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GENETIC ANALYSES FOR YIELD AND YIELD CHARACTERS IMPROVEMENT IN AROMATIC AND NON-AROMATIC RICE (*ORYZA SATIVA* L.) OF SELECTED CROSSES FROM GENOTYPES FROM MOZAMBIQUE AND MALAWI UNDER IRRIGATION

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ABSTRACT

An experiment was laid out in a randomized complete block design (RCBD) with three replications at Lifuwu Rice research station, Salima district, Malawi during winter 2015/16 cropping season. Genetic analyses for yield and yield components were performed in selected hybrids derived from aromatic and non-aromatic rice (*Oryza sativa* L.) crosses and their parental genotypes from Mozambique and Malawi. The results revealed that the hybrids and their parents differed significantly ($p < 0.05$) for all the traits studied except culm number, suggesting that conventional breeding program for yield and yield characters can start using these genotypes hence they constitute a pool of germplasm with adequate genetic variability. Genotypic coefficients of variation were lower than the corresponding phenotypic coefficients in all the characters. High broad sense heritability was found on vegetative vigour (0.70), plant height (0.70), 1000 grains weight (0.85) and grain yield (0.68) indicating that direct selection for yield and yield components improvement can be effectively performed using these traits. These results, indicate the potential for production of high grain yield recombinant inbred lines and also the design of a breeding program that aims to study agronomic characters to improve the productivity of rice varieties in both Mozambique and Malawi.

Keywords: Variability, heritability, rice, hybrid, genotypic coefficient of variation, phenotypic coefficient of variation, yield, selection.

INTRODUCTION

Rice (*Oryza Sativa* L) is one of the oldest grown crop in the worlds. This crop is widely cultivated in all continents from tropical and sub-tropical regions of the world (Pereira, 2002). Morphologically, it is an annual grass that belongs to family Gramineae (Jamal et al., 2009). The importance of rice is widely recognized and today more than half of the global human population depend on rice as their basic diet. According to Akinwale et al., (2011) the world population is expected to reach 8 billion by 2030 and rice production must be increased by 50% in order to meet the growing demand.

According to FAO (2014), the global paddy production of rice in 2014 was about 745 million tonnes (for a total area of 163 million ha), with a marginal decline of 0.2% from 2013 record estimated at 746 million tonnes

of paddy (Single, 2015) and (FAO, 2015). Rice production is very concentrated, geographically, in Asia that produces more than 90% of the total world rice production, with a production of approximately 675 million tonnes of paddy (Siriwardana and Jayawardena, 2014). China and India are by far the two biggest rice producers with a production of 205 million tonnes and 155 million tonnes of paddy, respectively, almost 50% of the world rice production (FAO, 2014; Siriwardana and Jayawardena, 2014).

Recently, rice consumption in Mozambique is growing either in rural or urban areas due to maize prices increment registered in the last few years (Donovan and Tostão, 2010). In Mozambique rice is on the fourth ranking of the most consumed crop after cassava, maize and wheat accounting for 15kg/person/year and 145kcal/person/day (Donovan and Tostão, 2010). In Malawi rice is the second main cereal food crop after maize which accounts for 60 percent of the cultivated

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land and it is also an industrial crop grown by the smallholder farmers (Magreta et al., 2013).

The yield levels of rice in Malawi have been revolving around the same levels and even getting lower (Magreta et al., 2013); In most flood plains the yield levels have been ranging from 1.0- 1.5 tons/ha⁻¹ (Magreta et al., 2013) and according to Mozambique Ministry Of Agriculture (Minag, 2013) yield of rice are around 0.8-1.2 tons/ha⁻¹ in Mozambique. However, under good management, the potential yield levels range from 4 - 5 tons/ha⁻¹. Use of improved varieties with high yield and best production practices can improve the production and productivity of rice.

Grain yield is the primary character targeted for rice productivity improvement in both favourable and unfavourable environments. Knowledge of the genetic architecture of genotypes is necessary to formulate efficient breeding methodology (Paikhomba et al., 2014). Thus, it is essential to find out the relative magnitude of genetic variances, heritability, phenotypic and genotypic coefficient of variation (PCV and GCV), with regard to the characters of concern to the breeder.

The systematic breeding programme involves the steps like creating genetic variability, practicing selection and utilization of selected genotypes to evolve promising varieties. According to Paikhomba et al., (2014) the large spectrum of genetic variability in segregating populations depends on the level of genetic diversity among genotypes that offer better scope for selection. Heritability, PCV and GCV are other important selection parameters (Nirmaladevi et al., 2015). The estimates of heritability help the plant breeder in determining the character for which selection would be rewarding.

The selection of superior genotypes based on their phenotypic expression is a method used by plant breeders adopting simple selection methods (Babu et al., 2012). The major function of heritability estimates is to provide information on transmission of characters from the parents to the progeny. Heritability estimates can indicate potential improvement by selection of useful characters. Nirmaladevi et al., (2015) suggested that high magnitude of GCV and PCV for quantitative characters reveal the presence of high degree of variability which is better for character improvement through simple selection.

The main objective of this research was to perform genetic analyses for yield and yield components in selected F1 progenies derived from aromatic and non-

aromatic rice (*Oryza Sativa L*) cross form rice genotypes sourced from Mozambique and Malawi grew under irrigation. Crosses were made to explore and enhance genetic variability among the genotypes selected for yield and grain quality character. The analysis centred on the determination of genetic variability, heritability, PCV and GCV, for grain yield and yield components.

MATERIAL AND METHODS

The trial was conducted at Lifuwu Research Station situated at the foot of the Lifuwu hill. The site is part of the expansive and seasonally flooded Katete dambo on the altitude of 500 metres above sea level (masl) with coordinates sited on latitude 13° 40' South and longitude 34° 35' Est. Lowland or paddy fields are predominantly vertisol types characterized by low nitrogen and phosphorus content, with pH 7 - 8. Lifuwu receives annual average rainfall of 1,200 mm. Mean minimum and maximum temperatures are 19°C and 29°C, respectively.

The materials for study was produced from crosses between four (3) parents of non-aromatic genotypes brought from Mozambique named and coded (Marista [D], Djissa [E] and Chibissa [G], respectively and three (3) parents of aromatic genotype from Malawi named and coded Faya [B], Kilombero [C] and Nunkile [F], respectively. From these crosses, only 11 hybrids with four reciprocals (FGRC-1, GFRC-1, FDRC-1, CERC-1, FERC-1, CGRC-1, CDRC-1, EFRC-1, BDRC-1, ECRC-1 and GCRC-1) were evaluated.

The hybrids (F1_s) were coded with four capital letters and one number for example ABRC-1. The first two letters refer to the parents crossed with (Female and Male, respectively) and the other two letters mean the rice crosses and the number symbolize the generation of the population (one for generation 1). The production in the field followed the best and recommended practices for rice productions as described by Sousa, (2012).

Data for agronomic, grain yield and yield component were recorded according to (Jarwar et al., 2014) and also earlier described by IRRI (2007); Days to germination (GD), vegetative vigour (Vg), tillering ability (Ti), days to 50% flowering (DFI50%), days to 85% flowering (DFI85%), plant height (Ht) [cm], days to 50% maturity (Mat50%), days to 85% maturity (Mat85%), culm number (CmN), panicle length (Pnl) [cm], weight of 1000 grains (GW) [g], and grain yield ha⁻¹ (Yld) [kg].

Analysis of variance appropriate for RCBD was done using the statistical package GenStat Seventeenth

Edition commercial licence and SPSS twentieth edition for means, standards errors separation and, correlation and regression estimates. The statistical model used for the design is:

$$Y_{igo} = \mu + B_i + T_{go} + E_{igo}$$

Where; Y_{igo} : The mean of block, genotypes and offspring; μ : overall mean; B_i : effect of the block, $i=3$; T_{go} : Effect of the treatments genotypes (g) parents and offspring ($g = B, C, D, E, F$ and G) and o ($o = FGRC-1, GFRC-1, FDRC-1, CERC-1, FERC-1, CGRC-1, CDRC-1, EFRC-1, BDRC-1, ECRC-1$ and $GCRC-1$); E_{igo} : the error of observations.

Six (6) parental genotypes: B= Faya; C = Kilombero; D = Marista; E = Djissa; F = Nunkile and G = Chibiça.

The estimation of broad sense heritability (H^2), phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was done according to the methodology used by Akinwale et al., (2011) and Jonah (2011) as follows:

$H^2 = \delta_g^2 / \delta_p^2$; Where; H^2 : Is the broad sense heritability; δ_g^2 : is the genotypic variance; δ_p^2 : is the phenotypic

variance; $GCV = (\sqrt{\delta_g^2})/X$ and $PCV = (\sqrt{\delta_p^2})/X$

Where; PCV = phenotypic coefficient of variation; GCV = genotypic coefficient of variation; X = grand mean; δ_g^2 (genotypic variance) = $(MSG - MSE)/r$, where MSG = mean square of genotypes, MSE = mean square of error, and r = number of replications; σE^2 = Mean square of error; δ_p^2 (phenotypic variance) = $(\sigma G^2 + \sigma E^2)$;

RESULTS AND DISCUSSION

Analysis of variance: The analysis of variance on this study revealed statistically significant differences at 5% of probability for most of the character evaluated except for culm number. The means and standard error presented in Table 1, show that hybrids performed better than their parents in most of the characters evaluated. The highest grain yield (8.73 tons/ha⁻¹) was obtained from the hybrid GFRC-1 derived from cross between genotypes Chibiça and Nunkile followed by GCRC-1 with 8.32 tons/ha⁻¹ which was derived from the cross between genotypes Chibiça and Kilombero, although the parental genotype, Kilombero, produced the lowest grain yield (4.31 tons/ha⁻¹). However, the hybrids had the longest time to reach physiological maturity (136 and 147 days, respectively).

The earliest maturity hybrid was EFRC-1 with 129 days which was derived from cross between Djissa and Nunkile. This hybrid produced the lowest yield among all hybrids (4.31 tons/ha⁻¹). The results show the

presence of high genetic variability among the genotypes (Babu et al., 2012). Highly significant differences found on the variables among the parental genotypes studied suggest the variability can be further utilized in crop improvement programme. Previous research results have shown high variability among hybrids and genotypes for yield and related characters (Can et al., 1982; Akram et al., 2007; Hassan, 2011; Oladosu et al., 2014). The efficiency of selection for yield mainly depends on the direction and magnitude of the association between yield and its components and among themselves (Siebenmorgen et al., 2012).

Broad sense heritability, phenotypic and genotypic coefficient of variation (PCV and GCV): The results for broad sense heritability, phenotypic and genotypic coefficient of variation showed variation for grain yield and yield components as presented in Table 2. The heritability results showed a range of high, medium and low heritability values (0.85; 0.37 and 0.03), respectively. In general, the parameter that presented non-significance on the analyses of variance (means squares of the genotypes) presented low heritability. The lowest heritability was observed on the culm number (0.03), the percentage of non-filled and filled grain (0.07), days to 50% flowering (0.26) and days to 50% maturity (0.28). The results suggest that genes contributed less to at all to phenotypic individual differences for the four characters. Environmental influences contributed much to the phenotypic expression. In other words, direct selection for those characters will be ineffective.

Medium heritability was obtained for tillering ability (0.52), days to 85% flowering (0.37), days to 85% maturity (0.53) and panicle length (0.60); while the highest heritability was observed on vegetative vigour (0.70), plant height (0.70), grain yield (0.68) and 1000 grain weight (0.85). The results for the character with high heritability suggest that genes account for a large component of the individual differences recorded for the phenotypic expression of the offspring variation. This is the portion which is exploited by breeders, whereby advanced selection can be made.

Akinwale et al., (2011) reported that high to medium broad sense heritability estimates were observed for days to heading (95.1%), days to maturity (92.1%), plant height (72.4%), grain yield (72.1%), number of grains per panicle (70.5%), panicle weight (68.1%) and panicle length (53.6%).

Table 1(a). Mean and standard error performance separation for eleven (11) hybrids and six (6) parental genotypes for 11 agronomic, grain yield and yield component grown under irrigation at Lifuwu research station in 2015.

Genotype	Days to germination	Vegetative vigour	Tillering Ability	Days to 50% flowering	Days to 85% Flowering	Plant height (cm)
FDRC-1	4.0±0.00a	7.70±0.66abcde	24.0±4.05ghi	96±2.081abc	101±3.179abcd	82.9±5.669abc
FGRC-1	4.0±0.00a	7.00±0.57ab	17.0±1.45abcdef	98±1.000abc	99±.855abcd	83.9±5.031bc
CGRC-1	4.0±0.33ab	14.7±0.33h	12.0±0.88a	93±0.881ab	97±1.666abc	102.6±3.08def
ECRC-1	4.0±0.33ab	7.30±0.88abcd	17.0±1.76abcdefg	92±5.174ab	102±1.000bcde	96.5±5.660def
FERC-1	4.0±0.33ab	10.3±1.20bcdefg	25.0±2.02hi	97±1452abc	101±1.855abcd	83.9±3.491bc
CERC-1	5.0±0.66abc	8.00±0.58abcde	14.0±2.00ab	95±1.333ab	100±1.855abcd	105.4±5.043ef
EFRC-1	5.0±0.00abc	8.00±1.15abcde	22.0±5.21cdefghi	91±3.055a	97±2.081abc	90.70±5.151bcd
GCRC-1	5.0±0.33abc	14.7±0.33h	27.0±1.66i	102±3.605c	109±1.527e	71.5±0.851a
GFRC-1	5.0±0.66abc	8.70±2.18abcde	23.0±1.45efghi	95±2.000abc	102±0.881abcd	96.5±4.672def
CDRC-1	5.0±0.57abc	11.0±2.00cefg	15.0±3.93abcd	92±0.333ab	98±0.577abcd	108.7±2.900e
BDRC-1	6.0±0.33cde	8.70±0.88abcde	20.0±4.33bcdefghi	91±3.214a	95±1.527a	107.6±2.718ef
Nunkile	5.0±0.33abcd	15.0±1.00h	22.0±0.88defghi	97±0.333abc	103±0.881bcde	78.6±0.850ab
Marista	7.0±0.66abcde	12.3±1.20fgh	18.0±1.16abcdefgh	97±0.577abc	104±1.154cde	97.71±5.311def
Djissa	6.0±0.00bcde	9.30±1.00abcdef	16.0±0.66abcde	91±1.763a	96±1.201ab	95.0±1.327cde
Chibiça	7.0±0.00de	7.30±0.88abc	23.0±0.89fghi	95±1.763ab	100±0.577abcd	95.0±4.886cde
Kilombero	7.0±0.00de	5.70±0.66a	15.0±1.21abc	95±1.201ab	103±1.452bcde	105.4±2.866ef
Faya	7.0±0.33e	13.3±0.66gh	22.0±0.86cdefghi	99±2.000bc	105±3.214de	98.13±4.948def
Grand mean	5.0±0.170	9.98±0.477	20.0±0.772	95.0±0.618	101.0±0.439	94.0±1.693
SE	0.6	1.89	3.6	3.7	3.7	6.6
LSD	1	3.14	6	6.2	6.1	11
Cv%	11.1	18.9	18.6	3.9	3.6	7.1
Fp>F	***	***	***	*	**	***

Table 1 (b). Mean and standard error performance separation for eleven (11) hybrids and six (6) parental genotypes for 11 agronomic, grain yield and yield components grown under irrigation at Lifuwu research station in 2015.

Genotype	Days to 50% Maturity	Days to 85% Maturity	Panicle length (cm)	1000 grains weight (gr)	Grain Yield (tons/ha-1)
FDRC-1	123±2.666abc	137±3.179bcd	22.93±0.133a	24.83±0.463a	5.62±0.753abcdef
FGRC-1	124±2.333abc	138±1.855bcd	23.27±0.066abc	24.96±0.185a	7.78±0.656ghi
CGRC-1	123±2.185abc	137±1.666bcd	23.40±0.642abc	28.35±2.487c	7.79±0.635ghi
ECRC-1	118±2.905a	130±2.027a	23.80±0.600abc	25.47±0.348ab	4.48±0.360abc
FERC-1	125±1.855abc	139±1.855bcd	22.73±0.176a	24.87±0.033a	6.03±0.338acdef
CERC-1	122±1000ab	136±1.855abcd	24.80±1.102cd	33.13±0.676d	5.98±0.145abcdef
EFRC-1	120±3.214a	129±0.881a	22.87±0.176a	26.14±0.328abc	4.31±0.416a

GCRC-1	128±1.000bc	147±1.732e	22.20±1.331a	25.50±1.715ab	8.32±0.202hi
GFRC-1	122±1.333ab	136±0.881abcd	23.27±0.405abc	23.80±0.655a	8.73±0.611i
CDRC-1	124±0.000abc	138±0.577bcd	23.20±0.461ab	32.97±0.366d	6.26±0.808defg
BDRC-1	125±1.000abc	139±1.527bcd	24.73±0.240bcd	32.07±0.433d	5.66±0.290abcdef
Nunkile	124±1.000abc	141±3.179cde	22.60±0.152a	24.73±1.120a	7.20±0.366fghi
Marista	128±0.577bc	142±1.154de	25.87±0.284d	33.87±0.185d	7.31±0.200fghi
Djissa	119±2.728a	133±2.185ab	22.77±0.533a	25.47±0.533ab	5.03±0.491abcd
Chibiça	121±2.962a	135±2.848abc	23.65±0.425abc	23.43±0.731a	5.23±0.497abcde
Kilombero	125±1.333abc	132±1.452ab	25.36±0.202d	32.77±0.448d	4.31±0.256ab
Faya	129±3.382c	141±3.382cde	25.40±0.115d	28.10±0.208bc	6.89±0.873efgh
Grand mean	124.0±0.598	137.0±0.735	23.70±0.187	27.70±0.322	6.30±0.218
SE	3.7	3.645	0.819	1.5	0.89
LSD	6.08	6.06	1.362	2.5	1.48
Cv%	3	2.7	3.5	5.4	14.2
Fp>F	**	***	***	***	***

Table 2. Broad sense heritability, phenotypic and genotypic coefficient of variation (PCV and GCV) for grain yield and yield component.

Variables	MS _g	(MSE)	σ^2_g	σ^2_p	H ²	PCV	GCV
Vegetative vigour (Vg)	28.561**	3.57	8.33	11.90	0.70 ^{Aa}	0.65	0.54
Tillering ability (Ti)	56.73**	13.22	14.50	27.72	0.52 ^{aa}	0.70	0.51
Days to 50% Flowering	28.93*	13.96	4.99	18.95	0.26 ^a	0.81	0.42
Days to 85% Flowering	36.58*	13.40	7.73	21.13	0.37 ^{aa}	0.76	0.46
Plant height (Ht) [cm]	348.53**	44.08	101.48	145.56	0.70 ^{Aa}	0.65	0.54
Culm number (CmN)	35.03 ^{NS}	32.06	0.99	33.05	0.03 ^a	0.97	0.03
Panicle length (Pnl) [cm].	3.73**	0.67	1.02	1.70	0.60 ^{aa}	0.67	0.52
Days to 50% Maturity	28.84*	13.41	5.14	18.55	0.28 ^a	0.80	0.42
Days to 85% Maturity	59.16**	13.29	15.29	28.58	0.53 ^{aa}	0.70	0.51
Grain Yield (tons/ha ⁻¹)	5.91**	0.79	1.71	2.50	0.68 ^{Aa}	0.65	0.54
1000 Grains weight	41.963**	2.26	13.23	15.49	0.85 ^{Aa}	0.61	0.56
Percentage of non-filled grain	4.12 ^{NS}	3.356	0.25	3.61	0.07 ^a	0.94	0.14
Percentage of filled grain	4.12 ^{NS}	3.356	0.25	3.61	0.07 ^a	0.94	0.14
Source of variation	df						
Genotype	16						
Replication	2						
Error	32						

Large differences reflect high environmental influence, while small differences reveal low

environmental differences (Can et al., 1982). The characters culm number and days to

The low broad sense heritability observed for the number of tillers per plant (19.2%) and 1000 grain weight (21.7%) indicate the great influence of the environment on these traits.

The highest phenotypic variance (145.97), genotypic variance (101.49) and environmental variance (44.48) was obtained by the plant height character. Panicle length had the lowest magnitude of the environmental variance (0.67) and phenotypic variance (1.70). The lowest the genotypic variance (0.25) was found for percentage of filled and non-filled grain.

The genotypic coefficients of variation were lower than the corresponding phenotypic coefficients in all the characters. Generally, genotypic coefficient of variation measures the variability of any character (Choudhury et al., 2013). The extent of the environmental influence on any character is indicated by the magnitude of the differences between the genotypic and phenotypic coefficients of variation.

flowering had the highest phenotypic coefficient of variation of 0.97 and 0.81, respectively, while

the lowest was obtained from the 1000 grain weight (0.61). The results indicate the presence of environmental influence to some degree in the phenotypic expression of the characters. Similar results were observed by Akinwale et al., (2011) on rice crop and Eid (2009) on wheat crop.

CONCLUSION

In general, the results indicated that there is suitable genetic variability present in the material studied and this genetic variability is adequate to start selection in an earlier generation for yield and yield component.

The values of broad sense heritability in this study indicate that direct selection for yield and yield characters improvement can be effectively performed through vegetative vigour, plant height, 1000 grains weight and grain yield. Selection through culm number, the percentage of non-filled grains, days to 50% flowering and days to 50% maturity cannot be effective. However, plant height, culm number and days to 50% flowering presented high PCV and GVC suggesting that this character is important for yield improvement.

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