



SELECTION INDEX FOR SELECTING PROMISING DOUBLED HAPLOID LINES OF BLACK RICE

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SUMMARY

Black rice is useful as source of carbohydrate as well as to prevent some diseases. Breeding on this rice is not as common as that of white rice. The objective of this research was to obtain potential doubled haploid (DH) black rice lines that have good agronomic performance based on selection index. The research was conducted during November 2017 to April 2018 using a randomized complete block design with three replications. The planting materials consisting of 54 DH lines produced from anther culture and three cultivars as check cultivars, i.e., Aek Sibundong, Inpari 24 and Ciherang were used in this study. Selection index was developed based on broad-sense heritability of traits, followed by various statistical techniques, such as correlation analysis, path analysis, and principal component analysis (PCA). The results of this research indicated that panicle density (PD), weight of 1000 grains (GWE) and the number of filled grains (NFG) showed significant and positive correlation with grain yield (GY), while days to 50% flowering (FL), flag leaf length (FLL) and number of unfilled grain (NUG) showed significant but negative correlation with grain yield. Path analysis suggested GWE, NFG and FL contributed directly to GY. Besides grain yield, selection of the right model based on the best PC with highest eigen vector value of grain yield gave three traits, i.e., FL, GWE and NFG, that can be used as selection criteria and constructed selection index model. The constructed model of selection index (I) was $I = (3 * 0.39 \text{ GY}) + (-0.42 \text{ FL}) + (0.23 \text{ GWE}) + (0.44 \text{ NFG})$. Based on the positive index values, 28 black rice DH lines were selected to be used in further yield trials.

Key words: Doubled haploid, heritability, selection index, path coefficient analysis, principal component analysis, black rice (*Oryza sativa* L.)

Key findings: The present investigation indicated that besides grain yield, there were three other traits, i.e., days to 50% flowering, 1000 grains weight and

number of filled grain that could be used as supporting traits in constructing selection index model for selecting potential doubled haploid black rice lines. Using the selection index, 28 DH black rice lines with good agronomic traits were selected.

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INTRODUCTION

Black rice is special food material intended for good health with a different market segment from white rice, especially for people in Asia (Muthayya *et al.*, 2014). Black rice belongs to *Oryza sativa* L., the same species as white rice, but natural anthocyanin plant pigments give them five times more antioxidants and a cultivar of extra benefits, such as anti-cancer, anti-heart disease, anti-diabetes, and anti-allergy activities (Pratiwi and Purwestri, 2017; Raghuvanshi *et al.*, 2017; Shao *et al.*, 2018). Treated as functional food, black rice has higher selling price than white rice (Manikmas, 2010). In Indonesia, local cultivars of black rice is abundant but breeding of black rice is not conducted as frequently as white rice. Recently, the Indonesian Ministry of Agriculture released four pigmented rice cultivars, i.e., three red rice cultivars, namely Arumba, Pamelen and Pamera, and for the first time released one black rice cultivar namely Jeliteng (Padi, 2019). In previous research efforts first generation of pure lines regenerated as doubled haploid (DH1) black and red rice lines had been obtained through anther culture technique and evaluated in the green house (Mawaddah, 2017; Mawaddah *et al.*, 2018). Those black rice pure lines need to be evaluated and selected

further in the field to obtain lines having good agronomic performance and high productivity.

Yield is the most important and complex trait, directly and multiply determined by yield-component traits (Hairmansis and Kustianto, 2010; Falconer and Mackay, 1996). Although high-yielding genotypes can be directly selected based on their yield, direct selection is not much effective on it because crop yield is a quantitative trait and has a complex genetic control mechanism (Islam *et al.*, 2017). Therefore, selection of high-yielding genotypes may be more effective if it also involves the determination of traits contributing to or affecting the yield traits. According to Via *et al.* (2017) this type of selection will be more effective if the heritability of those traits, which determines whether the traits can be used as a selection criteria or not is known.

Selection index method which combines information on all the high heritability traits associated with yield in a linear regression model can be used in selection process. The selection based on such an index is more efficient than selecting individually for the various traits (Islam *et al.*, 2017). Selection index can be constructed based on several analysis, such as correlation analysis, path coefficient analysis and principal component analysis. Correlation and

path coefficient analysis simultaneously can effectively explain the correlation among traits and the influence of a trait directly and indirectly to the dependent trait (Samonte *et al.*, 2013). Whilst, principal component analysis is used for further selection of traits so that a set of linear combinations can be obtained which can represent a large part of the variance of the original data (Nayak *et al.*, 2018; Maji, 2012). The coefficient of the selected principal components can be standardized and used to develop selection index formula. The coefficients when combined with economic weights for trait values can make a new selection index formula that can be used to rank the lines' performance (Jolliffe, 2002; Sabouri *et al.*, 2008). The superiority of selection based on index increases with an increase in the number of traits under selection (Raghuwanshi *et al.*, 2016). The objective of the research was to obtain potential DH black rice lines with good agronomic performance based on selection index.

MATERIALS AND METHODS

Plant material

A total of 54 DH black rice lines produced by anther culture were used in this research. The lines were derived from crossing as followed: Leukat Itam × IR 85627-46-1-2-3 (6 lines), Malang × WI-44 (20 lines), Malang × IR 85627-46-1-2-3 (21 lines), Purworejo × WI-44 (6 lines), Purworejo × IR 85627-46-1-2-3 (1 line) (Mawaddah, 2017). Leukat Itam, Malang, and Purworejo are black local rice cultivars, while WI-44, and IR 85627-46-1-2-3 are high yielding elite

lines. Two red rice varieties, i.e., Aek Sibundong and Inpari 24, and one white rice cultivar, i.e., mega cultivar Ciherang, were used as check cultivars. The anther culture protocol followed the method of Dewi *et al.* (2004) and the lines were developed as reported by Mawaddah (2017) and Mawaddah *et al.* (2018).

Experimental design and data collection

The experiment was conducted in Bogor (6° 33'43" South Latitude and 106°44'5" East Longitude) during November 2017-April 2018. The experiment was conducted in a randomized complete block design (RCBD) with three replications. The single factor used was the 54 genotypes of DH black rice lines and three check cultivars.

Twenty one-day old seedlings were transplanted into an experimental unit of 0.54 m × 4.32 m plot, with plant spacing of 27 cm × 27 cm. Plots were fertilized with the doses of 90, 36, and 60 kg ha⁻¹ N, P₂O₅ and K₂O, respectively. Nitrogen was divided at three applications, i.e., 1/3 each at basal, maximum tillering, and panicle initiation stage, while the P₂O₅ and K₂O were applied as a basal application. Vegetative phase plant height (VPH), generative phase plant height (GPH), number of vegetative tiller (VT), number of productive tiller (NPT), days to 50% flowering (FL), flag leaf length (FLL), panicle length (PL), panicle density (PD), 1000 grains weight (GWE), number of filled grains per panicle (NFG), number of unfilled grains per panicle (NUG), total grain number per panicle (TGS), and grain yield (GY) were observed and measured.

Data analysis

Broad sense heritability ($h^2_{(BS)}$) estimate of each trait was computed according to the procedure outlined by Falconer and Mackay (1996) as:

$$h^2_{(BS)} = \frac{\sigma^2_g}{\sigma^2_p} \times 100\%$$

σ^2_g = genotypic variance,
 σ^2_p = phenotypic variance

According to Stansfield (1988) the heritability is classified as:

$$\begin{aligned} \text{Low} &= h^2_{(BS)} < 20\% \\ \text{Moderate} &= 20\% < h^2_{(BS)} \leq 50\% \\ \text{High} &= h^2_{(BS)} > 50\% \end{aligned}$$

The Pearson's correlation and principal component analysis, which was used to determine the relationship between traits and determine important traits, were carried out using the Statistical Tool for Agricultural Research (STAR) 2.0.1 from IRRI. Path coefficient analysis to determine the causal relationship between traits was carried out using the R Program Statistic Tool Version 3.0.3.

The selection index was determined according to Falconer and Mackay (1996) by the following formula:

$$I = A_1Z_1 + A_2Z_2 + A_3Z_3 + \dots + A_nZ_n$$

I = Selection Index

A_n = weight of the n^{th} variable

Z_n = the standardized phenotype value of Z

RESULTS AND DISCUSSION

Estimation of heritability in broad sense and correlation analysis between traits

Heritability is a good index of transmission of characters from parents to its progeny. The results of the analysis showed that all traits, except for generative plant height, have high heritability (Table 1). The DH lines used in this experiment do not have heterozygous loci as a result from doubling of haploid chromosomes spontaneously during in-vitro culture of anthers (Dewi and Purwoko, 2012; Purwoko, 2017). DH plants show high homozygosity for every locus in the genome for which they do not have dominance gene action to affect their traits (Seymour *et al.*, 2011), and that make all traits highly heritable. High heritability indicates that genetic factors contributed more to the traits than environmental factors (Nirmaladevi *et al.*, 2015; Mishra *et al.*, 2015). Traits having moderate to high heritability can be used efficiently as selection traits (Bahar and Zein, 1993). Therefore, based on their heritability, all traits can be used as selection criteria.

Selection criteria as a key trait in the selection process should be constructed from number of those traits which have high correlation values (Falconer and Mackay, 1996). Therefore, besides high heritability, we also need to determine the closeness of the relationship between the traits. Correlation analysis

Table 1. Mean basis variance analysis and estimation of broad sense heritability of agronomic traits 54 DH black rice lines.

Traits	σ^2g	σ^2p	$h^2_{(BS)}$ (%)	Criteria of heritability
Grain yield or productivity	0.65	0.75	87.03	high
Vegetative phase plant height	18.68	27.66	67.53	high
Generative phase plant height	44.30	93.23	47.52	moderate
Number of vegetative tillers	12.75	17.30	73.70	high
Number of productive tiller	8.53	12.93	65.92	high
Days to 50% flowering	63.19	67.45	93.69	high
Flag leaf length	19.04	23.06	82.58	high
Panicle length	6.81	11.74	58.07	high
Panicle density	0.21	0.32	65.00	high
1000 grains weight	7.33	8.04	91.18	high
Number of filled grain	907.20	956.50	94.85	high
Number of unfilled grain	629.83	666.61	94.48	high
Total grains per panicle	378.00	414.12	91.28	high

σ^2g = Genotypic variance; σ^2p = Phenotypic variance; $h^2_{(BS)}$ = Broad sense heritability

performed here is one of the statistical methods that can be used to study the closeness of relationships between independent traits and the dependent trait, i.e., yield. This closeness is illustrated by -1 to +1 (Gomez and Gomez, 1984; Agahi *et al.*, 2007; Akhtar *et al.*, 2011; Seyoum *et al.*, 2012).

The results of the Pearson's correlation analysis showed that the trait of the panicle density (0.44), 1000 grains weight (0.65) and the number of filled grains (0.75) had a high-positive correlation with the grain yield. Meanwhile, the trait of days to 50% flowering (-0.80), the flag leaf length (-0.51) and number unfilled grains (-0.73) showed high-negative correlation with the grain yield (Table 2). Positive and negative correlation coefficient only indicated the absolute position of the independent trait

towards dependent trait (Shabana *et al.*, 2015). Therefore, the results indicated that the increase in panicle density, weight of 1000 grains and the number of filled grain contributed to high grain yield, whilst the decrease in flag leaf length, days to 50% flowering, and number of unfilled grain also contributed to less droopy flag leaf and early maturing genotypes with high grain yield. This result is similar to the study of Faza'a *et al.* (2016) on doubled haploid rice lines derived from anther culture and of Agahi *et al.* (2007) on several high yielding rice genotypes from IRRI.

Selection criteria for determining good agronomic performance

The degree of correlation among yield contributing characters is an important factor, especially the characters

related to economic and complex characters such as yield. Although the correlation coefficient may provide mathematical information on the level of closeness between traits, it can not imply cause and effect relationships (Roy, 2000). To make the correlation coefficient meaningful, many researchers use the path coefficient analysis in order to get a clear and complete picture of the cause and effect relationship among different traits (Eshghi *et al.*, 2011; Akhtar *et al.*, 2011; Seyoum *et al.*, 2012; Sanghera and Kashyap, 2012). In selection, besides providing the path coefficient values of the traits, this path analysis also serves to prove the effect of several traits on dependent trait in the form of direct and indirect effect (Kumar *et al.*, 2017).

Based on the results of path coefficient analysis, traits that have highly significant Pearson's correlation coefficient also have direct effect on grain yield (Table 2, Figure 1). These traits were days to 50% flowering, flag leaf length, panicle density, weight of 1000 grains, number of filled grains and number of unfilled grains. All direct effects towards grain yield per plant were positive except for days to 50% flowering and number of unfilled grain. Therefore, not only relationship between traits and dependent trait must have high correlation values, but also the direct and indirect effect of the traits to the dependent trait need to be known to confirm that the trait can be used as a selection criteria (Falconer and Mackay, 1996; Jolliffe *et al.*, 2002; Rabiei *et al.*, 2004; Yuniarti *et al.*, 2010). The model gave the residual effect of 0.46, which indicated that the contribution of those component traits on grain yield was 54%. However, only several traits that have high path coefficient as well as

high direct effect on grain yield can be selected to be used as selection criteria (Seyoum *et al.*, 2012). Thus, based on path coefficient analysis only three traits, i.e., days to 50% flowering (-0.27), weight of 1000 grains (0.36) and number of filled grain (0.34) were chosen as selection criteria.

Development of selection index and selection of DH black rice lines

Selection Index is a quantity calculated using standardized coefficients, where appropriate weights are assigned to each trait based on their relative importance, heritability and genotypic and phenotypic correlation between different traits. The component traits are combined into a score or an index in such a way that selection is applied to the index, as if, the index was a single trait (Falconer and Mackay, 1996). Sabouri *et al.* (2008) stated that trait coefficients could be combined with weighting based on economic values so that the resulting selection index model was a combination of true breeding value and trait economic value.

In developing effective selection index, principal component analysis (PCA) can be used to compress data sets of high dimensional vectors into lower dimensional ones (Jolliffe, 2002). In this research, the results of the principal component analysis showed 4 PCs which have eigen values of more than 1 and cumulative proportion more than 80%. Previously, according to Mattjik *et al.* (2011) the PC with eigen values of more than 1 are representative models to be used as selection indices because the variance can be highly

Table 2. Pearson correlation analysis between traits in 54 DH black rice lines

Traits	GY	VPH	GPH	VT	NPT	FL	FLL	PL	PD	GWE	NFG	NUG	TGS
GY	1												
VPH	0.14	1											
GPH	-0.04	0.18	1										
VT	-0.18	-0.30	-0.23	1									
NPT	0.06	-0.09	-0.11	0.72**	1								
FL	-0.80**	-0.12	0.04	0.35**	-0.02	1							
FLL	-0.51**	0.45**	0.11	0.20	0.07	0.68**	1						
PL	-0.06	0.09	0.29	-0.51**	-0.48**	0.06	0.02	1					
PD	0.44**	0.22	0.05	-0.29	-0.27	-0.32	-0.11	-0.16	1				
GWE	0.65**	0.00	-0.28	0.19	0.35**	-0.53**	-0.41**	-0.36**	0.17	1			
NFG	0.75**	0.08	0.09	-0.57**	-0.32	-0.83**	-0.62**	0.25	0.52**	0.32	1		
NUG	-0.73**	0.14	0.14	0.18	-0.10	0.89**	0.77**	0.16	-0.11	-0.55**	-0.76**	1	
TGS	0.24	0.29	0.32	-0.66**	-0.62**	-0.15	0.02	0.58**	0.67**	-0.21	0.57**	0.10	1

** = highly significant at $P < 0.01$; GY = grain yield or productivity, VPH= vegetative phase plant height, GPH= generative phase plant height, VT = number of vegetative tiller, NPT = number of productive tiller, FL = days to 50% flowering, FLL= flag leaf length, PL= panicle length, PD = panicle density, GWE = 1000 grains weight, NFG = number of filled grain per panicle, NUG = number of unfilled grain per panicle, TGS = total grains per panicle.

Figure 1. Diagram of path coefficient analysis of traits that influence grain yield of DH black rice lines

Description: \leftarrow = direct effect; \leftarrow ----- = indirect effect; GY = grain yield; FL = days to 50% flowering; FLL= Flag leaf length, GWE = 1000 grains weight; NFG = number of filled grains; NUG = Number of unfilled grains.

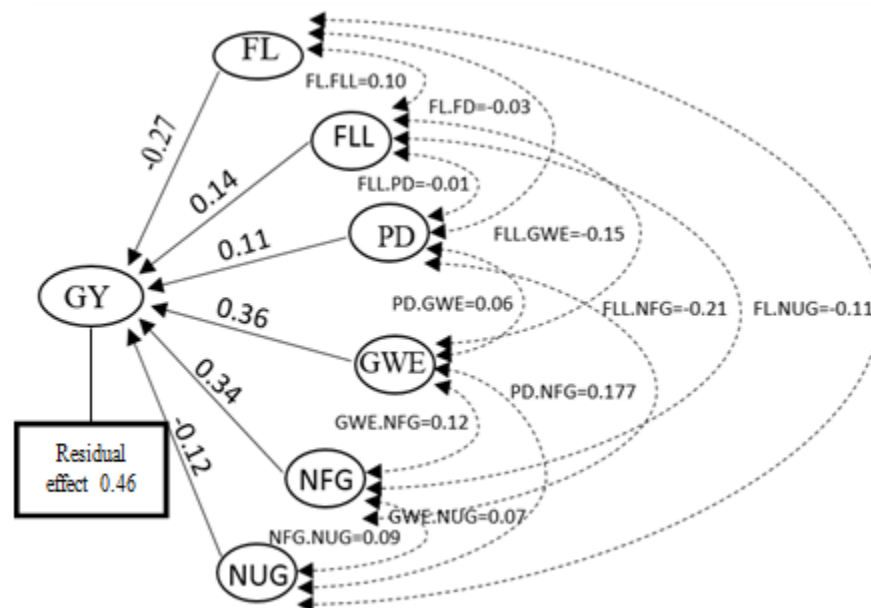


Table 3. Principal component analysis of agronomic traits of DH black rice lines.

Traits	PC1	PC2	PC3	PC4
Grain yield or productivity	0.39	-0.12	0.19	0.10
Vegetative phase plant height	0.04	0.20	0.59	0.35
Generative phase plant height	0.00	0.24	0.04	0.60
Number of vegetative tillers	-0.23	-0.38	0.12	-0.03
Number of productive tillers	-0.11	-0.41	0.21	0.32
Days to 50% flowering	-0.42	0.12	-0.02	-0.18
Flag leaf length	-0.33	0.17	0.42	0.08
Panicle length	0.04	0.38	-0.32	0.29
Panicle density	0.24	0.15	0.43	-0.49
1000 grains weight	0.23	-0.33	0.22	0.00
Number of filled grains	0.44	0.09	-0.05	0.02
Number of unfilled grains	-0.38	0.23	0.16	-0.15
Total grains per panicle	0.20	0.44	0.13	-0.17
Standard deviation	2.17	1.84	1.23	1.01
Proportion of variance	36%	26%	12%	8%
Cumulative proportion	36%	62%	74%	82%
Eigen values	4.69	3.40	1.50	1.03

explained. Furthermore, Kumar *et al.* (2016) and Anyaoha *et al.* (2018) stated that the selection of the right model also should be based on the high PC eigen vector value of the dependent trait. Therefore, the model with the highest PC eigen vector value of grain yield will be the true model to be used as a selection index, because in this research the dependent trait is grain yield or productivity.

The PC 1 is the true model to be used as a determinant of selection index because the trait of grain yield gives the highest PC coefficient or eigen vector value (Table 3). High PC eigen vector value on the grain yield (GY) trait will maximize the selection towards high productivity lines. PC1 also showed high eigen vector values on days to 50% flowering (FL) and the number of filled grain (NFG). The negative coefficient on FL indicates absolute position of trait variance towards grain yield. Therefore, negative coefficient on FL and the high eigen vector value on the NFG, will maximize the selection of good

agronomic performance lines that are early maturing and have large number of filled grains. Trait of a 1000-grains weight can also be added and used in selection index formulation by considering the high correlation value (0.65) and its direct effect on the grain yield trait as shown by Pearson’s correlation analysis (Table 2) and path analysis (Figure 1). The results of principal component analysis also indicated that each selected traits has a large PC coefficient that can be used in a model (Table 3). Before establishing the selection index model, the production traits were given a weight of 3 to maximize the model as suggested by Sabouri *et al.* (2008). Based on this state, the model of selection index (I) was formulated as follow:

$$I = (3*0.39 \text{ GY}) + (-0.42 \text{ FL}) + (0.23 \text{ GWE}) + (0.44 \text{ NFG}).$$

The selection using the standardized selection index showed that by considering the positive value

Table 4. Ranks of DH black rice lines based on selection index.

Rank	Genotypes	Agronomic Traits*				I **
		GY (ton ha ⁻¹)	FL (DAS)	GWE (g)	NFG (grain/panicle)	
1.	MW2-7-1-2	3.77	58.0	26.9	165.6	7.88
2.	MW2-7-1-1	3.14	60.0	27.4	129.7	5.24
3.	MW5-19-1-2	3.14	61.7	23.5	121.9	4.95
4.	MW2-7-1-3	2.32	60.3	25.6	136.5	3.73
5.	Ciherang	2.80	70.0	28.7	92.3	3.18
6.	Inpari 24	2.59	67.0	26.3	101.7	3.06
7.	MW3-58-1-1	2.95	69.0	26.1	75.7	2.92
8.	MW3-32-2-4	2.91	70.0	26.0	65.1	2.45
9.	MW3-19-1-2	2.82	69.3	27.0	68.1	2.36
10.	MW4-2-1-1	2.35	67.7	24.4	94.9	2.30
11.	MW4-11-1-3	2.62	71.7	27.4	67.3	1.91
12.	Aek Sibundong	2.29	70.0	29.9	85.5	1.85
13.	MW3-58-1-2	2.64	69.7	27.2	64.5	1.84
14.	MW4-2-2-1	1.70	66.7	24.3	114.0	1.58
15.	MW4-11-2-3	2.47	71.0	26.2	63.2	1.44
16.	MW4-62-2-1	2.40	70.7	27.9	63.4	1.30
17.	MW4-40-1-5	2.17	57.0	26.1	76.5	1.27
18.	MW3-24-1-1	2.25	70.0	28.2	69.5	1.18
19.	MW3-58-2-5	2.16	68.7	28.0	73.3	1.14
20.	MW3-58-1-3	2.21	69.0	28.5	68.7	1.09
21.	MW3-12-1-2	2.25	70.7	27.8	65.3	1.05
22.	MW3-9-2-1	2.28	77.7	21.4	62.3	0.97
23.	MW3-58-2-1	2.28	70.0	27.4	58.7	0.87
24.	MW4-19-1-1	2.15	72.0	28.3	59.3	0.61
25.	MW4-17-1-1	2.11	72.7	26.1	61.6	0.60
26.	MW3-24-2-5	2.27	72.0	26.2	49.3	0.52
27.	MW4-53-1-1	2.13	72.7	26.6	51.2	0.29
28.	MW3-24-1-4	2.09	71.3	25.8	50.6	0.17
29.	MW4-11-2-2	2.05	71.0	27.9	51.2	0.12
30.	MW4-11-2-1	1.88	71.3	28.9	59.9	0.06
31.	MW6-8-1-1	1.57	68.3	21.1	77.9	0.01
32.	MW3-24-1-2	1.95	71.0	27.3	53.8	-0.01
33.	MW3-24-1-3	1.84	71.0	27.5	60.2	-0.02
34.	MW5-5-1-3	1.53	57.0	24.7	78.1	-0.04
35.	MW3-13-1-3	1.95	77.0	27.1	50.7	-0.14
36.	MW4-2-1-2	1.41	75.0	21.5	79.0	-0.30
37.	MW4-11-1-1	1.79	71.7	27.4	53.9	-0.35
38.	MW3-13-1-2	1.76	76.0	26.3	51.0	-0.54
39.	MW3-13-1-1	1.83	74.7	26.7	43.8	-0.62
40.	MW3-24-2-6	1.69	72.3	27.3	48.4	-0.76
41.	MW3-13-1-4	1.62	74.7	27.4	46.3	-1.00
42.	MW4-53-1-2	1.69	74.0	26.5	39.3	-1.09
43.	MW5-72-1-1	1.28	73.7	23.9	62.6	-1.15
44.	MW4-62-2-2	1.52	73.0	28.7	45.8	-1.23
45.	MW4-11-2-5	1.40	71.7	27.4	51.6	-1.27

*GY = grain yield, FL = days to 50% flowering, GWE = 1000 grains weight, NFG = number of filled grain per panicle; DAS= days after sowing; ** I = standardized selection index.

Table 4. (cont'd).

Rank	Genotypes	Agronomic Traits*				I **
		GY (ton ha ⁻¹)	FL (DAS)	GWE (g)	NFG (grain/panicle)	
46.	MW5-6-1-2	0.87	75.7	22.1	69.7	-1.78
47.	MW2-2-1-1	1.29	87.3	20.7	36.0	-2.09
48.	MW3-9-3-1	1.22	81.0	23.8	36.1	-2.22
49.	MW5-5-2-1	0.89	76.7	22.2	52.8	-2.35
50.	MW5-6-1-1	0.62	74.3	22.8	63.4	-2.55
51.	MW2-2-2-2	0.32	88.7	19.0	28.2	-4.47
52.	MW4-46-1-1	0.06	91.0	19.8	18.4	-5.37
53.	MW2-2-2-1	0.11	80.3	19.0	10.8	-5.51
54.	MW4-6-1-3	0.09	90.7	21.2	10.4	-5.59
55.	MW4-46-1-2	0.10	94.0	26.5	4.5	-5.76
56.	MW4-6-1-2	0.11	88.7	22.0	3.0	-5.79
57.	MW4-6-1-1	0.04	91.0	19.7	3.2	-5.95

*GY = grain yield, FL = days to 50% flowering, GWE = 1000 grains weight, NFG = number of filled grain per panicle; DAS= days after sowing; ** I = standardized selection index.

of the index, 28 DH black rice lines were selected for further evaluation in a preliminary yield trial (Table 4).

CONCLUSION

Based on heritability, Pearson's correlation, path coefficient and principal component analysis there were four traits, i.e., grain yield (GY), days to 50% flowering (FL), 1000 grain weight (GWE) and number of filled grains (NFG) that can be used as selection criteria to obtain good agronomic performance and high yielding plants. Twenty-eight (28) DH black rice lines were selected by using positive value of the index derived from standardized selection index (zI) = (3 * 0.39 GY) + (-0.42 FL) + (0.23 GWE) + (0.44 NFG).

REFERENCES

Agahi K, Fotokian MH, Farshadfar E (2007). Correlation and path coefficient analysis for some yield-related traits in rice genotypes

(*Oryza sativa* L.). *Asian J. Plant Sci.* 47: 285-293.

Akhtar N, Nazir MF, Rabnawaz A, Mahmood T, Safdal ME, Asif M, Rahman A (2011). Estimation of heritability, correlation and path coefficient analysis in fine grain rice (*Oryza sativa* L.). *J. Anim. Plant Sci.* 21(4): 660-664.

Anyaocha C, Adegbehingbe F, Uba U, Popoola B, Gracen V, Mande S, Onotugoma E, Fofana M (2018). Genetic diversity of selected upland rice genotypes (*Oryza sativa* L.) for grain yield and related traits. *Int. J. Plant Soil Sci.* 22(5): 1-9.

Bahar M, Zein A (1993). Parameter genetik pertumbuhan tanaman, hasil dan komponen hasil jagung. *Zuriat* 4(1): 4-7.

Dewi IS, Purwoko BS (2012). Kultur antera untuk percepatan perakitan varietas padi di Indonesia. *J. Agron. Biogen.* 8(2): 78-88.

Eshghi R, Ojaghi J, Salayeva S (2011). Practical approaches to principal component analysis in the presence of missing values. *J. Machine Learning Res.* 11: 1957-2000.

Falconer DS, Mackay TFC (1996). Introduction to Quantitative

- Genetics (4th ed). Longman. New York. pp. 186.
- Fazaa M, Sabagh AEL, Anis G, El-Rewainy I, Barutçular C, Hatipoglu R, Islam MS (2016). The agronomical performances of doubled haploid lines of rice (*Oryza sativa* L.) derived from anther culture. *J. Agric. Sci.* 8(5):177-183.
- Gomez KA, Gomez AA (1984). *Statistical Procedures for Agricultural Research*. John Wiley & Sons.
- Hairmansis A, Kustianto B (2010). Correlation analysis of agronomic traits and grain yield of rice for tidal swamp areas. *Indonesian J. Agric. Sci.* 1(1): 11-15.
- Islam MA, Kayess MO, Hasanuzzaman M, Rahman MW, Uddin MJ, Zaman MR (2017). Selection index for genetic improvement of wheat (*Triticum aestivum* L.). *J. Chem. Biol. Phys. Sci.* 7(1): 1-8.
- Jolliffe IT (2002). *Principal Component Analysis* (2th ed). Springer-Verlag. New York.
- Kumar U, Laza MR, Soulié JC, Pasco R, Mendez KVS, Dingkuhn M (2017). Analysis and simulation of phenotypic plasticity for traits contributing to yield potential in twelve rice genotypes. *Field Crops Res.* 202: 94-107.
- Maji AT (2012). Application of principal component analysis for rice germplasm traitization and evaluation. *J. Plant Breed. Crop Sci.* 4 (6): 87-93.
- Mawaddah (2017). Pembentukan galur-galur dihaploid padi beras merah berpotensi hasil tinggi melalui kultur antera. Thesis. Bogor Agricultural University, Indonesia.
- Mawaddah, Purwoko BS, Dewi IS, Wirnas D. (2018). Karakterisasi sifat agronomi tanaman padi beras merah dihaploid berpotensi hasil tinggi diperoleh melalui kultur antera. *J. Agron. Indonesia* 46(2):126-132.
- Manikmas MOA (2010). Respon produsen dan konsumen terhadap varietas unggul padi beras merah dalam menciptakan peluang pasar. *J. Penel. Pert. Tan. Pangan.* 29(2): 88-96.
- Mattjik AA, Sumertajaya IM, Hadi AF, Wibawa GNA (2011). *Pemodelan Additive Main-effect & Multiplicative Interaction (AMMI): Kini dan yang akan datang*. IPB Press. Bogor. pp. 252-257.
- Mishra R, Narashima GJ, Nageswara R, Kaushal P (2015). Development and traitization of elite doubled haploid lines from two *indica* rice hybrids. *Rice Sci.* 22(6): 290-299.
- Muthayya S, Sugimoto JD, Montgomery S, Maberly GF (2014). An overview of global rice production, supply, trade, and consumption. *Ann. N.Y. Acad. Sci.* 13(24): 7- 4.
- Nayak P, Mukherjee AK, Pandit E, Pradhan SK (2018). Application of statistical tools for data analysis and interpretation in rice plant pathology. *Rice Sci.* 25 (1): 1-18.
- Nirmaladevi G, Padmavathi G, Kota K, Babu VR (2015). Genetic variability, heritability and correlation coefficients of grain quality traits in rice (*Oryza sativa* L.). *SABRAO J. Breed. Genet.* 47(4): 424-433.
- Padi BB (2019). Balai Besar Penelitian Padi - Empat varietas padi yang baru saja dilepas baik untuk kesehatan. Available at <http://bbpadi.litbang.pertanian.go.id/index.php/info-berita/info-teknologi/>
- Pratiwi R, Purwestri YA (2017). Black rice as a functional food in Indonesia. *Funct. Foods in Health Dis.* 7(3): 182-194.
- Purwoko BS (2017). Pengembangan teknik kultur antera dan aplikasinya pada percepatan pemuliaan tanaman padi di Indonesia. In: Sudarsono, BS Purwoko, editor. *Landasan Teoritis dan Penerapan Genetika serta Rekayasa Lingkungan untuk Peningkatan Produksi Tanaman*. IPB Press, pp. 135-182.

- Rabiei B, Valizadeh M, Ghareyazie B, Moghaddam M (2004). Evaluation of selection indices for improving rice grain shape. *Field Crops Res.* 8 (3): 359–367.
- Raghuvanshi RS, Dutta A, Tewari G, Suri S (2017). Qualitative characteristics of red rice and white rice procured from local market of Uttarakhand: a comparative study. *J. Rice Res.* 10 (1): 49-53.
- Raghuwanshi SS, Kachadia VH, Vachhani JH, Jivani LL, Malav AK, Shakti Singh Bhati SS (2016). Selection indices in groundnut (*Arachis hypogaea* L.). *Electr. J. Plant Breed.* 140-144.
- Roy D (2000). Plant Breeding: Analysis and Exploitation of Variation. Alpha Science Int'l Ltd.
- Sabouri H, Rabiei B, Fazlalipour M (2008). Use of selection indices based on multivariate analysis for improving grain yield in rice. *Rice Sci.* 15(4): 303–310.
- Samonte SOPB, Tabien RE, Wilson LT (2013). Parental selection in rice cultivar improvement. *Rice Sci.* 20(1): 45–51.
- Sanghera GS, Kashyap SC (2012). Genetic parameters and selection indices in F3 progenies of hill rice genotypes. *Not. Sci. Biol.* 4(4): 110-114.
- Seymour DK, Filiault DL, Henry IM, Monson-Miller J, Ravi M, Pang A, Comai L, Chan SWL, Maloof JN (2011). Rapid creation of *Arabidopsis* doubled haploid lines for quantitative trait locus mapping. *Proc. Natl. Acad. Sci. USA* 109(11): 4227-4232.
- Seyoum M, Alamerew S, Bantte K (2012). Genetic variability, heritability, coefficient and path analysis for yield and yield related traits in upland rice (*Oryza sativa* L.). *J Plant Sci.* 7(1): 13-22.
- Shabana R, El-Mohsen AAA, El-Haleem AKA, Saber AA (2015). Validity of conventional and restricted selection indices in selecting promising lines of sesame. *J. Agri-Food Appl. Sci.* 3 (4): 68-84.
- Shao Y, Hu Z, Yu Y, Mou R, Zhu Z, Beta T (2018). Phenolic acids, anthocyanins, proanthocyanidins, antioxidant activity, minerals and their correlations in non-pigmented, red, and black rice. *Food Chem.* 239: 733–741.
- Stansfield WD (1988). Theory and Problem of Genetics. McGraw Hill Book Co. New York. USA. pp. 220-221.
- Via ACM, Jonathan MN, Marie AR, Orbase, Nenita VD (2017). Selection in recombinant inbred lines of rice (*Oryza sativa* L.) by drought tolerant indices. *Int. J. Agric. Technol.* 13(7.3): 2679-2691.
- Yunianti R, Sastrosumarjo S, Sujiprihati S, Surahman M, Hidayat SH (2010). Kriteria seleksi untuk perakitan varietas cabai tahan *Phytophthora capsici* Leonian. *J. Agron. Indonesia.* 38 (2): 122 - 129.