Panicle Length and Weight Performance of F3 Population from Local and Introduction Hybridization of Rice Varieties

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Plant breeding program consists of establishment of the population, selection, and evaluation. The study aimed to observe the variability of yield components, the heritability, and the distribution of the yield component characters in the F3 populations. The experiment was conducted at Muara Experimental Farm Bogor, from April to August 2012 on Latosol soil. The F3 populations derived from crosses of Bintang Ladang x US2, Gampai x IR77674, and Progol x Asahan and their parental were used as plant materials. Twenty one-day-old seedlings from each population were planted in plots of 2 x 12 m, with planting space of 20 x 20 cm and 3-5 seedlings per hole. Panicle length and weight were observed on 300 randomly selected plant samples from each population. The results showed that there was a variation of agronomic characters among genotypes. The heritability of characters, the panicle length and weight was low to high. Panicle length and weight were controlled by many genes with additive gene action in the Gampai x IR77674 derived population, while panicle weight was controlled by few genes with complementary epistatic additive gene action in both Bintang Ladang x US2 and Progol x Asahan derived populations. The more genes controlling a character, the more distribution classes formed and the greater variance among genotypes.

Keywords: F3 population, yield components, heritability, variability

INTRODUCTION

Rice is an important staple food in most of the world's population, especially for the people of Indonesia. The increase in population and decrease of the land in Indonesia lead to a need to increase in rice productivity especially on marginal which have a potential for rice cultivation. Marginal lands are characterized with drought, salinity, Al toxicity, and heat stress. One of the potential strategies to improve productivity, quality and competitiveness of rice is through plant breeding approaches. Therefore, plant breeding activities is necessarily directed to the establishment and development of new cultivars for these lands (Witcombe *et al*. 2008; Kumar *et al*. 2008; Babu 2010; Cha-um *et al*. 2010).

Through breeding activities, it is expected to produce a variety of new high yielding rice cultivars and other characters that support the improvement of rice quality and competitiveness. In general, plant breeding program consists of the establishment of the population variability, selection, evaluation and testing of the selection results. Establishment of populations and their variability were gained through hybridization (Kanya *et al*. 2012; Ai-Yun *et al*. 2005), mutation (Lang *et al*. 2007; Shehata *et al*. 2009), varietal introduction (Dibba *et al*. 2012) or exploration (Singh *et at*. 2005). The next step that is considered to be important is the selection of the population and the evaluation and testing of the selected lines to obtain the new desired varieties desired with predetermined advantages.

It was known that local varieties have more characters advantages than others, such as resistance to marginal land or suboptimum conditions, resistance to pests and diseases, as well as good quality rice. Therefore local varieties could be a major genetic resource for breeders to develop new varieties with improved architecture. It is expected that genetic variability can be selected and obtained genotypes able to produce optimally on suboptimum soil conditions, resistant to pests and diseases, and

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good rice quality. Selection activities usually done in the next generation, after majority of the genetic was suspected homozygous.

This study aimed to observe the variability and heritability of panicle length and weight characters in three F3 populations obtained from crosses of local and introduced IRRI rice variety, as well as the distribution of both characters in those populations against.

MATERIALS AND METHODS

The experiment was conducted on the Latosol land at the Muara Experimental Farm Bogor, Indonesia starting from April to August 2012. Rice genotypes used in the experiment were rice genotypes from three F3 populations and their parental, i.e.: Bintang Ladang x US2, Gampai x IR77674, Progol x Asahan, Bintang Ladang, US2, Gampai, IR77674, Progol, Asahan. Each genotype was planted in plots of 2 x 12 m, planting space of 20 x 20 cm with 3-5 2-day-old seedlings from each seeds per hole. The plants were fertilized with 150 kg/ha urea, 100 kg/ha SP36 and 100 kg/ha KCl. Pests and diseases were controlled optimally. A total of 300 plant samples were randomly selected from each population, and the panicle length and weight were observed. Data was analyzed using Microsoft Excel 2007 and Minitab 15.

The average value and variance are used to estimate the heritability (Allard 1960). There were three heritability classes, i.e.: high ($h^2 > 0.5$), moderate ($0.2 < h^2 < 0.5$), low ($h^2 < 0.2$). Genetic variability was calculated by reducing the range of phenotypes F3 with a variety of environments, which is obtained from a variety of environmental averaging range of the parent.

$$\mu \frac{\sum x_i}{n} \qquad \sigma^2 = \frac{\sum x_i - \frac{1}{n}(\sum x_i)^2}{n-1}$$

$$h^2 = \frac{\sigma^2 g}{\sigma^2 F3} \qquad \sigma^2 e = \frac{\sigma^2 p2 + \sigma^2 p1}{2}$$

μ = general mean, h^2 = heritability, σ^2 = variance, $\sigma^2 g$ = genetic variance, x_i = observed value, $\sigma^2 e$ = environment variance, n = number of observation, $\sigma^2 p$ = parent variance.

Skewness (K3), the third degree statistics and kurtosis (K4), the fourth degree statistics estimated to understand the distribution of different character in a population (Roy 2000).

$$\text{Skewness} = K3 = \frac{\sum (xi - \mu)^3 / N}{\sum (xi - \mu)^2 / N} \times \sqrt{\sum (xi - \mu)^2 / N}$$

Skewness shows epistasis effected expression of a character. If K3 equals to zero, there is no epistasis, K3>0, there are complementary epistasis gene action, and K3<0, there are duplicate epistasis gene action.

$$\text{Kurtosis} = K4 = \frac{\sum (xi - \mu)^4 / N}{\sum (xi - \mu)^2 / N}$$

Kurtosis shows number of gene that controlling a character. If K4>3, has positive value, character is controlled by a few gene and if K4<3, has negative value, so that the character is controlled by many genes.

RESULTS

General Field Condition. Planting conditions at vegetative and generative phases were presented on Figure 1. In early condition, the plants were attacked by snails. The snails attack was then controlled by drying the fields for a week and removing the snails manually. By this way the snails would be difficult to move from one area to another to minimize the spread and plants damage. While in the generative phase when the plants enter seed filling period rice bug and birds attacked the plant. Rice bug was then sprayed with insecticide, while the birds were controlled manually by covering the planting area with net.

Plant Performance. Bintang Ladang had the longest panicle length (27.15 cm) followed by IR77674 (26.62 cm), while Gampai had the shortest panicle length (19.42 cm) (Table 1). The Bintang Ladang x US2 population had the highest average of panicle length (25.90 cm) over the other populations. Panicle weight also showed similar characteristics with panicle length, where the F3 population and parents with long panicles also has an average of panicle weight more than 3.5 g, such as Bintang Ladang x US2 (3.97 g), Bintang Ladang (3.81 g) and IR77674 (3.16 g). Progol x Asahan population also

Figure 1. Planting conditions. Preparation (upper), vegetative phase (lower left), and generative phase (lower right).

has a heavy panicles (3.76 g). Gampai was the parent that has the lighter panicle weight (1.92 g).

Heritability. Panicle weight and panicle length showed high and moderate heritability in the Progol x Asahan population, respectively (Table 2), which indicated the phenotypes were more influenced by genetic factors than that of the environment. High heritability of the characters was important in improving the effectiveness of selection. In addition, the selection against high heritability characters can be done at the beginning of the generation because the genetic factors dominantly influence the plant phenotype.

Unlike in the Progol x Asahan population, panicle length and panicle weight had a low heritability in both Bintang Ladang x US2 and Gampai x IR77674 populations, which means that character is more influenced by environmental factors rather than genetics factors and the selection against those

characters in both populations will be effectively carried out at the late generation.

Character Distribution. A skewness and kurtosis value was used to read the frequency distribution of genotypes and to detect gene interactions such as epistasis gene action, complementary epistasis, and duplicate epistasis rather than the analysis of variance (ANOVA). Quantitative characters in plant has always a negative values (sticking to the left) and positive skewness (sticking to the right). Value of skewness (K3) is the value of the distribution. K3 = 0 means there is no epistasis, K3 $\geq$ 0 means that there is an influence of complementary epistasis gene action, and K3 $\leq$ 0 means that there is an influence of duplicate epistasis gene action.

Recapitulation of skewness values for panicle length characters were presented in Table 3. The highest value of skewness for panicle length was 0.45 on Bintang Ladang x US2 population. Panicle length

Table 1. Mean values of panicle length and panicle weight of F3 population and the parents planted at Muara Experimental Station, Dry Season 2012

Population	Panicle length (cm)	SD	Panicle weigth (g)	SD
Bintang Ladang x US2	25.90	2.29	3.97	1.07
Gampai x IR77674	23.54	2.33	2.86	0.78
Progol x Asahan	24.20	2.68	3.76	1.25
Bintang Ladang	27.15	2.71	3.81	1.21
US2	24.99	1.94	2.67	0.65
Gampai	19.42	1.70	1.92	0.64
IR77674	26.62	3.08	3.16	0.93
Progol	24.13	2.29	2.80	0.75
Asahan	23.34	1.51	2.23	0.50

Table 2. Heritability of panicle length and panicle weight of F3 population planted at Muara Experimental Station, Dry Season 2012

Population	Heritability			
	Panicle length	Criteria	Panicle weight	Criteria
Bintang Ladang x US2	0.06	Low	0.17	Low
Gampai x IR77674	0.13	Low	0.06	Low
Progol x Asahan	0.47	Moderate	0.74	High

Table 3. Skewness value and gene action of panicle length and panicle weight characters of F3 populations planted at Muara Experimental Station, Dry Season 2012

Population	Panicle length		Panicle weight	
	Skewness	Gene action	Skewness	Gene action
Bintang Ladang x US2	0.45	Additive	0.80	Additive + complementary epistasis
Gampai x IR77674	-0.04	Additive	0.40	Additive
Progol x Asahan	0.13	Additive	1.10	Additive + complementary epistasis

Table 4. Kurtosis and expected gene number for panicle length and panicle weight characters of F3 population, planted at Muara Experimental Station, Dry Season 2012

Population	Panicle length		Panicle weight	
	Kurtosis	Number of controlled gene	Kurtosis	Number of controlled gene
Bintang Ladang x US2	0.42	A few	0.68	A few
Gampai x IR77674	-0.44	Many	-0.10	Many
Progol x Asahan	-0.34	Many	2.06	A few

kurtosis > 0 = a few gene, kurtosis < 0 = many gene (Roy 2000).

showed negative skewness values (K3 = -0.04) in the Gampai x IR77674, indicating that the selection would obtain a higher genetic advance than expected. Conversely, if the distribution of the data had positive skewness, then the selection will give a lower genetic advance than expected.

Based on the value of skewness, panicle length distribution was relatively normal in all populations. While the distribution for panicle weight, Gampai x IR77674 population classified as normal, Bintang Ladang x US2 and Progol x Asahan considered as abnormal distribution. If the distribution of genotypes of a character is not normal and has sticking to the left or right, the character is influenced by the presence of epistasis gene action. Based on the estimation gene action, panicle weight character in Bintang Ladang x US2 and Progol x Asahan have additive gene action and epistasis complementary gene action. In contrast, panicle weight in Gampai x IR77674 and panicle length for all populations were controlled by additive gene action and there is no epistasis gene action.

Kurtosis value (K4) indicated number of genes controlling the phenotypes. Characters that have spread with positive K4 means that the character was controlled by many genes, while a negative value of K4 means that the character is controlled by few genes. Based on the kurtosis, panicle length and panicle weight characters in Bintang Ladang x US2 and Gampai x IR77674 derived F3 populations were controlled by few and many genes, respectively. In Progol x Asahan derived F3 population, the panicle length character was controlled by many genes, while the panicle weight characters by few genes. The number of genes controlling a character will affect the level of difficulty in breeding programs. For example, the selection against panicle length and panicle weigth in Gampai x IR77674 derived population will be difficult since both characters were controlled by many genes (Table 4).

DISCUSSION

Estimates of the amount of variability for different characters and their heritable components available in the population are essential for dynamic and efficient plant breeding. Genetic parameters was necessary to split variability into heritable and non heritable characters (Samak *et al*. 2011). Low heritability value indicates that the genetic diversity of the characters was low or almost uniform; therefore diversity is more influenced by the environment. Conversely, the high heritability value indicates that the character is more influenced by genetic factors, and then the selection can be done in the early generations. In

genetic characters panicle length and panicle weight of Bintang Ladang x US2 and Gampai x IR77674 is more stable than Progol x Asahan population.

High to medium heritability estimates of the character of flowering, harvest, plant height, grain yield, panicle weight, and panicle length suggests high component of heritable portion of variation, which is the portion exploited by breeder and that selection for these characters can be achieved directly based on their phenotypic performance as reported by Akinwale *et al*. (2011). High heritability value was important in improving the effectiveness of selection. In character with high heritability, selection will be effective and can be done at the beginning of the generation so that genetic factors are more dominant in the appearance of plant genetic (Kumar *et al.* 2009).
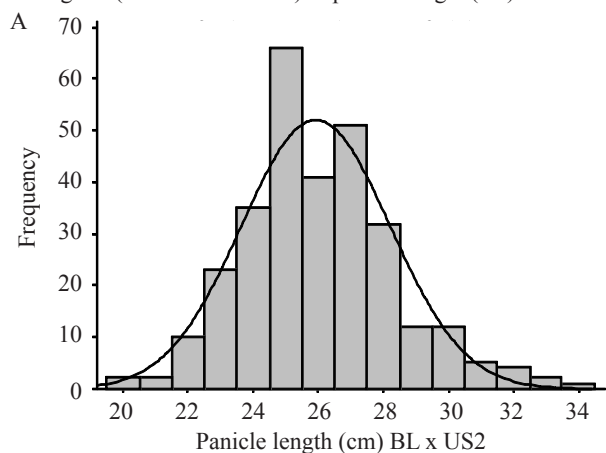
High heritability values followed by high genetic advances will further improve the efficacy of selection. Heritability will be more useful when it is guided by the standard deviation of the intensity of phenotypic and genetic selection to determine progress or response to selection of a character. High heritability of flowering age, harvesting time, plant height, and yield characters of rice lines was reported by Akinwale *et al*. (2011). Akhtar *et al* (2011) reported that high heritability values related to days to maturity, number of grains per panicle, number of tiller per plant and plant height were obtained which indicated reasonable variation for these traits. This suggests that selection can be practiced by using these traits to improve rice yield. The traits with high heritability, considerable phenotypic correlation and low seasonal variability can be used in further improvement of the progenies (Sabu *et al*. 2009). High heritability, followed by a high selection response is the result of additive gene action. The presence of additive gene action indicates that the progress of the selection of rice can be expected to obtain potential lines (Utami *et al*. 2006). Instead, a trait that has a high heritability values and followed by a low selection response due to the influence of genes is not additive (dominant epistasis) (Aryana 2010). Low heritability means that character is more influenced by environmental factors rather than genetics factors and the selection against those characters in both populations will be effectively carried out at the late generation (Kumar *et al*. 2009).

The study of distribution using skewness and kurtosis provides information about gene action and number of genes controlling a character, respectively (Samak *et al*. 2011). The number of genes affects the number of distribution classes. The more genes that
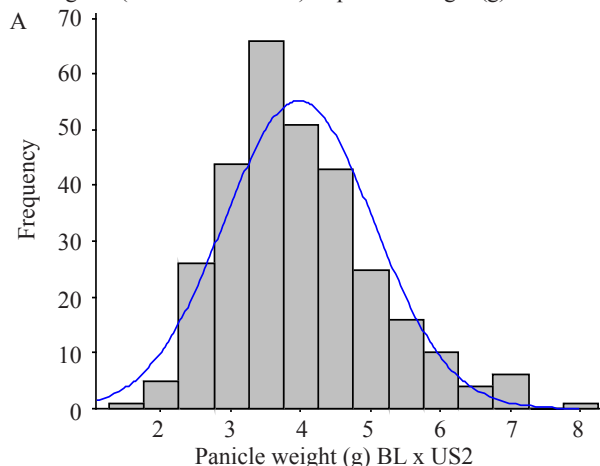
control, the more classes formed on the distribution and the greater variability among lines. The characters controlled by a smaller number of genes seem to be more pursed than characters controlled by many genes. Lines will be in the middle of the median area and the variability will be narrower in distribution (Roy 2000; Rohaeni 2010). The relationship was observed in the distribution patterns

of each character, presented in Figure 2 and 3. The distribution on the panicle length and panicle weight characters showed the class position of both parents in the three populations. In Bintang Ladang x US2, Bintang Ladang has means value greater than US2. It was similar with panicle weight character. IR77674 mean value of panicle length and panicle weight was also greater than Gampai. In the Progol x Asahan
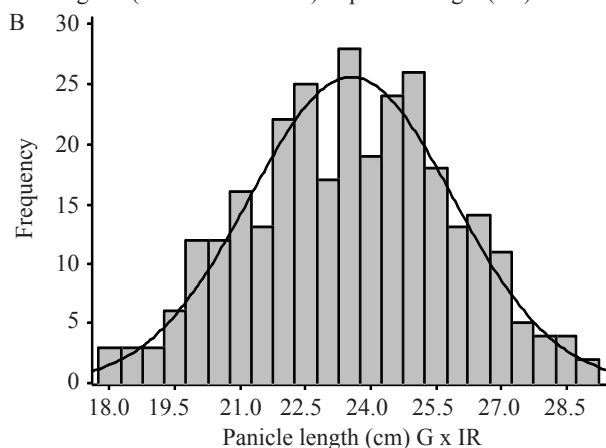
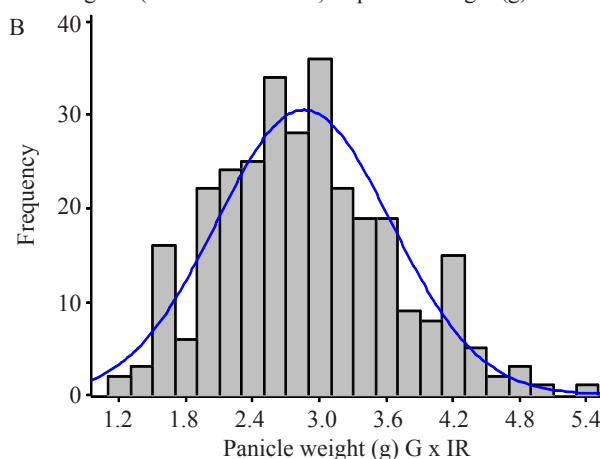Histogram (with normal curve) of panicle length (cm) BL x US2

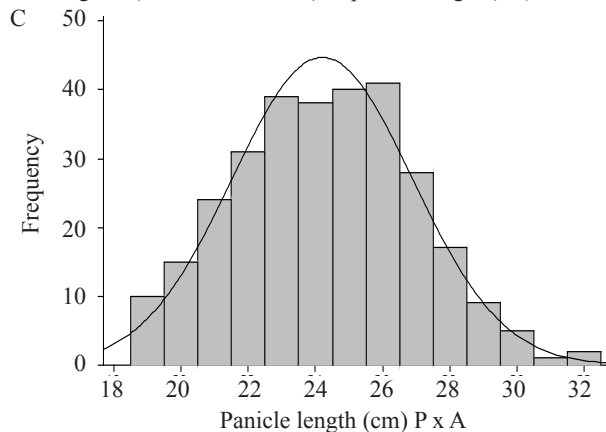
Histogram (with normal curve) of panicle length (cm) G x IR

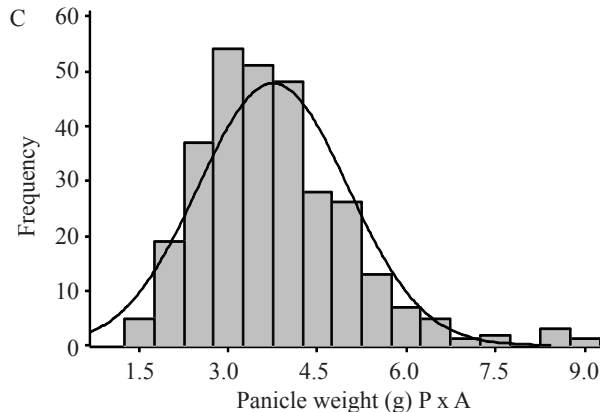Histogram (with normal curve) of panicle length (cm) P x A

Figure 2. Distribution of panicle length in (A) Bintang Ladang x US2, (B) Gampai x IR77674, (C) Progol x Asahan derived F3 populations planted at Muara Experimental Station in Dry Season 2012.

Histogram (with normal curve) of panicle weight (g) BL x US2

Histogram (with normal curve) of panicle weight (g) G x IR

Histogram (with normal curve) of panicle weight (g) P x A

Figure 3. Distribution of panicle weight in (A) Bintang Ladang x US2, (B) Gampai x IR77674, (C) Progol x Asahan derived F3 populations planted at Muara Experimental Station in Dry Season 2012.

population, mean value of Progol for panicle length and panicle weight was greater than Asahan.

From the discussion above, we concluded that there was a variability of panicle length and weight characters in the F3 populations. The spectrum of the heritability was from low to high with the highest value achieved in the Progol x Asahan derived F3 population for panicle weight character. Based on the prediction of gene action and number of genes controlling the characters, it was concluded that the difference in the number of genes controlling a character caused the differences in gene action. Panicle length and panicle weight in Gampai x IR77674 derived F3 population were controlled by many genes with additive gene action. However, the panicle weight character in Bintang Ladang x US2 and Progol x Asahan derived F3 populations was controlled by few genes with gene action is additive + different complementary epistasis. Number of genes controlling the character will determine the distribution pattern of the character in a population.

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