Agronomy Research **7**(1), 97-102, 2009

Analysis of heritability and genetic variability of agronomically important traits in *Oryza sativa* x *O. rufipogon* cross

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Abstract. Heritability is a measure of possible genetic advancement under selection. Estimation of variance components could imply partitioning of genetic variability over different sources of variation. This article describes statistical methods applied and some of the observations made on results of heritability and analysis of environmental variances of grain yield and related traits of progenies derived from a cross between wild and cultivated rice. The study shed light on the genetic information of grain yield and related traits such as their heritability, genetic and environmental effects in the F_1 progenies of a cross between *O. sativa* and *O. rufipogon*. A considerable amount of additive genetic variation was found in these families. The traits with high heritability, considerable phenotypic correlation and low seasonal variability can be used in further improvement of the F_1 progenies. The results obtained were highly promising and can be utilized to develop new rice cultivars.

Key words: *Oryza sativa*, *Oryza rufipogon*, advanced backcross, heritability, genetic variance

INTRODUCTION

The world population is expected to reach 8 billion by 2030 and rice production must increase by 50 percent in order to meet the growing demand (Khush & Brar, 2002). Genetic variability for agronomic traits is the key component of breeding programmes for broadening the gene pool of both rice and other crops. However, the genetic variability for many traits is limited in cultivated germplasm. During the past 30 yr, genetic diversity among improved indica rices has narrowed because of the massive international exchange of germplasm (Khush & Aquino, 1994). The genetic basis of changes associated with the process of rice domestication was studied in detail (Xiong et al., 1999). Studies in rice using advanced backcross QTL analysis provided evidence that certain regions of rice genome are likely to harbour genes of interest for plant improvement (Xiao et al., 1998; Moncada et al., 2001). However, genetic improvement from wild germplasm might result in transfer of undesirable traits as reported in some QTL mapping studies in rice (Moncada et al., 2001; Septiningsih et al., 2003b; Xiao et al., 1998). Hence it is imperative that a detailed understanding of genetic information of yield traits such as their heritability, genetic and environmental effects should be addressed properly before performing any genetic improvement programmes.

The objective of the study was to estimate heritability and environmental effects of yield and yield-related traits using parent-offspring regression in F_1 progenies. By doing so, genetic variability of traits affecting grain yield in rice could be identified. It was found earlier that genetic improvement of plants for quantitative traits requires reliable estimates of heritability in order to plan an efficient breeding program (Dudley & Moll, 1969).

MATERIALS AND METHODS

Oryza rufipogon (accession # IRGC 105491) was used as female parent and crossed to *O. sativa* cv. MR219 in December 2002. Field evaluation of F_1 progenies was conducted in 2 seasons during February 2003 and April 2004 (dry season (DS) plantings) and October 2004 (wet season (WS) planting) at the Malaysian Agricultural Research and Development Institute (MARDI) field experimental station in Seberang Perai, Penang, Malaysia (5°32´N, 100°27´E). Details of field planting, data recording and evaluation of agronomic traits of progeny and parental lines were summarized in Sabu et al. 2006.

Cultivation during DS planting depends on canal water supply as the amount of rain during this time is very low and the air temperature is high (Fig. 1). But there will be rain during WS planting and rice cultivation during this season mainly depends on rainwater. Availability of rainwater is not constant in contrast to the canal supply and this can be severe at the end of the growing season (probably after grain filling stage) which can affect yield. In all plantings, individual plants were evaluated for culm length, panicle length, tillers per plant, panicles per plant, filled grains per plant, empty grains per plant and 1000 grain weight besides estimating the grain yield per plant.

Parent and offspring regression coefficient was calculated using PROC REG of SAS version 6.12 (SAS Institute Inc., 1996). The parent-offspring regression data was standardized using PROC STANDARD of SAS and regression coefficients were also calculated as suggested by Frey & Horner (1957). This is due to the fact that the parent-offspring regression can be greatly influenced by environments resulting in higher or lower trait expression in the offspring relative to the parents (Nyquist, 1991).

Analysis of variance (ANOVA) was performed using PROC GLM.

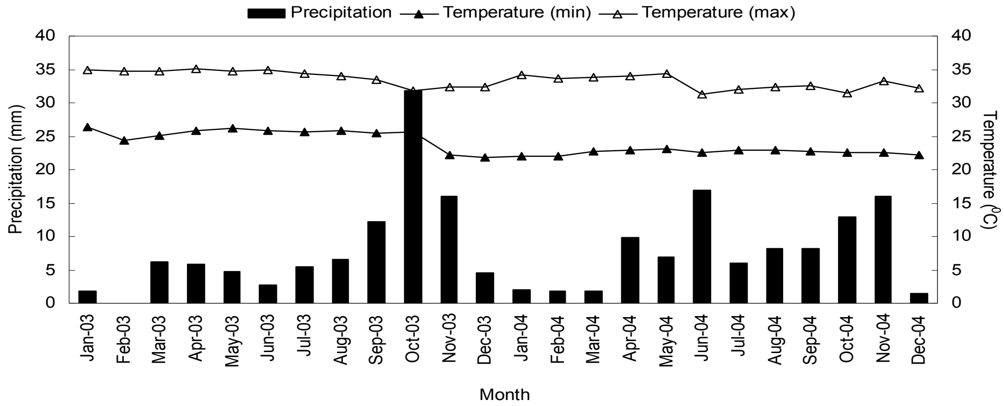

Fig. 1: Monthly changes in precipitation and air temperature in Seberang Perai, Penang in 2003-2004

RESULTS AND DISCUSSION

Rice requires relatively more water during peak tillering activity, flowering and grain filling stages of growth than any other cereals (Kuoko, 1997). Availability of bright sunlight during the entire growth period during WS is also a problem. Hence it is not surprising that most of the agronomic traits recorded lower values in the WS plantings for parents and F_1 progenies (Table 1).

The WS and DS data were combined and analyzed. The pooled data showed highest variability for empty grains per panicle. The coefficient of variation over seasons was moderate to high for the progenies for all traits except panicle length and 1000 grain weight. Between seasons the variability in the traits was low for *O. rufipogon* and high for the F_1 progenies. It shows a wider range of adaptability of *O. rufipogon* for various environmental conditions as reported in previous studies (Moncada et al., 2001).

Table 1: Means and coefficient of variation (CV) of the agronomic traits in parents and F_1 progenies.

Traits	*O. rufipogon*				MR219				F_1			
	DS	WS	Pooled^x	CV	DS	WS	Pooled^x	CV	DS	WS	Pooled^x	CV
CL	123.1	94.0	113.4	13.5	86.7	87.0	86.8	6.1	114.0	65.4	95.3	26.5
PL	24.0	21.2	23.0	9.2	27.2	25.6	26.8	31.2	26.2	25.4	25.9	6.0
TPL	36.2	25.0	32.4	33.1	19.0	16.2	18.3	35.6	40.3	16.2	31.1	44.6
PPL	35.5	24.0	31.7	33.7	19.0	15.6	18.1	36.5	39.4	12.6	29.1	51.1
FGP	86.8	67.0	79.2	28.9	138.8	89.4	125.8	26.2	90.4	66.6	81.2	38.8
EGP	13.0	11.9	12.6	54.9	26.3	91.6	43.5	75.8	34.7	44.8	38.5	68.6
GW	25.9	25.1	25.6	2.2	25.1	25.6	25.2	3.0	28.1	23.1	26.2	9.5

Abbreviations used: Culm length, cm (CL), panicle length, cm (PL), tillers per plant (TPL), panicles per plant (PPL), filled grains per panicle (FGP), empty grains per panicle (EGP), 1000 grain weight, g (GW)

DS=dry season planting, WS=wet season planting, ^{x}Off-season and season data combined.

It is interesting to note that the coefficient of variation in empty grains per panicle between WS and DS in F_1 progenies (69%) was lower than that of the cultivated parent, MR219 (76%). This reduction may be imparted by genetic factors from *O. rufipogon* (variability for empty grains per panicle was 55%). Besides, *O. rufipogon* was insensitive to season for most of the phenotypic traits and showed higher values for grain filling (86%) compared to MR219 (74%) and F_1 progenies (68%) for pooled data. The genetic advantage of F_1 progenies is that it is less sensitive to availability of water in grain filling (72% during DS and 60% during WS) compared to MR219 (84% during DS and 49% during WS).

The progenies recorded higher values for all traits except culm length and filled grains per panicle in contrast to the mid-parental value of the traits (Fig. 2). High levels of heterosis are common in yield component traits (Zhang et al., 1996). The grain yield per plant for the offspring (62 g) was phenomenal and it was about 210% higher than *O. rufipogon* (30 g) and 150% higher than MR219 (39 g). In a similar study conducted earlier, about 15% of the BC2 test cross families outperformed parents with respect to grain yield and grains per plant (Xiao et al., 1998).

Grain filling was highly influenced by the growing environment (e^2 = 0.91; Table 2) and the heritability estimates for filled and empty grains per panicle were the lowest (~0). In the case of culm length, tillers per plant, panicles per plant and 1000 grain weight the heritability estimates were higher, which may be due to influence from the maternal parent, *O. rufipogon* as evident from the comparatively higher common environmental effect for these traits (0.30, 0.13, 0.13 and 0.25 respectively). The range of values of agronomic traits among individuals was generally consistent for parents and F_1 progenies, and may explain why standardized heritability estimates were not appreciably different from actual heritability estimates.

Common environmental effects and heritability estimates were high for culm length, tillers per plant, panicles per plant and 1000 grain weight when pooled over seasons (Table 2). Negative heritability can be assumed to be zero (Robinson et al., 1955), but should be reported (Dudley & Moll, 1969). Based on the variance estimates of the parent-offspring regression model, the error mean squares (expressed as error variance, e^2) resulted in higher estimates for filled and empty grains per panicle and panicle length. Heritability estimates using standardized data did not differ greatly from the actual heritability estimates for any trait or season. The two traits showing differences were tillers per plant (0.06 and 0.08 for actual and standardized data respectively) in DS and panicles per plant (0.41 and 0.39 for actual and standardized data respectively) in pooled data sets. During the WS planting, grain weight data could not be recorded and hence heritability, common environmental effect and error variance for 1000 grain weight were not estimated.

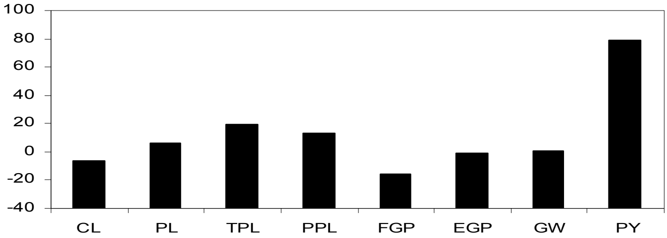

Fig. 2: Mid-parent heterosis in culm length (CL), panicle length (PL), tillers per plant (TPL), panicles per plant (PPL), filled grains per panicle (FGL), empty grains per panicle (EGL), 1000 grain wt (GW) and grain yield per plant (g) in F_1 progenies.

Table 2: Estimates of broad-sense heritability (h^2_b), common environmental effect (c^2) and error variance (e^2) for the agronomic traits in F_1 progenies.

Traits	h^2_b			c^2			e^2		
	DS	WS	Pooled[x]	DS	WS	Pooled[x]	DS	WS	Pooled[x]
CL	0.43	0.79	0.72	0.03	0.12	0.30	0.07	0.04	0.01
PL	0.20	0.28	0.04	-0.12	-0.01	-0.03	0.90	0.18	0.67
TPL	0.06	0.09	0.35	0.07	-0.07	0.13	0.16	0.76	0.03
PPL	0.11	0.77	0.41	0.08	-0.42	0.13	0.13	0.84	0.03
FGP	0.00	-0.06	0.02	-0.02	-0.01	0.01	0.75	0.92	0.34
EGP	-0.03	-0.06	-0.02	-0.01	-0.01	-0.01	0.74	0.98	0.91
GW	0.69	[xx]	0.51	0.35	[xx]	0.25	0.01	xx	0.01

Abbreviations used: Culm length, cm (CL), panicle length, cm (PL), tillers per plant (TPL), panicles per plant (PPL), filled grains per panicle (FGP), empty grains per panicle (EGP), 1000 grain weight, g (GW)

DS=dry season planting, WS=wet season planting, [x]Off-season and season data combined, [xx]Insufficient data.

CONCLUSIONS

This study shed light on the genetic information of grain yield and related traits such as their heritability, genetic and environmental effects in the F_1 progenies of cross between *O. rufipogon* and MR219. It is interesting to note that the coefficient of variation in empty grains per panicle between WS and DS in F_1 progenies was lower than that of the cultivated parent, MR219. This reduction may be imparted by genetic factors from *O. rufipogon*. The genetic advantage of F_1 progenies is that it is less sensitive to availability of water in grain filling compared to MR219. A considerable amount of additive genetic variation was found in these families. Grain yield was significantly correlated to tillers per plant, panicles per plant and filled grains per panicle. The traits with high heritability, considerable phenotypic correlation and low seasonal variability can be used in further improvement of the F_1 progenies.

ACKNOWLEDGEMENTS

This project is supported by the Ministry of Science, Technology and Innovation (MOSTI), Malaysia (IRPA 01-03-03-001 BTK/ER/01). Postdoctoral fellowship awarded to K.K. Sabu and National Science Fellowship awarded to Lim L.S. by MOSTI are highly appreciated.

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