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Genetic Diversity, Heritability, Correlation and Path Analysis Yields and Yield Component Local Rice Variety

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Abstract
More than 95% of Indonesia's population makes rice a staple food so that the need exceeds production, as a result, rice imports continue to be carried out by the government. Efforts should be made to increase production through genetic improvement of plants. This study aims to determine genetic diversity, heritability, correlation and path analysis between yields and yield components of local rice varieties. The study was conducted in the Sidondo Experimental Garden, Sidondo Village, Biromaru District, Sigi Regency, Central Sulawesi Province-Indonesia, from March to August 2015. Using a Randomized Block Design with 22 varieties of treatments and three groups so that there were 66 treatment units. The results showed that genetic influences were more dominant than environmental influences in expressing all observed characteristics except panicle length. Plant height, leaf area, age of flowering, age of harvest, angle of leaf flag, number of filled grains and panicle exit age have high heritability and genetic advance. Leaf width and weight of 1000 seeds have a high genetic correlation and are very real on yield. The weight of 1000 seeds has a high genetic correlation coefficient and a high direct effect on yield so that it can be used as a direct selection criterion to increase rice yield.

I. INTRODUCTION

The human population in the world in 2030 is estimated at 8 billion people and therefore the production of rice plants must be increased by 50% to meet the needs of the human population (Miah et al. 2013). Rice is the main high-value crop in the world and is the main source of food needed by more than one-half of the world's population and over 95% of the world's rice is used for human food (Rafii et al. 2014.). More than 95% of Indonesia's population uses rice as the main consumption material so that their needs exceed the products produced. According to (Handayani and Sulistyawati Badan Penelitian dan Pengembangan Provinsi Jawa Tengah 2013) over 37 years the average rice consumption per year is 27,859.14 thousand tons which are still higher than the average rice production per year which only reaches 26,725.78 thousand tons. This condition causes imports to continue to be carried out by the government to maintain national rice stock. Rice imports carried out continuously will harm domestic producers so that efforts to solve them need to be sought.

The development of high-yielding varieties through genetic improvement is one of the strategic ways that needs to be done. The development of these varieties requires some basic knowledge such as genetic diversity, heritability, and the correlation between traits. Knowledge of the genetic diversity of the traits that contribute to the outcome, the relationship between these traits and their relationship to the results is essential for the success of a plant breeding program(Singh, Singh and Singh 2014). The genotypic and phenotypic diversity coefficients are useful in predicting the diversity in germplasm (Idris et al. 2012). Genetic progress in selection depends mainly on the amount of genetic diversity (Selvaraj and Nagarajan 2011). The greater the genetic diversity, the easier we will get the desired genotype. The results of (Akhtar et al. 2011.) show that there are several characteristics of rice plants that have high genotypic diversity.

The genetic diversity coefficient along with heritability estimators will provide the best picture of the amount of progress expected from selection (Selvaraj and Nagarajan 2011). Thus, knowledge about heritability and genetic progress is very important to determine traits that can be passed on to further generations. The results of the study of (Paikhomba et al. 2014.) showed that high heritability in the broad sense of plant height, age of 50% flowering, panicle length, number of seeds filled per panicle and seed yield.

The correlation coefficient can help identify traits that have little or significant influence in the selection program. Knowledge of the relative contribution of individual traits to results can be known by correlation studies, therefore simple correlations cannot provide sufficient information about the contribution of each factor to the results (Rangare et al. 2012.). The cross print coefficient has been used extensively by breeders on many cultivated plants to understand complex relationships between traits and to identify sources of variation from yield. Analysis of path coefficients divides the genetic correlation between yields and their components into direct and indirect effects so that it is more effectively used to identify useful traits as selection criteria for improving rice crop yields (Gregorio and Nwilene 2011; Sadeghi, S.M. 2011.). Based on the description above, this study aims to determine genetic diversity, heritability, correlation and path analysis between yields and yield components of some local rice varieties.

II. MATERIALS AND METHODS

2.1. Place and Time of Research

Twenty-two local rice varieties used came from exploration results in three regencies namely Banggai Regency, Poso Regency and Sigi Regency in 2012. The 22 varieties are Kamba, golden Kamba, cashew Kamba, Kamba power, Kamba kolori, Kamba bulili, Raki, Sia, Halaka, Pancasila, Kahari, Habo, Ranta, Sampara, Landaeo, Bausarum, Dogan, Toni, Black, Lauda, Kelor and Lamala.

The study was conducted in the Sidondo Experimental Garden, Sidondo Village, Biromaru District, Sigi Regency, Central Sulawesi Province, from March to August 2015.

2.2. Research Implementation

The study used a Randomized Block Design with 22 varieties of treatments and three groups so that there were 66 experimental units. The soil was cleaned of grass and 66 plots were made with a size of 2.1m x 1.2m each. A week before planting, mature cow manure is given as much as 2 $kg.plot^{-1}$ (equivalent to 10 $tons.h^{-1}$) and mixed until blended. The day before planting, the plot is watered until it reaches the field capacity. The seeds are planted in a hole manner as deep as 2 cm, 3-5 seeds per hole (according to farmer's practice) with a spacing of 20 cm x 20 cm, 28 clumps per plot. Irrigation is done once a week. Observations were carried out randomly on 10 plants per plot. Variables observed included plant height at harvest, 50% flowering age, stem diameter, panicle length, leaf length, leaf width, flag leaf angle, harvest age, number of seeds per panicle, number of filled grains per panicle, number of empty grains per panicle, leaf area, panicle age, weight of 1000 seeds and yield.

2.3. Data Analysis

Data analysis using Minitab version 14.0 and excel program 2010. Genotypic and phenotypic diversity coefficients were calculated using the (Burton and DeVane 1953), heritability and genetic advance were calculated using the (Johnson et al. 1955.) formulation, correlation coefficients were calculated using the (Al-Jibouri et al. 1958.) and path analysis were calculated using the (Dewey, and Lu 1959.).

III. RESULTS AND DISCUSSION

3.1. Genetic Diversity and Heritability

The success of a plant breeding program depends on the genetic diversity of the traits to be improved in a population. There are variations or differences between genotypes used in research. The coefficient of genetic diversity ranges from 7.81 to 54.29 while the value of the phenotype diversity coefficient ranges from 7.01 to 52.44 (Table 1). There is a tendency that the coefficient of genetic diversity is greater than the coefficient of phenotype diversity in all observed traits except panicle length. That is, genetic influences are more dominant than environmental influences in expressing all observed traits except panicle length (Sravan et al. 2012). The same research results have also been found by several previous researchers on the same plant as (Idris et al. 2012; Sanghera and Kashyap 2012.; Singh and Pandey 2011.). In the selection process, the selection of superior genotypes will be obtained if the phenotype expression is more determined by genetic influences than the environment.

Heritability is a genetic parameter that is very useful in describing the roles that determine suitability and strategies for selecting certain characters (Idris et al. 2012). Heritability values in a broad sense range from 0.68 to 0.99 and all traits observed have high heritability values (Table 2). Similar results have been reported by (Abarshahr, Rabiei and Lahigi 2011; Jayasudha and Sharma 2010; Yadav et al. 2010.).

High heritability values indicate the effectiveness of selection based on phenotypic appearance, although it is not always that high heritability values alone will indicate high genetic advance when selection is made. Therefore, a high heritability value and supported by high genetic advance toward a trait will provide the best picture for genotype selection. The value of the genetic advance of all observed traits ranged from 0.19 to 98.19 with small to high value (Table 2). Stem diameter, panicle length, leaf width, number of tillers, weight 1000 grain and yield have relatively low genetic advance.

The length of leaves and the number of empty seeds are moderate while the other characteristics are high. Traits that indicate high genetic advance means that additive genes play a more important role than non-additive genes so that the inheritance of the parents to the offspring occurs more quickly

Table 1. Mean square, genotypic variance, environmental diversity, phenotypic variance, coefficient of genetic diversity and phenotype variance coefficient for all observed characteristics

Traits observed	Mean square	Genotypic diversity	Environment -tal diversity	Phenotypic diversity	Coef. genetic variation	Coef. Phenotype variation
Plant height	29.43**	623.43	61.46	684.88	17.62	16.81
Stem diameter	30.48**	0.01	0.00	0.01	32.82	31.36
Panicle length	11.49**	3.78	0.91	4.69	7.81	7.01
Leaf length	5.33**	77.75	36.84	114.60	16.71	13.77
Leaf width	13.13**	0.11	0.02	0.13	28.43	25.82
Leaf Area	40.60**	369.11	26.62	395.73	31.76	30.67
Flowering age	1190.76**	336.47	0.85	337.31	20.35	20.33
Harvest age	189.86**	194.91	3.06	197.97	11.38	11.30
Number of tillers	10.42**	2.75	0.72	3.47	42.07	37.44
Corner of the flag leaf	18.89**	1228.33	185.31	1413.64	38.20	35.61
number of seeds contained	40.88**	3591.28	257.28	3848.55	54.29	52.44
The number of empty seeds	7.79**	79.83	27.25	107.08	48.80	42.13
The panicle exit age	926.14**	336.93	1.09	338.02	20.61	20.57
1000 seeds weight	69.19**	12.55	0.54	13.09	14.79	14.49
Yield	16.61**	0.67	0.11	0.78	15.09	16.33

*Note: ** very significantly different*

(Rahman et al. 2014). High heritability does not always have high genetic advance. The results of this study are the same as those conducted by (Author, Elsadig Idris and Abdalla Mohamed 2013; Seyoum, Alamerew and Bantte 2012)

3.2. Correlation between Traits

Correlation analysis between the nature of the results and the components of the results shows that the genotypic correlation coefficient is greater than the phenotypic correlation coefficient (Table 3), meaning that the correlation is caused by genetic influences that are beneficial to plant breeders. The occurrence of correlation is caused by the influence of linkage or pleitropic of genes or the influence of physiological and developmental relationships or environmental influences or the effect of a combination of some of these components (Oad et al. 2002.). Plant height, age of harvest, number of seeds contained and age of panicle out were genotypically and negatively correlated to yield. In contrast, leaf width and weight of 1000 seeds had high and significant genotypic correlations with yields of 0.68 and 0.88, respectively. The results of this study are in line with the study of (Abarshahr, Rabiei and Lahigi 2011) for the weight of 1000 seeds and different from the research of (Kiani and Nematzadeh 2012.) which used 44 F2 populations of rice genotype. The direct effect between yield components on rice genotype yield ranged from 0.00 to 2.59 (Table 4). The weight of 1000 seeds is a trait that has the highest correlation with rice yield. The high correlation coefficient between the weight of 1000 seeds with the results not only influenced by the direct effect of the height is also a contribution of the indirect effect through plant height, stem diameter, leaf length, leaf width, leaf area, flowering age, number of tillers, corner of flag leaves, harvest age panicle length, number of filled grains, number of empty grains and panicle exit age. The results of this study differ from the results obtained by (Abarshahr, Rabiei and Lahigi 2011; Bagheri, Babaeian-Jelodar and Pasha 2011) who found a high direct effect between the number of seeds per panicle on rice yield. This difference is caused by the material used in the study. (Bagheri, Babaeian-Jelodar and Pasha 2011) used six local genotypes, five newly released genotypes, and 15 rice lines.

Table 2. Phenotypic standard deviation, heritability and genetic progress of some traits observed in local rice varieties

Traits observed	Phenotypic standard deviation	Heritability	Genetic Advance (%)
Plant height	26.170	0.91	39.80
Stem diameter	0.098	0.91	0.15
Panicle length	2.166	0.81	2.85
Leaf length	10.705	0.68	11.11
Leaf width	0.367	0.82	0.49
Leaf Area	19.893	0.93	31.31
Flowering age	18.366	0.99	31.30
Harvest age	14.070	0.98	23.75
Number of tillers	1.863	0.79	2.37
Corner of the flag leaf	37.598	0.87	53.87
number of seeds contained	62.037	0.93	98.19
The number of empty seeds	10.348	0.75	12.13
The panicle exit age	18.385	0.99	31.33
1000 seeds weight	3.618	0.96	5.93
Yield	0.885	0.85	1.26

Note: Genetic advance with 10% selection intensity (t = 1.75)

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Table 3. Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients between yields and yield components of local rice varieties

	TT	DB	PD	LD	LSD	UB	JA	SDB	UP	PM	JBB	JBH	UKM	1000	HSL
TT	**1.00**	-0.41ns	0.69**	-0.56*	-0.45ns	0.34ns	0.12ns	0.13ns	0.43ns	0.47ns	0.74**	-0.41ns	0.35ns	-0.63**	-0.54*
DB	-0.37ns	**1.00**	0.23ns	0.81**	0.75**	-0.53*	-0.86**	-0.22ns	-0.44ns	0.15ns	-0.73**	0.73**	-0.55*	0.59*	0.28ns
PD	0.56**	0.17ns	**1.00**	0.19ns	0.35ns	0.07ns	-0.53*	-0.34ns	0.10ns	0.68**	0.24ns	0.22ns	0.07ns	-0.13ns	-0.26
LD	-0.49*	0.70**	0.12ns	**1.00**	0.90**	-0.70**	-0.79**	-0.47ns	-0.64**	0.11ns	-0.90**	0.72**	-0.72**	0.89**	0.63**
LSD	-0.38ns	0.69**	0.36ns	0.81**	**1.00**	-0.52*	-0.79**	-0.54*	-0.52*	0.13ns	-0.78**	0.78**	-0.56*	0.72**	0.45ns
UB	0.32ns	-0.51*	0.05ns	-0.63**	-0.54*	**1.00**	0.46ns	0.42ns	0.85**	-0.02ns	0.80**	-0.54*	1.00**	-0.82**	-0.68**
JA	0.14ns	-0.68**	-0.33ns	-0.61**	-0.61**	0.40*	**1.00**	0.49*	-0.79**	-0.10ns	0.61**	-0.70**	0.47ns	-0.54*	-0.24ns
SDB	0.12ns	-0.17ns	-0.20ns	-0.36ns	-0.46ns	0.39ns	0.41ns	**1.00**	-0.54*	0.09ns	0.40ns	-0.39t	0.41ns	-0.41ns	-0.31ns
UP	0.40ns	-0.42ns	0.08ns	-0.58*	-0.50*	0.84**	-0.61**	-0.46ns	**1.00**	-0.20ns	-0.78**	0.78**	-0.56*	-0.82**	-0.79**
PM	0.44ns	0.16ns	0.40ns	0.09ns	0.12ns	-0.01ns	-0.05ns	0.08ns	-0.16ns	**1.00**	0.21ns	-0.12ns	-0.02ns	-0.06ns	-0.09ns
JBB	0.68**	-0.66**	0.16ns	-0.76**	-0.73**	0.77**	0.54*	0.36ns	-0.73**	0.16ns	**1.00**	-0.69**	0.81**	-0.89**	-0.67**
JBH	-0.31ns	0.58*	0.12ns	0.52*	0.61**	-0.45ns	-0.54*	-0.27ns	0.61**	-0.07ns	-0.57*	**1.00**	-0.56*	0.55*	0.31ns
UKM	0.33ns	-0.52*	0.05ns	-0.64**	-0.55*	1.00**	0.40ns	0.38ns	-0.55*	-0.02ns	0.78**	-0.47ns	**1.00**	-0.83**	-0.68**
1000	-0.58*	0.55*	-0.10ns	0.79**	0.69**	-0.80**	-0.47ns	-0.36ns	-0.79**	-0.01ns	-0.85**	0.44ns	-0.81**	**1.00**	0.88**
HSL	-0.48*	0.26ns	-0.16ns	0.51*	0.40ns	-0.62**	-0.23ns	-0.25ns	-0.70**	-0.03ns	-0.61**	0.27ns	-0.62**	0.40ns	**1.00**

*Note: * = significantly different; ** = very significantly different; ns = non-sicnificant; TT = plant height, DB = stem diameter; PD = leaf length; LD = leaf width; LSD = leaf area; UB = age of flowering; JA = number of tillers; SDB = corner of the flag leaf; UP = age of harvest; PM = panicle length; JGB = number of filled grains; JGH = number of empty grains; UKM = age of panicle; 1000 = the weight of 1000 seeds; HSL = yield*

Table 4. Direct and indirect effects between yields and yield components of local rice varieties

	TT	DB	PD	LD	LSD	UB	JA	SDB	UP	PM	JBB	JBH	UKM	1000	Coef. Corr.
TT	**0.24**	0.19	-0.52	1.24	0.11	-0.40	-0.10	-0.04	0.00	0.50	-0.62	-0.32	0.80	-1.62	-0.54
DB	-0.10	**-0.46**	-0.17	-1.78	-0.18	0.62	0.68	0.07	0.00	0.16	0.60	0.56	-1.24	1.52	0.28
PD	0.16	-0.10	**-0.76**	-0.42	-0.08	-0.08	0.42	0.11	0.00	0.72	-0.20	0.17	0.15	-1.62	-0.26
LD	-0.13	-0.37	-0.15	**-2.20**	-0.08	0.82	0.63	0.15	0.01	0.12	0.74	0.56	-1.63	0.89	0.63
LSD	-0.11	-0.34	-0.27	-1.99	**-0.24**	0.61	0.62	0.17	0.01	0.14	0.65	0.60	-1.28	1.88	0.45
UB	0.08	0.24	-0.05	1.55	0.12	**-1.16**	-0.36	-0.13	-0.01	-0.02	-0.67	-0.42	2.27	-2.13	-0.68
JA	0.03	0.39	0.40	1.75	0.19	-0.53	**-0.79**	-0.16	0.01	-0.11	-0.51	-0.54	1.06	-1.41	-0.24
SDB	0.03	0.10	0.26	1.04	0.13	-0.48	-0.39	**-0.32**	0.01	0.09	-0.33	-0.30	0.93	-1.06	-0.31
UP	0.10	0.20	-0.08	1.42	0.12	-0.99	0.62	0.17	**-0.01**	-0.22	0.65	0.60	-1.28	-2.13	-0.79
PM	0.11	-0.21	-0.52	-0.24	-0.03	0.02	0.08	1.06	-0.01	**1.06**	-0.17	-0.09	-0.05	-0.16	-0.09
JGB	0.18	0.33	0.10	1.98	0.19	-0.94	-0.49	-0.13	-0.01	0.22	**-0.83**	-0.53	1.84	-2.30	-0.67
JGH	-0.10	-0.33	-0.17	-1.59	-0.19	0.63	0.63	0.12	-0.01	-0.13	0.57	**0.77**	-1.27	1.43	0.31
UKM	0.08	0.25	-0.05	1.58	0.13	-1.16	-0.37	-0.13	0.01	-0.02	-0.67	-0.43	**2.27**	-2.15	-0.68
1000	-0.15	-0.27	0.10	-1.96	-0.17	0.96	0.43	0.13	0.01	-0.06	0.74	0.43	-1.89	**2.59**	0.88

Note: Residual effect = 0.19087; TT = plant height, DB = stem diameter; PD = leaf length; LD = leaf width; LSD = leaf area; UB = age of flowering; JA = number of tillers; SDB = corner of the flag leaf; UP = age of harvest; PM = panicle length; JGB = number of filled grains; JGH = number of empty grains; UKM = age of panicle ; 1000 = the weight of 1000 seeds; Coef. Cor. = Correlation coefficient

IV. CONCLUSIONS

Genetic diversity is more finite than environmental variability in appearance. The number of filled grains, corner of the flag leaf, leaf area, age of flowering, age of panicle exit and age of harvest have high heritability and genetic advance. The weight of 1000 seeds has a high correlation coefficient and a large direct effect so that they can be used as selection criteria for increasing the yield of local rice varieties.

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