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ASSESSMENT of GENETIC DIVERSITY and BIPLOT ANALYSIS in VARIOUS YIELD TRAITS to DETERMINE a HIGH YIELDING NEW TYPE of UPLAND RICE

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Abstract— The objective of this experiment was to identify the agronomic characters and to estimate the genetic diversity of F5 populations on various yield component variety and trait quality for developing a high-yielding upland rice. The experiment was carried out from April to August 2018 at Semarang Village, Bengkulu City, Bengkulu Province, Indonesia. Plant materials used in the experiment were 160 accessions of F4 Generations, obtained from a pedigree selection of crossing between two local landraces (Sriwijaya and Bugis) and two introduced accessions (IR-148 and IR-7858-1). The experiment was arranged in Augmented Design with a spaced planting system (20 cm x 20 cm). Each accession was planted in six rows with one seed per hole using a head-to-row system (about 800 population). The variance between populations was determined by Principal Component Analysis (PCA), correlation matrix, and biplot with XLSTAT version 9.0. Broad sense genetic diversity was found for the number of traits, such as number of panicles, the total number of grain per panicle, number of empty grain per panicle, number of filled grain per panicle, percentage of empty grain, the weight of 1000 grains, the weight of grain per hill, which potentially improved crop production. These genotypes were categorized into three groups, each of which had its own characteristics. The group I showed superior traits for the total number of grain per panicle, the number of filled grain per panicle, weight of 1000 grains, and weight of grain per hill. Group II had superior traits for panicle length, the number of empty grain per panicle, and the percentage of empty grain. Groups III was superior to the number of panicle traits.

Keywords— Genetic diversity, biplot analysis, high yielding, upland rice

I. INTRODUCTION

The contribution of upland rice to the national rice production in Indonesia has been very insignificant. Its productivity is only 2.5 ton.ha^{-1}, much lower than that of lowland rice, reaching 5.15 ton.ha^{-1}[1]. However, as the land for growing lowland rice has become limiting, increasing national rice production has to be done by growing upland rice at the upland soil, because of which improves the performance of upland rice has always been of paramount importance.

Many factors are contributing to the low productivity of upland rice, such as unfavorable environment, improper crop management, and lack of high-yielding seeds ([2],[3]). One way to cope with those problems is by developing a high-yielding new type of upland rice adaptive to such environmental conditions. Assembling a high-yielding and drought-tolerant variety of rice may be done by combining all excellent traits of two parental lines, like high yield and tolerance to drought. The parental lines come from either local landraces or introduced accessions, having desirable-superior traits ([4],[5]). An ideal new type of high-yielding rice paddy is expected to increase the potential yield, which is in line with the Indonesian government's program so-called food self-sufficient program.

Assembling a new variety of upland rice may start by crossing two or more parental lines to incorporate the expected superior traits within a new population. The population is then selected, evaluated, tested for environmental adaptability to get a promising line ready to be released as a new high-yielding variety. Selection is an effective method to obtain the essential traits, having a high chance of succeeding. If a certain trait has high genetic diversity, it must have a high intergroup diversity so that a selection process will be easier to get the expected traits. Because of this, it is essential to have information on the genetic diversity of a population to get an expected new variety. Trait variability of plants significantly determines

the yield potency and improves the efficiency of using the genetic materials in the breeding program for increasing yield ([6],[7],[8]).

Trait superiority must be prioritized during the assembly of the new variety program so that each promising variety owns a specific trait different from the existing variety. A specific trait identity must be identified thoroughly to prevent duplication and to ensure the identity of the newly released variety. Reference [9] suggested that to achieve the selection objective, one must identify the interspecific agronomic character, yield component, and yield so that a selection program for one or two traits could be done. A selection process will be effective, provided that the targeted traits have a high value of heritability. Heritability is essential to determine the choice of a selection method and at which generation selection of the expected trait should be made.

Genetic advance reflects how effective the selection process was taking place. A selection process will be effective provided that the value of genetic advance is high and supported by a high value of heritability. Furthermore, heritability value also determines the selection progress, in which the higher the heritability values, the higher the selection progress will be, and the faster a high-yielding variety will be obtained. The genetic diversity plays an essential aspect in which breeders always work ([10],[8],[11],[12]).

Principal component analysis might be used to determine trait diversity and to identify the general trait while biplot visualization can determine the specific trait of a certain genotype ([13],[14]). The objective of this experiment was to identify the agronomic characters and to estimate the genetic diversity of F5 populations on various yield component variety and trait quality for developing high-yielding new types of upland rice.

II. MATERIALS AND METHODS

The experiment was carried out from April to August 2018 at Semarang Village, Bengkulu City, Bengkulu Province, Indonesia. Plant materials used in the experiment were 160 accessions of F4 Generations, obtained from a pedigree selection of crossing between two local landraces (Sriwijaya and Bugis) and two introduced accessions (IR-148 and IR-7858-1). The experiment was arranged in Augmented Design with a spaced planting system (20 cm x 20 cm). Each accession was planted in six rows with one seed per hole using a head-to-row system (about 80 population). At ten days after planting (DAP) the crops were fertilized with 150 kg.ha^{-1} Urea, 100 kg.ha^{-1} SP36, and 100 kg.ha^{-1} KCl. At 30 DAP the crops were fertilized with 100 kg.ha^{-1} Urea, 100 kg.ha^{-1} SP36, and 100 kg.ha^{-1} KCl. Pests, diseases, and weeds were managed intensively. Variables measured included length of panicle, number of panicle per hill, number of total grain per panicle, number of filled grain per panicle, percentage of empty grain per panicle, the weight of 1000 grains, and weight of filled grain per hill.

Data Analysis

Data were analyzed with Microsoft Excel Statistical Program combined with Minitab 15. The variance between populations was determined by Principal Component Analysis (PCA), correlation matrix, and biplot with XLSTAT version 9.0.

Estimating Variance Component and Heritability

Data were analyzed for estimating the value of phenotype variance (σ^2p), genetic variance (σ^2g), the variance of the environment (σ^2e), coefficient of genotypic diversity (CGD), the standard deviation of genotypic variance ($\sigma\sigma^2$g), and broad sense of heritability (hbs) were measured with the following Formula:

$$\text{Variance } (\sigma2) = \frac{[\sum(xi - x^2)]}{n-1}$$

Phenotype variance (σ^2p) = σ^2F

Variance of environment $$(\sigma2e) = \frac{\sigma2P1 + \sigma2P2}{2}$$

Genetic variance (σ^2g) = σ^2p - σ^2e

$$\text{Heritability (hbs)} = \frac{\sigma2g}{\sigma2p}$$

We categorized heritability values based on [15] criteria, which were high when h$_{bs}$ were $\geq$ 0.50, medium 0.20 > h$_{bs}$ >0.50, and low h$_{bs}$ $\leq$ 0.20.

The CGD values were used for estimating how broad the genetic variance own by each trait estimated based on the following Formula [16]:

$$\text{CGD} = \frac{\sqrt{\sigma2g}}{X} \text{ x } 100\%$$

Where, σ^2g = genetic variance, x = population mean. Criteria: narrow (0-10%), medium (10-20%), and broad (>20%).

The following Formula could determine the value of genetic gain (GG):

GG = S.h2bs
GG (%) = $\frac{G}{X}$ x 100%

where S = selection differential, G= selction advance, G (%) = genetic gain in percentage, h2bs = broadsense heritability, X = average of initial population. Selection was done for seleceted individual from single trait at 10% of intensity.

III. RESULTS AND DISCUSSION

Genetic Diversity of F5 Population

The estimated value of plant genetic trait showed that the coefficient of genetic diversity (CGD) ranged between 7.63% and 62.46%. The lowest CGD value (7.63%) was found in the panicle length trait, while the highest value was found in the percentage of emptied grain per panicle (62.46%). The absolute value of CGD (0 –

62.46%) was then used to determine the relative value of CGD, in which 62.46% was assumed to be the 100% relative value. Therefore, the criteria for absolute value transformed to low (0.0% < x < 15.62%), medium-low (15.62% < x < 31.23%), medium-high (31.23% < x < 46.85%), and high (46.85% < x < 62.46%).

Traits having a low and medium-low of CGD values were categorized as traits with narrow genetic diversity. In contrast, traits having medium-high and high CGD values were categorized as traits with broad variability ([17],[18]). Based on those criteria, we found that the length of the panicle as a trait with narrow genetic variability while the number of panicles, total grain per panicle, and empty number grain per panicle as traits with medium broad genetic variability. Furthermore, the number of filled grain per panicle, percentage of empty grain per panicle, weight of 1000 grains, and weight of grain per hill

were categorized as traits with broad genetic variability. In other words, there was one trait having low genetic variability and seven traits having broad genetic variability, having the chance to improve the genetic performance of the rice through the following traits: number of panicles, number of total grain per panicle, number of empty grain per panicle, number of filled grain per panicle, percentage of empty grain, the weight of 1000 grain, and weight of grain per hill. A broad genetic variability means that the selection processes of the trait run effectively and be able to improve the genetic traits for the following generation ([19],[8]). The selection process could be done in a more convenient way for traits with broad genetic variability that can be used for crop improvement.

TABLE 1. THE ANALYSIS OF GENETIC VARIABILITY TRAIT OF THE F5 POPULATION

Characters	σ^2g*	σ^2p	CGD (%)	Criteria	h_{bs}	Criteria	GG	GG%
Panicle length	4.46	5.70	7.63	narrow	0.78	high	2.91	13.27
Number of panicle	350.88	352.20	30.21	moderate	0.99	high	32.84	89.67
Total number of grains per panicle	2942.34	3025.00	25.51	moderate	0.97	high	92.86	84.57
The number of fill grains per panicle	2588.42	2669.15	30.09	broad	0.97	high	86.83	59.39
The number of empty grains per panicle	31.93	33.04	17.70	moderate	0.97	high	9.61	26.24
Persentage of empty grain per panicle	159.74	162.58	62.46	broad	0.98	high	21.86	57.56
1000 weight grains	4889.26	4890.58	43.43	broad	1.00	high	123.03	335.88
Grain weight per hill	1019.49	1021.41	51.49	broad	0.99	high	56.09	153.13

*σ^2g=genetic variance; σ^2p= phenotype variance; CGD=Coeficient Genetic Diversity, h_{bs}= broadsense heritability; GG=genetic gain

The estimated value of trait heritability was 0.78 for panicle length and 1.0 for the weight of 1000 grain (Table 1.). Based on [15] criteria, the estimated heritability values of all traits were high. However, the high genetic advance was found only for the total number of grain per panicle, the number of filled grain per panicle, weight of 1000 grain, weight of grain per hill. Traits having high heritability determine the effectivity of the selection process and speed up the advance of crop improvement. High heritability values suggested that genetic factors are more dominant than the environmental factors, and that selection process could be done in the early generation ([20],[21],[7]).

Lines Performance of F5 Population

The panicle length produced in this experiment ranged from 24.22 to 31.04 cm, with 27.91 cm on average (Table 2.). The lines obtained from the hybridization produced lines with the shortest panicle (24.22 cm) and the longest panicle (31.04 cm). Some lines, however, showed shorter panicle than their parental lines. The length of the panicle is strongly correlated to the number of grain per panicle. The number of panicles ranged from 3.00 to 27.00, with an

average of 12.46. Refer to [22] that improving the potential yield of 10% higher than New Plant Type (NPT), some traits are needed, such as 330 panicles per m2 and 150 grain per panicle, 22 ton per hectare of biomass (with 14% of moisture content), and 50% harvesting index. Reference [23] have developed a strategy for getting a new type of rice with specific panicle trait and 150 grains per panicle. Further, [24] added that the number of panicles per m2, percentage of filled grain, total biomass, and harvesting index are needed for developing the new type of rice.

TABLE 2. THE MINIMUM, MAXIMUM, AVERAGE VALUES, AND STANDARD DEVIATION OF YIELD COMPONENT OF THE F5 POPULATION.

Characters	Min	Max	Mean	SD*
Panicle length	24.22	31.04	27.91	1.44
Number of panicle	3.00	27.00	12.46	7.18
Total number of spikelet/panicle	141.00	307.42	214.35	47.17
fill grain/panicle	106.67	268.75	166.43	45.64
Empty	20.07	109.25	47.92	27.59

grain/panicle				
Percentage of empty grain	7.54	46.65	22.01	11.07
1000 grains weight	26.84	55.52	40.74	6.93
Grains weight/hill	21.45	121.99	59.55	30.56

*SD=Standar deviation

The lines obtained from the crossing demonstrated the number of grain per panicle up to 141.00-307.42, with 214.35 on average, the highest number of the filled grain of 268.75 with 166.43 in average, and the low percentage of empty grain (22.01%), as shown in Table 2. Reported by [24] that poor grain filling is caused by the low level of apical dominance at the panicle, the poor arrangement of grain on the panicle, and the limiting activity of phloem in transporting assimilates. Furthermore, reference [25] found that the inefficient partition of assimilates causes the poor grain filling of the new rice paddy.

Reported by [26] that the NPT rice in Indonesia must have the reasonable number of tiller (12-18 tiller), but all of them must productive, with the number of grain per panicle up to 150-250, percentage of the filled grain of 85-95%, the weight of 1000 grain about 25-26 g, short but vigorous stem (80-90 cm), and early season (110-120 days). With those traits, the newly breed rice paddy is expected to yield 9-13 tons per hectare. The population of the F5 line demonstrated the high number of grain (307.42, 214.35 on average), a low percentage of empty grain (22.01%), and a high percentage of fille grain (268.67, 166.43 in average) per panicle. In short, these lines were potential for producing high yield because they demonstrated the high number of panicles per hill, 12.46 on average (Table 2.). Refer to [24] recommended avoiding an extreme trait when obtain newly breed rice paddy, such as high number of grain (200-250) per panicle leading to the poor grain filling, because of which IRRI set a standard for 150 grain per panicle to ensure a high percentage of filled grains. In addition, the weight of 1000 seeds of the new lines produced in this experiment was about 26.84-55.52 g, with an average of 40.74 g. Ideally, a new variety must weight 26.84-55.52 g for 1000 seeds [27]. Based on this standard, therefore, all newly bred lines resulted in this experiment were considered to have high potential yield. To increase the yield of newly bred rice, one needs to have parental lines having long panicles and the high number of grain per panicle ([28],[24]). Also, recommended by [27] that an ideal new variety has 180-240 grain per panicle, and 85% of the grain is fully filled.

Correlation and Analysis of Principal Component between Yield Component and Yield

The correlation values could determine the relationship between the yield component and yield. Correlation between characters was presented in Table 3. Panicle length was negatively correlated to and significantly different from the number of panicles (-0.59) and weight of grain per hill (-0.49), and positively correlated with and significantly different from the number of empty grain per panicle (0.64) and percentage of emptied grain (0.57)

TABLE 3. COEFfiCIENT OF CORRELATIONS BETWEEN AGRONOMICAL CHARACTERS AND GRAIN YIELD PER TILLER

Characters	PL	NP	NSP	FGP	EGP	PEG	1000GW	GW
PL	1	-0.6*	0.21	-0.17	0.64*	0.57*	-0.18	-0.46*
NP		1	-0.28	-0.04	-0.40	-0.37	0.09	0.42*
NSP			1	0.82*	0.35	0.02	0.45*	0.33
FGP				1	-0.25	-0.54*	0.66*	0.68*
EGP					1	0.93*	-0.33	-0.56*
PEG						1	-0.50*	-0.73*
1000GW							1	0.79*
GW								1

*Values in bold are different from 0 with a significance level alpha=0.05; PL= Panicle length; NP= Number of panicles; FGP=fill grain/panicle; EGP= empty grain/panicle; PEG= Percentage of empty grain; 1000GW=1000 grains weight; GW= Grains weight/hill

Number of panicles, number of filled grain, and weight of 1000 grains positively correlated to and significantly different from the weight of grain per hill. Consequently, those three traits could be used as selection criteria for increasing grain yield. The weight of 1000 grain is correlated to the size and degree of fullness of the grain. The high percentage of filled grain and the big size of grain lead to the high weight of 1000 grain (Table 3). Increasing the number of filled grain per panicle, increasing the number of grain per hill significantly. In contrast, increasing the number of empty grain per panicle reduces grain yield per hill. The high number of filled grain per panicle, combined with a high percentage of filled grain per panicle, will significantly increase grain yield per hill. Reported by [31] that sucrose synthetase (SUS3) actively involved during the grain filling period, at the proximal location, as well as increased density of spikelets on panicles affected SUS3 expression in the basal spikelets.
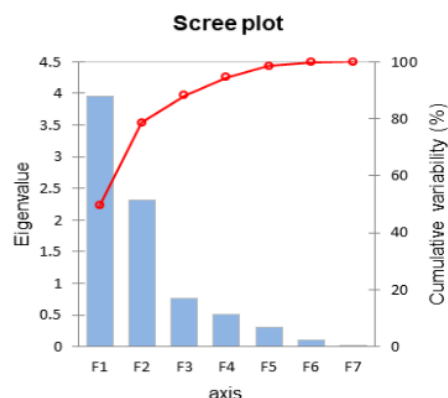

Scree plot

Fig 1. Eigenvalue for the main components and their contributionto total diversity and cumulative diversity

The results of principal trait analysis showed that some traits significantly affected the variability of the tested lines. The results reduced significantly total morphological traits evaluated to three main components (KU-1, KU-2, and KU-3), which represented the eigenvalue of >1 and the

variability of line performance up to 88.15% (Fig 1). Moreover, the trait with a higher coefficient value of the main component has a higher contribution to the main component [30].

Eigenvalue contributed significantly to total diversity. The first principal component (KU-1) with an eigenvalue of 3.96 contributed to 49.47% of total diversity. The second principal component (KU-2) with an eigenvalue of 2.33 contributed to 78.53% of total diversity among the tested lines, and the third component (KU-3) with an eigenvalue of 0.77 contributed to 88.15% of the total diversity of the lines tested.

Morphological characters Main component

Analysis of the identifier vector shows which trait contributes maximally to the diversity of the tested lines (Table 4), as the trait with the highest point of identifier vector and positive value [31]. For KU-1, the traits contributing to the diversity of tested lines included length of panicle, number of filled grain per panicle, number of empty grain per panicle, percentage of empty grain, the weight of 1000 grain, and weight of grain per hill. Besides, it was found in the number of total grain per panicle for KU-2 and the number of panicles for KU-3.

TABLE 4. IDENTIFIER VECTOR FOR YIELD COMPONENT TRAITS CONTRIBUTING TO THE DIFFERENCES OF THE TESTED LINES OF THE F5 POPULATION

Morfological Characters	Main Components		
	KU1	KU2	KU3
Panicle length	**0.424***	0.250	0.057
Number of panicle	0.223	0.305	**0.388**
Total number of spikelet/panicle	0.048	**0.846**	0.049
fill grain/panicle	**0.481**	0.436	0.000
Empty grain/panicle	**0.600**	0.232	0.158
Percentage of empty grain	**0.817**	0.037	0.102
1000 grains weight	**0.529**	0.192	0.000
Grains weight/hill	**0.837**	0.029	0.016

*Values in bold are significantly different on p-value =1% or p-value =5%.

The contribution of diversity explaining the indicators used to observe the relationship between yield potency and yield was 100%. However, by conducting biplot analysis, which reduced all of the indicators into two-side dimensions, the information that could be explained was only about 78.53%, meaning that the information that could be explained by biplot analysis was >70%. It meant that biplot analysis has already represented enough information on the relationship among those eight indicators.
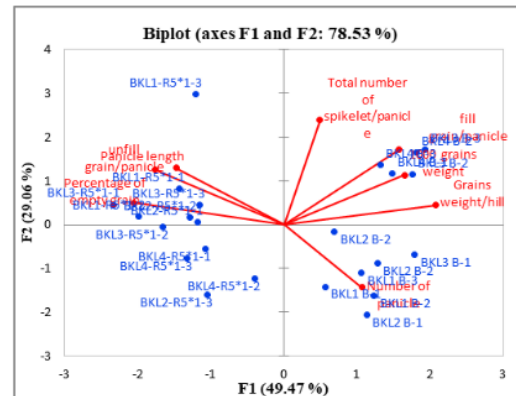

Fig 2. Biplot analysis showing the spreading of yield component and yield traits on genotypes obtained from the crossing

Fig 2 showed four traits a member of the Grup I Identifier superior in the total number of grain per panicle, filled grain per panicle, the weight of 1000 grains, and weight of grain per hill. The genetic population of the crossing included BKL4 B-2, BKL3 B-3, BKL4 B-3, BKL3 B-2. Group Identifier II was superior in the length of the panicle, the number of empty grain per panicle, and the percentage of empty grain. Members of these groups included BKL1-RS*1-3, BKL1-RS*1-1, BKL3-RS*1-1, BKL3-RS*1-3, BKL1-RS*1-2, BKL2-RS*1-2, and BKL2-RS*1-1. Group Identifier III was superior in the number of panicles, found in the next crossing: BKL2 B-2, BKL3 B-1, BKL1 B-1, BKL1 B-2, and BKL2 B-1. There was a significant positive correlation between each trait in the group has also been demonstrated in Table 3.

Analysis of the main coordinate was carried out to show the relative position of each tested line, as presented in Fig 2. The results demonstrated that the following traits, the total number of grain per panicle, filled grain per panicle, the weight of 1000 grain, weight of grain per hill, had a greater chance to yield the higher population average that the other traits. References ([24],[28]) reported that to improve the yield of new type rice, it needed parental lines having superior traits on grain per panicle and length of the panicle. One of the ideal traits for new rice paddy is that the number of grain must be 180-240, with the percentage of filled grain about 85% [27]. Report by [23] and [32] have used a number of filled grain as the indicator trait to develop a new type of rice paddy. In addition, an ideal new type of rice paddy must have 130 number of filled grain [23] or 160 number of grain [32]. From this discussion, it may be suggested that the traits of the total number of grain per panicle, filled grain per panicle, the weight of 1000 grain, weight of grain per hill have to be considered while selection for high yield as they expressed positive and significant correlation with grain yield. A positive inter-correlation was also noticed between these traits. Hence, a

balance should be maintained while selecting for these traits. It will bring up improvements in the yielding potential and also the traits themselves.

IV. CONCLUSIONS

Broad sense genetic diversity was found for the number of traits, such as number of panicles, the total number of grain per panicle, number of empty grain per panicle, number of filled grain per panicle, percentage of empty grain, the weight of 1000 grains, the weight of grain per hill, which potentially improved high yielding. These genotypes were categorized into three groups, each of which had its own characteristics. The group I showed superior traits for the number of grain per panicle, the number of filled grain per panicle, weight of 1000 grains, and weight of grain per hill. Group II had superior traits for panicle length, number of empty grain per panicle, and percentage of empty grain. Groups III were superior for the number of panicle trait.

ACKNOWLEDGMENT

REFERENCES

[1] Badan Pusat Statistik. Luas panen, produksi, dan produktifitas padi di Indonesia. 2018. https://www.bps.go.id/dynamictable/2019/04/15/1608/luas-panen-produksi-dan-produktivitas-padi-menurut-provinsi-2018.html

[2] H.M. Toha, K. Permadi, Prayitno, I. Yuliardi. 'Peningkatan produksi padi gogo melalui Pendekatan model pengelolaan tanaman dan sumberdaya terpadu (PTT)'. Seminar Puslitbang Tanaman Pangan. Bogor, Juli 2005. Badan Litbang Pertanian. 2005.

[3] Shah, Shoumik, D. Rashmi, B. Loitongbam, P. Bisen, V.K. Singh, Sandhya, U.S. Singh, and P.K. Singh. 'Genetic Analysis of F4:F Marker Assisted Derived Lines of Rice against Bacterial Leaf Blight (BLB) and their Marker Validation'. Vegetos, 30 (Special): 101-108. 2017. DOI: 10.5958/2229-4473.2017.00043.X

[4] R. Herawati, B.S. Purwoko, I.S. Dewi, N. Khumaida, B. Abdullah. "Pembentukan galur haploid ganda padi gogo dengan sifat-sifat tipe baru melalui kultur antera'. Bul. Agron. 36:181-187.2008.

[5] A. Hairmansis, Yullianida, Supartopo, dan Suwarno. "Rice Improvement for Upland Areas". Iptek Tanaman Pangan. 11(2):95-106.2016.

[6] M. Khodadadi, M.H. Fotokian, and M. Miransari. "Genetic diversity of wheat (Triticum aestivum L.) genotypes based on cluster and principal component analyses for breeding strategies". Aust. J. Crop Sci. 5(1): 17–24.2011. https://www.researchgate.net/publication/228410566

[7] J.M. Bitew. "Estimation of genetic parameters, heritability and genetic advance for yield related traits in upland rice (Oryza sativa L. and Oryza glaberrima steud) genotypes in Northwester Ethopia". World Sci. News. 47(2): 340-350. 2016.

[8] R. Herawati, Masdar, and Alnopri. "Genetic analysis of grain yield of F4 populations for developing new type of upland rice". SABRAO Journal of Breeding and Genetics. 51(1):68-79. 2019.

[9] Zen, S. "Parameter genetik karakter agronomi galur harapan padi sawah". Stigma10(4):325-330. 2002.

[10] G.R. Gowane, V. Prakash, A. Chopra, and L.L.L Prince. "Population structure and effect of inbreeding on lamb growth in Bharat Merino sheep". Small ruminant Research 114:72-79. 2013.

[11] O.T. Osundare, B.O. Akinyele, L.S. Fayeun, and O.S. Osekita. "Evaluation of qualitative and quantitative traits and correlation coefficient analysis of six upland rice varieties".Journal of Biotechnology and Bioengineering. 1(1):17-27.2017.

[12] A.K. Pachauri, A.K. Sarawgi, S. Bhandarkar, and G.C. Ojha. "Agro-morphological characterization and morphological based genetic diversity analysis of Rice (Oryza sativa L.) germplasm". Journal of Pharmacognosy and Phytochemistry 6(6): 75-80. 2017.

[13] R.M. Pacheco, J.B. Duarte, R. Vencovsky, J.B. Pinheiro, and A.B. Oliveira. "Use of supplementary genotypes in AMMI analysis". Theor. Appl. Genet. 110(5): 812–818. 2005.

[14] P. Sharifi, M. Mohammadi, and R. Karimizadeh. "Biplot analysis of diallel crosses for yield and some of morphological traits in wheat". Vegetos 32, 420–430.2019. https://doi.org/10.1007/s42535-019-00046-z

[15] W.D. Stanfield WD. Theory and Problems of Genetics. 2nd edition. Schain.s Outline Series. Mc.Graw Hill Book Co. New Delhi. 1983.

[16] R. Knight. "Practical in Statistic and Quantitative Genetics". Brisbane (AU): Australian Vice-Chancellors Committee. 1979.

[17] R. Herawati, B.S. Purwoko, and I.S. Dewi. "Characterization of Doubled Haploid Derived from AntherCulture for New Type Upland Rice". J. Agron. Indonesia 38(3) : 170 - 176 . 2010.

[18] R. Herawati, E. Inoriah, Rustikawati, Mukhtasar. "Genetics Diversity and Agronomic Characters of F3 Lines Selected by Recurrent Selection for Drought Tolerance and Blast Resistance of Bengkulu Local Rice Varieties". International Journal on Advanced Science, Engineering and Information Technology (IJASEIT). 7(3):922-927. 2017.

[19] P. Bisen, P. K. Singh, B. Loitongbam, Namrata, S.R. Rathi, S. Upadhyay and B. Sinha. "Genetic analysis and trait association for yield related traits in $F_{2.3}$ biparental population of rice under slightly sodic condition". Electronic Journal of Plant Breeding, 10 (3): 1105 – 1112. 2019. DOI: 10.5958/0975-928X.2019.00141.8

[20] M.G. Akinwale, G. Gregorio, F. Nwilene, B.O. Akinyele S.A. Ogunbayo, and A.C. Odiyi, "Heritability and correlation coefficient analysis for yield and its components in rice (Oryza sativa L.)". African Journal of Plant Science 5: 207-212. 2011.

[21] F. Corazon, E. Pacquiao and E.V. Aguinaldo. "Genetic variation and heritability of yield related traits in promising rice genotypes (Oryza sativa L.)". Int. J. Plant Breed. Genet. Vol. 2(3): 105-110. 2015.

[22] Khush. "Strategies for increasing the yield potential of cereals: case of rice as an example". Plant Breeding, 132:433–436. 2013. doi:http://dx.doi.org/10.1111/pbr.1991

[23] P.S. Virk, G.S. Khush, and S. Peng. "Breeding to enhance yield potential of rice at IRRI: the ideotype approach". (Mini Review). International Rice Research Notes. 29(1):59 . 2004.

[24] S. Peng, G.S. Khush, P. Virk, Q. Tang, and Y. Zou, "Progress in ideotype breeding to increase rice yield potential". Field Crops Research,108(1):32-38.2008. doi:http://dx.doi.org/10.1016/j.fcr.2008.04.001

[25] T. Kobata and K. Iida. "Low grain ripening in the new plant type rice due to shortage of assimilate supply". New directions for a diverse planet: Proceedings of the 4th International Crop Science Congress Brisbane, Australia, 26 Sep – 1 Oct 2004. 2004.

[26] B. Abdullah, I.S. Dewi, Sularjo, H. Safitri, A.P. Lestari. " Perakitan padi tipe baru melalui seleksi silang berulang dan kultur anter". Penelitian Pertanian Tanaman Pangan 27(1):1-8. 2008.

[27] J. Ma, W.B.Ma, D.F. Ming, S.M. Yang, Q.S. Zhu. "Characteristics of rice plant with heavy panicle". Agricultural Sciences in China 5(12): 911-918. 2006.

[28] W. Yang, S. Peng, R.C. Laza, R.M. Visperas, M.L.D. Sese. "Grain yield and yield attributes of new plant type and hybrid rice". Crop Sci. 47:1393-1400. 2007.

[29] B.B. Panda, A.K. Badoghar. A. Das, R. B. Panigrahi, E. B. Kariali B , S.R.C. Das, S.K.D. Dash, B.P.A. Shaw, and P.K. Mohapatra. "Compact panicle architecture is detrimental for growth as well as

sucrose synthase activity of developing rice kernels". Functional Plant Biology 42(9):875-887. 2015.

[30] S.H. Abdurrachman, H. Komalig, and N. Nainggolan. "Penggunaan analisis komponen utama dalam penggabungan data peubah ganda pada kasus produksi pertanian dan perkebunan di wilayah Bolaang Mongondow tahun 2008". Jurnal d'Cartesian, 3 (2), 1–7. 2014.

[31] A. Haydar, M.B. Ahmed, M.M. Hannan, and M.A. Razvy.. "Analysis of genetic diversity in some potato varieties grown in Bangladesh". *Middle-East Journal of Scientific Research*, 2 (3–4), 143–145. 2007.

[32] X.U. Zhengjin, C. Wenfu, Z. Longbu, and Y. Shouren. "Design principles and parameters of rice ideal panicle type". Chinese Science Bulletin. 50(19):2253-2256. 2005.
.

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