

## GENETIC DIVERSITY, HERITABILITY AND CORRELATION BETWEEN LOCAL CULTIVARS OF UPLAND RICE

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### ABSTRACT

Paddy is one of the important cereal crops as food a main food for a third of the world's population, including Asia. Production of paddy rice plants can be improved through plant genetic improvement. The objective of this study was to examine the genetic diversity, heritability, and correlation between the characteristics of several local upland rice cultivars. This study was carried out in Tamarenja Village, Sindue District, Donggala Regency, Central Sulawesi Province. It was begun in May to October 2018. A Randomized Block Design with eight cultivars as a genotypic treatment and repeated three times was used in this study. There were 24 trial plots in total. Variables observed included plant height, number of leaves, length of leaves, number of tillers, number of productive tillers, age of panicle exit, panicle length, harvest age, number of seeds per panicle, seed length, seed diameter, weight of 100 seeds, and total yield. The results showed that the genetic influences were more dominant than the environment on all observed variables except the weight of 100 seeds and seed diameter. The number of seeds per panicle, the number of tillers and the number of productive tillers were traits that have a high value on heritability and genetic progress. Panicle length, seed diameter and weight of 100 seeds were characteristics that have a high genetic correlation coefficient on upland rice yields. The weight of 100 seeds has a direct influence and high genetic correlation to the results so that it can be used as a direct selection criterion to increase upland rice yields.

**Keywords:** Correlation between characters, Genetic diversity, Heritability, Local upland paddy.

### INTRODUCTION

Paddy is one of the important cereal crops that belongs to the family members of Poaceae and is used as a main food for a third of the world's population including Asia. Rice is the first strategic food commodity and prioritized in agricultural development in Indonesia (Somantri, 2001). The production of rice in Indonesia in 2017 reached 81.382 million tons with productivity of 53.03 kw / ha-1. Thus, the contribution of upland field paddy is limited to the national rice production. The contribution was 4.64% with productivity of 30.27 kw/ha (Ministry of Agriculture, 2017). Therefore, the contribution of field paddy to national production needs to be increased.

To overcome this problem, expanding the planting area and increasing the productivity of field rice are possible. The local rice is currently only dependent on conventional cultivation by the local community there has not been sufficient conservation of genetic resources to protect the cultivars from extinction and genetic erosion (Hendra *et al.* 2002). In addition, the utilization of local paddy cultivars in paddy breeding programs for assembling superior varieties has not been optimized.

Non-technical constraints to meet the food needs of Indonesian people and self-sufficiency in rice are related to the shifting function of paddy fields into residential areas or plantation crops as well as the development of rice varieties that are more oriented to lowland rice. The land use

change causes a decrease in the carrying capacity of paddy fields to rice production. Upland can be alternatively substituted to paddy fields to meet rice needs (Saleh et al., 2009).

Estimation of genetic parameters must be done before fixing a trait needed to improve the yield of a crop. Genetic parameters usually include estimating the coefficient value of genetic diversity, heritability and correlation between traits (Samudin and Saleh, 2009). Information about genetic parameters in upland plants is still very lacking so this study aims to determine the coefficient value of genetic diversity, heritability and correlation between traits.

## METHODS

This study designed as a randomized block design with eight cultivars as a genotypic treatment and repeated three times. Therefore we had obtain 24 trial plots. The study located in Tamarenja Village, Sindue District, Donggala Regency, Central Sulawesi Indonesia. The research began from May to October 2018.

A total of eight paddy Gogocultivars were planted in different plot with 30 x 30 cm space between plants. The plants fertilized using NPK (Mutiara, Indonesia) at a dose of 200 kg ha<sup>-1</sup>. Observations began in the generative phase. The rice harvested during physiological ripe, indicated by changing colors from green to yellow.

The genotypic and phenotypic diversity coefficients were calculated according to the formula of Samudin (2005) as follows:

$$KKF = (\sqrt{\sigma_f^2/\bar{x}}) \times 100 = \sigma_f^2 = KTP/r$$

$$KKG = (\sqrt{\sigma_g^2/\bar{x}}) \times 100 = \sigma_g^2 =$$

$$KTG - KTG/r$$

where :

KKG = Genetic Diversity Coefficient  
 KKF = Phenotype Diversity Coefficient  
 r = repetition

The heritability was calculated by the formulation of Yawen et al. (1997), as follows:

$$h^2 = \frac{\sigma_g^2}{\sigma_f^2}$$

where :

$h^2$  = heritability  
 $\sigma_g^2$  = genetic diversity  
 $\sigma_f^2$  = phenotypic diversity

Genotypic and phenotypic correlation coefficients of trait pairs calculated according to the formula of Samudin (2005) as follows:

$$rp = \sigma_{pxy} / \sqrt{\sigma_p^2x \cdot \sigma_p^2y}$$

$$rg = \sigma_{Gxy} / \sqrt{\sigma_G^2x \cdot \sigma_G^2y}$$

Where :

$\sigma_{pxy}$  = phenotypic covariant pairs x character and y character

$\sigma_{Gxy}$  = genotypic covariant pairs x character and y character

$\sqrt{\sigma_p^2x \cdot \sigma_p^2y}$  = phenotypic correlation pairs of character x and y

$\sqrt{\sigma_G^2x \cdot \sigma_G^2y}$  = genotypic correlation pairs of character x and y

$\sigma_G^2x$  = genotypic diversity of x

$\sigma_G^2y$  = genotypic diversity of y

$\sigma_p^2x$  = phenotypic diversity of x

$\sigma_p^2y$  = phenotypic diversity of y

## RESULTS AND DISCUSSIONS

**Genetic Diversity Coefficient.** The coefficient of genetic diversity provides a comparison of genetic diversity in various quantitative traits (Toshimenla et al Changkija, 2013). Bekele et al (2013) divided the coefficient of genetic diversity into three groups, namely high if the coefficient of genetic diversity > 20%, classified as moderate if the coefficient of genetic diversity was 10-20% and classified as low if the coefficient of genetic diversity

<10%. Our study showed a high coefficient of genetic diversity on variables observed, except the weight of 100 seeds classified as moderate, and the seed diameter classified low genetic diversity.

The high genetic diversity coefficient showed that differences in the characteristics observed were influenced by genetic traits that were more dominant than environmental factor. Such conditions are greatly desired by breeders in making selections. In addition, the high coefficient of genetic diversity showed that in our selection process it is fast to separate superior genotypes from non-superior ones. Conversely, if the coefficient of genetic diversity in a population was small, then we will find it difficult to separate superior genotypes from non-superior ones.

The results of this study was in line with the results found by Vanisree et al. (2013). Bisne et al (2009) found a coefficient of high genetic diversity for the harvest index, total number of seeds contained, and weight of 100 seeds.

**Heritability.** Heritability is a genetic parameter used to measure the ability of a plant in terms of reducing its characters to its generation. The higher the value of heritability, the faster a trait is passed to the next generation. According to Stansfield, (1983) the value of heritability is high if > 50%; heritability of 20-50% is classified as

moderate, while heritability <20% is classified low. Hence, the crop yield, weight of 100 seeds, plant height, number of seeds per panicle, panicle length, number of tillers, seed length, leaf length, panicle exit age, number of productive tillers, and number of leaves were traits that had a high heritability. It is indicate that selection in the crossing above characters will give a chance to the reduce these traits in the next generation. This is in line with the statement of Kartika ningrum et al. (2005) which states that heritability is a genetic parameter that is used to measure the ability of a genotype in plant populations in inheriting character traits both controlled quantitatively and qualitatively.

Harvest age had a moderate heritability, while seed diameter had a low heritability value. Both of these traits had small chance to reduce their character to the next generation. In this case, improvements in the is difficult to achieve. According to Bisne et al., (2009) this difficulty is caused by the role of non-genetic influences and the role of non-additive genes. This is in line with the results of the study of Maryenti et al. (2014), if the heritability is low, the selection will relatively ineffective. In addition, the appearance of plant phenotypes is more affected by environmental factors compared to genetic factors.

Table 1. Coefficient of Genetic Diversity.

No	Observation Variables	Genetic Diversity	Coefficient of Genetic Diversity (%)
1	Plant height	114.837	83.90
2	Number of leaves	0.563	32.90
3	Length of leaves	41.544	78.81
4	Number of tillers	1.015	45.92
5	Number of productive tillers	0.670	38.73
6	Age of panicle produced	1.205	29.71
7	Length of panicle	12.759	63.12
8	Harvest age	1.051	23.79
9	Number of seed per panicle	1866.813	22.00
10	Length of seed	0.732	28.51
11	Diameter of seed	0.001	1.92
12	Weight of 100 seed	0.082	16.61
13	Yield	0.106	18.01

Table 2. The Heritability of Local Upland Rice Cultivar Properties.

No	Observation Variables	Heritability (%)	Genetic progress
1	Plant height	81.270	15,64
2	Number of leaves	55.752	28,50
3	Length of leaves	64.947	20,51
4	Number of tillers	74.292	47,63
5	Number of productive tillers	57.471	36,65
6	Age of panicle produced	59.471	16,41
7	Length of panicle	77.415	25,92
8	Harvest age	42.174	9,44
9	Number of seed per panicle	79.221	50,96
10	Length of seed	70.454	21,04
11	Diameter of seed	10.555	1,15
12	Weight of 100 seed	85.821	23,70
13	Yield	87.899	24,60

Table 3. Genotypic Correlation (above diagonal) and Phenotypic Correlation (below diagonal) Between Characters of Upland Paddy.

Characters	TT	JD	PD	JA	JAP	UKM	PM	UP	JBPM	PB	DB	100 seed	yield
TT	-	1.00*	-0.69*	0.75*	0.77*	1.00*	-0.16tn	0.90*	0.79*	0.22tn	-1.04*	-0.77*	-0.74*
JD	0.95*	-	-0.56*	0.98*	0.86*	1.10*	-0.24tn	0.83*	1.00*	0.37tn	-1.01*	-1.00*	-1.01*
PD	-0.43tn	-0.26tn	-	-0.35tn	-0.19tn	-0.05tn	0.63*	0.12tn	0.30tn	-0.05tn	-0.11tn	0.16tn	0.11tn
JA	0.58*	0.61*	-0.22tn	-	1.02*	1.00*	-0.47*	1.00*	0.42tn	0.92*	-0.50*	-0.24tn	0.22tn
JAP	0.51*	0.46*	-0.11tn	1.00*	-	1.06*	-0.37tn	1.00*	0.30tn	0.81*	-0.49*	-0.16tn	-0.13tn
UKM	0.87*	0.83*	-0.04tn	0.70*	0.61*	-	0.33tn	1.02*	1.03*	0.54*	-1.00*	-0.57*	-0.55*
PM	0.21tn	-0.18tn	0.45tn	-0.31tn	-0.30	0.09tn	-	0.55*	0.20tn	-0.10tn	0.81*	0.51*	0.50*
UP	0.48*	0.30tn	0.01tn	0.57*	0.47*	0.58*	0.48*	-	0.45tn	0.86*	-0.54*	0.21tn	0.26tn
JBPM	0.66*	0.83*	0.34tn	0.28tn	0.19tn	0.75*	0.13tn	0.25tn	-	0.09tn	-1.04*	-1.00*	-1.02*
PB	0.21tn	0.22tn	-0.07tn	0.75*	0.59*	0.30tn	-0.14tn	0.50*	0.03tn	-	0.41tn	0.37tn	0.41tn
DB	-0.35tn	-0.48*	-0.03tn	-0.08tn	-0.10tn	-0.27tn	0.10tn	0.11tn	-0.55*	0.31tn	-	1.02*	1.02*
100 seed	-0.07tn	-0.73*	0.11tn	-0.13tn	-0.04tn	-0.48*	0.47*	0.14tn	-0.90*	0.25tn	0.70*	-	1.03*
yield	-0.68*	-0.71*	0.09tn	-0.12tn	-0.04tn	-0.46*	0.46*	0.15tn	-0.91*	0.29tn	0.72*	1.02*	-

Note: TT:.....; JD: ....; PD: .... and so on.

Table 4. Direct and Indirect Effects of Local Upland Paddy Characteristics.

Characters	TT	JD	PD	JA	JAP	UKM	PM	UP	JBPM	PB	DB	100 seed	Yield
TT	<b>1,59</b>	3,49	-1,14	6,25	-7,76	-1,56	-0,17	3,77	-0,08	-2,48	-2,67	3,11	-0,74*
JD	3,49	<b>0,15</b>	-0,25	-3,49	3,71	1,78	-0,11	-2,61	1,37	2,52	1,40	-1,85	-1,01*
PD	-1,14	-0,25	<b>-0,01</b>	0,56	-0,63	0,43	-0,29	0,19	0,71	-0,13	-0,87	0,91	0,11tn
JA	6,25	-3,49	0,56	<b>0,21</b>	-1,76	-3,28	-2,44	1,44	3,08	6,83	-0,93	0,18	-0,22tn
JAP	-7,76	3,71	-0,63	-1,76	<b>-0,20</b>	7,54	3,10	-4,99	-5,21	-7,00	3,06	-2,66	-0,13tn
UKM	-1,56	1,78	0,43	-3,28	7,54	<b>-0,10</b>	1,59	-1,43	-1,63	-1,90	2,13	-2,56	-0,55*
PM	-0,17	-0,11	-0,29	-2,44	3,10	1,59	<b>0,01</b>	-1,13	-0,04	-0,33	1,29	-0,62	0,50*
UP	3,77	-2,61	0,19	1,44	-4,99	-1,43	-1,13	<b>0,14</b>	1,99	2,53	-1,85	2,35	0,26tn
JBPM	-0,08	1,37	0,71	3,08	-5,21	-1,63	-0,04	1,99	<b>-0,06</b>	0,65	-0,95	-0,26	-1,02*
PB	-2,48	2,52	-0,13	6,83	-7,00	-1,90	-0,33	2,53	0,65	<b>-0,11</b>	-1,01	1,98	0,41tn
DB	-2,67	1,40	-0,87	-0,93	3,06	2,13	1,29	-1,85	-0,95	-1,01	<b>-0,05</b>	-0,62	1,02*
100 seed	3,11	-1,85	0,91	0,18	-2,66	-2,56	-0,62	2,35	-0,26	1,98	-0,62	<b>1,09</b>	1,03*

Estimation of heritability has been understood to be useful in identifying the relative value of selection based on phenotypic expressions of different

characters. The value of heritability itself does not provide any indication of the level of genetic progress that will occur from the results of the best individual selection (Perera et al., 2014). According to Johnson et al. (1955) the value of heritability, which is pleasing to the estimation of genetic progress hope, is more useful than the estimated value of heritability itself in predicting the influence of selection. High heritability values are not always followed by high genetic progress values (Table 2). Characters that have a high heritability value and followed by high expectations of genetic progress indicate that such traits are controlled by additive genetic influences (Ahmadikhah, 2010, Bisne et al., 2009; Hosseini, et al., 2012). Based on the results of this study, the number of seeds per panicle, number of tillers and the number of productive tillers were traits that had high heritability values followed by high genetic progress. When associated with selection, the three traits can be selected to the initial generation (F2).

The character is a complex entity and the character inheritance depends on a number of characters that are often polygenic and strongly influenced by environmental factors (Nadarajan and Gunasekaran, 2005). The closeness of the relationship was measured through the correlation coefficient between the characters which was an important factor. According to Falconer and Mackay (1996) correlation between characters can be used to find out the correlated response in indirect selection.

The genotypic correlation coefficient found in this study was greater than the phenotypic correlation coefficient. This study justifying the previous studies by Kishore et al., (2015) and Idris et al., (2012). Greater genetic correlation coefficient than phenotypic is preferred by breeders since the character observed is not influenced by the environment.

Table 3 shows plant height, leaf length, panicle exit age and number of seeds per panicle have a high and significant

negative genetic correlation with upland paddy yields. Means that the higher the plant habitat, number of leaves, and number of seeds per panicle will reduce. In contrast, the faster the panicle comes out, the more the yield of the crop will increase. Generally, farmer like to harvest quickly with high yields. Panicle length, seed diameter and weight of 100 seeds had a high positive and significant genetic correlation with upland rice yields. Subsequently, the longer the panicle, the larger the size of the seeds and the higher the weight value of 100 seeds, and the higher the yield of upland paddy.

The increasing number of variables in correlation studies, indirect associations will become complex and important. In such situations, path coefficient analysis is useful for knowing the direct and indirect causes of the association. Path coefficient analysis allows a critical examination of specific factors that act to produce certain correlations and measure the relative importance of each factor (Ganapati, et al., 2014).

This study indicates the high direct influence is not always followed by a correlation between two high traits. Plant height has a high direct effect on yield but its correlation with results was not pronounced. Similarly, panicle length had a high correlation with upland rice yields but had a low direct effect on yield. Direct selection, what needs to be considered is a high correlation between traits and has a high direct effect on results. Based on these assumptions, the weight of 100 seeds is a trait having a high correlation coefficient with respect to results and has a high direct effect on results. Hossaini et al. (2012) found that flowering age had a high correlation and a high direct effect on crop yield.

## CONCLUSION

Based on the results of the study it can be concluded as follows:

All observed characters have a high coefficient of genetic diversity except the weight of 100 seeds and yields were classified as moderate while the seed diameter was low.

The number of seeds per panicle, the number of tillers and the number of productive tillers were the traits that had a high heritability and genetic progress.

Panicle length, seed diameter and 100 seed weight were characteristics that had a high genetic correlation coefficient on upland paddy rice yield.

## Recommendation

Panicle length, diameter of seeds, and weight of 100 seeds can be used as indirect selection criteria to improve rice yield. Selection can be done directly on the character of 100 seeds weight to improve paddy rice yield.

## BIBLIOGRAPHY

- Ahmadikhah, A., 2010. *Study on selection effect, genetic advance and genetic parameters in rice*. Annals of Biological Research, 1(4):45-51.
- Bekele, B. D., S. Rakhi, G. K. Naveen, P. J. Kundura, H. E. Shashidhar., 2013. *Estimation of Genetic Variability and Correlation Studies for Grain Zinc Concentrations and Yield Related Traits in Selected Rice (Oryza sativaL.) Genotypes*. Asian J. Exp. Biol. Sci. 4(3):391-397.
- Bisne, R., A. K. Sarawgian dan dS. B. Verulkar., 2009. *Study Of Heritability, Genetic Advance And Variability For Yield Contributing Characters In Rice*. Bangladesh J. Agril. Res. 34(2):175-179.
- Falconer, D.S, T.F.CMackay., 1996. *Introduction to Quantitative Genetics*. Fourth Edition. London: Longman
- Ganapati, R.K, M.G, Rasul, M.A.K, Mian and U. Sarker., 2014. *Genetic Variability and Character Association of T-Aman Rice (Oryza Sativa L)*. International Journal of Plant Biology & Research, 2(2):1013.
- Hendra M, E Guhardja, D Setiadi, E.B Walujo, Y Purwanto., 2002. *Cultivation Practices and Knowledge of Local Rice Varieties among Benuaq Farmers in MuaraLawa District West Kutai, East Kalimantan-Indonesia*. Biodiversitas 10: 98-103.
- Hosseini, S. J., Z, T, Sarvestani, H. Pirdashti, A. Afkhami and S. Hazrati., 2012. *Estimation of heritability and genetic advance for screening some rice genotypes at salt stress conditions*. International journal of Agronomy and Plant Production. 3(11): 475-482.
- Idris, A.E., F. J. Justin, Y. M. I. Dagash and A. I. Abuali., 2012. *Genetic Variability and Inter Relationship between Yield and Yield Components in Some Rice Genotypes*. American Journal of Experimental Agriculture 2(2): 233-239.
- Johnson, H.W., H.F. Robinson and R. Comstock., 1955. *Estimates of genetic and Environmental variability in Soybeans*. Agronomy Journal, 47(7): 314-318.
- Kartikaningrum, S. dan K.Efendi., 2005. *Keragaman genetik plasma nutfah anggrek Spathoglothis*. J. Hort. 15(4): 30
- Kementerian Pertanian, 2017. Pusat Data dan Sistem Informasi Pertanian, Kementerian Pertanian Republik Indonesia.
- Kishore, N.S., T. Srinivas, U. Nagabhushanam, M. Pallavi and S.k. Sameera., 2015. *Genetic Variability, Correlation And Path Analysis For Yield And Yield Components In Promising Rice (Oryza sativaL.) Genotypes*. SAARC J. Agri., 13(1):99-108.

- Maryenti, T, M. Bermwaidan J. Prasetyo., 2014. *Heritabilitas Dan Kemajuan Genetik Karakter Ketahanan Kedelai Generasi F2 Persilangan Tanggamus X B3570 Terhadap Soybean Mosaic Virus*. Jurnal Kelitbangan Vol. 02 (02)
- Nadarajan N and M. Gunasekaran., 2005. *Quantitative Genetics and Biometrical Techniques in Plant Breeding*. Kalyani Publishers.
- Perera, U.I.P., D. Ratnasekera, S.G.J.N. Senanayake, D. Sumith, Z. Abeysiriwardena, 2014. *Genetic parameter sand correlations of yield attributing characteristics of weedy rice in Sri Lanka*. J.Natn.Sci.Foundation Sri Lanka, 42 (4): 299-306
- Saleh, M.S., F. Pasaru., M. Yunus., 2009. *Eksplorasi Padi Gogo Lokal di Kabupaten Banggai*. Media Litbang Sulteng.
- Samudin, S. dan M. S. Saleh., 2009. *Parameter Genetik Tanaman Aren (Arenga pinnata L.)*. J. Agroland 16 (1) : 17 - 23,
- Samudin, S., 2005. *Penentuan Indikator Seleksi Untuk Perbaikan Hasil dan Mutu Tembakau Madura*. J. Agroland 12(4): 339-445.
- Somantri IH., 2001. Wild Rice (Oryza spp.): *Their Existence and Research in Indonesia*. Buletin Agro Bio 5(1):14–20
- Stansfield, W.D., 1983. *Theory and Problem in Genetics Schaum's out Lines Series*. Mc Graw Hill Book. Co.
- Toshimenla and S. Changkija, 2013. *Genetic Variability in Yields and its Component Characters in Upland Rice of Nagaland*. Indian Journal of Hill Farming 26(2):84-87.
- Vanisree, S., K. Swapna, Ch.D. Raju, Ch.S. Raju and M. Sreedar., 2013. *Genetic variability and selection criteria in rice*. Journal of biological and scientific opinion, 1(4):341-346.