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Genetic parameters of F₆ upland rice with lodging resistance derived from landraces x national varieties

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Abstract. Developing rice varieties with lodging resistance is important to maintain yields. The selection of lodging resistance lines should be related to genetic parameters to determine the genetic character of plants. This study aimed to determine the variability, heritability, and genetic advances of 6th generation [F₆] upland rice “*padi gogo*” and selected the promising lines that can be used as candidates for new superior varieties. The research was held in Experiment and Research Garden, Universitas Bangka Belitung. The study used an experimental method with a randomized block design. The treatment consisted of 10 F₆ genotypes, 4 parental plants, and 3 check plants, with 2 replications. Quantitative data were analyzed by calculating the values of variability, heritability, and expected genetic advance. The results showed broad phenotypic variability and high heritability for all characters. The expected genetic advance showed low criterion except for the number of grain filled. The F₆ lines that can be used as candidates for new superior varieties are 23A-56-20-07-20 and 23A-56-22-20-05 lines that have better lodging resistance scores and higher production than parental and check varieties.

Keywords: genetic advance, heritability, lodging resistance, red rice, variability

1. Introduction

Rice is a major staple food and strategic commodities of Indonesian and other Asian countries. Rice production of Indonesia in 2018 amounted to 56.54 million tons [1]. Meanwhile, rice imports in 2017 amounted to 305.3 thousand tons and 2.2 million tons in 2018 [2]. Another effort that can be made is to develop local rice. Three varieties of local rice in Yogyakarta have good stability and adaptation in a less than optimal environment [3]. However, there are also some disadvantages in local rice, including long harvest age, low productivity, and lack of lodging resistance [4]. Bangka's local rice crop has an average plant height of more than 100 cm which is at risk of high levels of lodging [5].

Lodging of the paddy plants causes a decrease in production. The rice yield loss due to lodging is 0-30% [6], in several studies reported that the yield could decrease up to 50% [7-8]. The solution is to develop rice varieties that are resistant to lodging through hybridization between local rice and national superior varieties. One of the ways to develop the new varieties is hybridization, which combines superior characters from the parental to acquire new genotypes [9].

The lines of rice used was the F₆ line from crossing between mutant red rice M8-GR150-1-9-13 X Inpago 8, M8-GR150-1-9-13 X Banyuasin, Banyuasin X Balok, Balok X Inpago 8, and Inpago 8 X Balok. Banyuasin and Inpago 8 varieties have been used as a parental donor for lodging resistant traits [10]. M8-GR150-1-9-13 was chosen because this rice has early maturity character and high yielding [11]. Balok accession is Bangka landrace red rice with lodging resistance trait and high yielding [12].



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Rice crops from crosses need to be selected to get offspring with superior character. Genetic parameter analysis is carried out on the characteristics that affect yield potency and lodging resistance. The selection of characters is determined based on the value of variability, heritability, and expected genetic advances [13]. Therefore, this research needs to be done to measure the value of the genetic parameter of the F₆ generation to obtain a superior variety candidate.

2. Materials and Methods

The Materials used are F₆ rice seeds, Balok, M8-GR150-1-9-13, Inpago 8 variety, Banyuasin variety, and check varieties seeds [Inpago 12 Agritan, Danau Gaung, and Rindang 1 Agritan]. The research was carried out in the Experimental and Research Garden, Universitas Bangka Belitung. The design used was a Randomized Block Design [RBD]. The treatment consists of 17 lines with 2 repeats and a total of 34 experimental units.

The procedure includes land preparation, seed preparation, planting and harvesting, maintenance, harvesting, and post-harvest observation. The character observed are quantitative [grain weight/plot, filled grains, panicles numbers, leaf length, flowering time, plant height, tillers numbers], and qualitative [lodging index] [14]. Quantitative data were analyzed by calculating the values of variability, heritability, and expected genetic advance.

Formula calculation of variability [15];

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

$$\sigma^2e = \frac{MSe}{r}$$

$$\sigma^2f = \sigma^2g + \sigma^2e$$

where, σ^2g = genotypic variance; σ^2e = environmental variance; σ^2f = phenotypic variance

The standard calculation formula for genotypic and phenotypic errors;

$$\sigma_{\sigma^2g} = \sqrt{\frac{2}{r^2} \left\{ \frac{MSg^2}{Dbg+2} + \frac{MSe^2}{Dbe+2} \right\}}$$

$$\sigma_{\sigma^2f} = \sqrt{\frac{2}{r^2} \left\{ \frac{MSg^2}{Dbg+2} \right\}}$$

where, σ_{σ^2g} = Standard error genotypic variance; σ_{σ^2f} = Standard error phenotypic variance

The criteria of heritability value are:

Genotypic variability ;

$\sigma^2g \geq 2 [\sigma_{\sigma^2g}]$ = wide

$\sigma^2g < 2 [\sigma_{\sigma^2g}]$ = narrow

Phenotypic variability

$\sigma^2f \geq 2 [\sigma_{\sigma^2f}]$ = wide

$\sigma^2f < 2 [\sigma_{\sigma^2f}]$ = narrow

Calculation of heritability based on variance analysis [16];

$$H = \frac{\sigma^2g}{\sigma^2f}$$

where, H= Heritability; σ^2g = genotypic variance; σ^2f = phenotypic variance

The heritability criteria are [17] :

$H < 0.20$, Low; $0.20 \leq H \leq 0.50$, Moderate; $0.50 < H$, High

The calculation formula calculation for Expected Genetic Advance [18];

$$EGA = i \cdot H \cdot \sigma_p$$

$$\%EGA = \frac{EGA}{\bar{x}} \times 100\%$$

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

3. Result and Discussion

Genotypic variability of F_6 lines varied criteria while phenotypic variability includes broad criteria as displayed in Table 1. The criterion of heritability is high and the value of expected genetic advance is varied. Lines 23A-56-20-07-20 and 23A-56-22-20-05 can be used as candidates for superior varieties. The lodging index of red rice is a resistant criterion while the lodging index of Balok and M₈-GR₁₅₀-1-9-13 is quite sensitive criteria.

Table 1. Variability of F_6 lines

Quantitative character	σ^2g	$2[\sigma_{\sigma^2g}]$	Criteria	σ^2f	$2[\sigma_{\sigma^2f}]$	Criteria
Flowering time [dap]	24,37	21,24	Wide	24,90	21,24	Wide
Tillers numbers	160,08	148,19	Wide	173,26	147,76	Wide
Plant height [cm]	50,17	50,57	Narrow	58,69	50,05	Wide
Leaf length [cm]	81,72	81,74	Narrow	94,93	80,96	Wide
Panicles numbers	134,64	120,31	Wide	140,93	120,19	Wide
Grain weight/plot [kg]	2,71	3,17	Narrow	3,61	3,07	Wide
Filled grains	178274,12	164947,55	Wide	192866,87	164477,42	Wide

Description: Genotypic variability $\sigma^2g \geq 2[\sigma_{\sigma^2g}]$ = wide, $\sigma^2g < 2[\sigma_{\sigma^2g}]$ = narrow; Phenotypic variability $\sigma^2f \geq 2[\sigma_{\sigma^2f}]$ = wide, $\sigma^2f < 2[\sigma_{\sigma^2f}]$ = narrow; σ_{σ^2g} = Standard error genotypic variance, σ_{σ^2f} = Standard error phenotypic variance.

The character of flowering time, tillers numbers, panicles numbers, filled grains indicate the genotypic variability is wide criteria and phenotype variability shows wide criteria in all characters [Table 1]. The wider the genetic variety/ phenotypic, the higher the chance of lines with superior traits [19]. The selection could be performed and will be more effective for characters with wide variability [20], while it will be less effective for characters with narrow variability because the offspring are in a population that tends to be homogeneous [21].

The heritability of F_6 lines is included in the high criteria and Expected Genetic Advance has varied criteria [Table 2]. The highest heritability value is the height of plants at 97.87%. The high value of heritability indicates the presence of genetic influence on the character of plants [22] and the selection will be efficient because of fewer environmental effects [23]. The high value of EGA should also be

considered in selecting a population. The character of the filled grains indicates high EGA criteria. High genetic advances have the opportunity to improve the character's traits through selection [24]. The characters with high heritability that are associated with high genetic advance indicates that selection would be more effective [12].

Table 2. Heritability [%] and EGA [%] of F₆ lines

Quantitative character	Hbs [%]	Criteria	% EGA	Criteria
Flowering time [dap]	97,87	High	0,24	Low
Tillers numbers	92,39	High	4,70	Quite low
Plant height [cm]	85,49	High	0,44	Low
Leaf length [cm]	86,07	High	1,47	Low
Panicles numbers	95,53	High	5,03	Quite low
Grain weight/plot [kg]	75,32	High	0,39	Low
Filled grains	92,43	High	169,69	High

Description: Low = Hbs < 20 %; moderate = 20 % ≤ Hbs < 50 %; high = Hbs ≥ 50 %; Hbs = heritability of broad. EGA Criteria Low = 0 < EGA < 3.3%; quite low = 3.3% < EGA < 6.6%; quite high = 6.6 % < EGA < 10%; High = EGA > 10%.

The lodging index [%] of F₆ lines is varied criteria [Table 3]. All of the F₆ lines showed resistance to lodging [6.24-10.62 %] while the lodging index of Balok [66.09 %] and M₈-GR₁₅₀-1-9-13 [78.12 %] is quite sensitive. Plants that have above-average plant height cause lodging [26]. Lodging tolerance index was positively correlated with plant height and bending moment [27].

Table 3. Lodging Index [%] of F₆ lines

Lines	Lodging Index [%]	Description
23A-56-20-07-20	10,62	Resistant
23A-56-24-22-13	6,24	Resistant
23 A-56-13-25-13	6,24	Resistant
23A-56-22-20-05	7,18	Resistant
19I-06-30-17-11	7,18	Resistant
23F-04-10-18-18	7,38	Resistant
21B-57-21-21-23	9,52	Resistant
19I-06-09-23-3	7,49	Resistant
23A-56-30-25-12	7,65	Resistant
21B-57-21-21-25	7,81	Resistant
Inpago 8	10,78	Resistant
Banyuasin	11,24	Resistant
M ₈ -GR ₁₅₀ -1-9-13	78,12	Quite sensitive
Balok	66,09	Quite sensitive
Danau Gaung	22,34	Quite resistant
Inpago 12	10,77	Resistant
Rindang 1	11,87	Resistant

Description: Plants no crumbs [very resistant], plants <20% [resistant], plants 21-40% [quite resistant], plants 41-60% [moderate], plants 61-80% [quite sensitive] and plants crumbs >80% [sensitive].

Table 4. Quantitative character LSI Test

Lines	Flowering time [dap]	Tillers numbers	Plant height [cm]	Leaf length [cm]	Panicles numbers	Grain weight/plot [kg]	Filled grains
19I-06-30-17-11[axc]	79.7 ^c	16.4 ^c	86.3 ^{cefg}	40,1	11,8	3.8 ^c	457.6 ^c
23 A-56-13-25-13[bxd]	63.4 ^{bdefgh}	21.4 ^{de}	73.1 ^{defg}	37.1 ^b	16.5 ^{de}	3,5	538.6 ^b
19I-06-09-23-3[axc]	71.0 ^{acefgh}	18.7 ^{ce}	82.1 ^{acefg}	45.5 ^a	15.9 ^{ce}	4.9 ^c	785.5 ^{aces}
21B-57-21-21-23[axd]	77.9 ^{defgh}	17.1 ^e	96.6 ^{defg}	48.6 ^{ah}	13.3 ^c	5.6 ^a	550,2
23F-04-10-18-18[axd]	73.6 ^{adefgh}	24.1 ^{defg}	88.2 ^{defg}	33,1	16.3 ^{de}	5.6 ^a	549,9
21B-57-21-21-25[axd]	73.3 ^{adefgh}	17.9 ^e	86.8 ^{defg}	44.4 ^a	12.3 ^e	2,8	494.9 ^b
23A-56-30-25-12[bxd]	75.5 ^{bdfh}	17.1 ^b	88.9 ^{defg}	40.5 ^b	13.7 ^e	4.2 ^b	652.9 ^b
23A-56-20-07-20[bxd]	71.8 ^{bdefgh}	44.2 ^{bdefgh}	92.3 ^{defg}	36.5 ^b	35.5 ^{bdefgh}	6.3 ^b	1676.5 ^{bdefgh}
23A-56-24-22-13[bxd]	75.8 ^{bdfh}	24.1 ^{bdefg}	75.7 ^{defg}	34.1 ^b	17.8 ^{bde}	5.1 ^b	655.5 ^b
23A-56-22-20-05[bxd]	80.7 ^b	54.8 ^{bdefgh}	76.3 ^{defg}	30,1	47.7 ^{bdefgh}	9.5 ^{beh}	1522.8 ^{bdegh}
Inpago 8+LSI [a]	77,1	26,3	82,6	42,9	20,2	5,5	676,1
Banyuasin+LSI [b]	84,5	22,8	56,8	32,5	17,3	3,8	381,4
M ₈ -GR ₁₅₀ -1-9-13+LSI [c]	86,9	17,9	151,4	63,1	14,6	3,6	388,5
Balok +LSI [d]	78,6	19,6	141,2	62,5	15,5	9,9	1302
Danau gaung+LSI [e]	75,2	15,9	114,9	54,3	11,9	6,9	774,7
Inpago 12+LSI [f]	77,8	21,9	103,7	51,5	18,5	13,2	1594,4
Rindang 1+LSI [g]	74,6	21,6	103,6	54,6	18,0	11,5	1286,4
\bar{x}_g +LSI [h]	78,1	33,7	72,5	46,4	26,3	8,1	1003,5
LSI	3,9	8,2	12,1	7,5	6,1	2,9	315,1

Description: 1. \bar{x}_g = The average lines of offspring; 2. The lowercase behind the number indicates better than parent/check plant; 3. Character of flowering age and height of plants, lines is better if the value of \leq check value – LSI.

4. Conclusion

The wide phenotypic variability and high heritability were found for all characters observed. The high expected genetic advance was only found for filled grains characters. All of the F₆ lines showed resistance to lodging. Two genotypes i.e. 23A-56-20-07-20 and 23A-56-22-20-05, have better results for tiller numbers, panicle numbers, and filled grains than other genotypes and check varieties. From the selection process, 23A-56-20-07-20 and 23A-56-22-20-05 genotypes can be used as candidates for new superior varieties.

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