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Genetic Parameter Contributing to Lodging Resistance of F₂ Population in Red Rice

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Abstract. The effectiveness and successful of selection depend on the value of genetic variability, heritability and genetic advance estimation. The purpose of this research is to measure the value of genetic parameters (variability, heritability and genetic advance) of F₂ lines derived from crossing of mutant red rice, local accession of red rice, and commercial upland rice varieties. This research used single plant design. The rice materials used in this research was the F₂ seeds derived from hybridization between MR1512 X Inpago 8, MR1512 X Banyuasin, Inpago 8 X Balok, Balok X Banyuasin and Balok X Inpago 8. Selection intensity used is 10%. The filled grains and grain weight have a wide phenotypic variability, whereas the plant height and the productive tiller numbers have wide genotypic variability. The high heritability value was found in the plant height, flowering time, and harvest time. The high genetic advance was found in plant height, productive tillers number, flowering time, and harvest time. In the present work, it has been shown that the plant height, productive tiller numbers, flowering time, and harvest time are the important traits for use in rice lodging tolerance breeding program.

1. Introduction

Local upland rice is one of important ecotypes of rice beside lowland rice because the upland rice contains the essential genetic resources for plant breeding program such as water saving, drought tolerance, and quality of grain. However, the local upland rice also has some weaknesses including low productivity and lack of lodging resistance [1]. Therefore, plant breeding program to mend this weakness is necessary. One of the varieties is red rice which has good quality of grain and high demand. However, the constraint to increase the production of this variety is the high level of lodging. The decrease of rice yield due to lodging is up to 50% according to several research [2-3]. One of the solutions is introgression of lodging resistance into such variety through hybridization.

Hybridization is one of the methods to extend genetic diversity, and combine desirable characters from the parents to obtain new populations and produce the new superior variety [4]. The value of variability and heritability are the important components to measure before determining the method and time to perform the further selection. The effectiveness and success of the selection depend of the value of genetic variability, heritability and genetic advance estimation [5]. The wide variability, high heritability, and high genetic advance in population will support the successful of selection [6].

The important parameter traits must be measured in relation to the purpose of the hybridization and characters associated with the major traits in breeding program. Recent progress in rice breeding, the genotypes that exhibit precocity, less dense panicles, low sterility and greater 100-grain weight should be prioritized for drought tolerance [7], meanwhile leaf area index and Na-Ca selectivity could be used as selection criterion for salt tolerance [8]. Analysis of genetic parameters is performed on the traits that affect lodging resistance and yield potency. Plant height, stem length, and stem diameter are the most correlated traits with lodging resistance [9-11]. In other study, plant height and bending



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moment were positively correlated with lodging tolerance index [12]. The identified characteristics can be used in the process of selecting resistant red rice lines.

This research aims to determine the value of variability, heritability and genetic advance of F₂ red rice lines. The F₂ lines used in this study were derived from crosses among the commercial rice varieties (Inpago 8 and Banyuasin (upland rice)), mutant red rice, and Bangka local red rice. Inpago 8 and Banyuasin have been chosen as donor for lodging resistant trait [13]. The mutant red rice (MR1512) was chosen because this rice have a high yield and early maturity in ultisol soil [14]. Balok variety is Bangka local red rice with high yielding which does not have lodging resistance.

4.6 Materials and Methods

This research was conducted in the Experimental and Research Garden, at University of Bangka Belitung. The materials used in this study are F₂ rice seeds from the hybrid between the varieties of MR1512 X Inpago 8, MR1512 X Banyuasin, Inpago 8 X Balok, Inpago 8 X Banyuasin, Inpago 8 X MR1512, Balok X Banyuasin, Balok X Inpago 8, Banyuasin X Balok, Banyuasin X MR1512, Banyuasin X Inpago 8, and the parental varieties i.e. Banyuasin, Inpago 8, MR1512, and Balok as check.

The method used was single plant design without replication. Each genotype consists of 90 rice seeds. The parameters observed are plant height, productive tillers numbers, flowering time, harvest time, filled grains, and grain weight. Plant height was measured from the plant base to the tip of the highest panicle. Productive tiller numbers were determined at 30 days after flowering for each plants. Flowering time was determined at 80% of the plants are heading. Harvest time was determined on which 80% of the grains on the panicles are fully ripened. Filled grains were separated from unfilled grains and measured with a seed counter meter. Grain weight was determined from filled grains in each plant.

The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were calculated following the procedures suggested by [15], thus

$$\%PCV = \left[(\sigma_p^2)^{1/2} (\bar{x})^{-1} \right] \times 100\% \text{ where } \sigma_p^2 = \frac{1}{N} \left[\sum_{i=1}^N (xi - \mu)^2 \right] \quad (1)$$

$$\%GCV = \left[(\sigma_g^2)^{1/2} (\bar{x})^{-1} \right] \times 100\% \text{ where } \sigma_g^2 = \sigma_p^2 - \sigma_e^2 \text{ and } \sigma_e^2 = \frac{1}{n} (\sigma_{P1}^2 + \sigma_{P2}^2 + \dots + \sigma_{Pn}^2) \quad (2)$$

where, \bar{x} = grand mean of the character, xi = value of plant-i, μ = mean of population, N = total of plant observed, σ^2 = variance, σ_p^2 = phenotypic variance, σ_g^2 = genotypic variance, σ_e^2 = environmental variance, Pn= check plant-n, n = total of check plant.

The analysis of the heritability (board sense) following the procedures suggested by [16], and expected genetic advance by [17].

$$\text{Broad Sense Heritability (H)} = (\sigma_g^2) (\sigma_p^2)^{-1} \quad (3)$$

Where, σ_p^2 = phenotypic variance, σ_g^2 = genotypic variance

The criteria of heritability value are [18] :

0 ≤ H < 0.20, Low; 0.20 ≤ H ≤ 0.50, Moderate; 0.50 < H ≤ 1.00, High

$$\text{Expected Genetic Advance (EGA)} = \frac{GA}{\mu} \times 100\% \text{ where } GA = i \cdot H \cdot \sigma_p \quad (4)$$

Where, GA = genetic advance, i = selection intensity (the value is 1.76 at 10%), H = broad sense heritability, σ_p = phenotypic standard deviation, μ = mean of population.

The criteria of EGA value are :

| | |
|-----------------------|--------------|
| $0 < EGA < 3.3\%$ | = low |
| $3.3\% < EGA < 6.6\%$ | = quite low |
| $6.6\% < EGA < 10\%$ | = quite high |
| $EGA > 10\%$ | = high |

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3. Results and Discussion

According to the results of the phenotypic and genetic variability parameters, the coefficient variation was range from 5.9 to 91.6% for PCV and from 0 to 26.4% for GCV as displayed in Table 1. The phenotypic and genetic coefficient of variation (PCV and GCV) were the basis of variability criteria. Based on the relative coefficient of variation, variability criteria were divided into four criterion [19]. The criterion of phenotypic variability is 0.0-23.0% (narrow), 23.0-46.0% (quite narrow), 46.0-69.0% (quite wide), and 69.0-92.0% (wide). The criterion of genotypic variability is 0.0-6.75% (narrow), 6.75-13.5% (quite narrow), 13.5-20.25% (quite wide), and 20.25-27.0% (wide). According to this value, the phenotypic variability for the flowering and harvest time is narrow, plant height is quite narrow, the productive tiller numbers is quite wide, and the filled grains as well as rain weight have a wide phenotypic variability. The genotypic variability for the filled grains and harvest time is narrow, flowering time and grain weight is quite narrow, plant height and productive tillers number have a wide genotypic variability.

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Table 1. Estimates of mean, phenotypic and genetic variability parameters.

| Parameters | \bar{x} | σ_p^2 | σ_g^2 | PCV (%) | Criteria | GCV (%) | Criteria |
|---------------------------|-----------|--------------|--------------|---------|--------------|---------|--------------|
| Plant height | 108.37 | 1188.25 | 647.27 | 31.81 | Quite narrow | 23.48 | Wide |
| Productive tiller numbers | 10.84 | 41.74 | 8.17 | 59.58 | Quite wide | 26.36 | Wide |
| Flowering time | 82.96 | 167.67 | 86.11 | 15.61 | Narrow | 11.18 | Quite narrow |
| Harvest time | 105.34 | 38.12 | 37.49 | 5.861 | Narrow | 5.81 | Narrow |
| Filled grains | 417.17 | 137437.02 | 10674.51 | 88.87 | Wide | 0 | Narrow |
| Grain weight | 11.19 | 23.14 | 1.62 | 91.63 | Wide | 11.36 | Quite narrow |

\bar{x} = grand mean of population, σ_p^2 = phenotypic variance, σ_g^2 = genotypic variance, PCV = phenotypic coefficient of variation, GCV = genotypic coefficient of variation

The broad variation in genotypic and phenotypic variability was probably caused by the F_2 population which has the highest level of segregation. Plant height and productive tiller numbers could be used as parameters selection rather than the other parameters with quite narrow and narrow genetic variability. The wide variability indicated that the selection on the parameters could be performed and would be effective [20]. Narrow genetic variability indicated that the individuals were in a relatively homogenous population so that the selection which is based on the character will be less effective [21].

According to the results of the heritability (broad sense) parameters, the heritability value was range from -0.1 to 0.98 as could be seen in Table 2. The negative heritability value was considered as 0 [22]. Based on this value, the heritability criteria for the filled grains and grain weight is low, the productive tillers numbers has a moderate heritability, and the plant height, flowering time, and harvest time has a high heritability.

In the current results, the plant height, productive tiller numbers, flowering time, and harvest time were the important traits in lodging traits selection and could be used in early selection rather than low. The selection of properties with high heritability values can be performed in the early generation, meanwhile if the heritability value is low, the selection can be performed in the final stage of selection program [23]. According to [24], heritability determines the progress of selection, the greater the heritability value, the greater the progress of selection, on the contrary, the lower the heritability value

makes the progress of selection slower. High heritability value means that the selection can be applied efficiently due to less effect of environment [25]. In contrast to the high heritability, the parameters with low heritability values indicates that it will be less effective as the next selection criteria [16]. This is due to the possibility of the characters change when planted in different environments, because the influence of environmental factors is quite large on the characters.

Table 2. Estimates of heritability parameters

| Parameters | Broad Sense Heritability (H) | Criteria |
|--------------------------|------------------------------|----------|
| Plant height | 0.54 | High |
| Productive tiller number | 0.2 | Moderate |
| Flowering time | 0.51 | High |
| Harvest time | 0.98 | High |
| Filled grains | -0.1 | Low |
| Grain weight | 0.02 | Low |

Criteria: Low = $0 \leq H < 0.20$, Moderate = $0.20 \leq H \leq 0.50$, High = $0.50 < H \leq 1.00$

Besides using wide variability and high heritability values, the high genetic advance should also be considered in selecting a population. The results of expected genetic advance (EGA) calculation in Table 3, showed that the EGA value was range from 0 to 30.5%. The parameters which have a high EGA were plant height, productive tillers number, flowering time, and harvest time. The plant height has the highest EGA value which is 30.5%. The parameters which has a low EGA were the filled grains and grain weight.

However, in the present study, the productive tiller number showed moderate heritability and high EGA. It may occur because the value of genetic advance was calculated using the value of phenotypic standard deviation [26]. Productive tillers number parameters can be either applied or not for the next selection, because even though the genetic advance is high, the heritability is moderate and poor for selection [27]. The characters with high genetic advance value that are aligned with high heritability indicate that subsequent selection of these characters will be more effective. The selection will be active if the population has wide genetic diversity, high heritability, and high genetic progress [28]. High heritability value accompanied by expectations of genetic advance indicates the effect of the additive gene that controls the trait [29]. The low genetic advance value is not necessarily caused by low heritability but may also be influenced by non-additive genes. Low genetic advance can be caused by the control of traits from non-additive genes [30], because non-additive gene is a temporary and inherited gene.

Table 3. Estimates of expected genetic advance (EGA) parameters

| Parameters | Mean | GA | EGA (%) | Criteria |
|--------------------------|--------|-------|---------|----------|
| Plant height | 108.37 | 33.05 | 30.5 | High |
| Productive tiller number | 10.84 | 2.23 | 20.53 | High |
| Flowering time | 82.96 | 11.7 | 14.11 | High |
| Harvest time | 105.34 | 10.69 | 10.15 | High |
| Number of pithy grains | 417.17 | 0 | 0 | Low |
| Weight of pithy grains | 11.19 | 0.28 | 2.48 | Low |

Criteria : Low = $0 < EGA < 3.3\%$, quite low = $3.3\% < EGA < 6.6\%$, quite high = $6.6\% < EGA < 10\%$, High = $EGA > 10\%$

Table 4. The average of promising lines selected from plant height, productive tiller numbers, flowering time, and harvest time parameters.

| No | Lines | Plant Height (cm) | Productive tiller numbers | Flowering time (dap) | Harvest time (dap) |
|----|-----------------|-------------------|---------------------------|----------------------|--------------------|
| 1 | F2-I8xBl-21B-45 | 71.5 | 20 | 71 | 97 |
| 2 | F2-I8xBl-21B-34 | 72.2 | 21 | 71 | 97 |
| 3 | F2-I8xBl-21B-26 | 75.5 | 11 | 72 | 97 |
| 4 | F2-I8xBl-21B-38 | 76.5 | 24 | 60 | 97 |
| 5 | F2-I8xBl-21B-28 | 80.2 | 15 | 60 | 97 |
| 6 | F2-I8xBl-21B-56 | 81.4 | 18 | 60 | 97 |
| 7 | F2-BlxI8-23F-34 | 84 | 20 | 74 | 103 |
| 8 | F2-MxI8-19J-59 | 84.4 | 30 | 83 | 106 |
| 9 | F2-I8xBl-21B-24 | 85 | 14 | 70 | 97 |
| 10 | F2-I8xBl-21B-33 | 86 | 22 | 71 | 97 |
| 11 | F2-I8xBl-21B-52 | 86.7 | 18 | 60 | 97 |
| 12 | F2-I8xBl-21B-35 | 92.8 | 17 | 60 | 97 |
| 13 | F2-MxI8-23E-54 | 100.5 | 16 | 74 | 106 |
| 14 | F2-BlxI8-23D-26 | 102 | 17 | 79 | 110 |
| 15 | F2-BlxI8-23D-13 | 107 | 19 | 79 | 110 |
| 16 | F2-BlxI8-23D-24 | 107 | 15 | 81 | 110 |
| 17 | F2-BlxI8-23D-53 | 113 | 11 | 58 | 110 |
| 18 | F2-MxI8-23E-52 | 113.5 | 14 | 70 | 106 |
| 19 | F2-I8xBl-21C-47 | 114.5 | 27 | 77 | 108 |
| 20 | F2-BlxI8-23F-44 | 114.8 | 27 | 70 | 103 |
| 21 | F2-MxI8-9D-5 | 115.7 | 17 | 75 | 104 |
| 22 | F2-BlxBa-23A-54 | 117 | 17 | 65 | 106 |
| 23 | F2-BlxI8-23D-59 | 117.2 | 19 | 58 | 110 |
| 24 | F2-BlxI8-23F-40 | 117.5 | 16 | 76 | 103 |
| 25 | F2-MxI8-23E-46 | 118 | 16 | 76 | 106 |
| 26 | F2-MxI8-23E-51 | 121.2 | 15 | 77 | 106 |
| 27 | F2-MxBa-15C-48 | 123.5 | 19 | 77 | 115 |
| 28 | F2-BlxI8-23F-47 | 124 | 31 | 65 | 103 |
| 29 | F2-BlxI8-23D-36 | 126.2 | 26 | 58 | 110 |
| 30 | F2-BlxI8-23D-46 | 126.8 | 20 | 58 | 110 |
| 31 | F2-I8xBl-25A-28 | 128.2 | 15 | 74 | 104 |
| 32 | F2-BlxI8-23F-38 | 128.2 | 19 | 70 | 103 |
| 33 | F2-BlxI8-23D-38 | 128.8 | 18 | 58 | 110 |
| 34 | F2-MxBa-13T-53 | 129 | 17 | 64 | 114 |
| 35 | F2-MxI8-9D-34 | 133.3 | 16 | 83 | 103 |
| 36 | F2-MxBa-15C-25 | 133.7 | 21 | 81 | 113 |
| 37 | F2-BlxI8-23D-17 | 137 | 29 | 79 | 112 |
| 38 | F2-MxI8-11A-33 | 140 | 14 | 86 | 113 |
| 39 | F2-MxI8-9R-39 | 140.3 | 17 | 74 | 103 |
| 40 | F2-MxI8-21B-45 | 140.5 | 20 | 71 | 107 |

Based on genetic parameters value, the selection was performed with 10% selection intensity. Thus, 40 out of 392 lines were selected as promising lines (Table 4). The selection was conducted based on plant height as a primary selection criteria, followed by productive tillers number, flowering time, and harvest time parameter. Plant height used as primary selection because it has wide GCV, high heritability, and high genetic advance value. In addition, plant height was considered to be the main trait for improving lodging resistance [2] [31-34]. From the selection process, 40 promising lines were obtained, considering that it has a height <141 cm, with the best-supporting characters (productive tillers number, flowering time, and harvest time) by rank method. Mostly selected lines were the F₂ lines derived of a cross between Inpago 8 and Balok (I8xBI). The I8xBI lines mostly selected because the plant height is short (<100 cm) and have many productive tillers. Supposedly, this is derived from the female parent of Inpago 8 which has short height and many tillers. According to [35], plant height is negatively correlated to the productive tillers number. More short plants probably mean more number of productive tiller.

The value of the genetic parameters influenced by parental genotype and growing environment [36]. According to [37], there is the role of parents in the effort to inherit the superior traits to the offspring. The role of the parents in the hybridization will also affect the genetic of offspring in addition to the influence of other factors such as the environment. Occurrence of lodging is common after strong wind accompanied by heavy rains during the grain filling period [2].

About 60 dwarf genes (*d1-d60*) genes and 7 semi-dwarf genes (*sd1-sd7*) have been found [38]. In our previous research, through molecular marker assessment showed that Inpago 8 varieties has an *sd-1* gene that controls plant height [39]. However, the *semi-dwarf1* (*sd-1*), a recessive, semi-dwarfing gene, one of the most important genes used in rice lodging resistance breeding program [40]. The *sd-1* gene has been reported to reduce plant height by 25% through approximately proportional reductions in lengths of the top five internodes; with practically no effect on panicle length [41]. The dwarf phenotype of *sd-1* which resulted from a deficiency in gibberellin (GA) plant growth hormones [42]. The presence of this gene resulted in a shortened culm with high lodging resistance. The adoption of semi-dwarfing rice varieties has significantly increased grain yield potential of rice [4]. MONOCULM 1 (MOC1), a gene that is important in the control of rice tillering. MOC1 may act as a master regulator in the control of rice tillering [43]. The *sd-1* and MOC1 genes could make a significant contribution to improve the lodging resistance and high yielding in rice breeding program.

4. Conclusion

The purpose of this research was to measure the value of genetic parameters of F₂ red rice lines. The filled grains and grain weight have a wide phenotypic variability, while the plant height and the productive tiller numbers have wide genotypic variability. The high heritability value was found in the plant height, flowering time, and harvest time. The high genetic advance was found in plant height, productive tillers number, flowering time, and harvest time. In the current study, it shows that the plant height, productive tiller numbers, flowering time, and harvest time are the important traits for use in rice lodging tolerance breeding program. From the selection process, 40 promising lines were obtained based on the approach of genetic parameters analysis.

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