

Grain Quality Performance and Heritability Estimation in Selected F₁ Rice Genotypes

(Prestasi Kualiti Bijian dan Anggaran Keterwarisan dalam Genotip F₁ Terpilih Padi)

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ABSTRACT

A total of 17 rice genotypes consisted of 12 F₁ progenies and five parental lines were evaluated for performance of grain qualities, yield and yield components and vegetative traits at the Malaysian Agricultural Research and Development Institute (MARDI) Research Station in Seberang Perai, Penang. Except grain length, all other grain quality characters, yield components and vegetative traits varied significantly among the genotypes. Among the studied characters, the highest heritability value was observed in plant height with 99.75% followed by panicle length having 96.90% and grain shape with 56.70% which could be successfully inherited to the next generations. The rest of the traits had low heritability values and ranged from 20.24 to 35.88%. This indicates that the characters are mainly influenced by environmental factors such as geographical effects and climate. However, in the quantitative traits such as grain qualities and yield components, they are usually difficult to inherit to the next generation due to low heritability values. The combinations of Q76 and MR84 had the highest in amylose content while Q76 and MRQ74 had the lowest. Several selected F₁ indica rice genotypes from this evaluation are useful for future breeding programme and biotechnological research for the improvement of valuable grain quality traits.

Keywords: Grain quality characters; heritability; indica rice genotypes; Oryza sativa L.

ABSTRAK

Sejumlah 17 genotip padi yang mengandungi 12 progeni F₁ dan 5 waris induk telah dinilai prestasi kualiti bijian, hasil dan komponen hasil serta ciri vegetatif di Stesyen Penyelidikan Institut Penyelidikan dan Pembangunan Pertanian Malaysia (MARDI), Seberang Perai, Pulau Pinang. Semua ciri kualiti bijian, komponen hasil dan vegetatif memberikan kesan progeni bererti kecuali panjang bijian. Dalam kalangan ciri tersebut, nilai keterwarisan tertinggi ialah tinggi pokok dengan 99.75%, diikuti panjang tangkai, 96.90% dan bentuk bijian, 56.70%; ciri tersebut boleh diwariskan dengan jayanya ke generasi seterusnya. Sementara itu ciri yang lain mempunyai nilai keterwarisan yang rendah iaitu antara 20.24 hingga 35.88%. Ini menunjukkan ciri tersebut adalah sangat dipengaruhi oleh faktor sekitaran seperti kesan cuaca dan geografi. Walau bagaimanapun, ciri kuantitatif seperti kualiti bijian dan komponen hasil kebiasaannya adalah sukar diperturunkan ke generasi seterusnya disebabkan nilai keterwarisan yang rendah. Kombinasi antara Q76 dan MR84 memberikan kandungan amilosa yang tertinggi dan sebaliknya kombinasi Q76 dan MRQ74 adalah yang terendah. Beberapa F₁ genotip padi indica terpilih daripada penilaian ini adalah sangat berguna untuk penyelidikan dalam program pembiakbakaan dan bioteknologi masa depan untuk memajukan ciri bernilai kualiti bijian.

Kata kunci: Ciri kualiti bijian; genotip padi indica; keterwarisan; Oryza sativa L.

INTRODUCTION

The world population is expected to reach 8 billion by 2030 and therefore, rice production must be increased by 50% in order to meet the growing demand (Khush 2005; Miah et al. 2013). Rice (*Oryza sativa* L.) is one of the world's highest value crops and second leading cereal crop after wheat that produced 430 million metric tons in world's rice production (IRRI 2009). It is the major food source for more than half of the world's population (IRRI 2010). Over 95% of the world's rice crop is used for human food. Malaysia produces 70% of its rice consumption. Hence, it needs to import the balance of 30% from other countries. So, there is a vital need to increase rice production in Malaysia. The

government is currently encouraging local production in order to obtain 100% self sufficiency by 2020.

Genetic improvement of rice following different breeding methods may help to achieve self sufficiency in rice through the development of high yielding varieties. Genetic variability for agronomic traits is the key component of breeding programmes for broadening the gene pool of both rice and other crops. Therefore, hybridization using different crossing programmes have extensively been used for studying the genetic components, combining ability and heritability of important agronomic traits or grain quality characters (Asfaliza et al. 2012; Iftekharuddaula et al. 2008; Pooni et al. 1992).

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 and having aroma with good yield. Sometimes the selection of progenies resulted in low quality progenies to fulfill breeding objectives due to a large number of plants within the segregating populations. Falconer (1989) reported that heritability estimates for agro-morphological 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 74.0, 74.0 and 89.0%, respectively. Vanaja and Babu (2008) evaluated 56 genotypes of high yielding rice 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.

Under the above context, research work has been planned to develop rice varieties to have higher grain yield potential with quality grain through crossing programme followed by selection in subsequent generations. The present study aimed to evaluate the grain quality performance, to study the variability in respect to yield and yield components and vegetative traits and to study phenotypic correlations among grain quality characters and other agronomic characters in selected F_1 Indica rice hybrids with parents which will help rice breeders in subsequent generations selection on the basis of heritability and characters associated with higher yield.

MATERIALS AND METHODS

PLANT MATERIALS AND SETTING THE EXPERIMENT

A total of 17 genotypes consisting of 12 F_1 genotypes and five parental lines (Table 1) were used in this experiment. The F_1 genotypes were produced using bi-parental mating system. The experiment was conducted at the Malaysian Agriculture Research and Development Institute (MARDI) Research station in Seberang Perai, Penang during May to September 2011. The 17 genotypes were planted using manual transplanting method in a randomized complete block design with three replications in order to ensure seedling growth uniformity and to give the rice plant ahead start over emerging weeds. Distance between

blocks was set at 50 cm. Within block each plot had three rows and in each row 10 hills were transplanted. Plant spacing was maintained at 20×20 cm². Fertilizer was applied as recommended by Azmi et al. (2008). Crops were harvested at 90% maturity when the flag leaves turned into yellowish color and the grains were fully ripened. Five hills were randomly selected from each plot from the middle of the rows to avoid border effect and harvested individually and dried. The dried panicles were then threshed and the seeds were kept in chiller ($23 \pm 2^\circ\text{C}$) for grain quality assessment.

DATA COLLECTION

Data were recorded on 11 quantitative characters of grain qualities, yield and its attributes and vegetative traits. After harvest, yield and its attributes such as panicle per hill, panicle length and plant height, yield per hill and weight of 1000 grain were measured. Two chemical properties, amylose content and gel consistency were determined according to Melissa et al. (2009) and Cagampang et al. (1973), respectively.

STATISTICAL ANALYSIS

All recorded data were analyzed by Statistical Analysis System (SAS) software. From the computation, the simple statistics for each trait such as mean, standard deviation (SD) and standard error (SE) were measured. The analysis of variance (ANOVA) was carried out by SAS programme. To evaluate the relationship among the different characters, correlation coefficients were determined by using SAS software. The variance components and values of heritability were estimated following the formulae given by Burton and De Vane (1953) and Johnson et al. (1955) and applied by Mazid et al. (2013).

σ_G^2 (Genotypic variance) = $(MS_G - MS_E)/r$, where MS_G = mean square of accession, MS_E = mean square of error, and r = number of replications; $\sigma_E^2 = MS_E$; σ_P^2 (Phenotypic variance) = $(\sigma_G^2 + \sigma_E^2)$; PCV (Phenotypic coefficient of variation) = $\sqrt{\sigma_P^2} / \bar{X} \times 100$, where σ_P^2 = phenotypic variance and \bar{X} = mean of the trait; GCV (Genotypic coefficient of variation) = $\sqrt{\sigma_G^2} / \bar{X} \times 100$, where σ_G^2 = genotypic variance and \bar{X} = mean of the trait; and h_B^2 (Broad sense heritability) = $\frac{\sigma_G^2}{\sigma_P^2}$, where σ_G^2 = genotypic variance and σ_P^2 = phenotypic variance.

TABLE 1. List of parental lines and hybrid progenies used in this experiment

Parental lines	F_1 hybrids
MR84, MR263, MR267, MRQ74 and Q76	MRQ74 \times MR84, Q76 \times MR84, Q76 \times MR263, MRQ74 \times MR267, Q76 \times MR267 MR84 \times MRQ74, MR267 \times MRQ74, Q76 \times MRQ74, MR84 \times Q76, MR263 \times Q76, MR267 \times Q76 and MRQ74 \times Q76

RESULTS AND DISCUSSION

GRAIN QUALITY CHARACTERS

The grain quality characters are important to determine the quality of a variety of the most popular and highly demanded. The results showed that except for grain length, all other grain quality characters differed significantly among the genotypes (Table 2). Overall mean data of grain quality traits has been presented in Table 3. Among the progenies, progeny of MRQ74 × MR84 had the highest filled grains followed by MR267 × Q76 while the progeny of MR84 × Q76 had the lowest. Progeny of Q76 × MRQ74 had the highest mean while Q76 × MR263 had the lowest mean for grain width. As reported by Shi et al. (2000), length and width are important quantitative traits closely related to the exterior quality of rice. Grain length and width are considered to be the fast-stable characters compared to other traits (Juliano 1993). The proportion of length to width reveals the grain shape of rice. All the progenies and parental genotypes has slender grain shape (>3.0 ratio). High grain length with low grain width could be lead to long shape of grain. As reported by Shi and

Zhu (1996), grain shape is simultaneously controlled by triploid endosperm, cytoplasmic as well as maternal genes. In all the progenies, gel consistency ranged between 58 and 95 mm and categorized as soft. This means that cooked rice has a tendency to become soft when cold. This result is in agreement with the findings of Bhonsle and Krishnan (2010). Amylose content, starch, gel consistency and non-reducing sugar content decrease with increased temperature (Pandey et al. 2007).

The progenies were tested for amylose content and classified as low, intermediate and high (Table 4). Amylose content varied among the progenies. The combinations of Q76 and MR84 had high amylose content while Q76 and MRQ74 had low (Table 3). Combinations of intermediate and high amylose or high and low amylose or intermediate and low amylose content resulted into the F₁ progenies with high or intermediate or low amylose content. Cooked rice becomes moist and sticky due to low amylose content. Amylose and amylopectin in kernels determine the texture of cooked rice and consumers prefer rice with intermediate amylose content.

TABLE 2. Mean squares for grain quality characters and yield components

Sources of variation	df	Filled grain (%)	Grain length (mm)	Grain width (mm)	Length/width (L/W)	Gel consistency (mm)	Amylose content (%)	Plant height (cm)	Panicle length (cm)	Panicles/hill (no)	Yield/hill (g)	1000-grain weight (g)
Genotypes	16	379.1*	0.09	0.004*	0.067**	658.53*	28.41*	145.09**	12.35**	25.42*	191.19**	4.95*
Replications	2	43.2	0.06	0.007*	0.104**	348.05	6.75	0.48*	0.68*	13.34	37.62	1.13
Error	32	147.5	0.05	0.002	0.013	293.30	11.85	0.12	0.13	11.41	71.37	1.98

*, ** indicate significant at $p \leq 0.05$ and $p \leq 0.01$, respectively

TABLE 3. Genotype means with standard errors for grain quality characters

Progeny	Filled grain (%)	Grain length (mm)	Grain width (mm)	Length/width (L/W)	Gel consistency (mm)	Amylose content (%)
MRQ74 × MR84	88.53 ± 1.33	9.90 ± 0.10	1.96 ± 0.03	5.00 ± 0.05	90.00 ± 0.57	22.86 ± 0.73
Q76 × MR84	82.86 ± 2.09	10.06 ± 0.10	2.00 ± 0.02	5.04 ± 0.04	66.0 ± 19.22	27.73 ± 1.61
Q76 × MR263	79.26 ± 10.02	10.15 ± 0.09	1.93 ± 0.03	5.26 ± 0.05	89.33 ± 6.67	21.94 ± 4.62
MRQ74 × MR267	69.86 ± 9.94	10.26 ± 0.26	2.01 ± 0.03	5.11 ± 0.05	90.67 ± 5.33	26.57 ± 1.19
Q76 × MR267	88.10 ± 1.78	10.15 ± 0.03	2.00 ± 0.01	5.11 ± 0.03	84.00 ± 6.43	26.45 ± 0.72
MR84 × MRQ74	87.53 ± 3.87	10.44 ± 0.10	1.96 ± 0.04	5.33 ± 0.15	62.67 ± 17.52	26.43 ± 2.93
MR267 × MRQ74	81.97 ± 2.38	9.86 ± 0.15	1.96 ± 0.03	5.04 ± 0.08	87.00 ± 1.53	18.60 ± 0.78
Q76 × MRQ74	67.10 ± 6.39	9.94 ± 0.19	2.06 ± 0.07	4.83 ± 0.08	92.00 ± 4.00	17.94 ± 3.00
MR84 × Q76	57.77 ± 12.01	10.38 ± 0.20	2.00 ± 0.01	5.25 ± 0.10	58.67 ± 2.40	20.94 ± 0.16
MR263 × Q76	75.63 ± 5.94	9.99 ± 0.19	1.96 ± 0.02	5.10 ± 0.12	78.0 ± 15.10	23.54 ± 1.60
MR267 × Q76	88.27 ± 6.16	9.97 ± 0.02	2.00 ± 0.03	5.00 ± 0.07	77.33 ± 18.67	26.53 ± 1.80
MRQ74 × Q76	58.10 ± 7.43	10.27 ± 0.13	2.00 ± 0.01	5.13 ± 0.07	95.00 ± 0.58	24.47 ± 2.58
MR84	95.63 ± 0.89	9.93 ± 0.14	1.97 ± 0.02	5.06 ± 0.13	72.0 ± 12.00	25.10 ± 0.20
MR263	65.93 ± 2.63	9.94 ± 0.07	2.00 ± 0.03	4.98 ± 0.03	68.00 ± 6.00	24.76 ± 1.46
MR267	69.13 ± 14.16	10.19 ± 0.14	1.91 ± 0.01	5.32 ± 0.06	40.00 ± 4.00	21.41 ± 1.91
MRQ74	84.63 ± 4.89	10.17 ± 0.12	1.90 ± 0.03	5.39 ± 0.02	70.00 ± 2.31	23.62 ± 1.61
Q76	77.30 ± 5.10	10.30 ± 0.04	1.97 ± 0.02	5.23 ± 0.07	59.33 ± 9.33	18.61 ± 0.40
Mean	77.51	10.11	1.97	5.13	75.29	23.38
Standard Error	2.064	0.036	0.008	0.026	2.873	0.576
CV (%)	19.02	2.56	2.81	3.62	27.25	17.61
LSD ($\alpha = 0.05$)	20.19	0.38	0.08	0.21	28.48	5.72

TABLE 4. Classification of amylose content

Amylose (%)	Classification	Progenies
10-19%	Low	MR267 × MRQ74, Q76 × MRQ74, MR84 × Q76
20-25%	Intermediate	MRQ74 × MR84, Q76 × MR263, MR263 × Q76, MRQ74 × Q76
>25%	High	Q76 × MR84, MRQ74 × MR267, Q76 × MR267, MR84 × MRQ74, MRQ74 × Q76

YIELD AND YIELD ATTRIBUTES

The results showed that grain yield per hill and its attributes such as plant height, panicle length, panicles per hill and 1000-grain weight differed significantly among the studied genotypes (Table 2). The mean performance of all the genotypes for yield and its components is presented in Table 5. The number of panicles is the result of number of tillers produced and the proportion of effective tillers, which survived to produce panicle (Hossain et al. 2008). Genotypic differences of grain yield per hill was reported by Biswas et al. (1998). The genotypes, which produced higher number of effective tillers per hill and higher number of grains per panicle also showed higher grain yield in rice (Dutta et al. 2002; Kusutani et al. 2000). Mondal et al. (2005) studied 17 modern cultivars of transplant among rice and reported that 1000-grain weight differed significantly among the studied cultivars and supported the present result.

HERITABILITY ESTIMATION

Heritability estimates and variance components of grain quality characters, grain yield and its components are shown in Table 6. Among the characters, panicles per

hill, yield per hill, 1000-grain weight, grain length, filled grains, gel consistency and amylose content showed comparatively higher differences between PCV and GCV indicating relatively higher influence of environment factors on the expression of these characters. Amin et al. (1992) observed the closeness of PCV and GCV for a few characters and much difference between PCV and GCV for others in a study with rice genotypes.

Heritability analyses estimate the relative contributions of differences in genetic and non-genetic factors to the total phenotypic variance in a population. Heritability is an important concept in quantitative genetics, particularly in selective breeding. Variance components with heritability values for grain quality characters, yield and its attributes are shown in Table 6. All the grain quality characters had low heritability values (<35%) except for length to width ratio. The present results indicated that grain quality characters are influenced more by environmental factors such as geographical effects and climate. These findings do not support the results from previous study by Vanaja and Babu (2008), who reported high degree of broad-sense heritability for grain quality characters. The filled grain had low heritability of 34.36%. This indicates that filled grain is not easily inherited character in the rice

TABLE 5. Genotype means with standard errors for yield components

PROGENY	Plant height (cm)	Panicle length (cm)	Panicles/ hill (no.)	Yield/ hill (g)	1000-grain weight (g)
MRQ74 × MR84	78.20 ± 0.46	26.00 ± 0.46	15.60 ± 1.30	44.54 ± 2.60	26.03 ± 0.77
Q76 × MR84	83.03 ± 0.18	27.63 ± 0.15	15.87 ± 0.76	64.32 ± 1.84	28.13 ± 0.53
Q76 × MR263	75.60 ± 0.23	27.80 ± 0.23	13.33 ± 1.91	39.22 ± 2.29	26.27 ± 1.68
MRQ74 × MR267	82.00 ± 0.23	23.80 ± 0.23	21.13 ± 1.67	56.70 ± 5.95	29.82 ± 0.38
Q76 × MR267	74.97 ± 0.03	26.07 ± 0.03	16.67 ± 2.10	45.19 ± 6.69	27.17 ± 0.40
MR84 × MRQ74	83.30 ± 0.06	29.30 ± 0.06	15.53 ± 2.82	45.90 ± 5.87	28.01 ± 0.79
MR267 × MRQ74	77.07 ± 0.32	26.77 ± 0.32	22.00 ± 2.42	64.27 ± 6.45	25.25 ± 1.01
Q76 × MRQ74	85.33 ± 0.18	23.63 ± 0.20	17.47 ± 1.83	54.11 ± 5.71	26.80 ± 0.56
MR84 × Q76	83.77 ± 0.26	22.07 ± 0.26	18.60 ± 1.11	51.31 ± 3.58	26.65 ± 0.31
MR263 × Q76	82.83 ± 0.19	24.70 ± 0.32	15.93 ± 1.04	47.41 ± 3.04	26.30 ± 0.78
MR267 × Q76	81.70 ± 0.40	25.50 ± 0.40	19.87 ± 2.19	55.84 ± 4.77	28.38 ± 0.54
MRQ74 × Q76	72.40 ± 0.11	27.40 ± 0.23	18.93 ± 4.04	54.41 ± 6.39	27.89 ± 0.35
MR84	82.30 ± 0.06	23.90 ± 0.06	21.40 ± 2.55	57.58 ± 4.11	27.00 ± 0.61
MR263	69.27 ± 0.20	26.37 ± 0.20	17.00 ± 0.76	48.20 ± 2.01	26.68 ± 1.10
MR267	60.17 ± 0.09	22.47 ± 0.09	20.27 ± 1.31	35.86 ± 6.43	27.22 ± 0.91
MRQ74	68.67 ± 0.03	23.37 ± 0.03	23.40 ± 0.70	44.27 ± 5.87	24.46 ± 0.31
Q76	71.20 ± 0.12	25.20 ± 0.12	22.33 ± 1.51	46.83 ± 2.63	25.70 ± 1.21
Mean	77.15	25.41	18.55	50.35	26.92
Standard Error	0.955	0.282	0.559	1.457	0.238
CV (%)	8.84	7.93	21.54	20.67	6.32
LSD ($\alpha = 0.05$)	0.51	0.51	5.61	14.04	2.35

TABLE 6. Variance components and heritability values (H^2_B) for grain quality characters and yields components

Traits	σ^2_G	σ^2_e	σ^2_{PH}	H^2_B (%)	PCV (%)	GCV (%)
Plant height	48.32	0.12	48.44	99.75	79.24	79.14
Panicle length	4.07	0.13	4.20	96.90	40.65	40.02
Panicles/hill	4.66	11.40	16.06	29.02	93.04	50.12
Yield/hill	39.93	71.37	111.3	35.88	148.67	89.05
1000-grain weight	0.98	1.98	2.96	33.11	33.15	19.07
Grain length	0.0137	0.053	0.0667	20.54	8.18	3.68
Grain width	0.00067	0.002	0.00267	25.10	3.68	1.84
Length/width	0.0179	0.0136	0.0315	56.70	7.82	5.89
Filled grain	77.20	147.46	224.66	34.36	170.24	99.79
Gel consistency	130.74	293.30	424.05	30.83	237.32	131.77
Amylose content	5.51	11.85	17.36	31.74	88.07	48.54

Notes : σ^2_G - Genotypic variance, σ^2_e - Error variance, σ^2_{PH} - Phenotypic variance, H^2_B - Broad sense heritability, PCV - Phenotypic coefficient of variation, GCV - genotypic coefficient of variation

population. Similar result, i.e. low heritability was also found in F_1 generation for filled grain by Sabu et al. (2009). Grain shape had high heritability of 56.70%. It has been established that grain shape and length are controlled by both of additive and non-additive gene actions (Savery & Ganesan 2003). According to Chen et al. (1998), grain shape is quantitatively inherited. Grain length and width can be considered as the fast-stable characters compared to other agronomic traits (Juliano 1993).

Breeding for yield and its component traits are difficult due to their low heritability. It means that for these traits the contribution of environmental factors is relatively high (Singh 2009). Present study showed that plant height and panicle length are easily inherited characters to the next generation as they possess high heritability (99.75 and 96.90%, respectively) and are less affected by environmental factors. Previous findings of Fahliani et al. (2010), Mohammad et al. (2002) and Rabiei et al. (2004), confirm the present result for plant height. However, the yield components are usually difficult to inherit due to involvement of many genes in controlling these traits. High heritability along with high GCV exhibited by plant height and panicle length imply that these two characters under additive gene effects and could be relied upon for further selection based on phenotypic performance (Vanaja & Babu 2008).

PHENOTYPIC CORRELATION

Phenotypic correlations were computed among all the characters studied (Table 7). Plant height had significant positive correlation with yield per hill, grain width and gel consistency, but had significant negative correlation with grain shape. Panicles per hill showed significant positive correlation with yield per hill, but significant negative correlation with panicle length. Panicle length has been reported to have negative association with number of panicles per plant which confirms the present

result (Ise 1992). Grain yield per hill was positively and significantly correlated with plant height, panicles per hill, grain width and gel consistency. This indicates that these traits influence positively towards grain yield. Positive associations of grain yield with panicles per plant have also been reported earlier by Babar et al. (2007), Kumar and Khush (1986) and Mirza et al. (1992). Grain length and width are the important traits for grain shape. Grain length had significant positive correlation while grain width had significant negative correlation with grain shape. This indicates that if grain length increased length to width ratio also increased but when grain width increased length to width ratio decreased.

CONCLUSION

From the results it can be concluded that among the grain quality and yield components, plant height, panicle length and grain shape could be easily inherited to their next generations due to high heritability. The rest of the component characters had low heritability which indicates that characters are mainly influenced by environmental factors. Grain shape can be considered as the first-stable characters compared to other agronomic traits. The combinations of crosses between Q76 and MR84 had high amylose content while Q76 and MRQ74 had low amylose. These rice genotypes are potential for consumer's preferences for amylose content and it could be used for breeding programmes and biotechnological research for the improvement of valuable grain quality traits.

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TABLE 7. Phenotypic correlations among grain quality characters and yield components

Characters	Panicle length	Panicle/hill	Yield/hill	Grain weight	Filled grain	Grain length	Grain width	Length/width	Amylose content	Gel consistency
Plant height	0.115	-0.216	0.428**	0.255	0.127	-0.071	0.389**	-0.354*	0.131	0.285*
Panicle length		-0.347*	0.102	0.089	0.246	0.046	0.050	-0.026	0.268	0.212
Panicles/hill			0.480**	-0.198	0.053	0.037	-0.005	0.035	-0.074	-0.070
Yield/hill				0.175	0.065	-0.131	0.312*	-0.343*	0.134	0.278*
Grain weight					-0.168	0.196	0.217	-0.041	0.317*	0.137
Filled grain						-0.052	-0.151	0.082	0.108	0.038
Grain length							0.078	0.641**	0.218	-0.248
Grain width								-0.711**	0.069	0.227
Length/width									0.097	-0.361**
Amylose content										0.004

* and ** indicate significant at $p \leq 0.05$ and $p \leq 0.01$, respectively

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