REGULAR ARTICLE

Genotype × environment assessment for grain quality traits in rice

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ABSTRACT

Physicochemical properties of 10 rice advanced breeding lines (BC₂F₇) across 3 environments in Malaysia were evaluated. Highly significant G × E interactions for all measured quality traits were detected using ANOVA, and the additive main effect and multiplicative interaction (AMMI) statistical model was applied to analyze them. The results showed that the grain quality parameters had large genotype by environment (G × E) interactions. Differences among genotypes and environments accounted for 16-73% and 0.5-56% of the total sum of squares, respectively, while the G × E interaction accounted for 15-52% of the total sum of squares. The first and second AMMI axes captured 67-96% and 4-33% of the total variation due to G × E interaction, respectively. The biplots of genotypes/environments means and scores on first Principal Component Axis (AMMI-1 biplot) for all traits accounted for most of the total treatment sum of squares. Genotypes G7 (in terms of head rice percentage and amylose content) and G16 (in terms of head rice percentage, protein and amylose content) were detected as winning genotypes in mega-environments, according to the AMMI-1 model. The best genotype in one environment was not always best in other test environments. However, most genotypes showed higher quality parameters in Bumbung Lima and Sungai Besar than in Gurun.

Key Words: *AMMI; biplot; genotype × environment; grain quality; rice.*

INTRODUCTION

Rice (*Oryza sativa*) is the most important food crop in the world, supplying over 21% of the calorific demands of the world population and up to 76% of the calorific intake of the

population of Southeast Asia. The main factors that plant breeders consider in developing new rice varieties are grain yield and quality. In countries where rice is consumed, traits of grain quality determine market value and have an important role in the selection of new varieties (Champagne et al. 1999, Fitzgerald et al. 2008). In order to extend the rice genetic base, which would make it possible to breed for increased crop yield, crosses have been made between elite cultivars and genetically distant relatives, such as landraces and varieties from different gene pools (e.g., *indica × japonica* crosses) (Wu et al. 1996, Zhuang et al. 1997). Furthermore, in spite of the overall inferior agronomic phenotypes observed in wild species, they have been a valuable source of favourable genes from the beginning of modern breeding. The introgression of wild rice alleles has been successfully used as an effective approach in cultivated rice breeding programs for further improvement of agronomic traits (Xiao et al. 1998, Moncada et al. 2001, Septiningsih et al. 2003, Thomson et al. 2003, Aluko et al. 2004, Fasahat et al. 2012a). Very widespread in South and Southeast Asia, wild rice *Oryza rufipogon* is the most important genetic resource for rice improvement. Using an introgression line population of rice developed from a cross between wild rice (*O. rufipogon* Griff.) and a *japonica* cultivar, Yuan et al. (2010) reported that the alleles derived from *O. rufipogon* had a desirable effect on amylose and protein content. *Oryza sativa* subsp. *indica* cultivar MR219 has good characteristics, such as a short maturation period (105-111 days), grain weight (27.10 g per 1000 grains), plant height (76-78 cm), resistance to diseases and pests, and intermediate amylose content (21.4%) (Alias 2002). Owing to its high yield potential, MR219 has been broadly accepted by farmers and is currently one of the most popular cultivars in Malaysia with good eating qualities (Alias 2002).

Grain shape and chalkiness ratio (i.e. the ratio between opaque and translucent grains) are the main factors in determining the appearance of grains in rice. The density of starch granules is lower in chalky grains in contrast to the translucent ones (Del Rosario et al. 1968). Since chalky grains are not as hard as the translucent ones, they are more likely to break during milling (Septiningsih et al. 2003). Head rice is a major factor in determining rice market value and is one of the most essential traits for milled rice (Aluko et al. 2004). Rice is consumed mainly as a whole grain and, as a result, the chemical property of the whole grain is a matter of primary concern. It is clear that the proportion of protein in rice is not very high but the quality of rice protein is far better than that of other cereals, thanks to higher amount of lysine (3.8 g/ 16 g N) than in grain of wheat (2.3 g/ 16 g N), sorghum (2.7 g/ 16 g N) and corn (2.5 g/ 16 g N) (James and McCaskill 1983). Amylose content, one of the important starch properties, affects the cooking and eating quality of rice grains (Juliano 1972, Fasahat et al. 2014). Rice with higher amylose content results in higher volume expansion ratio and higher degree of flakiness. Likewise, higher amylose content results in cooked rice that is dry and less tender, and turns hard upon cooling. On the contrary, low amylose rice tends to be moist and sticky when cooked.

G × E interaction is common when genotypes (G) are tested across a number of environments (E). Based on the extent of the interaction, ranking of genotypes can vary across environments. Various methods have been proposed to analyse the genotype-by-environment interaction, examples being the combined analysis of variance (ANOVA), linear regression analysis, additive main effects and multiplicative interaction (AMMI) analysis and joint regression analysis. The combined analysis of variance (ANOVA) can test the significance of interactions and main effects, but it does not help to explain the patterns of the G × E interaction. To this aim, AMMI is the model of first choice when main effects and interactions are both important (Zobel et al. 1988). This method integrates ANOVA and principal component analysis (PCA) into a unified approach. One key feature of this type of analysis is that adjustment may be carried out using information from other locations, to refine the estimates within a given location (Crossa et al. 1990, Gauch 2006, Ebdon and Gauch 2011). Gauch et al. (2008) argue that AMMI's relative merit depends on the ANOVA part, which can separate the genotype (G) and environment (E) main effects and G × E

interaction effects. Moreover, the principal component part of AMMI, which provides a multiplicative model, is applied to analyze the matrix of residuals from the additive ANOVA model. AMMI has been widely applied in various research situations. For instance, Makinde and Ariyo (2011) applied AMMI analysis to the yield data of groundnut performance trials, and suggested two favoured genotypes in their mega-environment trial in India. Campbell and Jones (2005) assessed the extent to which G × E interaction affected lint yield of cotton, and identified two regions within the South Carolina cotton production area as proper testing locations for lint yield performance.

In a previous paper, the result of introgression analysis was presented (Fasahat et al. 2012a). The objectives of this study were to evaluate the main quality traits of 10 advanced breeding lines under different environmental conditions and to investigate the pattern of G × E interactions.

MATERIALS AND METHODS

A set of advanced breeding lines were developed under an advanced backcross program (focusing on the development of high-yielding rice cultivars) from a cross between a Malaysian high yielding *indica* cultivar of *Oryza sativa*, MR219 and a common wild rice accession of *O. rufipogon* (Sabu et al., 2006; Fasahat et al., 2012b). After a successful pedigree selection in BC_2F_3 and BC_2F_4 generations, 26 transgressive variants were identified for cultivar performance trials. The selected genotypes were field tested in three rice growing areas (Supplemental Table S1a, b and c), including Bumbung Lima (E1), Gurun, Kedah in Pulau Pinang (E2) and Sungai Besar in Selangor (E3), over two (main and off) seasons. Ten rice transgressive variants (advanced breeding lines of BC_2F_7 generation) used in this study were selected based on yield performances (Table 1) in the BC_2F_5 and BC_2F_6 generations under the main growing season (September 2007 to February 2008). After harvest, the rice grains were dried directly under sunlight followed by drying in cool drying room down to below 14% moisture content, and stored at room temperature for 3 months. The samples were hulled by a de-husker machine (Motion Smith Co., Singapore) to produce brown rice. Then the brown rice samples were polished by a polishing machine (Satake Engineering, Co., Tokyo, Japan) and tested for physical properties. The rice flour of each variant was obtained by passing the milled rice grains through a 500 μm sieve screen (Foss cyclotec mill 1093) and was further evaluated for chemical constituents. The following physical properties were determined: head rice (HR) and immature grain (IMM) percentages, which were measured according to Septiningsih et al. (2003). The percentage values of the respective traits were calculated as follows:

Head rice (%) = weight of head rice × 100 / weight of milled rice sample.

Immature grain (%) = weight of immature grain × 100 / weight of milled rice sample.

Amylose content (AC) of milled rice was determined according to Fasahat et al. (2012c), using a flow injection analyser (FIA) (FOSS Co., Sweden). Protein content (PC) was measured by the Kjeldahl method (MS1194, 1991). The selected genotypes were considered as treatments and assigned to the experimental units in a completely randomized design with 2 replicates. A code for variants was used for easy reference in future studies (Table 1).

STATISTICAL ANALYSIS

SAS software version 9.1 (SAS Institute, Cary, NC, USA) was used to perform analysis of variance on the values of traits obtained per replication across environments. PROC GLM of SAS was run to calculate genotype-by-environment interactions and type III sum of squares. The Duncan multiple range test (α = 0.05) was used for mean separation and the genetic correlation between traits were determined as Pearson's correlation coefficients among genotype means by using the SAS software. Joint regression analysis and Additive Main Effect and Multiplicative Interaction (AMMI) analysis was done by MATMODEL Version 3.0 (Gauch and Furnas 1991, Gauch 2007). The AMMI-1 biplot shows mean trait values and the

first interaction principal component axis (IPCA1) scores. F tests were used to assess the significance of IPCAs, in the form devised by Gollob (1968).

Table 1. List of the evaluated genotypes in this study

Sl. No.	MARDI Rice Gene Bank Designation (BC$_2$F$_7$)	Variant Code	Average yield (t/ha) across 3 environments
1	R2-10-18-2-B-B	G4	5.8
2	R6-2-31-2-B-B	G7	6.2
3	R7-6-38-2-B-B	G8	6.2
4	R7-7-39-4-B-B	G9	5.6
5	R14-9-69-2-B-B	G13	5.9
6	R14-9-69-4-B-B	G15	5.8
7	R14-9-69-5-B-B	G16	6.0
8	R17-1-83-3-B-B	G19	6.0
9	R26-2-108-1-B-B	G25	5.6
10	R26-6-113-1-B-B	G26	5.3

RESULTS

ANALYSIS OF VARIANCE

The mean value of the 10 genotypes grown in 3 environments, the environment means, and the first PCA scores from AMMI analysis are presented in Table 2. Large differences among genotypes and among environments were observed. Mean head rice ranged from 52.0% (G15) to 81.6% (G7). Four genotypes, that is, G7, G16, G25, and G13, showed above average head rice percentages, and were also consistently above the environment average. Genotypes G4, G8, G9 and G15 produced head rice consistently below average in all environments. Environments E1 and E3 had large positive head rice main effects, while environment E2 showed a large negative head rice main effect. E3 recorded the highest mean head rice (78.5%), while E2 had the lowest mean head rice (46.1%).

Genotypes G9 and G25 showed consistently higher immature grain percentage with respect to environment averages. Mean immature grain percentage in E2 (12.7%) was lower than in the other environments.

In the case of protein content, the G × E interaction effect was significant ($p < 0.001$); this trait ranged from 8.5% (G9) to 9.3% (G16) and G16, G4, G19 and G25 showed a higher average content with respect to the average value across environments. E1 yielded higher protein content (9.4%) than E3 and E2, which showed mean protein contents of 8.8% and 8.4%, respectively.

Mean amylose content ranged from 19.5% (G25) to 23.9% (G13). Genotypes G4, G13 and G15 had amylose content consistently above the environment average, whereas genotype G8 had amylose content consistently below average in all environments. E1 and E3 showed slightly higher amylose content than E2.

The ANOVA revealed highly significant G × E interactions as well as significant differences among genotypes and among environments for all traits (Table 3). As for IMM, the proportion of variation contributed by the genotypic effect was much greater than that from the other sources of variation.

The dominant contribution of G × E interactions over that of the genotype was detected for amylose content, accounting for 52.5% of sum of squares, several times larger than the main environmental effect.

The percentage of sum of squares explained by G × E interactions ranged from 15.9% for head rice to 52.5% for amylose content. The interaction effect between genotypes and environments can be estimated by multiplying the score of a genotype by that of an environment (Van Oosterom et al. 1993). The AMMI analysis produced two significant

principal components for protein content and amylose content, whereas for head rice and immature grain percentage only the first PCA was significant (Table 3). IPCA1 was highly significant, capturing 67.0-96.0% and 55.6% of the interaction sum of squares and degrees of freedom, respectively. In comparison with IPCA1, the joint linear regression model captured 28% of G × E for IMM, 53% for protein content and nearly 100% for the other two traits.

Table 2. Physicochemical properties of 10 rice genotypes (G) in 3 environments (E), mean values and first IPCA scores for the AMMI model for analysis of interaction.

| Genotype | HR (%) | | | | | IMM (%) | | | | |
| | Environment | | | Mean | | Environment | | | Mean | |
	E1	E2	E3		IPCA1	E1	E2	E3		IPCA1
G4	75.7	34.9	77.2	62.6	1.29	17.2	9.1	13.0	13.1	-0.28
G7	83.5	72.9	88.5	81.6	-2.26	13.5	7.6	9.3	10.1	-0.38
G8	74.1	20.4	70.9	55.1	2.58	17.8	11.5	13.6	14.3	-0.37
G9	71.7	28.4	77.3	59.1	1.89	23.2	24.2	33.7	27.0	2.62
G13	81.0	61.5	81.2	74.5	-1.46	13.3	11.3	6.5	10.4	-1.16
G15	63.9	19.2	72.9	52.0	2.31	16.0	14.3	20.2	16.8	1.31
G16	83.9	74.4	82.7	80.3	-2.83	15.8	12.8	12.1	13.5	-0.40
G19	76.9	48.8	74.1	66.6	-0.59	19.5	12.3	15.4	15.7	-0.31
G25	80.1	69.6	81.6	77.1	-2.51	21.9	17.2	15.5	18.2	-0.96
G26	70.9	31.1	78.4	60.1	1.60	12.6	7.3	10.0	10.0	-0.05
Mean	76.2	46.1	78.5	66.9		17.1	12.7	14.9	14.9	
IPCA1	2.31	-5.27	2.95			-2.08	-0.53	2.62		
G4	9.6	8.2	9.4	9.1	-0.39	23.7	22.6	22.6	22.9	-0.06
G7	9.0	9.0	7.9	8.6	0.74	18.1	24.3	19.2	20.5	1.87
G8	9.4	8.0	8.8	8.7	-0.22	20.6	21.2	20.7	20.8	0.27
G9	9.6	7.8	8.1	8.5	-0.04	22.9	21.4	25.1	23.1	-0.74
G13	9.5	8.7	8.1	8.8	0.46	23.9	22.1	25.7	23.9	-0.79
G15	9.6	7.9	9.0	8.8	-0.40	23.5	22.4	25.7	23.8	-0.62
G16	9.4	9.4	9.2	9.3	0.37	24.2	22.8	20.6	22.5	0.25
G19	9.6	8.6	9.0	9.1	-0.02	22.6	20.6	22.7	22.0	-0.55
G25	9.3	9.2	9.2	9.2	0.29	22.1	18.2	18.4	19.5	-0.51
G26	9.2	7.5	9.5	8.7	-0.77	20.4	23.1	20.8	21.4	0.89
Mean	9.4	8.4	8.8	8.8		22.2	21.8	22.1	22.0	
IPCA1	-0.21	1.08	-0.86			-0.97	2.09	-1.12		

HR: head rice, IMM: immature grain, PC: protein content, AC: amylose content, IPCA 1: first PCA score

Table 3. Combined analysis of variance from GLM and AMMI analyses of variance for evaluated traits in the experimental environments.

| Source | DF | Head rice | | Immature grain | | Protein | | Amylose content | |
		SS	MS	SS	MS	SS	MS	SS	MS
Treatments	29	22950.95	791.41***	1912.65	65.95***	24.48	0.84***	245.94	8.48***
Genotypes (G)	9	6271.53	696.83***	1407.74	156.41***	3.99	0.44***	115.40	12.82***
Environment s (E)	2	13014.54	6507.27***	187.05	93.52***	10.24	5.12***	1.40	0.70***
G × E	18	3664.87	203.60***	317.85	17.65***	10.24	0.56***	129.12	7.17***
IPCA 1	10	3517.17	351.71***	266.73	26.67***	7.78	0.77***	86.56	8.65***
IPCA 2	8	147.70	18.46ns	51.11	6.38 ns	2.46	0.30***	42.56	5.32***
Error	30	326.12	10.87	183.64	6.12	1.30	0.04	0.35	0.01
Total	59	23277.07	394.52	2096.29	35.53	25.78	0.43	246.29	4.17

ns: not significant, ***significant at the 0.001 probability level

AMMI-1 BIPLOT DISPLAY

To further investigate the main and interaction effects across genotypes and environments, biplots were constructed (Figure 1). The genotype and environment means are plotted on the x-axis, while the IPCA1 scores for the same genotypes and environments are on the *y*-axis. Displacement along the x-axis shows differences in the main effects, whereas displacement along the *y*-axis reflects differences in the interaction effects. When a cultivar and an environment have the same sign on IPCA1, their interaction is positive; if the sign is different, their interaction is negative. Genotypes with dissimilar interaction scores have dissimilar interaction effects across environments, while genotypes with interaction scores close to zero have negligible interaction effects. The components of the biplot for each trait explained a high proportion of the total treatment SS, which ranged from 82.7% for amylose content to 99.4% for head rice; therefore, the AMMI-1 biplot was suitable to interpret the G × E interactions and the main effects.

Genotypes G9 and G19 have near-zero values on IPCA1, so they have small interactions with different environments (Figure 1a). G7 had the largest positive scores for protein content and amylose content (0.74 and 1.87), so they interacted positively with E2, although they also had below average means for both traits (Figure 1a and 1b, respectively). However, G7 had the highest mean head rice (81.6%) and negative interaction with E1 and E3 for HR and E3 for immature grain (Figure 1c and 1d, respectively). The genotypes G4, G16, G19 and G25 were similar in the main effect for protein content but varied appreciably in interaction. Genotypes G7, G8, G16 and G26 showed similar interaction for amylose content but varied considerably in the main effects (Figure 1b). G13 had the lowest score (-0.79) and the highest mean amylose content (23.9%), together with G15 (23.8%). G16 showed a similar trend to G13, G7, and G25 for head rice (Figure 1c). The environments were also variable in both main and interaction effects. Environments E1 and E3 had similar mean amylose content (Figure 1b).

A mega-environment is a group of locations that have the same or similar best cultivars (Gauch and Zobel 1997, Yan and Rajcan 2002). Genotype G7 was the highest performer in environments E3 and E2 (mega-environment 1) for head rice and amylose content, respectively (Table 4). Genotype G16 was selected as the winner in environments E1 and E2 (mega-environment 1 and 2) for head rice, environment E2 for protein content (mega-environment 1) and E1 (mega-environment 2) for amylose content. Genotype G9 was worst in all environments for having immature grain.

Table 4. AMMI-1 mega-environment and their winning genotypes

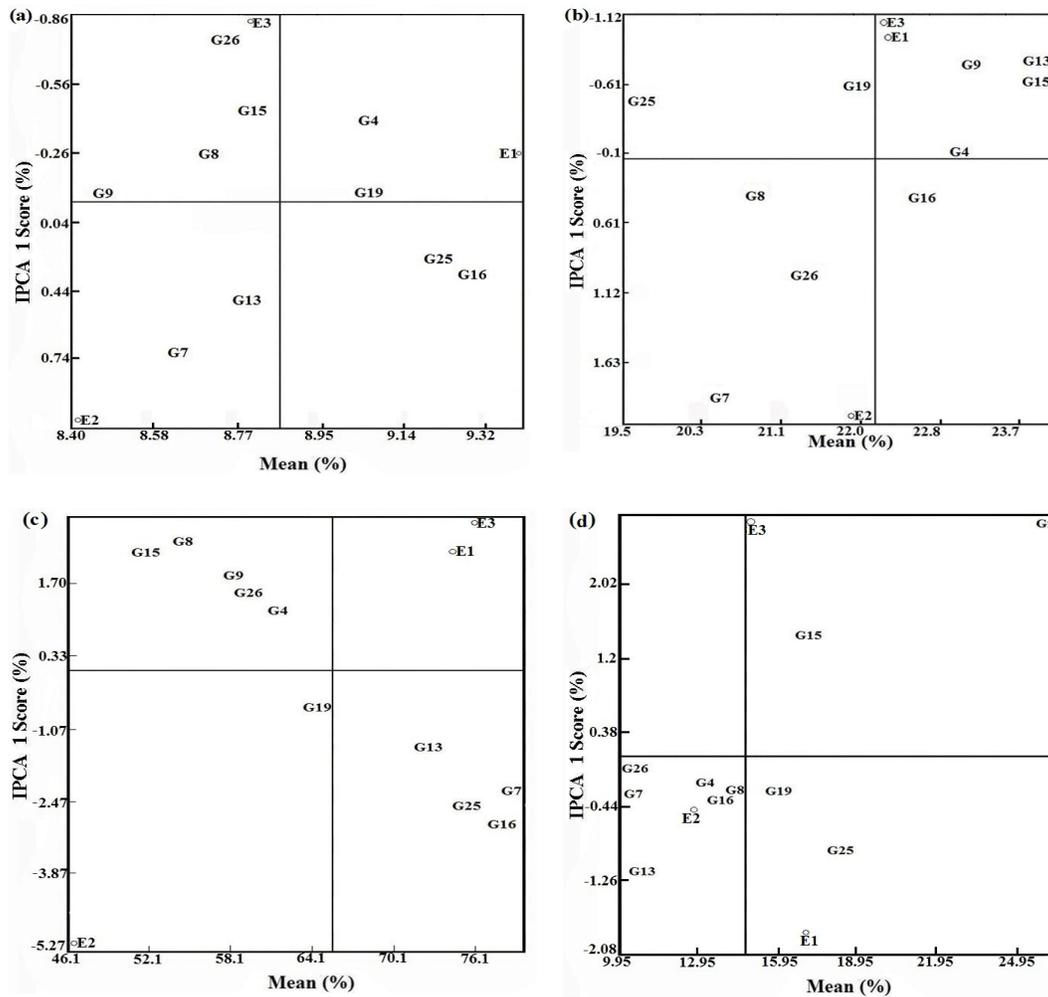| Trait	Mega-environments	Location	Genotype
HR	Mega-environment 1	E3	G7
		E1	G16
	Mega-environment 2	E2	G16
IMM	Mega-environment 1	E3	G9
		E2	G9
		E1	G9
PC	Mega-environment 1	E2	G16
		E1	G4
	Mega-environment 2	E3	G26
AC	Mega-environment 1	E2	G7
	Mega-environment 2	E1	G16

Figure 1. AMMI-1 biplot showing the means of genotypes (G) and environments (E) against their respective IPCA1 scores. Open circles denote environments, a) protein content %, b) amylose content %, c) head rice %, and d) immature grain %.

DISCUSSION

Before releasing a new variety on a commercial basis, plant breeders grow different varieties in different environments over several years to evaluate the magnitude of G × E interactions for confirming the stability of the variety across various environments (Sabaghnia et al. 2008). The AMMI model is suitable for the analysis of the G × E interaction in multilocation trials (Zobel et al. 1988). The analysis of variance of the AMMI model showed that G × E interactions were significant for all traits. This implied that selection for head rice and protein content in rice, according to the additive model alone, would be misleading. The results clearly indicated that better milling traits were obtained in E1 and E3 compared to E2, which can be due to differences in environmental factors such as temperature, relative humidity and rainfall (Cooper et al. 2006, Thompson and Mutters 2006). The lowest head rice percentage was found in G15 (52.0%) and G8 (55.1%), across all the environments. Immature grains reduce head rice yield and quality. Immature rice kernels are too slender and chalky, which results in extreme production of bran, broken grains and brewer's rice. With an increase in temperature, the grain filling period in rice will decrease, which results in high immature grain percentage (Thompson and Mutters 2006).

Genotype G9 had the highest (27%) while G26 the lowest (10%) percentage of immature rice grain across the environments.

Even though milled rice has a low level of protein (i.e., between 5.8 and 9.4%), rice is the major source of protein in many rice-consuming regions of the world. Thus, protein content is important from a nutritional perspective. In the present study, protein content was rather high (> 8%) for all genotypes. Various factors affect protein content, e.g. fertilization (Eggum and Juliano 1975, Juliano 1985), short growth periods, and soil salinity or alkalinity (Fasahat et al. 2012a). A large proportion of the total variability in protein content is nonetheless to be attributed to the environment (Shobha Rani et al. 2006). A positive correlation was found between protein content and head rice percentage ($r = 0.62$, $p < 0.001$). As a result, head rice percentage appears to increase with increased content of protein. Increased grain protein makes brown rice more resistant to cracking and breakage during abrasive milling than low protein rice of the same variety (Hatfield and Follett 2008). Normally there is a tight, positive correlation between grain protein content and head rice yield. For example, in a study by Perez et al. (1996), head rice percentage was 58% of the rough rice for high-protein rice that was achieved when nitrogen fertilizer was applied at flowering. On the other hand, only 47% head rice was obtained when the last nitrogen topdressing was applied at panicle initiation (Hatfield and Follett 2008).

Amylose content of rice grain determines whether it will be firm and fluffy on cooking, or it will turn sticky and glutinous. In the present study, the average amylose content of rice grown in three different environments was intermediate, which results in extreme elongation during cooking and soft texture of cooked rice (Juliano and Pascual 1980). Previous studies (Bao et al. 2002, Tian et al. 2005, Sharifi et al. 2010) showed that rice grain quality traits such as amylose content and protein content were readily affected by various environmental factors, such as temperature, solar radiation and field location. Nagarajan et al. (2010) found that, similar to grain yield, all the tested grain quality parameters were significantly influenced by genotype, environment, and G × E interaction, except for aroma, which had no significant interaction with environment. In the study by Lou et al. (2009), G × E interaction explained 7.3% of the variation in amylose content.

The significant genotype regression for protein and amylose content indicates that some amount of G × E can be explained by the linear response of genotypes to cultivation environments. The relatively large percentage (52.5%) of interaction SS attributed to genotype regression of amylose content tended to indicate that genotypes were probably very diverse and responded differently to different environments, whereas environments alone did not dictate genotype performance. However, the significant residual effect for immature grain percentage and protein and amylose content implies that some variation within the data still remains unexplained.

AMMI biplot analysis is an efficient tool to analyze G × E interaction patterns graphically (Gauch 2013). In a biplot display, genotypes or environments lying almost on a perpendicular line have similar means for the trait under investigation, while those lying almost on a horizontal line have similar interactions (Crossa et al. 1990). Genotype G7 not only showed higher head rice in environment E3, as compared to the other genotypes, but it also showed higher yield in the same environment (Bhuiyan 2010). Genotype G16 ranked among the best across the three environments for all traits except IMM and can be reasonably recommended for any environment with good cropping techniques and optimal climate factors.

The results of the present study indicated that quality traits of rice genotypes were mainly controlled by both the genetic and environmental factors.

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Table S1a. Summary of soil and climatic conditions of Environment 1 (E1)

		Sept, 2007	Oct, 2007	Nov, 2007	Dec, 2007	Jan, 2008	Feb, 2008
Temp (°C)							
	Max.	32.7	32.3	33.4	34.2	34.8	35.0
	Min.	21.7	20.4	23.1	21.0	20.0	20.1
	Ave.	29.8	25.4	26.7	25.8	25.9	26.1
Rainfall (mm)							
	Total	544.4	NA	90.0	169.4	NA	72.4
	Freq. (days)	28		13	12		4
Soil							
	Series	Ketai					
	p^H	4.3-4.5					
Season		Main season					
Location		Bumbung Lima, Pulau Pinang					

NA= data not available
Source: Weather Department of Malaysia, Department of Agriculture in Malaysia and MARDI

Table S1b. Summary of soil and climatic conditions of Environment 2 (E2)

		Sept, 2007	Oct, 2007	Nov, 2007	Dec, 2007	Jan, 2008	Feb, 2008
Temp (°C)							
	Max.			*31-32			
	Min.			*22-23			
	Ave.			*26-29			
Rainfall (mm)							
	Total	476.5	269.5	199.6	150.0	5.0	175.0
	Freq. (days)	17	21	11	12	1	5
Soil							
	Series	Kundur					
	p^H	4.0-4.5					
Season		Main season					
Location		Gurun, Kedah					

*average data of the growing season
Source: Weather Department of Malaysia, Department of Agriculture in Malaysia and MARDI

Table S1c. Summary of soil and climatic conditions of Environment 3 (E3)

		Sept, 2007	Oct, 2007	Nov, 2007	Dec, 2007	Jan, 2008	Feb, 2008
Temp (°C)							
	Max.	33.2	32.7	33.8	34.1	34.0	34.8
	Min.	21.2	21.8	21.4	21.2	21.9	21.8
	Ave.	30.3	29.8	30.1	30.1	31.1	30.7
Rainfall (mm)							
	Total	38.0	16.5	36.5	44.5	3.0	12.0
	Freq. (days)	8	2	6	7	2	6
Soil							
	Series	Jawa					
	p^H	4.2-4.5					
Season		Main season					
Location		Sungai Besar, Selangor					

Source: Weather Department of Malaysia, Department of Agriculture in Malaysia and MARDI