

Estimation of Genetic Parameter in New Plant Type Aromatic Rice Lines

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ABSTRAK. Pendugaan Parameter Genetik Galur-Galur Padi Aromatik Tipe Baru. Informasi keragaman genetik dan heritabilitas karakter tanaman sangat penting guna mendukung program seleksi padi. Penelitian dilakukan dengan tujuan untuk mengetahui keragaman genetik karakter tanaman dan hasil dari 35 galur Padi Tipe Baru (PTB) pada dua lingkungan yang berbeda dengan varietas Ciherang dan Sintanur sebagai pembanding. Percobaan dilakukan di dua lokasi (Bogor dan Pusakanagara) pada Musim Kemarau (MK) 2009 dan musim hujan (MH) 2009/2010 menggunakan rancangan acak kelompok (RAK) dengan tiga ulangan. Bibit padi berumur 21 hari ditanam satu bibit per lubang dengan jarak tanam 20 cm x 20 cm, ukuran plot 2 m x 5 m per galur. Hasil analisis gabungan menunjukkan bahwa galur, lingkungan, dan interaksi galur dengan lingkungan berbeda nyata pada seluruh karakter PTB yang diuji. Hasil penelitian menunjukkan nilai keragaman genetik, heritabilitas, dan kemajuan genetik yang tinggi dijumpai pada karakter jumlah anakan produktif, jumlah gabah total per malai, dan hasil gabah total. Ketiga karakter tersebut berkorelasi positif dengan hasil gabah.

Kata kunci: keragaman genetik padi, heritabilitas, galur PTB

ABSTRACT. Genetic Parameter Estimation on New Plant Type of Aromatic Rice Lines. Information on genetic variability and heritability of plant characters is important to support the rice selection program. A study was conducted to determine the genetic variability of characters and grain yields of 35 New Plant Type Rice Lines (NPTs) under two different environments, with varieties Ciherang and Sintanur as checks. The trials were conducted at two locations (Bogor and Pusakanagara, West Java) during dry season (DS) 2009 and wet season (WS) of 2009/2010. Each trial was arranged in a randomized block design (RBD) with three replications. Twenty one day-old rice seedlings of each entry were planted in 2 m x 5 m plots at a 20 cm x 20 cm plant spacing, one seedling per hill. Results of the combined analysis showed that strains, environments, and its interaction was significantly affecting the whole characters of NPTs. High variabilities were observed on genetic, heritability, and genetic advance characters among the new rice type lines, particularly on the number of productive tillers, total number of grains per panicle, and total grain yield. These three characters were positively correlated with rice grain yield, and could be used as indicators for superior lines.

Key words: new plant type rice, genetic variability, heritability.

Two major objectives in rice improvement program are increasing yield potential and yield stability. Improvement of high yielding potential could be enhanced through the establishment of new plant type rice (NPT). The desired NPT characteristics are 80-100 cm plant height, sturdy stem, 8-10 productive tillers, erect

leaves, thick-dark green leaves, long panicle, total grain of 200-250 grains/panicle, 100-130 maturity days, resistant to pests and major diseases (Khush 2000). In 1995, the International Rice Research Institute (IRRI) began to breed the second generation of NPTs by crossing between elite tropical japonica varieties with indica varieties. NPTs improvement is aimed at increasing the percentage of filled grains and high biomass production (Peng *et al.* 2008).

The development of rice breeding lines with an aromatic flavor character is still in progress. In this effort, Bogor Agricultural University (BAU) used aromatic upland rice varieties from South Sulawesi as parental sources of the aromatic gene. These varieties are Pulu Mandoti, Pinjan, Pare Bau, Lambau, and Sintanur. Indonesian Center of Rice Research (ICRR) has currently developed breeding lines for aromatic NPTs with gene source from variety Gilirang.

In selecting plant characters, attention should be given to the magnitude of the genetic variation, heritability, and expected genetic advance (Heliyanto *et al.* 1998). Information on genetic variability (CGV) is necessary to obtain the expected genetic gain on selection, of which selection should be effective if there is a wide genetic variability in the population. With a wide genetic variability means that by using the right selection criteria it is expected to be effective to improve the genetic potential of the characters in the next generation (Zen and Bahar 2001). Selection could be done broadly on to characters that have wide genetic variability to improve the respective character of the genotype. Karim *et al.* (2007) reported high coefficient of genetic variation (CGV) for 1000-grain weight followed by grain yield per hill and number of filled grains per panicle, whereas days to maturity showed very low CGV. The research of Karim *et al.* (2007) using 41 lines of aromatic rice in Bangladesh concluded that the number of grain per panicle also had high CGV values in addition to the 1000 grain weight and yield. On different breeding population, a high CGV for the number of productive tillers, number of grains per panicle, and total number of grains were also reported by Herawati *et al.* (2009).

Heritability is very important in determining the selection method and on which the generation of the desired character should be selected. Selection would be effective if a high value of genetic variability is supported by high heritability. Thus, these parameters determine the success of the breeding programs (Wicaksana 2001). Heritability is critical in determining the success of a selection, because it indicates as to whether a character is affected by genetic or environmental factors. Heritability determines the genetic progresses to be achieved, and the generations of selections need favorably be made to improve a certain character (Zen and Bahar 2001). High heritability values for the character of grains per panicle and days to maturity were also reported by Karim *et al.* (2007). Meanwhile, Sutaryo (2000) reported high heritability values on all agronomic characters at four locations in Central Java. High heritability values indicate that the variability of plant traits is more affected by genetic factors than by the environmental factors, and selection of these characters can be made at the early breeding generations.

The objective of this study was to quantify the genetic parameters of yield and yield components of aromatic NPT rice lines.

MATERIALS AND METHODS

Field trials were conducted at two locations, i.e., at a farmer's field in Bogor (200 m above sea level, ASL) and at Pusakanagara Experimental Farm, Subang (8 m ASL) in the Dry Season (DS) 2009 and Wet Season (WS) 2009/2010. A randomized complete block design (RCBD) with three replications was used. Materials tested were 35 aromatic rice lines and two check rice varieties Ciherang and Sintanur (Table 1). Twenty one day-old seedlings of each entry were planted in a 2 m x 5 m plot at a 20 cm x 20 cm plant spacing, 250 plants per plot. The plants were fertilized with urea, SP36, KCl at the rate of 250 kg ha⁻¹, 100 kg ha⁻¹, and 100 kg ha⁻¹, respectively. Pest and disease controls were done optimally. Data collection were done on days to flowering, days to maturity, plant height (cm), number of productive tillers, total grains per panicle, percentage of filled grains, weight of 1000 grains (g), and grain yield (t ha⁻¹).

The genetic parameters were analyzed using a combined analysis of variance according to Singh and Chaudary (1979) (Table 2).

$$\text{Variance of genotype } (\sigma_g^2) = \frac{(M3 - M2)}{r}$$

$$\text{Variance of G x E interaction } (\sigma_{ge}^2) = \frac{(M2 - M1)}{r}$$

$$\text{Variance of the environments } (\sigma_e^2) = M_1$$

$$\text{Variance of phenotypes } (\sigma_p^2) = \sigma_g^2 + \frac{\sigma_{ge}^2}{l} + \frac{\sigma_e^2}{rl}$$

Table 1. New Plant Type (NPT) rice genetic lines used in the study on genetic parameters.

No.	Lines	Parental
1	IPB 113-F-1	Pare Bau* x Fatmawati
2	IPB 113-F-2	Pare Bau x Fatmawati
3	IPB 115-F-3-2	Fatmawati x Lambau*
4	IPB 115-F-11	Fatmawati x Lambau
5	IPB 116-F-3-1	Pinjan* x Fatmawati
6	IPB 116-F-44-1	Pinjan x Fatmawati
7	IPB 116-F-46-1	Pinjan x Fatmawati
8	IPB 117-F-1-3	Fatmawati x Pulu Mandoti*
9	IPB 117-F-4-1	Fatmawati x Pulu Mandoti
10	IPB 117-F-6-1	Fatmawati x Pulu Mandoti
11	IPB 117-F-14-2	Fatmawati x Pulu Mandoti
12	IPB 117-F-15-2	Fatmawati x Pulu Mandoti
13	IPB 117-F-17-4	Fatmawati x Pulu Mandoti
14	IPB 117-F-17-5	Fatmawati x Pulu Mandoti
15	IPB 117-F-18-3	Fatmawati x Pulu Mandoti
16	IPB 117-F-45-2	Fatmawati x Pulu Mandoti
17	IPB 140-F-1-1	Sintanur* x (Fatmawati x I PB26-d-14j-1-1-2)
18	IPB 140-F-2-1	Sintanur x (Fatmawati x IPB26-d-14j-1-1-2)
19	IPB 140-F-3	Sintanur x (Fatmawati x IPB26-d-14j-1-1-2)
20	IPB 140-F-4	Sintanur x (Fatmawati x I PB26-d-14j-1-1-2)
21	IPB 140-F-5	Sintanur x (Fatmawati x I IPB26-d-14j-1-1-2)
22	IPB 140-F-6	Sintanur x (Fatmawati x I IPB26-d-14j-1-1-2)
23	IPB 140-F-7	Sintanur x (Fatmawati x IPB26-d-14j-1-1-2)
24	IPB 149-F-1	Lambau* x Fatmawati
25	IPB 149-F-2	Lambau x Fatmawati
26	IPB 149-F-3	Lambau x Fatmawati
27	IPB 149-F-4	Lambau x Fatmawati
28	IPB 149-F-5	Lambau x Fatmawati
29	IPB 149-F-7	Lambau x Fatmawati
30	IPB 149-F-8	Lambau x Fatmawati
31	B11249-9C-PN-3-3-2-2-MR-1	B10589F-KN/Memberamo/IR64
32	B11738-MR-1-2-Si-1-2	Gilirang*/BP342F-MR-1-3//Gilirang*
33	B11742-RS*2-3-MR-34-1-2-1	BP360E-MR-79-PN-2/IR71218/BP360E
34	B11823-MR-3-15-1	BP140F-MR-1-KN-1/Code/BP140F-MR-1
35	B11955-MR-84-1-4	B11738-MR-2-5/B11738-MR-6B
36	CIHERANG**	
37	SINTANUR**	

* Donor parent for the aromatic characters. ** check varieties.

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

$$\text{Coefficient of genetic variance (CGV)} = \frac{\sqrt{\sigma^2_g}}{X} \times 100\%$$

$$\text{Coefficient of phenotypic variance (CPV)} = \frac{\sqrt{\sigma^2_p}}{X} \times 100\%$$

$$\text{Genetic advance (GA)} = k \times \sqrt{H^2\text{bs}} \times \sqrt{\sigma^2_p}$$

$$\text{GAP (\%)} = \frac{GA}{X} \times 100\%, \text{ is the value of genetic improvement in the percent of the average value of the population, where:}$$

k = selection differential in standard unit, k = 2.06 at 5% selection intensity

X = general mean

RESULTS AND DISCUSSION

Combined analysis of variance showed significant affects among the lines, environments, and interaction between lines and environments for all characters (Table 3). There was no significant different value of panicle

length on single environment. This means that variability of the characters was influenced by the line differences, environments, as well as interaction between lines and environments. The results suggest possibility of improving genetic characters through lines selection.

The value of genetic parameters indicated that the coefficient of genetic variance (CGV) and coefficient of phenotype variability (CPV) for all the characters ranged from 1.11-16.34% and 1.55-18.18%, respectively (Table 4). The lowest value of CGV was obtained from the days to maturity, while the highest value was obtained from the total number of grains per panicle. The CGV values from 0-16.34% were determined as absolute values; while CGV 100% was considered as the relative value of 16.34% (Murdaningsih *et al.* 1990). Criteria on the relative value of CGV were grouped into: low ($0 < x \leq 25\%$), rather low ($25\% < x \leq 50\%$), high ($50\% < x \leq 75\%$), and very high ($75\% < x \leq 100\%$). The absolute values of these criteria were: low ($0 < x \leq 4.09\%$), rather low ($4.09\% < x \leq 8.17\%$), high ($8.17\% < x \leq 12.25\%$), and very high ($12.25\% < x \leq 16.34\%$). Based on the value of these criteria, four characters showed low values, namely days to flowering, days to maturity, 1000 grain weight, and yield. Three characters were considered as rather low values, namely plant height, panicle length, and percentage of filled grain. The other three characters showed high values, i.e., number of productive tillers,

Table 2. Combined analysis of variance (Singh and Chaudary 1979).

Source of variance	Degree of freedom	Mean Square (MS)	Expected MS
Environment (E)	(l-1)	-	$\sigma^2_e + g \sigma^2_{ge} + g \sigma^2_{r(2l)} + r_g \sigma^2_e$
Replication within env.	(m-1)	-	$\sigma^2_e + g \sigma^2_{r(l)}$
Genotype (G)	(g-1)	M3	$\sigma^2_e + r \sigma^2_{ge} + r l \sigma^2_g$
G x E	(g-1) (l-1)	M2	$\sigma^2_e + r \sigma^2_{ge}$
Error	(g-1) (r-1) l	M1	σ^2_e

Table 3. Mean squares (MS) of combined analysis of variance of plant characters of 35 New Plant Type rice lines in four environments.

Plant character	Value of MS				
	Environment (E)	Replication in Environment	Line (G)	G x E	CV (%)
Days to flowering	8771.52**	50.06**	77.78**	27.45**	2.8
Days to maturity	2741.17**	58.55**	41.94**	20.45**	2.1
Plant height	2406.28**	485.74**	519.31**	100.62**	5.5
Number of productive tiller	595.58**	26.98**	24.12**	7.65**	15.3
Panicle length	15.43**	2.47ns	34.40**	9.22**	4.6
Number of filled grain per panicle	9315.19**	2683.98**	9655.73**	2270.62**	15.8
Total grain per panicle	114348.66**	3806.24**	24503.7**	4727.69**	13.7
Percentage of filled grain	6413.97**	347.14**	317.98**	161.96**	11.4
1000 grain weight	132.37**	21.38**	19.22**	11.96**	7.4
Yield	717.68**	8.45**	2.67**	2.14**	17.5

Notes: MS = mean squares; ns = not significant; ** = significant at 1%; * = significant at 5%.

Table 4. Combined genetic variabilities and phenotypic correlations of yield characters of 35 New Plant Type rice lines in four environments.

Plant character	VG	VP	h ² bs	GCV	PCV	GA	GAP (%)	Avg.	r yield
Days to flowering	4.19	6.48	0.65	2.22	2.76	3.39	3.68	92.28	-0.46**
Days to maturity	1.79	3.50	0.51	1.11	1.55	1.97	1.64	120.48	-0.43**
Plant height	34.89	43.28	0.81	5.31	5.91	10.93	9.82	111.22	0.04
Number of productive tillers	1.37	2.01	0.68	10.63	12.87	1.99	18.10	11.02	0.46**
Panicle length	2.10	2.87	0.73	4.96	5.79	2.55	8.73	29.23	0.01
Number of filled grains per panicle	615.43	804.64	0.76	15.28	17.47	44.69	27.52	162.40	0.19**
Total grains per panicle	1648.00	2041.98	0.81	16.34	18.18	75.13	30.23	248.50	0.21**
Percentage of filled grains	13.00	26.50	0.49	5.46	7.79	5.20	7.88	66.07	-0.03
Weight of 1000 grains	0.61	1.60	0.38	2.73	4.44	0.98	3.45	28.51	-0.10*
Yield	0.04	0.22	0.20	3.23	7.26	0.19	2.97	6.50	

Notes: VG = genetic variances; VP = phenotypic variances; h²bs = broad sense heritabilities;

CGV = coefficient of genetic variances; CPV = coefficient of phenotypic variances;

GA = genetic advances; GAP = genetic advance percentages; r yield = coefficient correlations to yield.

number of grains per panicle, and total number of grains. A rather low criterion was just called low.

Characters with rather low CGV values were considered as having a narrow genetic variability. Conversely, characters with high CGV values were classified as having a wide genetic variability. Hence, the number of productive tillers, number of filled grains per panicle, and number of total grains had wide genetic variabilities. These means that there were chances to improve genetic characters of the NPT rice through the number of productive tillers, number of grains per panicle, and total number of grain.

In a broad sense, heritability values of the NPT's grain yield was low, the percentage of filled grain and 1000-grain weight were medium, while those of the other 6 characters were high. The high heritability values of the 6 characters indicated the strong influences of genetic factors on the phenotypes. Selections for characters with high heritability could generally be done at early plant generations.

The genetic value (GA) could be used to predict the amount of added value of certain characters that can be attained as a result of selection, over the average value of the population. The GA values of the tested lines ranged from 0.04 (on yield) to 75.13 (on total grain). In this study, the GA values were determined from α 5% selection intensity, so that the 5% value was used to determine the range of high and low percentage of genetic advance (GAP) (Murdaningsih *et al.* 1990). Subsequently, it was determined that the low GAP values were between 0 to 1.67%; rather low between 1.67-3.33%, high enough between 3.33-5.00%, and high GAP if more than 5%. Using these criteria, there were characters with high-values of GAP, namely plant height, number of productive tillers, panicle length, number of filled grain per panicle, total number of grains, and percentage of filled grain. Character with a high GAP value were days to flowering and 1000

grain weight, while that classified as rather low and low was days to maturity. The coefficient of phenotypic correlation for the number of productive tillers, number of grains per panicle, and total grains, with grain yield each was positive and significantly (Table 4).

The combine data correlation values of each character were in accordance with the single location data correlation. The total number of grain, number of grains per panicle, and number of productive tillers were positively correlated with the grain yield (t ha⁻¹). For example, at Bogor in the DS 2009, the lines that had yield potentials more than 10 t ha⁻¹ of IPB 140-F-7 and B11738-MR-Si-1-2-1-2, decreased to 3 t ha⁻¹ in the WS 2009 and they were proportional to the decrease in the total number of grains, number of grains per panicle, and number of productive tillers. This fact was also true for varieties Sintanur and Ciherang, the checks. The same phenomenon was also observed at Pusakanagara in the DS 2009 and WS 2009.

The number of productive tillers, number of grains per panicle, and total grain numbers showed heritability, CGV, and GAP in high criteria (Table 5). High heritable characters with high GAP could further be improved through individual line selection, where selection to be made in accordance with the breeding objectives, because there were significant effects of the genotypes (G), environment (E) effects as well as the G x E interactions (Laxuman *et al.* 2010; Bahar *et al.* 2000).

Significant negative correlations of the plant characters with the grain yield were found on days to flowering, days to maturity and 1000 grain weight. The correlations between the character values with the rice yield were used as indicators for selecting improved rice varieties. Using the correlation values between the grain yield with other characters for selection criteria is better if there is a high heritability value (Sudarmadji *et al.* 2007). Then, based on the results of correlation and heritability,

Table 5. Criteria of the genetic parameter values of 35 New Plant Type rice lines.

Plant character	h ² bs	GCV	GAP (%)
Days to flowering	High	Low	High
Days to maturity	Medium	Low	Low
Plant height	High	Low	High
Number of productive tillers	High	High	High
Panicle length	High	Low	High
Number of filled grains per panicle	High	High	High
Total grains	High	High	High
Percentage of filled grains	Medium	Low	High
1000 grain weight	Medium	Low	High
Yield (t.ha ⁻¹)	Low	Low	Low

Notes: h²bs = board sense heritability; GCV = Genetic coefficient of variance; GA = genetic advance.

characters for the number of productive tillers, number of grains per panicle and total grains are targets to be improved to increase the rice yields.

Wide yield gaps between the NPT lines planted in the DS and WS were also reported by Peng *et al.* (2004) on NPTs at the IRRI Experimental Farm. In the DS 2002, the rice yields ranged from 8-9 t ha⁻¹, but they declined to only 4-5 t ha⁻¹ or by 50% in the WS 2002/2003. The grain yield decreases in the WS 2002/2003 were due to the less number of productive tillers per m², less number of filled grains, and low 1000 grain weight.

CONCLUSIONS AND SUGGESTIONS

Combined analysis of variance of 35 NPT rice lines conducted at Bogor and Pusanagara in the DS 2009 and WS 2009/2010 showed that rice lines, environment, and interaction between the rice line and the environment were significantly different for all plant characters. The genetic variabilities showed high values of coefficient of genetic variability (GCV), heritabilities, genetic advances on productive tillers, number of grains per panicle, and total grains of the rice lines. There were significant positive correlations among the productive tillers, number of grains per panicle, and total grains to the grain yield. It is suggested, therefore, that the selection to obtain new high-yielding NPT rice lines was carried out on these characters.

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