marginal effects for the study. Thirteen (13) qualitative and quantitative traits for these plants were observed. These are culm habit (CH), leaf blade color (LBC), basal leaf sheath color (BLS), awn, tiller count (TL), Number of grain per panicle (NGP), Grain yield (GY), number of days to 50% flowering (50%FLW), plant height (PH), panicle length (PL), number of panicle per plant (NPP) and 1000-grain weight (1000GW) according to IRRI. (2013). Data recorded were analysed using chi-square (X^2), most commonly used to test hypothesis concerning the frequency distribution of one or more populations. In this study, we used X^2 for a fixed ratio hypothesis using data from F_3

segregating population of each cross as described by Gomez and Gomez (1984).

Results and Discussion

The application of Mendalian genetics has clearly led to many breeding advances in rice as well in other crops (Rutger and Mackill 2001). There was variation on segregation pattern among different characters studied. Selection based upon the knowledge of gene action is a prerequisite in the breeding program. The joint segregation as shown in Table 1, for each pair of character was investigated in order to find out the relative position of gene involved. In the F_3 segregation population derived from Tog5384 x Tog7236 for leaf blade colour, with a segregation ratio (light green: dark green) was 283:95 ideally fitting the 3:1 ratio for a single-gene model ($X^2=6.49$, $P=6.63$) while, joint segregation between Tog5384 and Binta Kouroure for leaf blade color with a segregation ratio (light green: dark green) was 180:180 fitting the 1:1 ratio with Tog5384 showing heterozygous dominant gene and BintaKouroure with homozygous recessive gene. The X^2 for segregation of basal leaf sheath color for the population derived from Tog5384 x Tog7236 on Table 1 was significant at 1 percent probability on (green: purple) coloration. The results indicated that basal leaf sheath colour, ratio of 9:7 (green: purple) was recorded; this implied that, leaf sheath colour was controlled by two genes with complementary interaction. This is in agreement with the findings of Pusapati *et al.* (2012), who ascertained that lamina colour alone was considered (purple or green) irrespective of the midrib, margin and sheath, the segregation ratio was 9:7, suggesting the role of two complementary loci. In the F_3 population derived from Tog5384 x Binta Kouroure for basal leaf sheath colour, a segregation ratio of (green: purple) 9:7 controlled by two complimentary genes ($X^2=1.65$) was observed, but there was no significant difference ($P>0.01$). However, the joint segregation for grain colour of population derived from Tog5384 and BintaKouroure on (black: brown) was 270:90 ideally fitting the 3:1 ratio for a single-gene model ($X^2=6.53$, $P=6.63$) at 1 percent probability. Contrast to the findings of Pusapati *et al.* (2012) who reported that, a single dominant gene control of pigmentation was inferred when analyzed using suitable crosses. Among F_3 progenies of crosses between

Tog 5384 x Tog7236, the result in Table 2 shows low number of tillers Tog5384 was dominant over high number recorded from Tog5384 with segregation ratio of 9:7; this implied that tillering ability was controlled by two genes with complementary interaction. This result contrast Tang *et al.* (2001) who ascertained that, genetic analysis in the BC_2F_2 population showed that, the traits of few or high tillering and yellowing apex and margin on the mature leaves were controlled by one recessive gene. In the F_3 progenies derived from Tog5384 x BintaKouroure, a segregation ratio of (low tillering: high tillering) was 270:90, ideally fitting the 3:1 ratio revealed the presence of monogenic gene action for phenotype.

Flowering time is another important agronomic trait, controlled by different endogenous genetic factors as well as environmental signals (Yano *et al.*, 2001). In the F_3 population derived from Tog5384x Tog7236 for number of days to 50% flowering, segregation ratio of (early flowering: late flowering) was 189:189, ideally fitting a ratio of 1:1 in which Tog5384 is heterozygous dominant and Tog7236 is homozygous recessive. This contrast the result of Kulkarni *et al.* (2013) who reported monogenic control of flowering time in rice. The X^2 for population from crosses between Tog5384 x BintaKouroure on number of days to 50% flowering was significant at 1 percent probability, fitting the X^2 ratio of 9:7, this revealed that number of days to 50% flowering for this population is controlled by two genes with complementary interaction.

Grain number per panicle is determined by the Panicle length, spikelet number and density, seed setting rate and grain plumpness. Joint segregation for the population derived from Tog5284 x Tog7236 on number of panicles per plant (Table 2), revealed that there was no significant difference at 1 percent probability. Low number of panicles per plant from Tog5384 was dominant over the high number of panicles per plant from Tog5384 with segregation of 213:165, ideally fitting X^2 ratio of 9:7, this implied that, the number of panicle per plant is controlled by two genes with complementary interaction. While for the segregation population from Tog5384 x BintaKouroure, was not significant at 1 percent probability, revealed segregation ratio of 270:90,

fitting the 3:1 ratio for a single-gene model ($X^2=0.014$, $P=6.63$), this is in contrast to the finding of Sripichitt (2013) who reported that, inheritance of number of grains per panicle in F_2 populations showed segregation ratio of 63:1 (low-mediate: high grain per panicle). However, the continuous distribution of F_2 populations indicated that, number of grains per panicle was quantitative trait controlled by three major genes. Similarly, Lin and Yan (2004) reported that number of grains per panicle was controlled by polygenes. Number of grains per panicle further depends on number of spikelets; which is primarily number of panicles per plant it depends on the tillering ability of the plant (Sakamoto *et al.*, 2006). In the F_3 population derived from crosses between Tog5384 x Tog7236 on grain yield, segregation ratio of the phenotypes (low yield: high yield) was 283:95, ideally fitting a single-gene model 3:1 ratio ($X^2=0.056$, $P=6.63$). However, in the F_3 population on grain yield derived from Tog5384 x BintaKouroure with (low yield: high yield) was 180:180, ideally fitting a ratio of 1:1; this revealed that Tog5384 is heterozygous dominant and BintaKouroure is homozygous recessive. The X^2 for segregation of population derived from Tog5384 x BintaKouroure for number of grains per panicle was not significant at 1 percent probability. Therefore, this result indicates that, the number of grain per panicle is governance by monogenic gene (Table 2), however the X^2 ratio is 270:90, fitting a single-gene model 3:1 ratio ($X^2=4.8$).

Conclusion

Leaf sheath color was controlled by two genes with complementary interaction. The crosses between Tog5384 x Tog7236 on tillering ability was controlled by two genes with complementary interaction, while progenies derived from Tog5384 x Binta Kouroure revealed the presence of monogenic gene action for tillering. Number of days to 50% flowering of population derived from Tog5384 x Tog7236 indicates heterozygous dominant gene and homozygous recessive gene. The crosses between Tog 5384 x Binta Kouroure on number of days to 50% flowering revealed that, number of days to 50% flowering for this population was controlled by two genes with complementary interaction. Grain yield of population derived from Tog5384 x Tog7236,

revealed monogenic gene action with ratio of 3:1 while Tog5384 x Binta Kourourewith ratio of 1:1. This revealed that Tog5384 is heterozygous dominant and BintaKouroure is homozygous recessive. The progenies developed from these crosses could be valuable not only for enriching the gene pool but also for other uses in rice breeding program.

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Table 1. Phenotype of qualitative characters of parents, F₃ segregation population 1 and 2

Population 1							
Traits	Scale	Test Ratio	Observed	Expected	X²	t X²=6.63 P @ 1%	
	Tog 5384	Tog 7236	Tog 5384: Tog 7236	Tog 5384: Tog 7236			
CH	Erect	Open	1:1	200 : 178	189 : 189	0.64	ns
Awn	Absent	Present	1:1	212 : 166	189 : 189	2.798	ns
LBC	Light green	Dark Green	3:1	240 : 138	283 : 95	6.499	ns
BLS	Green	Purple	9:7	429 : 36	213 : 165	19.99	*
Population2							
	Tog 5384	BintaKouroure	Tog 5384: BintaKouroure	Tog 5384: BintaKouroure			
CH	Erect	Open	3:1	246 : 114	270 : 90	2.133	ns
LBC	Light green	Dark Green	1:1	179 : 181	180 : 180	0.05	ns
BLS	Green	Purple	9:7	357 : 3	203 : 157	1.658	ns
GC	Black	Brown	3:1	312 : 48	270 : 90	6.533	ns

*- Significant, ns- Not significant @p<0.05

Table 2. Phenotype of quantitative characters of parents, F₃ segregation population 1 and 2

Population 1							
Traits	Tog 5384	Scale Tog 7236	Test Ratio	Observed Tog 5384: Tog 7236	Expected Tog 5384: Tog 7236	X²	t X²=6.63 P @ 1%
TL	Low	High	9:7	198 : 183	213 : 165	0.232	ns
PH	Tall	Short	9:7	151 : 227	213 : 165	2.756	ns
50%FLW	Early	Late	1:1	110 : 268	189 : 189	7.130	*
NNP	Low	High	9:7	119 : 259	213 : 165	5.939	ns
GY	High	Low	3:1	287 : 91	283 : 95	0.056	ns
1000 GWT	High	Low	3:1	310 : 68	283 : 95	2.562	ns
Population 2							
	Tog 5384	BintaKouroure		Tog 5384:Binta Kouroure	Tog 5384:Binta Kouroure		
TL	Low	High	3:1	229 : 131	270 : 90	6.225	ns
PH	Tall	Short	9:7	95 : 265	203 : 157	8.23	*
PL	Long	Short	3:1	241 : 119	270 : 90	3.114	ns
50%FLW	Early	Late	9:7	58 : 302	203 : 157	14.842	*
NPP	High	Low	3:1	272 : 88	270 : 90	0.014	ns
GY	Low	High	1:1	156 : 204	180 : 180	3.2	ns
NGP	Low	High	3:1	306 : 54	270 : 90	4.8	ns
1000 GWT	High	Low	1:1	191 : 169	180 : 180	0.672	*

*- Significant, ns- Not significant @p<0.05