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Assessment of variability in performances of F3 rice populations on inland swampland in Indonesia

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Abstract

Rice improvement program for swampland areas is mainly addressed to develop high yielding varieties with the desirable agronomic characteristics along with the improved adaptability to all growth limiting factors inherent in the ecosystem. This study was implemented to evaluate the growth and yield performances of 10 rice F_3 populations generated from the crosses involving Bengkulu swamp rice landraces (Hanafi Putih, Batubara, Harum Curup, Tigo-tigo, and Lubuk Durian) and the cultivated varieties (Diah Suci, Bestari, and Sidenuk) on a swampland. The experiment was laid out on a shallow inland swamp with stagnant inundation up to 50 cm depth during the plant growth period. Data were collected for plant height, tiller number, number of productive tillers clump^{-1}, heading date, maturity date, panicle length, number of grain panicle^{-1}, 100-grain weight, and grain yield clump^{-1}. High variability among the populations was observed for most of the traits and readily explored for the development of rice varieties well adapted to swampland. The principal component analysis showed that the populations were distinguishable on the basis of the observed traits. The magnitude of broad sense heritability and genetic advance estimates denoted that simple phenotypic selection should be sufficient for gaining genetic improvement for the majority of the traits, excluding panicle length.

Keywords: Genetic advance, Heritability, Inland swamp, Local rice varieties, Principal component

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Introduction

Rice serves as an essential staple diet for the majority of Indonesian, contributing around 44% average daily consumption of calorie (BPS, 2016). With annual milled rice consumption amounted to 114 kg per capita (Kadarmanto, 2018), it is easy to perceive that Indonesians have a high dependency on rice as the dietary energy source. Although the annual rice consumption per capita among Indonesians tended to decline in recent years, the trend of rice demand is steadily increasing along with the population growth. The current Indonesia rice production was 75 million tons resulted from 14 million hectares of harvested areas, while the total consumption was 32.4 million tons of milled rice (BPS, 2018). These figures have ranked Indonesia as the third largest rice producing and consuming countries after China and India (World atlas, 2019ab). Moreover, about 52 to 53% of national rice supply was produced in Java Island with a total harvested area around 6 million hectares. By the lessening the harvested areas due to land conversion in this densely populated island, the Indonesian government has targeted the less productive areas outside Java Island for maintaining the national food supply.

The availability of vast swampy areas that are currently neglected or underutilized could be considered as potential fields for the future food source to feed the growing population. Swamplands of Indonesia are spread over four major islands outside Java, namely: West Papua, Sulawesi, Kalimantan, and Sumatera, covering 20.13 million hectares of tidal swamps and 13.28 million hectares of inland swamps. However, only about 1.18 million hectares of the areas are used for rice production and 1.53 million hectares for other agricultural activities and infrastructures (Nursyamsi and Noor, 2013). Swampland reclamation is not always the best option for rice production as it cost intensive in term of both financial and environmental risks (Houterman et al., 2004). Therefore, the use of improved varieties especially adapted to intrinsic characteristics of swampy areas appears to be a more sensible alternative to optimize swamplands for maintaining food self-sufficiency.

With all constraints inherent in the swamplands, including seasonal water level fluctuation and physicochemical properties of the soil, the development of superior rice varieties well adapted to such environmental characteristics would be challenging. In this case, a diverse genetic background in the breeding materials for agronomic performances, yield potential, and adaptability in marginal conditions should be devised at the beginning of the breeding program (Tigerstedt, 1994).

The availability of landrace varieties currently grown traditionally on swampy areas could serve as valuable genetic materials for improving the crop adaptation to swampland conditions. Landrace rice varieties might be low in their yield potential, but they have characteristics required to grow well under biotic and abiotic stresses (Silitonga, 2004; Bailey-Serres et al., 2010). Moreover, Rumanti et al. (2016) have demonstrated that the involvement of landraces in the breeding program had resulted in high-yielding elite lines with good adaptation in swampland agro-ecosystem.

A clear insight on the amount and nature of variability obtained in the breeding material and evidence of the heritable desired traits are essential for gaining the effectiveness of the selection efforts, especially in the segregating population. This study was performed to evaluate the growth and yield characteristics of ten F_3 rice populations generated from crosses involving Bengkulu swamp rice landraces on an inland swamp and to estimate the genetic parameters concerning the expected crop improvement from selection program.

Material and Methods

Experimental site characteristics

The trial was carried out on a shallow inland swamp of Agriculture Faculty, University of Bengkulu (03° 45’ 324” S, 102° 16’ 310” E, 10 m above sea level). The soil was histosol with sapric peat $\leq$ 75 cm thick, and pH = 4.0. Fluctuated stagnant inundation occurred during the plant growing period at depth 5 to 50 cm from the soil surface without submerging the plants.

Genetic materials and experimental design

The F_3 populations evaluated in this study were generated from the ten crosses of Hanafi Putih x Sidenuk, Batubara x Harum Curup, Harum Curup x Tigo-tigo, Tigo-tigo x Sidenuk, Lubuk Durian x Diah Suci, Harum Curup x Sidenuk, Lubuk Durian x Sidenuk, Hanafi Putih x Lubuk Durian, Tigo-tigo x Bestari, and Harum Curup x Bestari. Hanafi Putih, Batubara, Harum Curup, Tigo-tigo, and Lubuk Durian are Bengkulu swamp rice landraces, while Diah Suci, Bestari, and Sidenuk are the cultivated varieties for irrigated lowland released by Nation Nuclear Agency of Indonesia (BATAN). The parental crosses were made through a half diallel crossing scheme to produce 21 F_1 hybrids. However, only ten populations were selected and maintained based on their performances in the inland swamp during the F_1 and F_2 generations screening processes by bulk population breeding method. A randomized block design (RBD) was employed with three replications to assign 100 plants from each population on 2.5 m x 2.5 m plots spaced 0.5 m apart with 1 m inter-block distance.

Crop management

The planting area was prepared by spraying the existing vegetation with a systemic herbicide at two weeks before transplanting and harrowing the land to incorporate the plant residue with the soil. The crop establishment was made by transplanting 18-day old seedlings on the experimental plots with single seedling hill^{-1} in a square pattern 25 cm x 25 cm apart. The basal dressing of fertilizers was applied to the soil a day after transplanting using 50 kg ha^{-}1of Urea, 200 kg ha^{-1} of SP36, and 75 kg ha^{-1} KCl. The following urea applications at 50 kg ha^{-1} were done at four and seven weeks after transplanting. Weed, pest, and disease controls were carried as necessary. Harvest was conducted when the plants produced 85 % straw-colored grains.

Data collection

Data were recorded from the observations of nine agro-morphological traits. Plant height, total tiller number $clump^{-1}$, number of productive tillers $clump^{-1}$, panicle length, number of grains $panicle^{-1}$, 100-grain weight, and grain yield $clump^{-1}$ were observed at maturity stage on samples of twenty-five plants randomly selected in each plot, excluding the border plants. Heading date and maturity date were recorded on a plot basis.

Statistical Analysis

The pattern of variation among the populations was examined using principal component analysis (PCA). The PCA was performed on the correlation matrix to provide an equal footing on each trait (Jolliffe, 2002. The analysis of variance was employed based on a randomized block design. Both principal component analysis and analysis of variance were performed using PROC PRINCOMP and PROC VARCOMP of SAS version 9 (SAS Institute Inc., 2004), while the graphs of the principal components were drawn using XLSTAT version 9.0 (Adinsoft, 2010).

Genetic parameters estimation

The mean squares derived from the analysis of variance were used to estimate the phenotypic variance and genotypic variance as suggested by Soomro et al. (2010) and Alkuddsi et al. (2013).

$$\text{Phenotypic variance } (\sigma^2_P) = MS_G$$

$$\text{Genotypic variance } (\sigma^2_G) = \frac{MS_G - MS_E}{r}$$

where MS_G is genotype mean square; MS_E is error mean square; r is number of blocks. The phenotypic and genotypic coefficients of variation were estimated according to Singh and Chaudhary (1985).

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{\sqrt{\sigma^2_P}}{\bar{x}} \text{ x } 100\%$$

$$\text{Genotypic coefficient of variation (GCV)} = \frac{\sqrt{\sigma^2_G}}{\bar{x}} \text{ x } 100\%$$

where $\bar{x}$ is the grand mean of the trait . Broad-sense heritability was derived using formula as suggested by Allard (1999).

$$\text{Broad-sense heritability } (h^2_B) = \frac{\sigma^2_G}{\sigma^2_P}$$

The genetic advance from selection was estimated using the formula provided by (Becker, 1984). The genetic advance was also expressed as a percent of the trait mean as suggested by Johnson et al. (1955).

$$\text{Genetic advance (GA)} = \sqrt{\sigma^2_P} \text{ x } h^2_B \text{ x } i$$

$$\text{Genetic advance as percent of the mean (GAM)} = \frac{GA}{\bar{x}}$$

where i represents the standardized selection differential and i = 2.06 for 5% selection intensity.

Results and Discussion

General performances of the experimental plants

Table 1 summarizes the general performances of the plant population under study. In most cases, the observed traits showed a wide range of performances, indicating that the current breeding populations were readily exploitable for the development of varieties with the desired characteristics. However, the scope of selection for bringing about the improvement in the desirable direction would vary among the traits depending on their extent of variation. A coefficient of variation (CV) can be considered as a simple measure for comparing the relative amount of variability among traits in a given population (Sharma, 2006). The higher CV of a trait implies the more significant potential of favored improvement for the trait through a selection process, and vice versa. Grain yield $clump^{-1}$ exhibited the most substantial variation followed by number of productive tillers $clump^{-1}$ and total tiller number $clump^{-1}$, whereas the lowest variation was exhibited by panicle length. These results suggest that grain yield $clump^{-1}$, number of productive tillers $clump^{-1}$, and total tiller number $clump^{-1}$ comprised a higher amount of utilizable genetic variability than the remaining traits.

Table 1: Summary statistics for the traits observed from 10 F$_3$ rice populations grown on an inland swamp

Observed trait	Minimum	Mean	Maximum	CV (%)
Plant height (cm)	69	106.9	161	10.2
Total tiller number clump^{-1}	6	23.1	70	17.3
Heading date (DAT)	75	93.4	115	3.3
Maturity date (DAT)	106	125.6	149	3
Number of productive tillers clump^{-1}	5	18.9	68	20.4
Panicle length (cm)	16	22.4	29	2.4
Number of grains panicle^{-1}	55	116.1	183	5.9
100-grain weight (g)	1.9	2.5	3.3	6.9
Grain yield clump^{-1} (g)	5.1	32.7	108.3	21.6

CV = coefficient of variation, DAT = days after transplanting

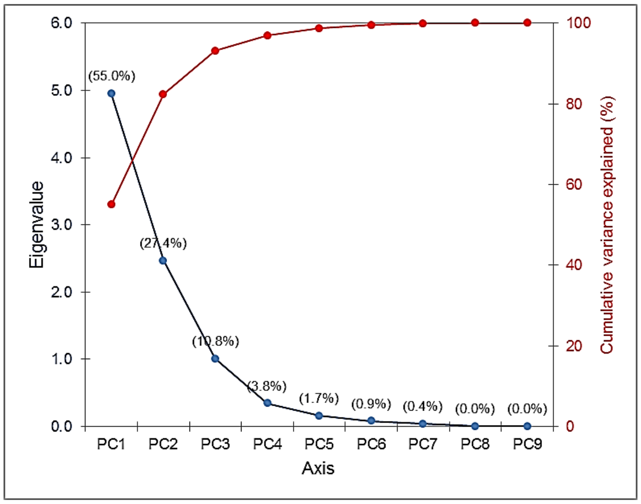

Figure 1. Scree plot indicating the eigenvalues for the PCs along with their contributions to the total variance (values in brackets) and their cumulative variances explained

Pattern of variation

The principal component analysis (PCA) has summarized the patterns of variations in the data set into a fewer number of independently uncorrelated variables, known as principal components (PCs). Using the eigenvalues-greater-than-one criterion proposed by Kaiser (1960), the PCA yielded three PCs accounted for 93% of the total variance of the data and worth further exploration, while the remaining axes were ignored as they were decreasingly uninformative (Figure 1).

Table 2 presents the loadings of each trait for the three PCs. The magnitude of a trait's loading indicates the importance of the trait to the corresponding PC and loading with an absolute value greater than 0.30 is considered as significant (Ogasawara, 2002). PC1 accounting for 55% of the total variance had approximately equal loadings for all traits, except number of grains panicle^{-1}and grain yield clump^{-1}, indicating that nearly all traits contribute equally in discriminating the populations.

Table 2: Loading of first 3 PCs for the observed traits on 10 F$_3$ rice populations

Observed trait		Loading	
	PC1	PC2	PC3
Plant height	**0.37**	0.23	**-0.34**
Total tiller number clump^{-1}	**0.32**	**-0.32**	0.00
Heading date	**0.37**	**0.30**	-0.18
Maturity date	**0.40**	0.22	-0.22
Number of productive tillers clump^{-1}	**0.37**	**-0.43**	-0.11
Panicle length	**-0.30**	**0.34**	0.10
Number of grains panicle^{-1}	0.19	**0.57**	0.09
100-grain weight	**0.37**	-0.23	**0.38**
Grain yield clump^{-1}	0.24	0.19	**0.79**

PC1, PC2, and PC3 denote the first, the second, and the third principal components, respectively. The values of component loading in the row for each trait indicate the strength of correlation between the trait and the eigenvector of the corresponding PC. The absolute value of component loadings larger than 0.30 (bold font) were considered important in defining the PC.

It means that a population possessing higher PC1 score could be expected to have taller plants, more total tiller number clump^{-1}, delayed in attaining flowering and maturity stages, more productive tillers, shorter panicle, and larger grain size. PC2 explaining 27% of the total variance was characterized by total tiller number clump^{-1}, heading date, number of productive tillers clump^{-1}, panicle length, and number of grains panicle^{-1}. Therefore, a population with the higher PC2 score to some extent would have more extended panicle and a higher number of grains panicle^{-1}, but lower numbers of the total tiller, delayed flowering date, and less productive tiller. PC3 was mainly characterized by grain yield clump^{-1} with some contribution given by 100-grain weight and plant height. However, by contributing only 10% to the total variance, PC3 provided less discriminatory power in discerning the populations.

Figure 2 visualizes the pattern of variation among the populations as plotted on the three PC axes. It can be noted that the populations could be assigned into three groups with respect to their common performances based on the description provided by Shoba-Rani et al. (2006), Biodiversity International, IRRI and WARDA (2007), IRRI (2013), and Sinha et al. (2015). Group I consisted of Lubuk Durian x Sidenuk, Harum Curup x Sidenuk, Hanafi Putih x Lubuk Durian, and Batubara x Harum Curup. These populations shared in common performances by having short plant stature (82.8 - 98.9 cm), good tillering ability (19 - 21 tillers), early heading (83 - 91 days after transplanting), early maturing (114 - 120 days after transplanting), medium number of productive tillers (13 - 18), medium panicle length (20.8 - 24.2 cm), low number of grain panicle^{-1} (98 - 125), medium high 100-grain weight (2.1 - 2.5 g), and medium-high grain yield clump^{-1} (29.2 - 40.6 g). Group II consisted of Tigo-tigo x Sidenuk, Harum Curup x Tigo-tigo, Tigo-tigo x Bestari, Lubuk Durian x Diah Suci, and Harum Curup x Bestari. These populations shared in other common performances, namely medium tall plant stature (116 - 134 cm), high tillering ability (20 - 31 tillers), medium late heading (101 - 113 days after transplanting), medium-late maturing (122 - 144 days after transplanting), medium to high number of productive tillers (14- 27), medium panicle length (19.0 - 23.6 cm), low number of grain panicle^{-1} (106 - 142), medium high 100-grain weight (2,1- 2.7 g), and medium-high grain yield clump^{-1} (19,6 - 36.8 g). Group III only consisted of Hanafi Putih x Sidenuk. This population had similar performances to the populations in Group II, except it had very high tillering capacity (36), very high number of productive tillers (33), high 100-grain weight (3,1 g), and high grain yield clump^{-1} (44,6 g).

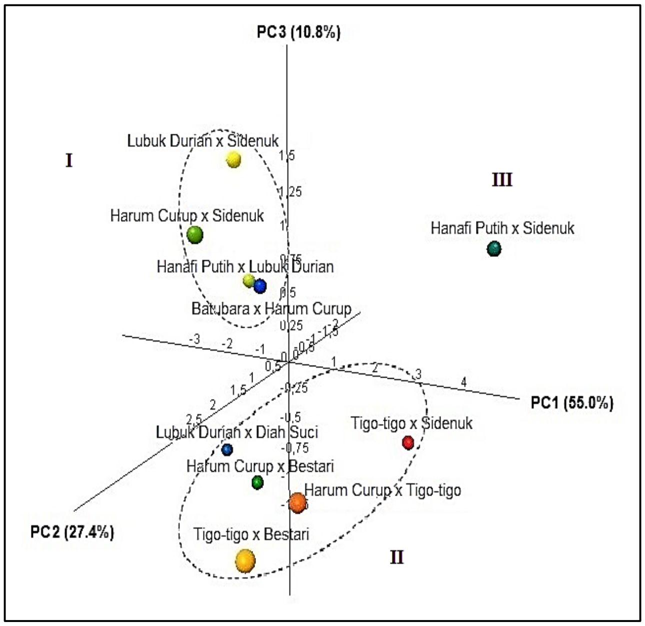

Figure 2. The pattern of variation among 10 F_3 rice populations as plotted on 3 PC axes

Swampland areas often experience *fluctuations* in *water* level due to the seasonal rain: prolonged inundation in the rainy season and drought in the dry season. Such phenomena would also dictate the course of the rice breeding program toward the development of varieties best suited to the ecological conditions of the growing areas. Phillip et al. (2018) suggested that short varieties should only be used for production on favorable areas with low flooding or drought risk. In this regard, the populations of Group I would meet such a requirement. Taller varieties as the populations in Group II and III, on the other hand, would become the option for the production on the flood-prone areas because the risk of completely submerged is lower for taller than shorter plants (Undan et al., 1989).

Estimates of genetic parameters

Table 3 presents the estimates of the genetic parameter for the nine traits studied. The estimates of genotypic coefficient of variation (GCV) were ranged from 3.59 to 29.00%, whereas phenotypic coefficient of variation (PCV) was ranged from 11.67 to 36.20%. It has been commonly adopted that GCV and PCV were considered as low, moderate, and high when their values are 0-10%, 10-20%, and 20% or above, respectively (Gunasekaran et al., 2017).

Table 3: Values of genetic parameters for the traits observed on 10 F_3 rice populations grown on an inland swamp

Observed trait	σ^2_P	σ^2_G	**PCV (%)**	**GCV (%)**	h^2_B	**GA**	**GAM (%)**
Plant height	354.92	315.48	17.63	16.62	0.89	34.50	32.27
Total tiller number clump^{-1}	36.78	31.83	26.21	24.39	0.87	10.81	46.73
Number of productive tillers clump^{-1}	112.52	109.43	11.36	11.21	0.97	21.25	22.76
Heading date	153.59	148.78	9.87	9.71	0.97	24.73	19.69
Maturity date	26.65	21.35	27.36	24.48	0.80	8.52	45.15
Panicle length	3.61	0.65	8.46	3.59	0.18	0.70	3.14
Number of grains panicle^{-1}	224.43	208.96	12.90	12.45	0.93	28.73	24.74
100-grain weight	0.08	0.07	11.53	10.81	0.88	0.51	20.87
Grain yield clump^{-1}	66.43	49.77	24.94	21.58	0.75	12.58	38.48

σ^2_P = phenotypic variance, σ^2_G = genotypic variance, PCV = phenotypic coefficient of variation, GCV = genotypic coefficient of variation, h^2_B = broad sense heritability, GA = genetic advance, GAM = genetic advance as percent of mean.

The higher values of a trait for both parameters indicate the existence of utilizable genetic variability for the trait with a higher chance of improvement through selection based on the phenotypic performance. Total tiller number clump^{-1}, maturity date, and grain yield clump^{-1} were among the traits exhibited high GCV and PCV, revealing a considerable amount of improvement could be expected from these traits. Moderate GCV and PCV were recorded on plant height, number of productive tillers clump^{-1}, number of grains panicle^{-1}, and 100-grain weight, indicating that these traits were amenable for improvement. Rest of the traits, viz. heading date and panicle length, appeared to have limited utility in selection for the improvement by having low GCV and PCV. Accordingly, either hybridization or mutation would be needed to enhance the variability of these traits (Tiwari et al., 2011). For all traits studied, PCV was higher than the corresponding GCV suggesting that both the genetic makeup of the traits and environmental effect had contributed to the expression of the traits. The closer values between GCV and PVC indicate the higher genetic control and the smaller effect of environment on the expression of the traits.

High broad sense heritability (h^2_B >0.60) was observed on all observed traits, except panicle length. A low estimate of broad sense heritability for panicle length presented in the study was in line with those previously reported by Lestari et al. (2015). Broad-sense heritability provides the ideas on the relative influence of genetic makeup to the observable trait's variation and the effectiveness of selection based on the phenotypic performances. Nevertheless, it does not provide information on the extent of genetic improvement made by selecting the best individuals.

Genetic advance (GA) is a good indicator of the expected gain by selecting the best performing genotypes for the targeted trait (Islam et al., 2015). High GA for the desired traits indicates that the selection will bring an improvement in the new population performance. To facilitate comparison in the selection gain among traits under study, however, the genetic advance is more useful when expressed in term of genetic advance as percent of the population mean (GAM). Johnson et al. (1955) categorized GAM as high (> 20%), moderate (10 - 20%), and low (< 10%). Thus, by selecting the top 5% of the population, high genetic improvement can be expected for maturity date, grain yield clump^{-1}, total tiller number clump^{-1}, plant height, number of grains panicle^{-1}, and a number of productive tillers clump^{-1}, whereas moderate improvement can be expected for heading date and 100-grain weight.

Combining the information obtained from h^2_B and GAM would elucidate the mode of gene action governing the trait inheritance and, thus, provide a measure for the efficacy of selection implemented in the varietal development (Shukla et al., 2004). High or moderate h^2_B along with high GAM was expressed on plant height, total tiller number clump^{-1}, number of productive tillers clump^{-1}, maturity date, number of grains panicle^{-1}, and grain yield clump^{-1}, implying that the additive gene action was preponderance in governing the traits inheritance and, hence, offering for straight phenotype-based selection to improve these traits (Acquaah, 2012). High h^2_B paired with moderate GAM was recorded on heading date and 100-grain weight, implying the involvement of non-additive gene actions in governing these traits inheritance and the improvement through simple selection would possibly be hindered by non-additive gene effects (Bughio et al., 2009). Low h^2_B paired with low GAM was found on panicle length, indicating that this trait was predominantly governed by environment and phenotypic selection for the trait may not be worthwhile.

Conclusion

The present study signified the presence of an adequate variability among 10 F_3 rice populations readily exploitable for the development of rice varieties well adapted to swampland. The principal component analysis sorted the populations into distinguishable groups on the basis of the observed traits and helped the breeders in assigning the populations with respect to suitability for different swampland hydrological conditions. The magnitudes of broad sense heritability and genetic advance signified that that selection based on phenotypic performances would bring about appreciable genetic improvements for all traits except panicle length. As grain yield improvement is also an important embedded task in the rice breeding program for swampland areas, future selection activities would be addressed on maximizing the grain yield with the reference to the inherent hydrological conditions of targeted swampland production areas.

Contribution of Authors

Chozin M: Conceived Idea, Statistical Data Analysis and Interpretation, Manuscript Writing

Sumardi S: Designed Research Methodology, Data Collection, Manuscript final reading and approval

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References

Acquaah G, 2012. Principles of plant genetics and breeding, 2nd Edition. John Wiley & Sons.

Addinsoft SARL, 2010. XLSTAT software, version 9.0. Addinsoft, Paris, France.

Allard RW, 1999. Principles of plant breeding. John Wiley & Sons, New York.

Alkuddsi Y, Patil SS, Manjula SM, Patil BC, Nadaf HL and Nandihali BS, 2013. Genetic variability studies in segregating generation of *Gossypium barbadense* lines in cotton. Mol. Plant Breed. 4(25): 209-213.

Bailey-Serres J, Fukao T, Ronald P, Ismail A, Heuer S and Mackill D, 2010. Submergence-tolerant rice: SUB1's journey from landrace to modern cultivar. Rice. 3(2-3): 138-147.

Becker WA, 1984. Manual of quantitative genetics. 4th Edition. Academic Enterprises, Pullman, Washington.

Bioversity International, IRRI and WARDA, 2007. Descriptors for wild and cultivated rice (*Oryza* spp.). Bioversity International, Rome, Italy; International Rice Research Institute, Los Banos, Philippines; WARDA, Africa Rice Center, Cotonou, Benin.

BPS, 2016. Consumption of calorie and protein of Indonesia and province. National Socio-Economic Survey, Book 2. BPS-Statistic Indonesia.

BPS, 2018. Dynamic table: Rice production and harvested areas 2011-2015. BPS-Statistics Indonesia. https://www.bps.go.id.

Bughio HR, Asad MA, Odhano IA, Arain MA and Bughio MS, 2009. Heritability, genetic advance and correlation studies of some important traits in rice. Int. J. Biol. Biotechnol. 6(1/2): 37-39.

Gunasekaran K, Sivakami R, Sabariappan R, Ponnaiah G, Nachimuthu VV and Pandian BA, 2017. Assessment of genetic variability, correlation and path coefficient analysis for morphological and quality traits in rice (*Oryza sativa* L.). Agric. Sci. Digest. 37(4): 251-256.

Houterman J, Djoeachir M, Susanto RH and van Steenbergen F, 2004. Water resources management during transition and reform in Indonesia: Toward an integrated perspective on agricultural drainage. Agriculture and Rural Development Working Paper 14. World Bank.

IRRI, 2013. Standard evaluation system (SES) for rice, 5th edition. International Rice Research Institute, Manila.

Islam MA, Raffi SA, Hossain MA and Hasan AK, 2015. Analysis of genetic variability, heritability and genetic advance for yield and yield-associated traits in some promising advanced lines of rice. Prog. Agric. 26(1): 26-31.

Johnson HW, Robinson HF and Comstock RE, 1955. Estimates of genetic and environmental variability in soybeans. Agron. J. 47(7): 314-318.

Jolliffe IT, 2002. Principal component analysis. 2nd edition. Springer-Verlag, New York.

Kadarmanto. 2018. Improvement of Indonesian rice statistics using area sample frame (ASF) approach. Asia and Pacific Commission on Agricultural Statistics Working Paper APCAS/18/9.2.3P. http://www.fao.org/3/bu598en/bu598en.pdf.

Kaiser HF, 1960. The application of electronic computers to factor analysis. Educ. Psychol. Meas. 20(1): 141-151.

Lestari AP, Sopandie D and Aswidinnoor H, 2015. Panicle length and weight performance of F3 population from local and introduction hybridization of rice varieties. Hayati J. Biosci. 22 (2): 87-92.

Nursyamsi D and Noor M, 2013. Swampland as barns for the future. Indonesian Agency for Agricultural Research and Development (IAARD), Jakarta.

Ogasawara H, 2002. Exploratory second-order analyses for components and factors. Jpn. Psychol. Res. 44(1): 9-19.

Philip D, Jayeoba O O, Ndripaya YD and Fatunbi AO (2018). Innovation Opportunities in the Rice Value Chain in Nigeria. FARA Research Report Vol. 2(3) PP 48.

Rumanti IA, Nugraha Y, Wening RH, Gonzaga ZJC, Nasution A, Kusdiaman D and Septiningsih EM, 2016. Development of high-yielding rice varieties suitable for swampy lands in Indonesia. Plant Breed. Biotechnol. 4(4): 413-425.

SAS Institute Inc, 2004. SAS/STAT User's Guide Version 9, 4th edition. Statistical Analysis Institute Inc., Cary, North Carolina, USA.

Sharma JR, 2006. Statistical and biometrical techniques in plant breeding. New Age International, New Delhi, India

Shobha Rani N, Subba Rao LV and Viraktamath BC, 2006. National Guidelines for the conduct of tests for Distinctness, Uniformity and Stability: Rice (*Oryza sativa* L). Technical Bulletin 20, Directorate of Rice Research, Directorate of Rice Research, Rajendranagar, Hyderabad, India.

Shukla S, Bhargava A, Chatterjee A and Singh SP, 2004. Estimates of genetic parameters to determine variability for foliage yield and its different quantitative and qualitative traits in vegetable amaranth (*A. tricolor*). J. Genet. Breed. 58(2): 169-176.

Silitonga TS, 2017. Management and utilization of rice germplasm in Indonesia. Buletin Plasma Nutfah 10(2): 56-71. [In Indonesian with abstract in English]

Singh RK and Chaudhary BD, 1985. Biometrical methods in quantitative genetic analysis. Kalyani Publishers, Ludhiana, India.

Sinha AK, Mallick GK and Mishra PK, 2015. Diversity of grain morphology on traditional rice varieties of lateritic regions of West Bengal. World J. Agric. Sci. 11(1): 48-54.

Soomro ZA, Kumbhar MB, Larik AS, Imran M and Brohi SA, 2010. Heritability and selection response in segregating generations of upland cotton. Pak. J. Agric. Res. 23(1-2): 25, 30.

Tigerstedt P, 1994. Adaptation, variation and selection in marginal areas. Euphytica. 77(3): 171-174.

Tiwari DK, Pandey P, Tripathi S, Giri SP and Dwivedi JL, 2011. Studies on genetic variability for yield components in rice (*Oryza sativa* L.). Adv. Agric. Bot. 3(1): 76-81.

Undan RC, Bhuiyan SI and Agua MM, 1989. Characterizing flood-prone rice areas and predicting flooding hazards. J. Hydrol. 107(1-4): 297-307.

World Atlas, 2019a. 10 largest rice producing countries. https:// www.worldatlas.com/ articles/ the-countries-producing-the-most-rice-in-the-world.html.

World Atlas, 2019b. Top 10 rice consuming countries. https://www.worldatlas.com/ articles/top-10-rice-consuming-counties.html