Variation of panicle characteristics in seven rice genotypes and F$_2$ populations
(Variasi ciri-ciri panikel tujuh genotip padi dan populasi F$_2$)

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Abstract
Rice variety MR276 has high values number of filled grain per panicle, the number of primary branches per panicle and 100-grain weights. There is a positive and highly significant relationship between number of primary branches per panicle and number of filled grain per panicle ($r = 0.79*$). All the panicle component characters had high heritability estimate. The variation of panicle characters of rice in the F$_2$ generation was studied. The F$_2$ population of IR64 x MR276 showed wide variations for the traits of primary branches with the range of 7 – 19 primary branches per panicle, 56 – 248 for the filled grain per panicle, 28 – 38 g for the 1000-grain weight and 3 – 8 g for the grain weight per panicle. The F$_2$ plants showed normal distribution for all the panicle traits in each population. The variations of primary branches and filled grain per panicle in the F$_2$ population for MRQ86 x IR73895-33-1-3-2 showed a wide range from 7 – 14 primary branches and 85 – 219 filled grains per panicle. The distributions of the 1000-grain weight and grain weights per panicle were uniform. Therefore, it is concluded that the large panicle type of rice is contributed by genotypes with more number of primary branches and number of filled grain. It is recommended to use these characters as new selection criteria in breeding for improve rice yield production. The F$_2$ plants performed better than the parents for the number of primary branches and filled grain per panicle.

Keywords: rice (*Oryza sativa*), panicle component, rice genotypes, yield and yield component, rice breeding

Introduction
Increase rice yield potential is one of the most important factor in rice breeding for development of better varieties. To meet increasing demands for rice, breeder has the option of selecting adaptable and high yielding genotypes from multilocational evaluations in breeding for high yield production. Yield is a complex character that can be determined by several components (Özer et al. 1999). It is necessary to determine the relationship between yield and some of the components that have a great effect on yield. This information is important to breeders in selecting desirable genotypes (Özer et al. 1999). Grain yield is a response variable caused by the interaction of yield components or yield-related traits.

Yield components in rice are categories in three orders (Samonte et al. 1998). The first-order comprises of panicle number per unit area or per plant, and panicle weight per unit area or per plant. The product of these two traits can be used

for the indirect estimate of grain yield in rice (Gravois and McNew 1993). The second order yield components are divided into two sub-groups. The first sub-group comprises components of panicle number which includes plant height, panicle length, and number of days to flowering or maturity. The second sub-group comprises components of panicle weight which are the number of filled grains per panicle and 1000-grain weight. Third-order components include the total number of grains per panicle and other traits that influence the number of filled grains per panicle and the 1000-grain weight (Gravois and McNew 1993).

In rice breeding, the panicle traits can be used for the indirect estimate of grain yield in rice. Studies had found that there are significant linear correlations between total spikelet numbers per panicle with total primary branch per panicle (Tay and Othman 1992). Furthermore, the panicle characteristic such as size, weight and the number of primary branches of the panicle is one of the solutions to overcome the yield stagnancy (Alias 1994). In addition, selection conducted for high values of the yield components, correlations between grain yield and yield components and heritability values revealed that the number of grains per panicle could be used as selection criteria in rice breeding (Halil and Necmi 2005). The spikelet on the primary branches of the rice panicles are usually heavy, well-developed and have high density (Patena and Vergara 1998).

In this paper, the panicle component characters of the seven rice genotype and the F_2 generation derivatives were observed. The purpose of this study essentially was to understand the panicle component aspects and indirectly may provide plant breeders with an idea of the general feature of a genetic resources in breeding and selection for increase yield potential.

Materials and methods
Fields experiment
The study was conducted in MARDI Seberang Perai Research Station, Pulau Pinang in main season 2009/2010. A total of seven genotypes namely, MR270, MR272, MR276, SPD184, MRQ86, IR73895-33-1-3-2 and IR64 were used in this experiment. MR270, MR272 and MR276 were high yield varieties obtained from Advanced Yield Trial (AYT). SPD184 and MRQ86 were also advanced lines obtained from MARDI. These lines were selected in this study because of their unique characters such as very long and heavy panicle, good grain shape and as well as quality rice. SPD184 is a line that has a very long and heavy panicle, while MRQ86 is an aromatic rice. IR64 is a high yielding *indica* variety developed in IRRI, Philippines in 1985. IR73895-33-1-3-2 was an International Network for Genetic Evaluation of Rice (INGER) obtained from IRRI rice breeding programme. The seeds of each genotypes were first germinated on rice hull in trays in the nursery. At 25 days seedling age, the seed were transplanted in field plots at 25 cm x 25 cm, with single seedling per point. Each of genotype was represented by two rows consisting of 10 plants for each row. Standard practices on fertilisations and plant protections were carried out for all the genotypes during the growth period. At physiological maturity stage, (95% heading), five panicles per plants was measured for the number of filled grain per panicle, number of primary branches per panicle and 100-grain weight.

Population development
A total of two separate population consists of 250 F_2 individuals derived from a cross between IR64 x MR276 and MRQ86 x IR73895-33-1-3-2. In this experiment, the F_1 seeds and their parent were soaked in distilled water at 30 °C for 2 days until the seeds germinated. Germinated seeds were sown on a paddy field. The plants were transplanted into a paddy field with single

seedling per hill. The space between hills was 25 cm. The field management was similar to that under normal rice production conditions. Plant protection agents were used as required, following the standard practices of MARDI experimental station. At physiological maturity stage, when 95% of the grains turn yellow, only one panicle representing one plant was harvest individually to prevent loss from over-ripening. The panicles of the parent and 250 of F_2 individual plant from two crosses were measured for the number of filled grain per panicle, number of primary branches per panicle and 1000-grain weight.

Data collection
In the first experiment, the panicle traits were recorded from 20 plants in each plot at near maturity, while in the second experiment, 250 of F_2 individual plants from two crosses were measured. The data collection were done according to Alias (1994). The panicles were measured by holding all the tillers together and then selected the longest panicle. The number of primary branches were measured by counting the primary branches on the panicle. Mean values of the traits were computed from all the panicles from each plant. All the panicles, were used to record filled grains per panicle. The 1000-grain weight was calculated in grams (g) as the mean weight of 1000 fully filled grains. Yield per plant, expressed in g, was calculated from the weight of bulked grain harvested from the panicles in each plant.

Data analysis
The mean values of each character under this study were analysed using the General Linear Model (GLM) procedure assuming a random effects model and type III sum of squares was used for the data analysis using individual plant data (SAS Institute Inc. 2006). Genotypic and phenotypic variance were calculated according to Burton and Devane (1953).

Source	Df	MS	EMS
Replications	(r^{-1})	MSR	$\sigma e^2 + g\sigma r^2$
Genotypes	(g^{-1})	MSG	$\sigma e^2 + r\sigma g^2$
Error	$(r^{-1})(g^{-1})$	MSE	σe^2

Genotypic variance, $\sigma g^2 =$

$$\frac{MSG - MSE}{r} + \frac{(\sigma_e^2 + r\sigma_g^2) - \sigma_e^2}{r}$$

$\sigma p^2 = \sigma g^2 + \sigma e^2$
where:
$\sigma p^2 =$ Phenotypic variance,
$\sigma g^2 =$ Genotypic variance,
$\sigma e^2 =$ Error variance (error means square)

The genotypic (GCV) and phenotypic (PCV) coefficients of variation were estimated according to the procedure outlined by Burton and Devanve (1953) and Johnson et al. (1955):

$$PCV (\%) = \frac{\sqrt{\sigma^2_p}}{\overline{X}} \times 100 \quad GCV (\%) = \frac{\sqrt{\sigma^2_g}}{\overline{X}} \times 100$$

where:
$\overline{X} =$ grand mean

The broad sense heritability values were estimated for the number of filled grain per panicle, number of primary branches per panicle and 1000-grain weight. The heritability were calculated as suggested by Allard (1960):

$$\text{Heritability } (H\%) = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where:
H^2 = Heritability in broad sense.

The variation on panicle traits was studied through an analysis of the distribution of frequencies at the generations F_2 in each of crosses. The correlation analysis was estimated from 20 samples for each of panicle components by using SAS version 9.13 (SAS 2006).

Results and discussion
Assessment of panicle traits in seven rice genotypes
The analysis of variance (*Table 1*) of the three panicle component: number of filled grain per panicle, number of primary branches per panicle and 1000 grain weight shows highly significant different (p <0.05) between seven rice genotypes. The number of filled grain per panicle varied from 86.40 ± 3.81 for IR64 to as high as 206.00 ± 6.10 for MR276 (*Table 2*). Besides, variety MR276 also has the highest mean value with 13.05 ± 0.16 for the number of primary branches per panicle. Then, followed by MR272 with the means value of 11.85 ± 0.26. The results showed no significant different between the MR270 and IR73895-33-1-3-2 and the mean value are 10.95 ± 0.21 and 10.65 ± 0.20 respectively. Genotype SPD184 and MRQ86 did not show significant different with the mean value of 9.25 ± 0.27 and 9.15 ± 0.15, respectively. IR64 has lowest number of primary branches with mean values of 8.05 ± 0.18 (*Table 3*).

The 1000-grain weight (g) varied from as high as 31.21 ± 0.25 g, 31.07 ± 0.60 g and 30.89 ± 0.30 g for IR73895-33-1-3-2, MR270 and MR276 respectively to as low as 25.56 ± 0.28 g and 24.56 ± 0.38 g for MR272 and MQ86 respectively (*Table 4*). Among the seven rice genotype, MR276 with relatively higher number of the entire panicle component studied was the highest yielder; whereas IR64 followed by MRQ86 with relatively smaller values for these characters were the poorer yielders. Therefore, MR276 can be proposed for breeding to produce better high yielding new rice variety. Similar result was also reported by Tay and Othman (1992), Alias (1994) and Abdus Salam et al. (2009) which concluded that the large panicle type of rice could be bred by using genotypes with more number of primary branches and number of filled grain for yield improvement in rice.

Table 5 shows the correlation between the panicle component characters of seven different rice genotypes. The number of primary branches per panicle was positive and high significantly correlated with the number of filled grain per panicle ($r = 0.79^{**}$). In general, the panicle component character; 1000-grain weight (g) was negative correlated with number of filled grain per panicle ($r = 0.31$) and number of primary branches per panicle ($r = 0.37$). These characters show significantly correlated with the 1000-grain weight but with low correlation. However, it is suggested that the 1000-grain weight criteria could be used as an indicator to gain heavy grain (Takeda and Saito 1983). The other character was found to be positive and highly correlated, number of primary branches per panicle and number of filled grain per panicle. Spikelets on the primary branches were usually heavy and have 100% probability filled. It is suggested that these characters could be contribute to high yield production (Patena and Vergara 1998). Changhua et al. (2007) concluded that

potential lines with great number of filled grain, number of primary branches and grain weight were the some panicle characters that can enhance yield. Besides, Haibin et al. (2009) suggested that it would be better to used primary branches as new criteria in selection for yield improvement in rice breeding.

Heritability is a property of the trait, population and environment. Changing any of these factors will result in a different estimate of heritability. The heritability broad sense was estimated using the total genetic variance, σ_g^2. It tends to yield high value. The narrow sense heritability was the additive component of genetic variance determines the response to selections. It is estimated as variance additive, σ_a^2/ variance phenotype, σ_p^2 (Acquaah 2007).

The variability, heritability and estimated components of variation are shown in Table 6. Low genotypic and phenotypic coefficients of variation were observed for 1000-grain weight (g), whereas high genotypic and phenotypic coefficients of variation were expressed by number of filled grain per panicle followed by number of primary branches per panicle. High phenotypic variations were composed of high genotypic variations and less of environmental variations, which indicated the presence of high genetic variability for different character and less influence of environment (Rita et al. 2009). According to Acquaah (2007), variance component method of estimating heritability uses the statistical procedure of analysis of variance (ANOVA). Variance estimates depend on types of populations in the experiment. Estimating genetic components suffer from statistical weaknesses. Variations are less accurately estimated than means.

High heritability were observed for all the characters studied; number of filled grain per panicle, number of primary branches and 1000-grain weight (*Table 6*). High heritability indicates the scope of genetics improvement of these characters through selection. High primary branches number, high grain number and heavy grain will contribute to high yield production of rice. Yield components in selection were preferred to be used for yield since their heritability values are normally higher than yield itself. In addition, with regards to these particular characters and to improve the yield potential, new characters which can further increase the yield production were identified and utilised in the selection program. Some of the new characters are the proportion of the number of panicle primary branches (Alias 1994). The magnitude of heritability estimates depends on the genetic population used, the sample size and the method of estimation. In this experiment, heritability was estimated by using the type of parent-offspring regression. This method was based on parents are non in-bred are less accurately estimated than means and there is no environment correlation between the performance of parent and offspring. The parent-offspring method of heritability is relatively straight forward (Acquaah 2007).

Table 1. Analysis of variance for panicle component characters in seven rice genotype.

Source	Df	filled grains per panicle	primary branches per panicle	1000-grain weight (g)
Replication	19	309.32	1.15	0.03
Genotypes	6	32267**	59.65**	1.07**
Error	114	474.01	0.88	0.03

**Significance at p =0.05 level

Table 2: Mean values filled grain per panicle for seven rice genotype

Genotype	Mean	Standard error (SE)	Range	Coefficient of variation % (CV)
MR270	102.45	4.92	74.00 – 156.00	21.51
MR272	23.50	2.66	5.00 – 46.00	50.67
MR276	206.00	6.10	151.00 – 257.00	13.24
SPD184	110.80	4.53	74.00 – 149.00	18.29
MRQ86	99.65	4.52	58.00 – 147.00	20.28
IR73895	131.80	4.88	100.00 – 172.00	16.59
IR64	86.40	3.81	61.00 – 111.00	19.72

Table 3: Mean values number of primary branches per panicle for seven rice genotype

Genotype	Mean	Standard error (SE)	Range	Coefficient of variation % (CV)
MR270	10.95	0.21	9.00 – 13.00	8.62
MR272	11.85	0.26	10.00 – 15.00	9.97
MR276	13.05	0.16	12.00 – 15.00	5.81
SPD184	9.25	0.27	7.00 – 12.00	13.52
MRQ86	9.15	0.15	8.00 – 11.00	7.33
IR73895	10.65	0.20	9.00 – 13.00	8.76
IR64	8.05	0.18	6.00 – 9.00	10.25

Table 4: Mean values 1000 grain weight for seven rice genotype

Genotype	Mean	Standard error (SE)	Range	Coefficient of variation % (CV)
MR270	31.07	0.60	25.60 – 39.40	8.73
MR272	25.56	0.28	23.48 – 27.94	4.92
MR276	30.89	0.30	28.06 – 34.26	4.39
SPD184	27.06	0.30	93.00 – 165.00	16.43
MRQ86	24.56	0.388	22.04 – 30.62	7.07
IR73895	31.21	0.25	29.26 – 33.52	3.66
IR64	26.82	0.21	25.08 – 28.60	3.51

Table 5: Correlation between some panicle components of rice

	filled grains per panicle	primary branches per panicle	1000-grain weight (g)
Primary branches per panicle	0.79**		
1000-grain weight	0.31	0.37	
Grain yield per plant	0.92**	0.79**	0.55**

Table 6: Estimated components of variation of some panicle component characters of rice

Traits	Filled grains per panicle	Primary branches per panicle	1000-grain weight (g)
GCV %	31.81	16.44	9.95
PCV %	36.24	18.75	11.46
h^2_b	77.04	76.93	75.29
Genotypic variance ($\delta^2 g$)	1589.70	2.93	0.07
Phenotypic variance ($\delta^2 p$)	2063.37	3.81	0.10
Environmental variance ($\delta^2 e$)	474.00	0.88	0.02

Variation of panicle traits in the F_2 generation

Some F_2 progenies showed extremes performance for nearly all traits (*Fig. 1*), indicating transgressive segregation for all traits in the populations. Transgressive segregation was found in F_2 population from the cross between IR and local rice varieties. These result indicated that several genes are involved in the genetic control of the studied traits. Quantitative inheritance was concerned with inheritance of multigenic traits. Multiple genes are the genes at different loci that affect the expression of the same phenotypic character. The location of these genes on the chromosomes controlling quantitative traits was referred to as a quantitative traits locus (QTL) and they are more complex to manipulate than qualitative genes. The inheritance of multiple genes at each locus follows the same principles of inheritance as with genes for qualitative traits, yet there are characteristics differences in number and the expression of multiple genes inheritance shows transgressive segregates. A portion of the progeny falls outside the range of the parent values. This phenomenon is very useful to the plant breeder in obtaining superior cultivar (David and John 2006).

The frequency distribution for number of primary branches per panicle in both populations showed normal distribution. This is supported by Haibin et al. (2009). The frequency distribution for filled grain per panicle appeared to be negatively skewed to the right for F_2 population of the cross between IR73895-33-1-3-2 x MRQ86 with the range is from 85 to 219 grain per panicle. According to David and John (2006), it is noted that the quantitative characters are measured and exhibited continuous variation. Phenotypic values for most traits tend to be normally distributed if measured from a sufficiently large number of observations. Changhua et al. (2007) reported that a high significant variation for the number filled of grains per panicle for different genotypes. Other factors such as soil fertility, plant nutrients translocation and weather condition might also be responsible. The frequency distribution for 1000-grain weight appeared to be normal distribution for both populations. This suggests that most of the alleles for 1000-grain weight would not be effective in early generations. It is indicated that non-additive gene action for this character, suggesting that selection for this trait should start in late generations. According to Mirza et al. (1992), the grain weight might be due to the environment or the correlation with the various yield contributing characteristics like fertility of soil, flag leaf area, grain per panicle and number of grain per panicle.

Conclusion

The number of filled grains per panicle, number of primary branches per panicle and the grain weight were three panicle component characters which have been used effectively in increasing yield rice genotypes. Increasing the grain filing and the primary branches were two new characters identified and recommended. Therefore, the panicle weight is the most panicle component character that contributes high yield production, while the panicle number must be followed with suitable agronomy package. As such further studies on the genetic resources, gene action, components correlation etc. have to be conducted and exploited.
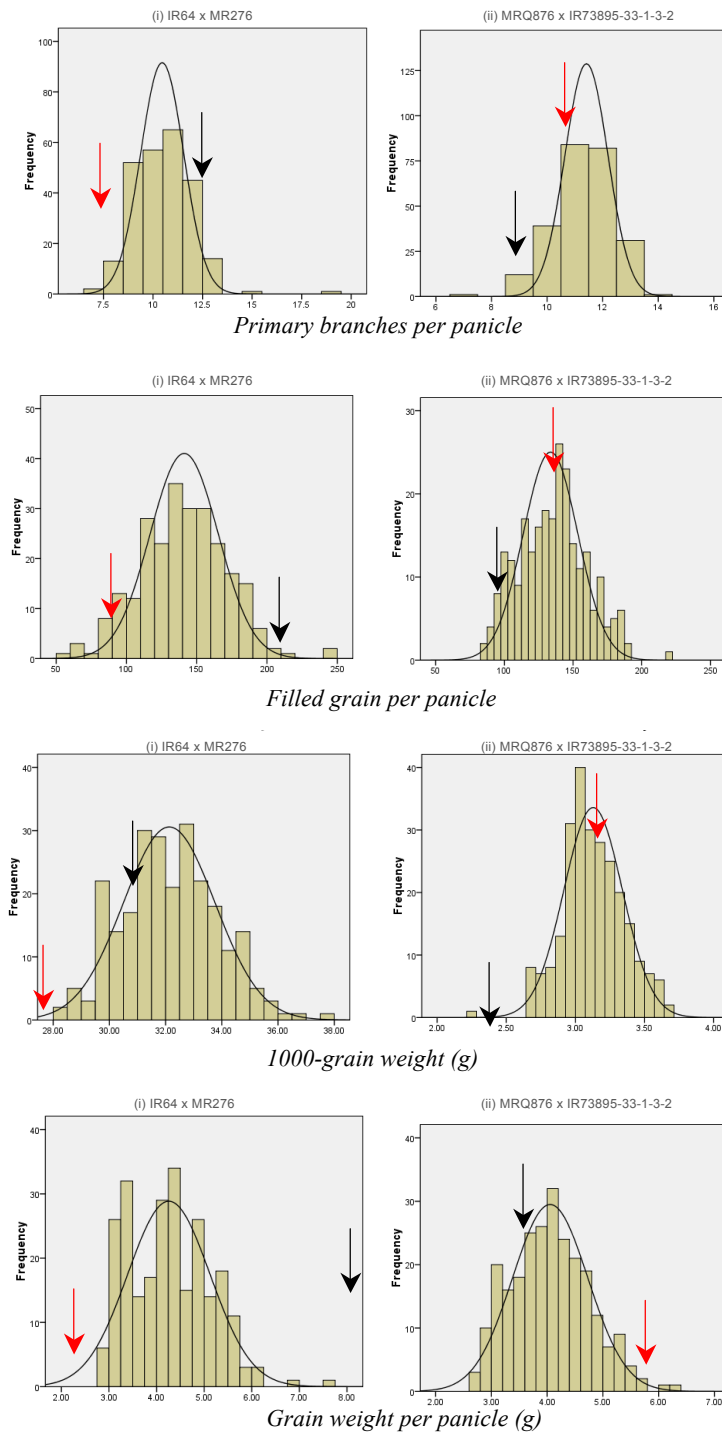
Primary branches per panicle

Filled grain per panicle

1000-grain weight (g)

Grain weight per panicle (g)

Figure 1: Frequency distribution of the traits measurements in the F_2 populations.
Arrow indicates mean value of female (red) and male (black) parents.

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Abstrak

Varieti padi MR276 mempunyai ciri panikel yang sangat baik. Ciri-ciri tersebut adalah bilangan biji bernas per panikel, bilangan cabang utama per panikel dan berat 1,000 biji. Terdapat hubungan positif dan signifikan antara bilangan cabang utama per panikel dan bilangan biji bernas per panikel (r = 0.79 *). Keputusan juga mendapati komponen panikel mempunyai nilai keterwarisan yang tinggi. Selain itu, variasi untuk ciri-ciri panikel dalam generasi F_2 juga dikaji. Populasi F_2 IR64 x MR276 menunjukkan variasi yang luas untuk ciri cabang utama dengan julat perbezaan 7 – 19 cabang utama per panikel, 56 – 248 biji bernas per panikel, 28 – 38 g berat 1,000 biji dan 3 – 8 g berat biji per panikel. Variasi untuk ciri cabang utama dan biji bernas per tangkai populasi F_2 MRQ86 x IR73895-33-1-3-2 menunjukkan julat perbezaan daripada 7 – 14 cabang utama dan 85 – 219 untuk ciri biji bernas per panikel. Taburan untuk ciri berat 1,000 biji dan berat biji per panikel adalah seragam. Kesimpulannya, varieti padi yang mempunyai ciri-ciri panikel yang baik dapat dijadikan sebagai kriteria untuk menentukan hasil padi. Kajian juga mendapati taburan untuk ciri-ciri panikel dalam populasi F_2 dengan kacukan IR64 x MR276 dan MRQ86 x IR73895-33 1-3-2 adalah sangat baik berbanding dengan induk.