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Combining ability and heritability of selected rice varieties for grain quality traits

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Abstract

This study was conducted to determine the combining ability and heritability of rice grain quality traits. Some grain quality traits such as grain length, grain width, milled grain length, milled grain width, length to width ratio, milled rice recovery, head rice recovery, amylose and gel consistency were analyzed using a full diallel mating design in Malaysian rice varieties. This study was commenced by crossing the selected rice varieties based on a full diallel mating design. The F₁ was harvested at the end of the season. In the following season, the crossed, reciprocal and parental lines were planted in randomly complete block design with three replications. Analysis of variance indicated that genotypes were significantly different for all traits evaluated except for milled rice recovery. Mean square values for general combining ability were significant for the evaluated grain quality traits which indicated the importance of additive gene effects in inheritance of these traits. The specific combining ability effects were significant for several populations derived from crosses involving MR 263, MR 267, MRQ 74, Q 85 and MRQ 76. Reciprocal effects were significant for eight combinations for grain quality traits. Broad sense heritability showed that the AMYL and GC had the lowest value. The GL showed moderate value while GW, MGL, MGW, LW and HRR were the highest. The narrow sense heritability for grain physical properties was higher than grain chemical properties. The highest heritability was observed for LW, MGL, HRR, MGW, GW and GL.

Keywords: Rice variety, Grain quality traits, General and specific combining ability, Heritability.

Abbreviation AMYL-amylose; GC-gel consistency; GL_grain length; GW_grain weight; MGL_milled grain length; MGW_milled grain width; LW_length to width ratio; MRR_milled rice recovery; HRR_head rice recovery; GCA_general combining ability; SCA_specific combining ability; REC_reciprocal effect; MAT_maternal, NMAT_non-maternal.

Introduction

Rice (Orvza sp.) belongs to grass family (Gramineae). It is the second largest cereal crop and is a staple food of nearly half of the world's population (FAO, 2008). Rice species are substantial but only Oryza sativa and Oryza glaberrima, which were originated from Southeast Asia and Niger basin in Africa, respectively, are cultivated. O. sativa is extensively cultivated due to its better adaptation to local growing conditions and produces better yield. Genetic improvement for rice has thoroughly been studied worldwide. Generally a rice breeding program will look into several objectives. Therefore, one way cross, top cross and backcross have extensively been used including diallel cross for study of genetic components, combining ability and heritability of agronomic traits or grain properties (Pooni et al., 1992 and Iftekharuddaula et al., 2008). Recently, a major concern of rice breeding is the grain quality such as appearance of the cooked rice, texture and aroma. The selection of breeding materials is usually focused on the long and slender grain, soft to semi-hard cooked rice texture, having aroma with good yield. Sometime the crosses and selection of progenies result in low quality progenies to fulfill breeding

objectives. This is probably due to numerous plants to work within the segregating populations. Diallel serves as important breeding technique for grain quality traits in rice such as grain length, grain width, grain shape and elongation (Sharifi et al., 2009). Diallel cross analysis helps to identify the best parents and their combinations for further selection and suggests the breeder the appropriate stage for selection as some traits are fully expressed after generations become uniform. Thus, the combining ability analysis, which is derived from a diallel mating design, is usually the appropriate method for choosing the parents and progenies with high general combining ability (GCA) and high specific combining ability (SCA), respectively. The GCA and SCA can further determine the heritability. Falconer (1989) mentioned that heritability estimates for agromorphological traits in rice are sparse and contradictory depending on the genetic materials. This statement is in agreement with Kato (1990) who postulated that selection for grain size is effective even in early segregating generations after crossing. Rabiei et al. (2004) estimated the broad sense heritability of grain length, grain width and grain shape of 0.74,

Table 1. Analysis of variance (Mean squares) of grain quality traits.

Source of	ource of df Mean squares									
variation		AMYL	GC	GL	G W	MGL	MGW	LW	MRR	HRR
Genotypes	48	31.98*	869.42**	0.117^{**}	0.005^{**}	0.107^{**}	0.003^{**}	0.047^{**}	42.80 ^{ns}	235.41**
Replications	2	189.95	1356.11	0.05	0.01	0.481	0.004	0.165	149.68	596.83
Error	96	18.37	357.83	0.06	0.001	0.404	0.001	0.012	37.30	55.43

***,*ns, non- significant, at $p \le 0.01$ and $p \le 0.05$ respectively, AMYL : amylose, GC: gel consistency, GL: grain length, GW: grain weight, MGL: milled grain length, MGW: milled grain width, LW: length to width, MRR: milling recovery and HRR: head rice recovery.

Table 2. Analysis of variance for combining ability.

Source of	df		Mean squares								
variation		AMYL	GC	GL	G W	MGL	MGW	LW	HRR		
GCA	6	45.311**	989.13**	0.339**	0.018**	0.417**	0.012**	0.209**	818.076**		
SCA	21	14.664 ^{ns}	524.11 ^{ns}	0.063 ^{ns}	0.003 ^{ns}	0.033 ^{ns}	0.002**	0.016^{ns}	149.428**		
REC	21	45.48**	1180.15**	0.108*	0.004*	0.094*	0.002*	0.033**	154.927**		
MAT	6	76.35**	1960.63**	0.081 ^{ns}	0.002 ^{ns}	0.174**	0.002 ^{ns}	0.052**	354.642**		
NMAT	15	33.14*	868.46**	0.119*	0.005**	0.062 ^{ns}	0.002*	0.024*	75.041**		
Error	96	18.369	357.831	0.059	00.002	0.0405	0.0012	0.012	55.431		

**, *ns, non- significant, at $p \le 0.01$ and $p \le 0.05$ respectively, AMYL: amylose, GC: gel consistency, GL: grain length, GW: grain weight, MGL: milled grain length, MGW: milled grain width, LW: length to width and HRR: head rice recovery.

0.74 and 0.89 respectively. Vanaja and Babu (2006) evaluated 56 genotypes of high yielding varieties and revealed that the broad sense heritability was 96.9, 92.1% and 96.4% for grain length, grain width and length to width ratio, respectively.

The aim of this study is to determine the combining ability of selected rice varieties for its grain quality traits and to estimate the heritability of the evaluated traits.

Results

Analysis of variance for genotypes

Analysis of variance (ANOVA) showed significant differences among genotypes for all the traits under study except for milling recovery. Thus, this trait was not evaluated for its combining ability in the subsequent analysis (Table 1).

Combining ability analysis

Estimation of GCA, SCA and reciprocal indicated the important role of additive or non-additive gene effect or both for the parents and the progenies derived from a 7×7 full diallel crosses. The mean square values of SCA revealed significant differences for the GCA for the entire grain quality traits and non-significant for AMYL, GC, GL, GW, MGL and LW while the reciprocal effects (REC) were significant for all grain quality traits (Table 2). The significance of GCA and SCA indicate the importance of additive and non-additive gene effects, respectively. These results were further partitioned into performance of the parents *per se* as revealed by the GCA value and performance of the hybrids for each trait as determined by the SCA value.

General combining ability (GCA)

The GCA effects of the grain quality traits are listed in Table 3. Generally, a parent with a positive value would contribute towards high value while parent with negative value would contribute to a low value of these traits. The performances of the parents were revealed as significant GCA. For instance, MR 84 is a good combiner for AMYL, GL, GW, MGL, MGW

and LW. However, for GL, MGL and LW the significant negative values possessed low value (short character) for the traits and could not be considered as the best performed parents. In contrast to these, the negative value for GW and MGW was the best to obtain long and slender grain shape (LW). MR 267 was considered as the best combiner for most of the grain quality traits namely GL, GW, MGL, MGW, LW and HRR. MRQ 74 showed significant effects as a combiner for AMYL, GW, MGW and HRR but due to its low value it could not be considered as a combiner. Of all the quality varieties tested as a combiner, Q 85 performed as a good combiner for GC, GL and HRR.

Specific combining ability (SCA)

The SCA effects indicate the interaction of hybrids for a specific trait. Twenty one combinations were derived from the diallel and the performance of each combination for grain quality traits differed significantly (Table 4). The superior combination which revealed the significant value for GC, GW and MGW was the hybridization between MR $263 \times Q$ 84 while MR $263 \times MRQ$ 74 was an excellent combination for GL and HRR. MR $267 \times MRQ$ 74 was a good combiner for LW. AMYL and MGL were not significant for any SCA combinations. Similar to the GCA value, negative and positive values of SCA effects indicate a tendency towards low and high value of these traits. For example, a population with highest positive value of gel consistency is associated with soft and sticky rice.

Reciprocal effects (REC)

The reciprocal crosses accounts for 21 combinations and the findings showed no significance for almost all the grain quality traits (Table 5). AMYL showed significant influence of maternal in three out of 21 combinations namely MRQ 76 × MR 84, MRQ 76 × MRQ 74 and Q85 × Q84. Furthermore, MRQ 76 × MRQ 74 showed significant effect for GL and HRR while Q 84 × MR 263 was significant for MGW and LW.

Table 3. General combining ability (GCA) effects of grain quality traits

Parents	AMYL	GC	GL	GW	MGL	MGW	LW	HRR	
MR 84	1.38*	4.11 ^{ns}	-0.190**	0.009*	-0.158**	0.023**	-0.112**	1.292 ^{ns}	
MR 263	0.35 ^{ns}	3.39 ^{ns}	0.0007 ^{ns}	0.029**	-0.037 ^{ns}	0.012*	-0.036*	-0.006 ^{ns}	
MR 267	0.900 ^{ns}	-3.89 ^{ns}	0.07*	-0.010*	0.145**	-0.013*	0.090**	2.346*	
MRQ 74	-1.43*	3.63 ^{ns}	-0.01 ^{ns}	-0.031**	0.016 ^{ns}	0.016**	0.031 ^{ns}	-4.08**	
MRQ 76	-1.47 ^{ns}	-3.08 ^{ns}	0.04 ^{ns}	0.019**	-0.032 ^{ns}	0.018**	-0.043*	-7.717**	
Q 84	-0.29 ^{ns}	3.68 ^{ns}	0.02 ^{ns}	$-0.002^{\text{ ns}}$	-0.033 ^{ns}	-0.009 ^{ns}	-0.002 ^{ns}	3.846**	
Q 85	0.15 ^{ns}	-7.84**	0.03*	-0.013	0.098**	-0.016**	0.072**	4.321**	

**,*ns, non-significant, at p≤0.01 and p≤0.05 respectively, AMYL: amylose, GC: gel consistency, GL: grain length, GW: grain weight, MGL: milled grain length, MGW: milled grain width, LW: length to width and HRR: head rice recovery

Table 4. S	pecific com	bining	ability	(SCA)	effects	of grain	quality	traits.
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Combination	AMYL	GC	GL	GW	MGL	MGW	LW	HRR
MR 84 x MR 263	-1.134 ^{ns}	-11.489 ^{ns}	-0.047 ^{ns}	-0.006^{ns}	-0.067^{ns}	$-0.002^{\text{ ns}}$	-0.026 ^{ns}	2.404^{ns}
MR 84 x MR 267	1.179 ^{ns}	-7.204 ^{ns}	-0.035 ^{ns}	0.023 ^{ns}	-0.008 ^{ns}	-0.013 ^{ns}	0.013 ^{ns}	0.077 ^{ns}
MR 84 x MRQ 74	-0.132 ^{ns}	2.939 ^{ns}	-0.039 ^{ns}	0.011 ^{ns}	0.016 ^{ns}	-0.022 ^{ns}	0.042 ^{ns}	1.501 ^{ns}
MR 84 x MRQ 76	-0.496 ^{ns}	9.986 ^{ns}	0.035 ^{ns}	0.023 ^{ns}	$-0.009^{\text{ ns}}$	-0.012^{ns}	0.013 ^{ns}	1.276 ^{ns}
MR 84 x Q 84	-0.233 ^{ns}	7.891 ^{ns}	-0.017 ^{ns}	-0.006 ^{ns}	0.005 ^{ns}	0.011 ^{ns}	-0.019 ^{ns}	1.352 ^{ns}
MR 84 x Q 85	0.477 ^{ns}	6.286 ^{ns}	-0.289 ^{ns}	0.012 ^{ns}	0.028 ^{ns}	-0.026^{ns}	0.048^{ns}	-5.192 ^{ns}
MR 263 x MR 267	0.145 ^{ns}	-3.489 ^{ns}	$0.024^{\text{ ns}}$	0.024 ^{ns}	-0.031 ^{ns}	0.003 ^{ns}	-0.023 ^{ns}	3.442 ^{ns}
MR 263 x MRQ 74	-1.124 ^{ns}	1.653 ^{ns}	0.173 *	0.019 ^{ns}	$-0.042^{\text{ ns}}$	-0.010 ^{ns}	-0.006 ^{ns}	6.345*
MR 263 x MRQ 76	0.630 ^{ns}	-0.632 ^{ns}	-0.081 ^{ns}	0.023 ^{ns}	0.038 ^{ns}	0.028 ^{ns}	-0.025 ^{ns}	1.989 ^{ns}
MR 263 x Q 84	0.058 ^{ns}	17.605*	0.076 ^{ns}	-0.039*	0.076 ^{ns}	-0.051**	0.124 ^{ns}	-5.169 ^{ns}
MR 263 x Q 85	-0.541 ^{ns}	9.905 ^{ns}	0.209 ^{ns}	0.055 ^{ns}	-0.122^{ns}	-0.010 ^{ns}	-0.038 ^{ns}	13.914 ^{ns}
MR 267 x MRQ 74	-0.276 ^{ns}	9.605 ^{ns}	0.006 ^{ns}	-0.031 ^{ns}	0.147 ^{ns}	0.003 ^{ns}	0.091*	1.549 ^{ns}
MR 267 x MRQ 76	0.835 ^{ns}	13.653 ^{ns}	0.095 ^{ns}	0.006^{ns}	0.081 ^{ns}	0.014 ^{ns}	0.036 ^{ns}	-2.346 ^{ns}
MR 267 x Q 84	2.778 ^{ns}	11.224 ^{ns}	-0.098 ^{ns}	0.023 ^{ns}	-0.065 ^{ns}	0.017 ^{ns}	-0.054 ^{ns}	$-0.470^{\text{ ns}}$
MR 267 x Q 85	2.624 ^{ns}	16.619 ^{ns}	0.147 ^{ns}	0.041 ^{ns}	0.096 ^{ns}	-0.005 ^{ns}	0.055 ^{ns}	-1.450 ^{ns}
MRQ 74 x MRQ 76	-0.321 ^{ns}	-10.537 ^{ns}	0.048^{ns}	-0.003 ^{ns}	-0.108 ^{ns}	$0.004^{\text{ ns}}$	-0.060 ^{ns}	-15.035**
MRQ 74 x Q 84	-2.074 ^{ns}	-1.632 ^{ns}	-0.159 ^{ns}	0.026 ^{ns}	-0.061 ^{ns}	0.022 ^{ns}	-0.065 ^{ns}	-1.910 ^{ns}
MRQ 74 x Q 85	-5.891 ^{ns}	8.476 ^{ns}	-0.180 ^{ns}	0.025 ^{ns}	-0.273 ^{ns}	-0.051 ^{ns}	-0.052 ^{ns}	-3.911 ^{ns}
MRQ 76 x Q 84	2.127 ^{ns}	-8.251 ^{ns}	-0.116 ^{ns}	0.005 ^{ns}	0.041 ^{ns}	0.013*	-0.003 ^{ns}	2.596 ^{ns}
MRQ 76 x Q 85	1.621 ^{ns}	0.762 ^{ns}	-0.176 ^{ns}	0.043 ^{ns}	0.214 ^{ns}	0.001 ^{ns}	0.105 ^{ns}	-1.89 ^{ns}
Q 84 x Q 85	-2.705 ^{ns}	6.523 ^{ns}	0.037 ^{ns}	-0.011 ^{ns}	0.045 ^{ns}	0.013 ^{ns}	0.075 ^{ns}	2.218 ^{ns}

**,* ns, non-significant, at $p \le 0.01$ and $p \le 0.05$ respectively, AMYL: amylose, GC: gel consistency, GL: grain length, GW: grain weight, MGL: milled grain length, MGW: milled grain width, LW: length to width and HRR: head rice recovery

These populations also could be considered for further phenotypic selection in the subsequent generations.

Estimation of genetic parameters on grain quality traits

From the combining ability analysis, the additive variance, dominant variance, heritability, genetic ratio and GCA: SCA ratio were calculated (Table 6) according to Singh and Chaudary (1977) and Zhang et al. (2005). The genetic ratio showed values close to unity for most of the traits except GC. The grain quality traits were all showed additive effect as revealed by their GCA to SCA ratio.

The broad and narrow sense heritability was derived from the respective genotypic and additive variances of the evaluated traits. Broad sense heritability showed that the AMYL (45.45%) and GC (45.78%) had the lowest value while the other traits were either moderate or high in heritability (Table 6). Similar trends were observed in narrow sense heritability of all traits evaluated.

Discussion

Combining ability of parents is important for rice varietal improvement. Rice breeding methods are usually comprised of several breeding techniques such as bulk breeding, backcross breeding and the most popular is pedigree breeding. In each breeding course, single cross, top cross, double cross and backcross are extensively used. In line with restraint of land, labor and cost, a rice breeder should illustrate their breeding programme in affordable methods and diallel mating design is one of the most appropriate one.

In this study, the additive gene action was important for the grain quality traits such as AMYL, GC, GL, GW, MG and LW which suggest that a selection process could be done in the early generations where less segregation would be observed for these traits. As for MGL and LW, the result was in agreement with Savery and Ganesan (2003) and Sharifi et al. (2009) who worked with Indian and Iranian rice varieties, respectively. However, for MGW and HRR, the result was in contrary with Sharifi et al (2009) as in present study both additive and non-additive gene action were important. Hence, delay in selection

Table 5. Reciprocal (REC) effects of grain quality traits

Combination	AMYL	GC	GL	GW	MGL	MGW	LW	HRR
MR 263 x MR 84	0.636 ^{ns}	-26.00 ^{ns}	0.137 ^{ns}	-0.011 ^{ns}	$0.037^{\text{ ns}}$	-0.018 ^{ns}	0.045^{ns}	-1.370 ^{ns}
MR 267 x MR 84	0.572 ^{ns}	-21.000 ^{ns}	-0.211*	-0.032 ^{ns}	-0.012 ^{ns}	-0.004 ^{ns}	0.003 ^{ns}	1.305 ^{ns}
MRQ 74 x MR 84	$-0.050^{\text{ ns}}$	11.333 ^{ns}	0.028 ^{ns}	0.008^{ns}	-0.137 ^{ns}	$0.002^{\text{ ns}}$	$-0.070^{\text{ ns}}$	-0.087 ^{ns}
MRQ 76 x MR 84	4.898**	-13.000 ^{ns}	0.063 ^{ns}	-0.032 ^{ns}	-0.002 ^{ns}	0.008 ^{ns}	-0.013 ^{ns}	9.083*
Q 84 X MR 84	-2.571 ^{ns}	6.333 ^{ns}	-0.040 ^{ns}	-0.023 ^{ns}	-0.137 ^{ns}	$0.002^{\text{ ns}}$	-0.070 ^{ns}	3.017 ^{ns}
Q 85 X MR 84	1.348 ^{ns}	19.000 ^{ns}	-0.190 ^{ns}	0.033 ^{ns}	-0.367**	0.039**	-0.238**	-4.74 ^{ns}
MR 267 x MR 263	-0.771 ^{ns}	7.333 ^{ns}	0.195 ^{ns}	0.037 ^{ns}	-0.090 ^{ns}	-0.005 ^{ns}	-0.037 ^{ns}	-3.175 ^{ns}
MRQ 74 x MR 263	0.655 ^{ns}	-8.000 ^{ns}	-0.148 ^{ns}	$0.017^{\text{ ns}}$	$-0.079^{\text{ ns}}$	-0.005 ^{ns}	-0.031 ^{ns}	2.748 ^{ns}
MRQ 76 x MR 263	-2.375 ^{ns}	24.333 ^{ns}	0.157 ^{ns}	-0.002^{ns}	0.041 ^{ns}	-0.012 ^{ns}	0.038^{ns}	7.182*
Q 84 X MR 263	-1.267 ^{ns}	-3.333 ^{ns}	-0.060 ^{ns}	-0.037 ^{ns}	-0.001 ^{ns}	-0.065**	0.108*	-7.177*
Q 85 X MR 263	-0.443 ^{ns}	22.667 ^{ns}	$0.002^{\text{ ns}}$	0.003 ^{ns}	-0.077 ^{ns}	0.001 ^{ns}	-0.037 ^{ns}	0.738 ^{ns}
MRQ 74 x MR 267	0.185 ^{ns}	-7.333 ^{ns}	0.237 ^{ns}	0.013 ^{ns}	0.060 ^{ns}	-0.010 ^{ns}	0.045 ^{ns}	2.002 ^{ns}
MRQ 76 x MR 267	2.818 ^{ns}	16.000*	-0.057 ^{ns}	0.015 ^{ns}	0.011 ^{ns}	-0.010 ^{ns}	0.022^{ns}	5.818 ^{ns}
Q 84 X MR 267	-0.105 ^{ns}	5.000 ^{ns}	0.048^{ns}	$-0.000^{\text{ ns}}$	-0.066^{ns}	-0.003 ^{ns}	-0.030 ^{ns}	0.948 ^{ns}
Q 85 X MR 267	-0.376 ^{ns}	6.667 ^{ns}	-0.186 ^{ns}	-0.015 ^{ns}	0.036 ^{ns}	0.001 ^{ns}	0.017 ^{ns}	0.345 ^{ns}
MRQ 76 x MRQ 74	6.238**	4.667 ^{ns}	0.250*	-0.005 ^{ns}	0.116 ^{ns}	-0.006 ^{ns}	$0.067^{\text{ ns}}$	11.686**
Q 84 X MRQ74	-2.44 ^{ns}	13.667 ^{ns}	-0.098 ^{ns}	-0.008 ^{ns}	0.153 ^{ns}	-0.021 ^{ns}	0.107*	7.071*
Q 85 X MRQ 74	1.989 ^{ns}	11.667 ^{ns}	-0.112 ^{ns}	-0.023 ^{ns}	-0.249**	-0.031 ^{ns}	-0.072 ^{ns}	-4.070 ^{ns}
Q 84 X MRQ 76	-0.247 ^{ns}	17.667*	-0.065 ^{ns}	-0.035 ^{ns}	-0.018 ^{ns}	-0.013 ^{ns}	0.011 ^{ns}	-4.538 ^{ns}
Q 85 X MRQ 76	-3.138 ^{ns}	6.667 ^{ns}	0.002 ^{ns}	0.030 ^{ns}	-0.011 ^{ns}	0.008 ^{ns}	-0.017 ^{ns}	-6.365 ^{ns}
Q 85 X Q 84	7.121**	1.000 ^{ns}	-0.015 ^{ns}	-0.055**	-0.157 ^{ns}	-0.008 ^{ns}	-0.062^{ns}	-0.427 ^{ns}

**,* ns, non-significant, at p \leq 0.01 and p \leq 0.05 respectively AMYL: amylose, GC: gel consistency, GL: grain length, GW: grain weight, MGL: milled grain length, MGW: milled grain width, LW: length to width and HRR: head rice recovery

Table 6. Genetics parameters of grain quality traits.

Genetics	AMYL	GC	GL	GW	MGL	MGW	LW	HRR
parameters								
σ_{e}^{2}	6.123	119.277	0.020	0.0007	0.014	0.00040	0.004	18.477
σ^2_{gca}	2.203	33.888	0.020	0.0011	0.027	0.00072	0.014	47.978
σ^2_{sca}	0.695	32.952	0.004	0.0002	0.002	0.00013	0.001	10.659
σ^2_{rec}	19.679	530.437	0.044	0.0015	0.040	0.00080	0.015	68.225
σ^2_A	4.407	67.776	0.040	0.0021	0.055	0.00143	0.028	95.956
σ^2_{D}	0.695	32.952	0.004	0.0002	0.002	0.00013	0.001	10.659
h ² n	39.26	30.81	63.05	71.42	78.45	73.00	84.73	76.71
H _B	45.45	45.78	68.71	78.34	80.72	79.63	87.73	85.23
genetic ratio	0.864	0.673	0.918	0.912	0.972	0.917	0.966	0.900
GCA:SCA	3.169	1.028	5.571	5.162	17.301	5.505	14.134	4.501

AMYL: amylose, GC: gel consistency, GL: grain length, GW: grain weight, MGL: milled grain length, MGW: milled grain width, L/W: length to width and HRR: head rice recovery

Table 7. Parentals gr	rain physical pro	perties and chemical	characteristics used for	or diallel mating design.

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variety	AMYL (%)	AROMA*	GC (mm)	MGL (mm)	MGW (mm)	L/W ratio	
MR 84	28	0	59	6.62	2.06	3.20	
MR 267	20	0	66	6.93	1.95	3.53	
MR 263	17	0	75	6.60	2.06	3.20	
MRQ 74	27	2	38	6.62	1.88	3.56	
MRQ 76	16	2	70	6.44	2.04	3.16	
Q 84	27	0	77	6.73	2.24	3.00	
0.85	23	0	75	6.91	1 97	3 51	

 Q 85
 23
 0
 75
 6.91
 1.97
 3.51

 AMYL: amylose, GC: gel consistency MGL: milled grain length, MGW: milled grain width, LW: length to width, *0-not scented 1-scented 2-highly

scented

for the improvement of these characters is suggested in later generations, where the genes has fully expressed and fixed. In addition, environment could play a major role in attaining the acceptable head rice percentage.

The parents are divided into non aromatic rice which, comprised of MR 84, MR 263, MR 267, Q 84 and Q85 while MRQ 74 and MRQ 76 are the aromatic rices. The performance of each parent for each trait could be group-dependant. For instance, Q 85 and MR 84 were suitable combiners for most traits evaluated. Hence, we suggest this variety as the parent for specific crossing objectives. However, the combining ability with the new variety is yet to be determined. This finding is in agreement with Pooni et al. (1996) and Sharifi et al. (2009) who mentioned that good general combiner are usually revealed by the significant of the GCA effect and should be selected as parental lines. High GCA effects mostly contribute to additive gene effects which represent a fixable portion of genetic variation. Though it is common to observe that parental lines would have several significant GCA but to produce the best progeny, parents with highest GCA for a specific trait should be used. The SCA value, which is derived from the interaction effect of the parents, is essential to breeders in term of selection

In this study, five combinations were selected for second generation evaluation instead of 21, where more attention is required for desired plant characters. These findings have reduced the number of populations to be planted for the next generation selection, by which the selection is practically focused. Therefore, the selected combinations were from a cross between normal rice (MR 263, MR 267, Q 84 and Q 85) with aromatic varieties (MRQ 74 and MRQ 76). Generally, high additive gene action indicates higher heritability. In relation to GCA : SCA ratio, genetic ratio is also used to predict gene action based on performance of the GCA alone. The closer genetic ratio to unity and greater GCA: SCA reveal the additive gene effect of grain quality traits. Similar results were observed in studies by Shi et al. (2000) for grain shape (LW), Chen et al. (1988) for MGL and Zhang et al. (2006) for MGW. However, Sarawgi et al. (1991) and Ku and Liu (1986) reported a contrary results for LW and MGW, where non-additive gene action was important.

Narrow sense heritability trend was also similar to the broad sense heritability but with lower value, which indicates the earliest selection could be done as the genes are fixed in early generations. Narrow sense heritability reflects the phenotypic variance due to additive genetic variability. It is classified as low, moderate and high. In present study, narrow sense heritability of grain quality traits were high for GW, MGL, MGW and LW and moderate for AMYL, GC and GL. The narrow sense heritability for GW, MGL, MGW and LW were in agreement with Zhang et al. (2006) and Sharifi et al. (2009). Lower narrow sense heritability suggests that some other factors may influence the expression of the traits such as environmental factors. Thus, selection process has to be prolonged (more generations compared to high heritability trait) in order to obtain acceptable traits.

Materials and methods

Breeding materials

Seven Malaysian rice varieties namely MR 84, MR 267, MR 263, Q74, Q76, Q84 and Q85 composed of released varieties

and advanced lines were obtained from Agriculture Research and Development Institute (MARDI) and selected as parental lines in this study. These parents had differences in some of the quality studied traits (Table 7). For instance, MR 84, MRQ 74, Q 85 have intermediate to high amylose content, while MR 263, MR 267 and MRQ 76 were resided in low to intermediate amylose class. Other differences were grain shape and fragrance. For example, the MRQ 76 variety had medium and slender grain while MRQ 74 and Q 85 were long and slender and both fragrant.

Crossing program

The parental lines were planted in main season during 2009-2010. These lines crossed in a 7×7 full diallel mating design were conducted in late December 2009. The F₁, selfed and reciprocal seeds were harvested and oven dried (14% moisture content) and kept in air conditioned room (23 ⁰C ±2).

Experimental design and crop maintenance

In the off season 2010, a total of 49 populations of F_1 , reciprocal and parents were transplanted in Seberang Perai. Each population was comprised of 3 lines with 10 plants in one line following randomized complete block design (RCBD) with 3 replications. Fertilizer applications were as recommended with minor modification to suit the transplanting system (MARDI, 2009). Water level was at 7-10cm from transplanting to 90 days and slowly drained out prior harvesting.

Data collection and statistical analysis

Five plants from the middle row were randomly chosen for data collection. The selected plants were individually harvested and processed for grain physical properties such as grain length (GL), grain width (GW), milled grain length (MGL), milled grain width (MGW), length to width ratio (LW), milling recovery (MRR) and head rice recovery (HRR). The chemical properties like amylose (AMYL) and gel consistency (GC) were determined according to Melissa et al. (2010) and Cagampang et al. (1973), respectively.

Data were analyzed using SAS (SAS 2002). DIALLEL-SAS procedure developed by Zhang et al. (2005) was used for analyzing the diallel according to Griffing's (1956) model 2 method 1 which the F_1 , reciprocal and the respective parents were included. This procedure had estimated the mean squares and standard error values for general combining ability (GCA), specific combining ability (SCA), reciprocal (REC), maternal (MAT) and non-maternal (NMAT). The partitioning of these effects was shown as the following model;

$$Y_{ij} = \mu + g_i + g_j + s_{ij} + r_{ij} + \varepsilon_{ij}$$

Where; μ : overall mean, g_i : GCA effects of parents i or j, s_{ij} : SCA effects of the cross between parents i and j, r_{ij} : REC effects and ϵ_{ij} : error of observation.

 σ^2_{gca} , $\sigma^2_{sca} \sigma^2_{rec}$ were determined according to Singh and Chaudary (1977). From these variances, additive and dominant variances were calculated as the following formula which is similar to Zhang et al. (2005);

 $\sigma_{A}^{2} = 2\sigma_{gca}^{2}$ while $\sigma_{D}^{2} = \sigma_{sca}^{2}$. Broad sense heritability was determined as the ratio of genetic variance (V_{G}) to phenotypic variance (V_{P}) and the narrow sense heritability as the ratio of genetic variance (V_{A}) to phenotypic variance (V_{P})

Conclusions

Diallel mating design for rice varieties served as the most important step in breeding programs. The derived information such as the parents performance (revealed by GCA) and interaction of parents (revealed by SCA) can directly be used by breeders. In both cases, parents with high GCA value and combinations with significant SCA value can be selected for further breeding approach. This study indicated that most of the grain quality traits are controlled by additive gene action, which correlates with high heritability. However, the chemical properties trait like AMYL and GC showed moderate to low heritability, respectively. The genetics parameters obtained from this study may benefit rice breeder, in term of choosing appropriate parental varieties such as MR 263 × Q 84, MR 263 \times MRQ 74 and MR 267 \times MRQ 74 for the quality traits. However, there is a need to study environmental interaction with the traits, so an effective selection method could be applied.

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