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Population Characteristics and Genetic Relationship on 25 Bengkulu Heirloom Rice Based on Morphological Traits

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ABSTRACT

Bengkulu Province has many local rice germplasms that have adapted to specific areas. The germplasm has certain character advantages so that it is maintained by farmers. The characteristics of each germplasm need to be identified in order to improve the properties of the existing germplasm. This study aimed to determine the performance, to estimate the value of genetic parameters, and to determine the genetic relationship of heirloom collected from four districts in Bengkulu. The results showed that the 'Kuning Sulaowangi' genotype was the earliest in maturityand possessed the highest number of tillers amongst genotypes. Genotypes which have the highest yield components were 'Kunig Air Dingin' and 'Impera'. A high heritability value was obtained on `100-seed weight (91.046%) and grain weight per panicle (80.252%). The 100-seed weight also has the highest genetic variability value. Thus increasing of heirloom production is possible to be done. The heirloom could be seperated into two groups with the similarity coefficient of 55% for all traits. Group I consisted of 9 genotypes namely 'Kuning Pendek', 'Humbur', 'Cantik', 'Pandak Kelabu', 'Cisadane Putih', 'Kuning Sulaowangi', 'China Abang', 'China Putih' and 'Impera'. Other genotypes were in Group II. Trait improvement can be done through hybridization between individuals of different groups. To develope varieties with early in maturity and high-yielding can be done through hybridization of the 'Kuning Sulaowangi' and 'Kunig Air Dingin'.

INTRODUCTION

Developing new varieties can be done if the genetic material used has high genetic diversity. The genetic diversity can be obtained through both natural (Herison, 2018) and artificial as mutation induced (Rustikawati, 2012). Exploration on germplasm adaptive to certain environments can increase the genetic diversity of collected population. Heirloom cultivars are cultivars that have undergone mutations due to natural selection occurred for years. Heirloom rice cultivars are still maintained by farmers because it has good adaptability to the sub-optimal environment and has superior characteristics according to farmer preferences in certain areas. Among these superior traits, delicious taste, fragrant

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and abiotic stress tolerance characteristic are the most desirable. They are gaining in popularity because of their unique flavors and cultural significance to local cuisine, and their role in sustainable food production for small-scale farmers (Dwivedi, *et al*., 2019). However, heirloom rice are now in a critical condition. Thousands of heirloom rice have disappeared due to widespread land conversion and the entry of new rice varieties (IRRI, 2016). heirloom rice nomenclature is often based on easily identified morphological trait or the name of the adaptation area. The main morphological characteristics that are often used to differentiate heirloom rice are plant height, number of productive tillers, stem color, leaf color, leaf surface, number of grains per panicle, grain shape, grain color, and grain surface. In addition, the character of flowering can also distinguishes rice cultivars. Plant height characteristics, productive tillers, and stem surface color are the characters used by the Indonesian Rice Research Institute to distinguish superior rice (IRRI. 2016). Observed variances in rice were mostly explained by flag leaf attitude, apiculus color, pallea-lemma color, grain tip color, and awning while that in quantitative data were number of grain per panicle, plant height at both flowering and harvesting, flowering date and harvesting date (Mau *et al*., 2017).

Based on some morphological traits identified, it can be determined the most useful trait for selection process by estimating the value of genetic parameters. The estimated value of heritability is a very important parameter in breeding because it is very influential on the effectiveness of selection (Bekele and Rao, 2014). Broad sense heritability is defined as the proportion of the total variability attributed to genetic factors to the phenotypic variability of a character (Adhikari, 2018). Some methods commonly used to estimate the value of heritability include the methods for estimation of variance component, regression methods for parents and heredity, and methods for estimating environmental variances indirectly (Fehr, 1987). Classification of high and low heritability of a character is determined by the high and low estimated value obtained. According to Acquaah (2012), heritability is considered low if $h^2 < 0.2$, moderate if $0.2 < h^2 < 0.5$, and high if $h^2 > 0.5$.

Determination of the selection procedure is commonly based on the phenotypic value of the individual depending on the value of heritability. Individual selection is used in situations of high heritability where deviations in families and between large families, selection in families in situations of moderate heritability where deviations in large families and between small families, and selection of families in conditions of low heritability where deviations in families are small and between families quite large (Falconer, 1981). Relationship information and genetic parameters are very important to determine the right breeding program. Genetic Relationship is needed to determine the highest genotypic distance as the crossing parent. Cluster analysis based on agro-morphological diversity assessment in rice was also reported in several studies, such as Mathure *et al*. (2010); Li *et al*. (2010); Zhang *et al*. (2010) and Nascimento *et al*. (2011).

The aims of this study were to evaluated the performance, estimate the value of genetic parameters and determine the genetic diversity of 25 Bengkulu heirloom rice.

MATERIALS AND METHODS

The study was conducted in low land experimental station of the Agronomy Laboratory, Faculty of Agriculture, University of Bengkulu. This study was arranged in a Complete Randomized Block Design (RCBD) with three replications. As the treatment was 25 heirloom rice. The experimental units were plots each of which was 1 m x 5 m, with a distance between plots 50 cm apart. In each block there were 4 rows of plants. Ten plant samples observed in each genotype.

Nursery was carried out with soil and manure mix media with a ratio of 2:1. Each tray was filled with media of 15 cm height. Rice seeds were spread one genotype per tray and grown until the age of 21 days. Transplanting was carried out manually with plant spacing of 20 cm in rows and 25 cm apart between rows.

The rate of fertilizers were 200 kg Urea, 100 kg SP36 and 100 kg KCl per hectare. Observations were made on vegetative and generative variables including plant height, number of leaves, number of productive tillers, age of harvesting, panicle length, grain weight per panicle, number of grain per panicle and 100-seed weight.

The data was analyzed for variance (ANOVA) and the means were cluster analysis with Scott-Knot test using Infostat software. Genetic parameters were calculated following the method of Singh and Chaudhary (1979). Cluster analysis was performed by software NTSys 2.01.

RESULTS AND DISCUSSION

The Diversity of Bengkulu Heirloom Rice Population

The results revealed a widw range of variability among 25 heirloom rice. The genotype of Manggar and Rantau Mudik showed a good vegetative growth indicated by plant height, number of leaves and the number of high productive tillers. Both genotypes were classified as long-lived, 128.3 days and 120 datype was 8.9. Heirloom that has an early maturity (106 days) were genotypes of ys, respectively. The Manggar genotype has 8.5 productive tillers, while Rantau Mudik genoBujang, Cantik, Padang Bakung, Kuning Sulaowangi and Kuning Air Dingin. Early maturing rice was more favorable for the farmers. Kuning Sulaowangi genotype was the earliest maturity and the highest number of tiller, which was 10.1 tiller per hill. Bujang and Cantik genotypes had a relatively small number of productive tillers, 5.5 and 6.0, respectively. Padang Bakung genotype, in addition to being short-lived, they also had high number of productive tiller, 9.7 tiller per hill (Table 1). A wide range in growth variability of upland rices was also recorded by Khatun *et al*. (2015).

Genotypes that had significantly higher average yield characteristics were Impera and Kuning Air Dingin. Their panicle lengths were 22.85 and 21.80 cm; grain weight per panicle 75.27 g and 68.25 g; the number of grain per panicle 126.7 and 152.5 and weight of 100.13 g

Table 1. Average plant height, number of leaves, number of productive tillers and harvest age of 25 Bengkulu local rice genotypes

Genotype	Plant height		Number of leaf		Number of productive tiller		Days to harvest	
Abang Pintal	119.93	a	63.9	c	8.6	b	118.7	b
Bangkok	113.07	a	62.1	c	9.5	b	118.7	b
Bujang	132.40	b	57.5	b	5.5	a	106.0	a
Beram	148.53	c	51.7	b	8.1	b	125.0	b
Cantik	145.53	c	65.9	c	6.0	a	106.0	a
Cina Abang	122.80	a	54.0	b	8.0	b	128.0	b
Cina Putih	115.27	a	78.9	d	7.5	a	125.0	b
Pandak Kelabu	160.47	d	40.4	a	7.6	a	115.7	b
Galur	163.73	d	74.2	d	7.7	a	130.3	b
Humbur	131.47	b	41.3	a	8.9	b	118.7	b
Impera	108.67	a	62.1	c	8.7	b	112.3	a
Kuning Air Dingin	149.47	c	48.5	b	8.5	b	106.0	a
Manggar	160.47	d	54.7	b	8.5	b	128.3	b
Kuning Pendek	127.87	b	41.8	a	8.4	b	118.7	b
Kuning Sulaowangi	131.87	b	43.7	a	10.1	b	106.0	a
Kuning Tinggi	153.47	c	65.3	c	8.4	b	123.3	b
Padang Bakung	134.40	b	51.2	b	9.7	b	106.0	a
Bunga Macang	142.13	c	77.2	d	8.9	b	128.3	b
Putih Halus	151.40	c	54.2	b	5.9	a	128.3	b
Pino Raya	159.33	d	37.2	a	6.7	a	106.0	a
Pendek Putih	145.60	c	51.7	b	7.4	a	125.0	b
Putih Cisadane	131.07	b	54.3	b	8.7	b	106.0	a
Rantau Mudik	141.47	c	84.4	d	8.9	b	120.0	b
Simpat Abang	136.33	b	75.3	d	8.9	b	117.0	b
Siung Kancil	168.87	d	66.7	c	7.2	a	128.3	b

Note: Numbers in the same clumn followed by the same letter were not significantly difference base don Scott-Knot Test at a=5%

Table 2. Average panicle length, grain weight per panicle, number of grains per panicle and weight of 100 grains 25 Bengkulu local rice genotypes

Genotype	Panicle length (cm)	Grain weight per panicle (g)	Number of grains per panicle	100-seed Weight (g)
Abang Pintal	19.69 c	11.96 a	121.1 b	9.06 a
Bangkok	19.91 c	28.20 a	118.0 b	13.67 b
Bujang	22.07 d	12.31 a	122.1 b	9.78 a
Beram	18.51 b	17.09 a	113.1 b	9.99 a
Cantik	20.50 c	23.78 a	93.1 a	11.53 a
Cina Abang	21.67 d	58.89 b	130.9 b	13.79 b
Cina Putih	21.00 c	37.67 a	162.0 b	13.65 b
Pandak Kelabu	22.53 d	58.18 b	145.8 b	13.67 b
Galur	21.40 d	20.98 a	113.9 b	10.70 a
Humbur	20.40 c	41.74 b	91.6 a	10.73 a
Impera	22.65 d	75.27 c	126.7 b	13.13 b
Kuning Air Dingin	21.80 d	68.25 c	152.5 b	12.81 b
Manggar	21.80 d	21.01 a	135.3 b	9.74 a
Kuning Pendek	22.13 d	29.72 a	95.5 a	14.77 b
Kuning Sulaowangi	20.85 c	54.82 b	132.9 b	12.31 b
Kuning Tinggi	22.13 d	11.46 a	114.8 b	8.66 a
Padang Bakung	19.30 c	22.29 a	84.6 a	10.90 a
Bunga Macang	22.60 d	21.79 a	115.5 b	10.36 a
Putih Halus	14.63 a	21.64 a	80.9 a	11.22 a
Pino Raya	22.20 d	27.01 a	116.0 b	8.71 a
Pendek Putih	21.80 d	10.98 a	135.3 b	8.83 a
Putih Cisadani	15.73 a	43.53 b	129.3 b	13.41 b
Rantau Mudik	21.67 d	18.55 a	96.7 a	11.77 b
Simpat Abang	17.67 b	70.59 c	114.1 b	11.47 a
Siung Kancil	22.51 d	10.40 a	125.6 b	8.95 a

Note: Numbers in the same clumn followed by the same letter were not significantly difference base don Scott-Knot Test at a=5%

and 12.81 g, respectively. The China Abang and Kuning Sulaowangi genotypes also had high grain weight per panicle, even though the panicle length were shorter than that of the previous genotypes (Table 2).

Bengkulu heirloom rice diversity was reflected through vegetative and generative variables. Diversity was shown through phenotypic and genotypic coefficient of variation. High diversity was reflected by high phenotypic coefficient of variation (84.36%) (Khatun, 2015). The grain weight per panicle and 100-seed weight exhibited very high genotypic diversity values, 60.057 and 77.13, respectively (Table 3 and Table 4). Characters with large CVs can be used to form contrasting segregation populations which was of high value for future breeding program.

The estimated genetic parameter values were calculated based on all 8 variables measured. All variables had high broad sense heritability except the number of productive tillers which were classified as moderate. This means that there were opportunity for good variety development through these parameters. The weight of 100 grains had the highest broad sense heritability value of 91.05%. Genetic factors predominantly determined the grain size. The genetic variability of those variable was also high so improvement in varieties by increasing seed size was very possible. Another variable that also had high heritability estimate (80.252%) was the grain weight per panicle. This variable was the main yield component. Meanwhile, the value of genetic diversity was also high, 386.427. Thus an increase in yield of varieties generated from Bengkulu's local rice germplasm is very possible. Similar results

Table 3. The genetic parameters of plant height, number of leaves, number of productive tillers and harvest age of 25 Bengkulu local rice genotypes

Parameter	Plant height	Number of leaf	Number of productive tiller	Days to harvest
Phenotypic variance	347.350	220.067	2.090	110.607
Genetic variance	241.060	145.037	1.000	63.877
Coefficient of phenotypic variation	13.329	25.430	17.839	8.908
Coefficient of genetic variation	11.104	20.644	12.340	6.769
Boad sense heritability estimate (%)	69.400	65.906	47.847	57.751

Table 4. The panicle length parameter values, grain weight per panicle, number of grains per panicle and weight of 100 grains 25 Bengkulu local rice genotypes

Parameter	Panicle length (cm)	Grain weight per panicle (g)	Number of grains per panicle	Weight of 100 grains (g)
Phenotypic variance	5.570	481.517	618.290	1208.003
Genetic variance	3.940	386.427	316.500	1099.723
Coefficient of phenotypic variation	11.409	67.057	20.949	77.131
Coefficient of genetic variation	9.596	60.072	14.989	73.593
Boad sense heritability estimate (%)	70.746	80.252	51.190	91.046

were presented by Adhikari *et al*. (2018). Higher phenotypic variation (PCV) was observed for grain yield (24.87%), number of grains/panicles (22.45%). High genetic advance coupled with heritability in maize was observed for plant height and grain yield per plot (Bekele and Rao (2014).

Genetic Relationship Analysis

Cluster analysis was needed to evaluate genetic relationship based on all variables observed including vegetative and generative variables. Two major groups were observed among 25 heirloom rice based on multivariate analysis at a 55% similarity coefficient. Group I consisted of 9 genotypes namely Kuning Pendek, Humbur, Cantik, Pandak Kelabu, Putih Cisadane, Kuning Sulaowangi, China Abang, China Putih and Impera. The other genotypes included in group II. The improvement of traits can be done through crossing between different groups according to the desired character.

If related to the results of growth performance and the estimation of genetic parameters suitable for heirloom traits improvement programs, Kuning Sulaowangi was the most appropriate genotype to be engineered. The genotype was known to have an early maturity (106 days) and the highest number of tillers (10.1). The genotype can be increased its productivity by increasing grain weight per panicle which has a broad sense heritability of 80.252%. As the donor parent for the high weight per panicle was the Kuning Air Dingin or China Abang genotype, both of which had the highest grain weight per panicle, 68.25 g and 70.9 g, respectively.

CONCLUSIONS

The Kuning Sulaowangi genotype had the highest early maturity and the highest number of tillers. Kuning Air Dingin and Impera had high average yield components. All variables had high broad sense heritability except the number of productive tillers, classified as moderate. The value of genetic diversity was also high. Bengkulu heirloom rice formed two major groups. Group I consisted of Kuning Pendek, Humbur, Cantik, Pandak Kelabu, Putih Cisadane, Kuning Sulaowangi, China Abang, China Putih and Impera. The other genotypes were belonged to group II. To develop short-lived and high-yielding varieties

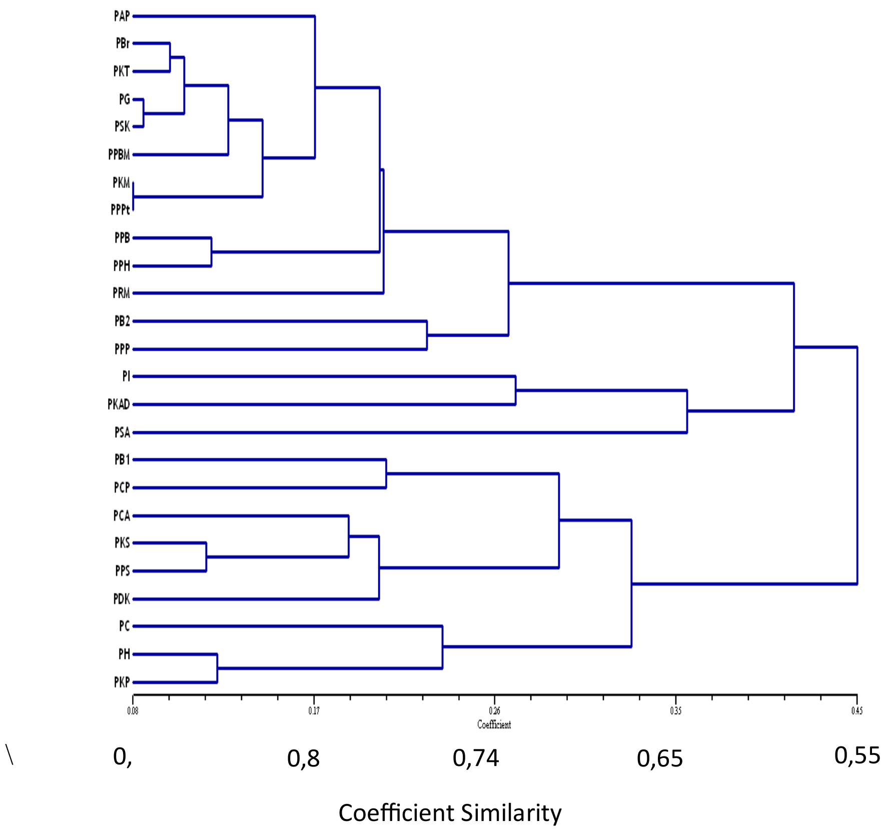

Figure 1. Dendrogram 25 Bengkulu heirloom rice based on quantitative observations in the vegetative and generative phases

can be started by crossing of Kuning Sulaowangi genotype with Kuning Air Dingin.

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