

Genetic diversity of local red rice cultivars collections of Yogyakarta AIAT, Indonesia based on morphological character

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Abstract. Identification of local red rice was important to study for genetic diversity. The objective of the study was to identify the morphological characteristics to estimate the genetic diversity and heritability in the broad sense of 11 local red rice cultivars. The quantitative data (plant height, leaf length, leaf width, number of productive tillers, panicle length, 1,000-grain weight and number of grain per panicle) were measured by their CVg values for determining their relationships and heritability. The results can be used for parent selection in a breeding program. Results showed that the number of productive tillers, leaf length and the number of grain content per panicle for 11 local red rice from Yogyakarta were efficient and effective characters in selection because the characters have wide of the coefficient of variation genetics and high heritability value.

Keywords: genetic diversity, relationship, morphology, local red rice, Yogyakarta AIAT.

1. Introduction

Red rice, a staple food source known since 2,800 BC, has long been known to be very beneficial to health, as well as staple foods. This red rice could prevent food shortages and nutrition and cure diseases of vitamin A deficiency (farsightedness) and vitamin B. According to Frei [1], rice especially red rice is a major source of carbohydrates, also contains proteins, beta-carotene, antioxidants, and iron. Red rice fibre was relatively easy to be absorbed by intestine than wheat, so it can lighten the intestine burden in performing a peristaltic movement [2] and launching the gastrointestinal system. Thus, conservation of the genetic resources of red rice needs to be addressed and put in high effort, so that the value of benefits can be enjoyed for the community welfare.

The exploration activity of genetic resources team of Yogyakarta AIAT obtained 15 local red rice cultivars which are still cultivated by some farmers in the region of Yogyakarta, Indonesia. Fifteen red rice cultivars have different names depending on the area of origin and farmers who cultivate. Besides, the difference in the name of red rice was thought to be due to the diversity of morphological appearance of the plant to the colour diversity [3].

The genetic resources of local red rice are indispensable in addition to cultivated for consumption required by plant breeders as a parent. Breeders need to use wide genetic diversity for the parent to improve varieties. Utilization of existing genetic resources becomes easier if characterization and



evaluation have been conducted. Characterization of the desired properties is able to estimate the kinship relationship between the cultivars. The phenotype appearance as an expression of genetic diversity can distinguish an individual with other individuals. The study of genetic diversity can be done based on morphological, biochemical and molecular markers [4].

The encoding of morphological properties was heavily influenced by the environment, but morphological properties have been of great benefit in forming several of excellent cultivars since the 1950s. Morphological enrichment can be used to identify multiple germplasm collections. Matching at the morphological level is primarily phenotype recognition and its associated changes in its ecotype [4].

Morphological identification was an easier step at the early stage compared to molecular identification. The morphological markers used were based on simple Mendelian inheritance, such as shape, colour, size and weight. The morphological properties can be used as real clues to specific genes and markers of genes in chromosomes because the properties that affect morphology can be inherited [5]. The phenotype of plants was determined by the genetic and environmental factors [6].

Extensive genetic diversity and high heritability were among the requirements for valid selection [7]. High heritability values indicate that most of the phenotypic diversity caused by genetic diversity, in which selection will gain genetic progress [8]. Based on these matters, this study aimed estimate the genetic diversity and heritability in the broad sense of 11 local red rice cultivars of Yogyakarta AIAT collection based on morphological characters.

2. Materials and methods

2.1. Plant material

The plant materials used in this study were 11 local red rice of Yogyakarta AIAT collection, Indonesia (Table 1). All materials used were planted in plastic pots in a greenhouse using a completely randomized design with three replications. Plant maintenance included watering, fertilizing and pest control were applied if needed.

Table 1. Red rice cultivar of Yogyakarta AIAT collection.

Red rice cultivars	Origin
Merah Pepen	Sleman, Yogyakarta
Sembada Merah	Sleman, Yogyakarta
Saodah Merah	Bantul, Yogyakarta
Mandel	Gunungkidul, Yogyakarta
Cempo Kenanga	Gunungkidul, Yogyakarta
Segreng	Gunungkidul, Yogyakarta
Cempo Jalen	Gunungkidul, Yogyakarta
Mayangan Gundil	Gunungkidul, Yogyakarta
Tangkulan	Gunungkidul, Yogyakarta
Gogo Lembayung	Gunungkidul, Yogyakarta
Andel Merah	Bantul, Yogyakarta

2.2. Observation

A number of morfo-agronomical characters were observed. The parameters included plant height, leaf length, leaf width, number of productive tillers, panicle length, 1,000-grain weight and number of grain per panicle.

2.3. Analysis

Quantitative morphological characters (plant height, leaf length, leaf width, number of productive tillers, panicle length, 1,000-grain weight and number of grain per panicle) were analyzed of variance using completely randomized design (CRD) estimation of genetic variation (Table 2) according to Singh and Chaudhary [9].

Based on results of the analysis the variants, further analysis to determine the genetic diversity shown by the coefficient of genetic diversity (CGD) value was done and calculated according to the Singh and Chaudhary [9] formula.

$$\sigma^2_g = \frac{MSg - MSe}{r}$$

$$CVg = \frac{(\sqrt{\sigma^2_g})}{\bar{X}} \times 100\%$$

According to Moedjiono and Mejaya [10], the CGD that has been obtained can be classified into four criteria, i.e. low diversity (0–25% of the highest CVg), medium diversity (25–50% of highest CVg), high diversity (50–75% of the highest CVg) and very high/very wide (>75% of the highest CVg). Furthermore, the estimated genetic variance of the mean square value of variance analysis follows the Moedjiono and Mejaya [10] formula, which are further used to calculate the value of broad-sense of heritability:

$$H^2 = \frac{\sigma^2_g}{\sigma^2_g + \sigma^2_e / r}$$

σ^2_g = genetic diversity, σ^2_e = EMSe, MSe = mean square of error, r = sum of block.

According to Mc Whirter [11], broad-sense of heritability estimates divided into three categories, low: $H^2 < 0.20$, medium: $0.20 < H^2 < 0.50$ and high: $H^2 > 0.50$.

Table 2. Analysis of varian of completely randomized design.

Source	Degree of freedom (Df)	Sum of square (SS)	Mean square (MS)	Expected mean square (EMS)
Genotipe/g	g-1	SSg	MSg	$\sigma^2_e + r\sigma^2_g$
Error/e	g(r-1)	SS s	MSe	σ^2_e
Correction total	rg-1			

SSg = sum square of genotype, MSe = mean square of error, σ^2_e = EMSe, σ^2_g = genetic diversity, g = genotype, r = sum of block.

3. Results and discussion

Phylogenic tree resulted from the clustering of eleven red rice local from Yogyakarta (dendrogram was not shown) showed that there was no duplication between cultivars. Moreover, other characters, such as anatomy, biochemical content, mineral Fe, Zn and other important components need to be observed. There was a correlation between morphological or phenotypic properties and certain biochemical compounds. As reported by Yawadio et al. [13], that pigmented rice has the potential as a source of antioxidants and feasible as a useful food source. Characterization based on morphological markers was usually influenced by macro and microenvironments, and plant life. Therefore, morphological characterization needs to be supported by characterization using molecular markers. According to Dwiatmini et al. [14], molecular markers can give a more accurate picture of the phylogenic tree, because DNA analysis as genetic material is not affected by environmental conditions.

3.1. Genetic variation

Analysis of variance of the coefficient of variation genetic (CVg) of 11 local red rice cultivars was presented in Table 3. The number of productive tillers has the highest value of CVg of 41.83%. According to Moedjiono et al. [10], very high and high CVg values mean of wide or high genetic variability, while those with relatively moderate and low CVg criteria were classified as narrow genetic variability. The number of productive tillers, leaf length and the number of grain content per panicle revealed wide genetic diversity. While characters of leaf width, plant height, panicle length, and 1,000-grain weight have a narrow genetic diversity. A trait that has a very high and high genetic variation value indicates that improvement through selection was possible on this trait.

Table 3. Genetic variation of some morphological properties.

Character	\bar{x}	σ_g^2	CVg (%)	Relative value	Criteria of diversity
Leaf width	12.82	5.11	17.63	42.15 (M)	Narrow
Leaf length	49.12	147.84	24.75	59.17 (H)	Broad
Number of productive tillers	15.26	40.74	41.83	100.00 (VH)	-
Plant height	129.14	505.41	17.41	41.62 (M)	Narrow
Panicle length	22.75	12.94	15.81	37.80 (M)	Narrow
1,000-grain weight	24.26	3.15	7.32	17.50 (L)	Narrow
Number of grain per panicle	137.12	2042.07	32.96	78.80 (VH)	Broad

CVg = coefficient of variation genetic, σ_g^2 = genetic diversity, \bar{x} = average, VH = very high/very broad, H = high/broad, M = medium, L = low.

3.2. Estimating heritability of results and results components

The value of heritability of 11 red rice cultivars was presented in Table 4. Results showed that the value was classified as high, suggesting that the character can be inherited to the next offspring [14]. Selection is an important stage on plant breeding, particularly on characters that contribute to crop adaptation. It will be more effective when the characters have genetic information on estimated heritability, as well as number and type of gene that control the particular traits [15]. Heritability was the most important of a genetic parameter. The heritability probability indicates whether a character was controlled by genetic or environmental factors [14].

Table 4. Heritability of 11 red rice cultivars.

Character	σ_g^2	σ_e^2	R	H ²	Criteria
Leaf width	5.11	0.30	3	0.98	High
Leaf length	147.84	3.77	3	0.99	High
Number of productive tillers	40.74	1.49	3	0.99	High
Culm height	505.41	10.42	3	0.99	High
Panicle length	12.94	3.40	3	0.92	High
1,000-grain weight	3.15	1.67	3	0.85	High
Number of grain per panicle	2,042.07	8.61	3	1.00	High

σ_g^2 = genetic diversity, σ_e^2 = error mean square, R = replication, H² = heritability.

Characters with high heritability values can represent that the effect of genetic factors is more significant on phenotypic appearance than on environmental influences [16]. This was consistent with Welsh [17], which reports that the overall variation in a population was the result of a combination of

genotype and environmental influences. The heritability value 0 to 1. The value 0 was when all the variations are caused by environmental factors, while the value of 1 when all variations are caused by the genetic factors of the crop varieties. Estimation of heritability value was used as a first step of the selection proses of a segregated population. Consequently, such character can be selected in the early generation and the possibility for further selection addressing on the desired genetic progress.

Concerning to the value of coefficients of genetic diversity, a selection will be efficient and effective when performed on characters with broad genetic diversity coefficient values and high heritability values [18]. Overall, characterization of plant height, stem height, leaf length, number of productive tillers and number of grain per panicle in the local red rice Yogyakarta, Indonesia was an efficient and effective way in selection because the characters have wide of the coefficient of variation genetics and high heritability.

4. Conclusions

The number of productive tillers, leaf length and the number of grain content per panicle on the local red rice Yogyakarta, Indonesia had wide of coefficient of variation genetics and high heritability. Such morphological paramaters in this study was an efficient and effective character included in the selection activity on red rice genetic resources management.

5. References

- [1] Suardi K 2005 The potential of brown rice to improve food quality *J. Agric. Res. Dev.* **24** 93–100
- [2] Indrasari S 2006 Rice of Aek Sibundong: functional food *News Agric. Res. Dev.* **28** 1–3
- [3] Sudarmaji, Widyayanti S, Iswadi A, Sutaryo B, Sutardi, Wiranti E W, Hendrata R, Hatmi R U and Sutarno 2014 *Final Report on the Management of Specific Genetic Resources Location of Yogyakarta in 2014* (Yogyakarta)
- [4] Marzuki I, Uluputty M, Sandra A and Memen S 2008 Memen, S *Karakterisasi Morfoekotipe dan Proksimat Pala Banda (Myristica fragrans Houtt)* **36** 145–51
- [5] Sofro A S 1994 *Genetic Diversity* (Yogyakarta: Andi Offset)
- [6] Sungkono, Trikoesoemaningtyas, Wirnas D, Soepandi D, Human S and Yudiarto M 2009 Estimation of genetic parameters and selection of sorghum mutant strains (*Sorghum bicolor* [L.] Moench) in acidic soils *J. Agron. Indones.* **37** 220–5
- [7] Hakim L 2010 Genetic diversity, heritability, and correlation of several agronomic characters on the F₂ strain resulting from crossing of mung beans (*Vigna radiata* [L.] Wilczek) *Biol. News* **10** 23–32
- [8] Suprpto and Kairudin N M 2007 Genetic variations, heritability, genetic action, and genetic advance of soybean (*Glycine max* [L.] Merrill.) on ultisol *J. Indones. Agric. Sci.* **9** 183–90
- [9] Singh and Chaudhary B 1979 *Biometrical Method in Quantitative Genetics Analysis* (New Delhi: Kalyani Publishing)
- [10] Moedjiono and Mejaya M 1994 Genetic variability of several characters of germplasm of corn collection of Malang food research center *Zuriat* **5** 27–32
- [11] Martono B 2004 Genetic diversity and heritability of yam bean characters (*Pchyrhizus erosus* [L.] Urban) *Res. Inst. Spice Plants Var. Ind. Plants*
- [12] Yawadio R, Sanimori S and Morita N 2007 Identification of phenolic compounds isolated from pigmented rices and their aldose reductase inhibitory activities *Food Chem* **101** 1616–25
- [13] Dwiatmini K, Mattjik N, Aswidinnoor H and Toruan-Matius N 2003 Clustering and kinship relations analysis of *Phalaenopsis* orchid species based on determination key and RAPD molecular marker *Hortycultura J.* **XIII** 16–27
- [14] Lestari A, Dewi W, Qosim W, Rahardja M, Rostini N and Setiamihardja R 2006 Genetic variability and heritability of yield component and results of fifteen red chili genotypes *Zuriat* **17** 94–102
- [15] Roy D 2000 *Plant Breeding. Analysis and Exploitation of Variation* (New Delhi: Narosa

Publishing House)

- [16] Falconer D and Mackay T 1996 *Introduction to Quantitative Genetics* (Longman)
- [17] Welsh J 2005 *Fundamentals of Plant Genetics and Breeding* (New York: John Wiley and Sons)
- [18] Yunianti R, Sastrosumarjo S, Sujiprihati S, Surahman, M and Hidayat S 2010 Selection criteria for the assembly of chili-resistant varieties of *Phytophthora capsici* Leonian *J. Agron. Indones.* **38** 122–9