Estimation of Heritability and Association Analysis of Agronomic Traits Contributing to Yield on Upland Rice (Oryza sativa L.)

by Eries Dyah Mustikarini

RESEARCH ARTICLE

Estimation of Heritability and Association Analysis of Agronomic Traits Contributing to Yield on Upland Rice (*Oryza sativa* L.)

Dewi Nawank Sary[1], Lailatul Badriyah[1], Ricoh Darisman Sihombing[1], Thoriq Ahmad Syauqy[1], Eries Dyah Mustikarini[2], Gigih Ibnu Prayoga[2], Ratna Santi[2], Budi Waluyo[1]*

[1]Department of Agronomy, Faculty of Agriculture, Brawijaya University, Malang 65145, Indonesia
[2]Department of Agrotechnology, Faculty of Agriculture, Fisheries, and Biology, Bangka Belitung University, Bangka Regency 33172, Indonesia

ABSTRACT Rice (*Oryza sativa* L.) is an important commodity with a major influence on the country's economy. Plant breeding activities must be conducted to develop high-yielding potential genotypes with desired agronomic traits. The purpose of this research is to study the heritability and coheritability of agronomic traits as well as to study the direct and indirect effects through genotypic and phenotypic correlations among agronomic traits contributing to yield on genotypes of rice. The research was carried out from March to July 2022 at the Experimental Field of the Faculty of Agriculture, Brawijaya University, Jatimulyo, Lowokwaru, Malang, East Java. Ten genotypes of rice were used as genetic materials. The research used a Randomized Block Design (RBD) method with 3 replications. Data were analyzed using analysis of variance, analysis of covariance, and path analysis. The results revealed that there were very significant differences among upland rice genotypes for all observed traits. All observed agronomic traits had high heritability estimates. Plant height with time of inflorescence emergence had the highest coheritability, and flag leaf length with yield per plot had the lowest coheritability. The traits of the number of spikelets per panicle and weight of milled dry grains positively correlated with yield. Weight of milled dry grains had the highest positive direct effect through genotypic correlation and phenotypic correlation with yield.

Keywords Path analysis, Heritability, Correlation, Upland rice, Agronomic trait

INTRODUCTION

Rice (*Oryza sativa* L.) is a commodity that has a major influence on the economy of the country. Indonesian people consume rice as their main energy source. Based on data (Badan Pusat Statistik 2020), the population growth rate over the last 10 years has reached an average of 1.25%. The annual increase in population in turn increases the demand for basic foods, particularly rice. Increasing rice productivity can be accomplished by increasing planting area, but this is difficult to achieve, given that many agricultural fields are currently being converted into non-agricultural areas. Pest and disease attacks, as well as environmental incompatibility, are issues in rice cultivation (Akram et al. 2019).

The development of high-yielding potential genotypes with desirable agronomic traits for a variety of environments, including dry land, is an important undertaking to make. The lines used in this research are lines that have been selected from the preliminary yield test of the F6 line (Mustikarini et al. 2021). It is important to develop lines into superior varieties that are drought-resistant and have high yield potential in order for them to be able to be cultivated in different seasons and to have adaptability. The development of a variety to improve plant traits and increase yields can be done through activities of plant

breeding namely selection. The genetic parameter that can be used as the basis for selection is heritability. Estimation of heritability can help to obtain information and measure the ability of genotypes to pass on their traits. Heritability shows the genetic contribution to traits, and thus traits with high heritability estimates will be the target of selection (Herlinda *et al.* 2018).

In addition to heritability estimates, knowledge of the relationships among traits is required to determine selection criteria in order to design an efficient breeding program. The association between traits can be measured through correlation analysis. Knowledge of the associations among traits and the direct and indirect contribution from agronomy traits contributes to yield through path analysis. Path analysis provides information about the correlation of each trait with the results, which are divided into direct and indirect effects (Singh *et al.* 2018). As such, the purpose of this study is to determine the estimation of heritability of agronomic traits and their relationships on yield. The obtained information can be used as selection criteria for choosing the best agronomic traits that can contribute to yield and can be inherited in rice.

MATERIALS AND METHODS

The research was conducted from March to July 2022 at the Experimental Field of the Faculty of Agriculture of Brawijaya University, located in Jatimulyo, Lowokwaru, Malang, East Java. The utilized genetic materials were 10 genotypes of upland rice from Bangka Belitung University collections that consisted of lines 19I-06-09-23-03, 21B-57-21-21-23, 23A-56-20-07-20, 23A-56-22-20-05, and 23F-04-10-18-18, as well as varieties of Danau Gaung, Inpago 8, Inpago 12, PBM UBB 1 and Rindang. The utilized lines were upland rice lines that are resistant to lodging from crosses of accessions (Balok and Mutant M_8-GR_{150}-1-9-13) and national superior varieties (Banyuasin and Inpago 8) (Mustikarini *et al.* 2022). Other materials used in this research were pesticides, fertilizers (urea, SP-36 and KCl), envelopes, label paper, ropes, sacks, and descriptors for rice. The tools were scissors, hoe, tractors, analytical scales, machetes, ticks, temperature data logger, rulers, measuring tape, sprayer, net, alphaboard, stationery, and camera.

The method used in this research was experimental research. The experiment was conducted with a Randomized Block Design (RBD) method, consisting of treatments of 10 rice genotypes of as with 3 replications. Each treatment was planted in plots measuring 5 m × 4 m with a distance of 1 m between plots. Each plot consisted of 320 planting holes with each hole being filled with 3 seeds. The utilized spacing was 25 cm × 25 cm. Observation of variables used a sample of 10 clumps in each plot. Quantitative observation of traits was based on the guide descriptor for rice from the International Union for the Protection of New Varieties of Plants (UPOV) (2017) and the International Rice Research Institute (IRRI) (1965). The observed traits consisted of plant height, flag leaf length, number of total tillers, number of productive tillers, time of inflorescence emergence, time to maturity, panicle length, number of spikelets per panicle, weight of 1000 grains, weight of milled dry grain, and yield per plot.

Quantitative data were analyzed by using analysis of variance, analysis of covariance, and path analysis. Analysis of variance (ANOVA) was used to determine the level of significance among the genotypes for different traits through the mean square values and to calculate variance components. After obtaining the variance component of the ANOVA, it is then followed by an analysis of covariance (ANCOVA) to estimate the coheritability of the trait which is related to the correlation response. Genotypic correlation and phenotypic correlation were based on the variance components in ANOVA. Path analysis was carried out to explain the complex association between observed traits by dividing the influence of trait into direct effect and indirect effect. Statistical analysis was carried out using SMARTSTAT and OPSTAT (Sheoran *et al.* 1998).

The estimate of heritability was calculated based on using the formula given by Singh and Chaudhary (1979):

$$H^2 = \frac{genotypic\ variance}{phenotypic\ variance} = \frac{\sigma_g^2}{\sigma_p^2} = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_e^2}$$

Explanation:

Error variance: $\sigma_e^2 = MSe$

Genotypic variance: $\sigma^2_g = \dfrac{MSg - KTe}{r}$

Phenotypic variance: $\sigma^2_p = \sigma^2_e + \sigma^2_g$

Criteria of broad sense heritability value based on Stansfield and Elrod (2002): low ($h^2_{bs} < 0.2$), moderate ($0.2 \leq h^2_{bs} \leq 0.5$), high ($h^2_{bs} > 0.5$)

Covariance analysis was used to calculate coheritability and correlation coefficient based on Singh and Chaudhary (1979):

Error Covariance: Cov e = MPe

Genotypic Covariance: Cov g = $\dfrac{MPg - MPe}{r}$

Phenotypic Covariance: Cov p = cov e + cov g

The coheritability values were entered into the following equation:

$$\text{Coheritability} = \frac{genotypic\ covariance}{phenotypic\ covariance}$$

To find out the associations among the observed quantitative traits, a correlation approach was used with the formula:

$$r_g(x,y) = \frac{Cov_g(x,y)}{\sqrt{Var_g(x)\,Var_g(y)}}$$

$$r_p(x,y) = \frac{Cov_p(x,y)}{\sqrt{Var_p(x)\,Var_p(y)}}$$

Explanation:

r(x,y) = correlation coefficient between trait x and trait y

Cov(x,y) = covariance between trait x and trait y

Var x = genotypic variance of trait x

Var y = genotypic variance of trait y

r_g symbolizes genotypic correlation and r_p symbolizes phenotypic correlation.

The statistical significance of the genotypic and phenotypic correlation coefficients was calculated using the t-test at a 5% level.

$$t = r\sqrt{\frac{n-2}{1-r^2}}$$

Explanation: r = correlation, n = amount of data

The following is the interpretation of the strength of the correlation coefficient based on Oladosu et al. (2018):

0- 0.30: Low

0.31- 0.70: Moderate

0.71-1.00: Strong

Path analysis was calculated according to the method of Singh and Chaudhary (1979). The following is the description for equations in path analysis:

Direct effect path coefficient (P):

$$\frac{\sigma X1}{\sigma Y} = P1,\ \text{path coefficient from X1 to Y}$$

Correlation equation (r) of agronomic traits to yield:

$$(X1,Y) = P1 + r(X1,X2)P2 + r(X1,X3)P3$$

Explanation:

P1 = Direct effect X1 to Y

r(X1,X2)P2 = Indirect effect X1 to yield through X2

r(X1,X3)P3 = Indirect effect X1 to yield through X3

RESULTS

Analysis of variance

Analysis of variance was carried out to assess the genotypic effects and the resulting estimates of variance components were used to calculate heritability estimates. Futhermore, the variance components (genotypic variance and phenotypic variance) were used for standardize in the correlation coefficients. Mean squares for analysis of variance (ANOVA) of agronomic traits on ten upland rice genotypes are presented in (Table 1). Analysis of variance revealed that among genotypes was very significant differences ($P < 0.01$) for all the observed agronomic traits, including plant height, flag leaf length, number of total tillers, number of productive tillers, time of inflorescence emergence, time to maturity, panicle length, number of spikelets per panicle, weight of 1000 grains, weight of milled dry grains, and yield per plot. All agronomic traits analyzed were significantly affected by the upland rice genotypes indicating that all genotypes of upland rice differed with each other.

Table 1. Mean squares analysis of variance for 11 traits of 10 upland rice genotypes from collections of Bangka Belitung University.

Source of variation	df	Traits										
		PH	FFL	NTL	NPL	TIE	TM	PL	NSP	WTG	WMDG	YP
Replication	2	19.05	1.48	4.76	2.91	34.30	30.63	2.54	0.83	47.02	1.56	0.23
Genotypes	9	1489.89**	100.88**	78.82**	72.41**	76.74**	4.30**	30.87**	8634.70**	66.77**	9.50**	42.45**
Error	18	12.65	1.67	3.08	2.55	2.55	0.71	1.05	16.08	3.03	0.04	0.43

**Significance test at 0.01.
PH: plant height, FFL: flag leaf length, NTL: number of total tillers, NPL: number of productive tillers, TIE: time to inflorescence emergence, TM: time to maturity, PL: panicle length, NSP: number of spikelets per panicle, WTG: weight of 1000 grains, WMDG: weight of milled dry grains and YP: yield per plot.

Table 2. Variance components and heritability estimates for 11 traits in upland rice genotypes from collections of Bangka Belitung University.

Agronomic Traits	σ^2_e [z]	σ^2_g [y]	σ^2_f [x]	H_{bs} [w]	Criteria H_{bs} [v]
Plant Height	12.65	495.41	508.06	0.98	High
Flag Leaf Length	1.67	33.07	34.74	0.95	High
Number of Total Tillers	3.08	25.24	28.33	0.89	High
Number of Productive Tillers	2.55	23.29	25.83	0.90	High
Time to Inflorescence Emergence	2.52	24.74	27.26	0.91	High
Time to Maturity	0.71	1.20	1.90	0.63	High
Panicle Length	1.05	9.94	10.99	0.90	High
Number of Spikelets Per Panicle	16.08	2872.87	2888.96	0.99	High
Weight of 1000 Grains	3.03	21.25	24.28	0.88	High
Weight of Milled Dry Grains	0.04	3.15	3.20	0.99	High
Yield Per Plot	0.43	14.01	14.44	0.97	High

[z]σ^2_e = error variance.
[y]σ^2_g = genotypic variance.
[x]σ^2_f = phenotypic variance.
[w]H_{bs} = broad sense heritability.
[v]Criteria of broad sense heritability value based on Stansfield and Elrod (2002): low ($h^2_{bs} < 0.2$), moderate ($0.2 \leq h^2_{bs} \leq 0.5$), high ($h^2_{bs} > 0.5$).

Estimation of heritability on agronomic traits

Estimated heritability values with high criteria were obtained for all observed traits based on the heritability analysis (Table 2). Heritability estimates for the observed traits with high criteria ranged from 0.63 to 0.99. The trait with the highest heritability estimation value was number of spikelets per panicle, while the lowest was time to maturity.

Coheritability analysis

Based on (Table 3), the range of coheritability values was from 0.3 to 2.23. The trait of flag leaf length with yield per plot had the lowest coheritability value. The highest coheritability value was for the relationship between plant height with time of inflorescence emergence. The obtained coheritability values were generally in the range of 0.9 to 1.

Correlation coefficient among agronomic traits

In this research, the genotypic correlation coefficient and phenotypic correlation coefficient showed positive, negative, and uncorrelated relationships between agronomic traits and yield, as shown in (Table 4). The value of the genotypic correlation coefficient was greater than that of the phenotypic correlation, but there was the same relationship among traits in genotypic correlation and phenotypic

Table 3. Coheritability agronomic traits to yield on upland rice genotypes from collections of Bangka Belitung University.

	PH	FFL	NTL	NPL	TIE	TM	PL	NSP	WTG	WMDG	YP
PH											
FFL	0.99										
NTL	1.02	0.97									
NPL	1.03	0.97	0.92								
TIE	2.23	1.36	1.03	1.03							
TM	0.98	1.23	1.01	0.98	0.88						
PL	1.00	0.96	0.98	0.98	1.18	1.09					
NSP	0.99	0.99	0.99	1.00	1.03	1.11	0.98				
WTG	1.08	0.72	0.98	1.01	0.99	1.16	1.04	1.02			
WMDG	0.44	1.26	1.29	1.12	0.86	0.42	1.01	1.00	1.06		
YP	1.17	0.30	0.91	0.93	0.92	0.85	0.99	1.00	0.82	1.00	

correlation. Traits with positive and very significant genotypic correlation and phenotypic correlations were plant height with flag leaf length (0.898**, 0.876**), panicle length (0.92**, 0.863**), and number of spikelets per panicle (0.599**, 0.594**); flag leaf length with panicle length (0.863**, 0.838**) and number of spikelets per panicle (0.72, 0.711); number of total tillers with number of productive tillers (0.943**, 0.921**), time of inflorescence emergence (0.543**, 0.474**), and time to maturity in genotypic correlation (0.577**); number of productive tillers with time of inflorescence emergence (0.663**, 0.584**) and time to maturity (0.621**, 0.478**); time of inflorescence emergence with time to maturity (0.758**, 0.654**); and panicle length with number of spikelets per panicle (0.864**, 0.833**). The number of spikelets per panicle positively and significantly correlated with weight of milled dry grain (0.457*, 0.452*), yield per plot (0.427*, 0.42*), and total of productive tillers in phenotypic correlation (0.425*). The weight of dry milled grain had a positive and very significant correlation with yield per plot (1.00**, 0.983**).

Traits with negative and very significant genotypic correlations and phenotypic correlations were plant height with number of total tillers (−0.725**, −0.664**) and number of productive tillers (−0.636**, −0.582**); flag leaf length with number of total tillers (−0.809**, −0.77**) and number of productive tillers (−0.692**, −0.66**); number of total tillers with panicle length (−0.684**, −0.627**), number of spikelets per panicle (−0.588**, −0.557**), and weight of 1000 grains (−0.502**, −0.543**); number of

productive tillers with panicle length (−0.641**, −0.589**), number of spikelets per panicle (−0.552**, 0.524**), and weight of 1000 grains (−0532**, −0.47**); and weight of 1000 grains with time of inflorescence emergence (−0.687**, −0.615**) and time to maturity (−0.951**, −0.61**).

Path analysis between agronomic trait to yield

The results of path analysis through genotypic correlation (Table 5) and phenotypic correlation (Table 6) on agronomic traits to yield. The trait that had the greatest direct positive effect on yield through genotypic and phenotypic correlations was weight of milled dry grain, with 1.046 and 0.986 respectively. Traits that had a positive indirect effect through either genotypic correlation or phenotypic correlation were the number of spikelets per panicle through weight of milled dry grain, with 0.47844 and 0.44560, respectively. Traits that had the largest negative indirect effect were panicle length through number of spikelets per panicle (−0.1539) through genotypic correlation, and number of productive tillers through number of total tillers (−0.16609) through phenotypic correlation. The residual value of path analysis was −0.01618 through genotypic correlation and 0.02646 through phenotypic correlation.

DISCUSSION

Analysis of variance

The result from the mean squares of the analysis of variance for each agronomic trait showed highly signi-

Table 4. Genotypic correlation coefficients (below diagonal) and phenotypic correlation coefficients (above diagonal) among 11 traits in upland rice genotypes from collections of Bangka Belitung University.

	PH	FFL	NTL	NPL	TIE	TM	PL	NSP	WTG	WMDG	YP
PH		0.876**	−0.664**	−0.582**	0.006NS	−0.129NS	0.863**	0.594**	0.065NS	0.011NS	−0.02NS
FFL	0.898**		−0.77**	−0.66**	−0.066NS	−0.215NS	0.838**	0.711**	0.12NS	0.018NS	−0.016NS
NTL	−0.725**	−0.809**		0.921**	0.474**	0.425*	−0.627**	−0.557**	−0.453**	−0.065NS	−0.058NS
NPL	−0.636**	−0.692**	0.943**		0.584**	0.478**	−0.589**	−0.524**	−0.47**	−0.075NS	−0.06NS
TIE	0.015NS	−0.097NS	0.543**	0.663**		0.654**	−0.146NS	−0.282NS	−0.615**	−0.143NS	−0.125NS
TM	−0.161NS	−0.342NS	0.577**	0.621**	0.758**		−0.121NS	−0.073NS	−0.61**	−0.057NS	−0.028NS
PL	0.92**	0.863**	−0.684**	−0.641**	−0.19NS	−0.173NS		0.833**	−0.067NS	0.225NS	0.191NS
NSP	0.599**	0.72**	−0.588**	−0.552**	−0.307NS	−0.102NS	0.864**		−0.094NS	0.452*	0.42*
WTG	−0.077NS	0.094NS	−0.502**	−0.532**	−0.687**	−0.951**	−0.079NS	−0.103NS		−0.077NS	−0.103NS
WMDG	0.005NS	0.023NS	−0.09NS	−0.09NS	−0.131NS	−0.03NS	0.241NS	0.457*	−0.088NS		0.983**
YP	−0.024NS	−0.005NS	−0.057NS	−0.06NS	−0.123NS	−0.031NS	0.203NS	0.427*	−0.092NS	1.007**	

Table 5. Path analysis through genotypic correlation of the direct (bold) and indirect effects in upland rice genotypes from collections of Bangka Belitung University.

	PH	FFL	NTL	NPL	TIE	TM	PL	NSP	WTG	WMDG	rg[z]
PH	**−0.16006**	0.14602	−0.00399	0.00007	−0.00081	0.00614	0.08182	−0.10677	0.00841	0.00555	−0.024NS
FFL	−0.14369	**0.16265**	−0.00445	0.00008	0.00531	0.01301	0.07676	−0.12832	−0.01029	0.02387	−0.005NS
NTL	0.11601	−0.13151	**0.00550**	−0.00011	−0.02980	−0.02192	−0.06087	0.10467	0.05514	−0.09379	−0.057NS
NPL	0.10183	−0.11253	0.00519	**−0.00011**	−0.03638	−0.02361	−0.05700	0.09825	0.05842	−0.09396	−0.060NS
TIE	−0.00235	−0.01574	0.00299	−0.00008	**−0.05487**	−0.02883	−0.01694	0.05464	0.07537	−0.13705	−0.123NS
TM	0.02584	−0.05568	0.00317	−0.00007	−0.04161	**−0.03801**	−0.01544	0.01814	0.10443	−0.03167	−0.031NS
PL	−0.14718	0.14032	−0.00376	0.00007	0.01045	0.00659	**0.08898**	−0.15390	0.00864	0.25256	0.203NS
NSP	−0.09595	0.11718	−0.00323	0.00006	0.01683	0.00387	0.07688	**−0.17810**	0.01133	0.47844	0.427*
WTG	0.01226	0.01525	−0.00276	0.00006	0.03768	0.03617	−0.00700	0.01838	**−0.10976**	−0.10976	−0.092NS
WMDG	−0.00085	0.00371	−0.00049	0.00001	0.00719	0.00115	0.02147	−0.08143	0.00967	**1.04642**	1.007**

Residual: −0.01618.
[z] rg = genotypic correlation coefficient.

Table 6. Path analysis through phenotypic correlation of the direct (bold) and indirect effects in upland rice genotypes from collections of Bangka Belitung University.

	PH	FFL	NTL	NPL	TIE	TM	PL	NSP	WTG	WMDG	rp[z]
PH	**−0.09107**	−0.04877	0.11968	−0.02645	0.00009	−0.00078	0.04269	−0.03092	0.00487	0.01109	−0.020 NS
FFL	−0.07982	**−0.05564**	0.13874	−0.03000	−0.00101	−0.00130	0.04145	−0.03697	−0.00891	0.01736	−0.016 NS
NTL	0.06045	0.04282	**−0.18030**	0.04189	0.00722	0.00259	−0.03103	0.02898	0.03378	−0.06408	−0.058 NS
NPL	0.05296	0.03671	−0.16609	**0.04548**	0.00889	0.00290	−0.02915	0.02727	0.03503	−0.07409	−0.060 NS
TIE	−0.00056	0.00369	−0.08552	0.02658	**0.01522**	0.00397	−0.00723	0.01465	0.04587	−0.14146	−0.125 NS
TM	0.01173	0.01195	−0.07670	0.02173	0.00995	**0.00608**	−0.00596	0.00378	0.04545	−0.05594	−0.028 NS
PL	−0.07857	−0.04661	0.11307	−0.02679	−0.00222	−0.00073	**0.04948**	−0.04331	0.00503	0.22210	0.191 NS
NSP	−0.05413	−0.03954	0.10044	−0.02384	−0.00429	−0.00044	0.04119	**−0.05202**	0.00702	0.44560	0.420*
WTG	0.00595	−0.00665	0.08171	−0.02137	−0.00936	−0.00371	−0.00334	0.00490	**−0.07453**	−0.07634	−0.103 NS
WMDG	−0.00102	−0.00098	0.01171	−0.00343	−0.00218	−0.00034	0.01114	−0.02350	0.00577	**0.98630**	0.983**

Recidual: 0.02646.
[z] rp = phenotypic correlation coefficient.

ficant differences for all observed traits, so that there were very significant differences in realizing the genetic performance of the upland rice genotypes. The upland rice genotypes differed very significantly for all observed traits indicating the presence of sufficient genetic variability in the genetic material. The more diverse the traits, the greater of the comparison ratio between genotype mean square with error mean square (Priyanto et al. 2018). The traits responded differently to each the upland rice genotypes. The very significant difference among the genotypes for agronomic traits is due to genetic component difference among the genotypes. Thus, the existences variability among analyzed genetic materials or genotypes provided opportunity for the improvement of upland rice through a plant breeding program namely selection. Similar result was observed by Fentie et al. (2014) found a significant difference between upland rice genotypes for days to 50% heading, days to 75% maturity, panicle length, plant height, number of fertile tillers per plant, number of spikelets per panicle, number of filled grains per panicle, biomass yield, 1000 grain weight and grain yield. The results of the analysis of variance will also produce variance components to help estimate genotypic correlation and phenotypic correlation, so that a more comprehensive study of the closeness of the association can be obtained.

Estimation of heritability on agronomic traits

The results of analysis of variance revealed that all observed traits were significantly different in each genotype, indicating that there was variability in each trait. All of the observed traits had a high broad-sense heritability. The high estimated heritability values for the observed traits reflect the combined effect of additive and non-additive gene action on broad-sense heritability. Traits with high heritability were influenced more by genetic factors. This shows that a high response to selection on these traits will be more effective and efficient than on traits with low heritability values (Shrestha et al. 2021). The expression of traits is more influenced by the environment when traits with low heritability values are used in the selection, and thus the percentage of inheritance of these traits is small. High heritability suggests that a large component of the proportion of variation will be heritable

in the selection of superior genotypes based on phenotypic performance (Nithya *et al*. 2020). This phenotypic performance will indicate the traits that will be expressed through appearances of plant phenotypes that result from the interaction of genetic and environmental factors.

Coheritability analysis

Coheritability is represented through calculating the covariance value, which is used to determine the magnitude of two linearly related traits that in concept are changing at the same time. This indicates the genetic association between two traits in terms of their mutual inheritance. The components of the covariance determine the magnitude of the coheritability value. Generally, the value for the estimation of inheritance ranges from 0 to 1. However, because it is taken from the covariance calculation, for which the value is not limited, it does not indicate the extent of the simultaneous change of the two traits. As covariance is obtained from the mean square of treatment and error, a high number indicates greater dependence. Smaller error results in a higher coheritability value. This is reflected in the obtained mean product error, which has a negative value. A small error indicates that the trait association is more influenced by genetics, whereas a large error indicates that environmental factors are more influential. Habiba *et al*. (2012) reported on the coheritability values of rice agronomic traits, including plant height, number of total tillers, productive tillers, panicle length, and number of spikelets per panicle with yield per plot, which ranged from 0 to 1.7.

The highest coheritability value was found for the traits of plant height with time of inflorescence emergence. This shows that the magnitude of the shared inheritance of the two traits is the largest among all other relationships between two traits. Coheritability is defined as a genetic component description, as the measure of the shared inheritance of two traits that represents the genetic contribution to their phenotypic correlation (Vasquez-Kool 2019). The lowest coheritability value was found for flag leaf length with yield per plot. This shows that the magnitude of the shared inheritance of the two traits is the smallest among all other relationships between two traits. The presence of traits is related to coheritability. Coheritability is associated with the presence of a shared genetic effect, thus reflecting the extent of the influence of shared genetics on the observed trait associations.

Correlation coefficient among agronomic traits

The relationship between two or more traits is referred to as correlation. Correlation analysis can help identify how these traits contributed to the results. A positive correlation indicates that an increase in one trait causes a rise in the correlated trait, and conversely, a negative correlation indicates that an increase in one trait results in a decrease in the correlated trait (Kampe *et al*. 2018). Correlation analysis revealed that plant height positively correlated with flag leaf length, panicle length, and number of spikelets per panicle. The increase in plant height will be followed by an increase in the flag leaf length. The results of a study (Oladosu *et al*. 2018) showed that plant height positively correlated with flag leaf length. Similar to plant height, flag leaf length also positively correlated with panicle length and number of spikelets per panicle. The formation of grains is influenced by photosynthesis that occurs in the upper part of the plant, along the length of the flag leaf. The flag leaf is the uppermost leaf beneath the panicle, which provides photosynthetic energy during reproduction. A longer flag leaf means more light that can be absorbed for photosynthesis, resulting in more carbohydrates as food reserves in the growth process (Rahman *et al*. 2013). The number of spikelets per panicle has a positive relationship with the panicle length trait.

Number of total tillers positively correlated with the number of productive tillers. This means that a clump of rice plants with a large number of total tillers also has a large number of productive tillers. There is a positive correlation between the number of total tillers and the number of productive tillers, which also positively correlated with time of inflorescence emergence and time to maturity. The time of inflorescence emergence correlated positively with the time to maturity. Similar findings reported by Rashid *et al*. (2014) revealed positive correlation relationships of the total number of tillers with the number of productive tillers, the number of total tillers with time of inflorescence emergence and time to maturity, and the number of productive tillers with time of inflorescence emergence and time to maturity. Time of inflorescence

emergence had a positive and very high correlation with time to maturity. When the inflorescence of a plant grows more quickly, the harvest age is also faster and vice versa. Therefore, selection of plants that grow inflorescences quickly will result in plants with a short harvest age, though the correlation to grain yield is negative.

The number of spikelets per panicle showed positive correlations with weight of milled dry grain for both genotypic and phenotypic correlations. The increase in number of spikelets per panicle will be followed by an increase in the weight of milled dry grain. The weight of dry milled grain is obtained from dry grain that is ready to be milled with a maximum moisture content of 14%, for which the filled grain is selected by separating it from the unfilled grain. The number of spikelets per panicle and the weight of dry milled grain both positively correlated with yield per plot. The positive association between the weight of dry milled grain and the yield per plot reaches a value of one for the genotypic correlation coefficient and nearly one for the phenotypic correlation coefficient. Therefore, these traits have a very strong genotypic relationship, for which the correlation value is greater than that of the phenotypic correlation. This suggests a higher genetic contribution (Karim *et al*. 2014). The genotypic correlation coefficient, which is in the same direction as the phenotypic correlation coefficient show different genotypes affect phenotypic appearance. Correlation is classified into two types: genotypic correlation and phenotypic correlation. The association between two traits caused by genetic and environmental factor is known as phenotypic correlation. Genotypic correlation is defined as the association between two traits caused by genetic factor so that can be inherited due to pleiotropism and linkage disequilibrium (Mochado *et al*. 2017). Pleiotropism results in a high correlation because one gene can influence the expression of multiple traits. The emergence of several traits controlled by two or more genes on the same chromosome is referred to as linkage disequilibrium. A higher genotypic correlation coefficient indicates a genetic explanation where a strong association between traits is caused by genetic, but their expression is also inseparable from environmental influences, so that phenotypic correlation is also important to study. Significant and strong associations coupled with high estimates of heritability can be selected as selection targets. Hence, the selection of these traits is important to be able to improve grain yield (Fentie *et al*. 2014).

Both the number of total tillers and number of productive tillers negatively correlated with plant height and flag leaf length. The genotypic correlation between these traits was greater than the phenotypic correlation, indicating that genetic factors have a greater influence on expression. Differences in the genetic composition of each genotype cause differences in traitistics and traits, which affect variability of plant performance. The ability of each genotype to produce offspring is caused by genetic factors. The number of tillers will be maximized if an individual plant has good genetic traits and support from a favorable growing environment (Yulina *et al*. 2021). Short rice plants generally have a greater number of tillers, and thus these plants tend to be more resistant to lodging. The trait of the weight of 1000 grains negatively correlated with time of inflorescence and time to maturity. The value of the weight of 1000 grains is determined by the shape and size of the seeds.

Some of the traits had non-significant correlations for both genotypic and phenotypic correlations. Yield component traits did not affect yield, except for the number of grains per panicle and the weight of dry milled grain. The associations between traits are not only influenced by genetic factors but also by the contribution of genetics and environment. Environmental contributions may allow an improvement in the vegetative phase of plants but have no effect on yield. Time of inflorescence emergence and time to maturity showed non-significant correlations with plant height, flag leaf length, panicle length, number of spikelets per panicle, weight of dry milled grain, and yield per plot. In addition to the state of the vegetative organs, pollen survival is very important for pollination (Rahman *et al*. 2013). Changes in temperature can also cause incompatibility of ready pollen with the pistil. This causes the filling of grains to be imperfect, resulting in unfilled grains. The weight of grains is determined by whether the grains are filled or unfilled. Correlation coefficient analysis reveals that the improvement of the phenotypic traits that possess positive and significant correlations with grain yield can then increase grain yield.

Path analysis between agronomic trait to yield

Path analysis is performed by separating the components of the correlation coefficients into direct and indirect effects of trait relationships. The weight of dry milled grain had the greatest direct positive effect on yield through both genotypic and phenotypic correlations. Furthermore, the weight of dry milled grain had a high correlation coefficient of nearly one, indicating a very strong relationship between the trait and yield. An increase in the weight of dry milled grain increases the yield per plot of rice. Islam *et al.* (2020) reported that filled grains positively and very significantly correlated with yield (0.78). Therefore, the selection will be effective which aims to get a genotype that has high yields is carried out through of the weight of dry milled grain trait.

Number of spikelets per panicle had the greatest indirect effect on yield through both genotypic and phenotypic correlation by weight of milled dry grain with a positive value. The weight of dry milled grain becomes an intermediate factor for the number of spikelets per panicle and achievement of high yield per plot. According to Singh and Chaudhary (1979), if a correlation coefficient is positive but its direct effect is negative, then the indirect effect seems to be cause of correlation. The number of spikelets per panicle resulted in a positive moderate correlation coefficient for both genotypic and phenotypic correlation on plot yield. Path analysis is very important for the results by showing the contribution of traits to those results through the division of the main correlation components during selection (Muthuramu and Sakthivel 2018). In this case, the indirect causal factors must be considered simultaneously. The target trait for selection based on path analysis is the weight of milled dry grains. This trait has a high positive direct effect, and serves as an intermediary for the highest positive indirect effect, on the trait of the number of grains per panicle. Furthermore, the correlation coefficient of the weight of dry milled grains is nearly one, indicating a very strong relationship. Weight of dry grains had a significant impact on grain yield.

In path analysis, there is also the residual value, which becomes another influence in addition to the effect caused by the independent variable, and is thus often referred to as the residual effect. The very small residual value, which is nearly zero, indicates that the applied path analysis was more effective in explaining the causal relationship. This causal relationship is derived from the correlation value, and the observed trait provides a more complete explanation of direct and indirect effects (Kartina *et al.* 2016). Estimation of residual effects through genotypic correlation (−0.01618) and phenotypic correlation (0.02646) revealed that the traits examined in path analysis contributed 100% and 97% of the yield variability per plot respectively. Only 3% of the pathways are still unknown through phenotypic correlation. Both environmental factors and cultivation practices can have an impact on yield (Islam *et al.* 2020).

CONCLUSION

There were very significant differences among upland rice genotypes for all observed traits. All of the observed traits had high heritability. The highest coheritability value was for plant height with time of inflorescence emergence and the lowest was for flag leaf length with yield per plot. The traits that positively correlated on yield are the number of grains per panicle and the weight of milled dry grains. The weight of milled dry grains has the main direct influence on the increase in yield (per plot). The high estimated heritability values for the traits and strong associations among traits, especially those that have a direct positive effect on grain yield, can become indicators in the selection criteria.

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REFERENCES

Akram HM, Ali A, Sattar A, Rehman HSU, Bibi A. 2013.

Impact of water deficit stress on various physiological and agronomic traits of three basmati rice (*Oryza sativa* L.) cultivars. J. Anim. Plant Sci. 23(5): 1415-1423.

Badan Pusat Statistik (BPS). 2020. Produksi padi dan beras menurut Provinsi 2020. [Online]. https://www.bps.go.id/indikator/indikator/view_data_pub/0000/api_pub/d3ZjM280TU9FanlkdDRETUV5aVdndz09/da_05/1. [Retrieved January 5, 2022].

Fentie D, Alemayehu G, Siddalingaiah M. 2014. Genetic variability, heritability and correlation coefficient analysis for yield and yield component traits in upland rice (*Oryza sativa* L.). East Afr. J. Sci. 8(2): 147-154.

Habiba U, Bishwas BK, Aktaruzzaman M, Sarkar ENS, Sultana S. 2012. Covariance and coheritability of different traits against the prevalence of major diseases in fine rice. Bangladesh J. Prog. Sci. & Tech. 10(1): 109-112.

Herlinda G, Soenarsih, DAS, Syafi S. 2018. Keragaman dan heritabilitas jagung merah (*Zea mays* L.) lokal. Techno J. Penelitian. 7(2): 191-199.

IRRI. 1965. The morphology and varietal traititics of the rice plant. Los Banos, Laguna, Philippines.

Islam SS, Anothai J, Nualsri C, Soonsuwon W. 2020. Correlation and path analysis of phenological traits of thai upland rice genotypes. J. of Plant Sci. 7(2): 133-142.

Kampe AK., Tassew AA, Gezmu AT. 2018. Phenotypic and genotypic correlation and path coefficient in rainfed upland rice (*Oryza sativa* L.) genotypes at Guraferda, Southwest Ethiopia. Food Sci. Qual Manag. 76: 41-46.

Karim D, Siddique MNA, Sarkar U, Hasnat Z, Sultana J. 2014. Phenotypic and genotypic correlation co-efficient of quantitative traits and trait association of aromatic rice. J. Biosci. Agric. Res. 1(1): 34-46.

Kartina N, Wibowo B, Widyastuti Y, Rumanti I, Satoto. 2016. Correlation and path analysis for agronomic traits in hybrid rice. J. Ilmu Pertanian Indonesia. 21(2): 76-83.

Mochado BQV, Nogueira APO, Hamawaki OT, Rezende GF, Jorge GL, Silveira IC, *et al.* 2017. Phenotypic and genotypic correlations between soybean agronomic traits and path analysis. Genet. Mol. Res. 16(2): 1-11.

Mustikarini ED, Prayoga GI, Santi R, Hairul. 2021. Genetic parameters of F6 upland rice with lodging resistance derived from landraces x national varieties. Earth Environ. Sci. 741: 1-7.

Mustikarini ED, Prayoga GI, Santi R, Murti WW. 2022. Potensi hasil dan uji keseragaman famili F7 padi gogo tahan rebah hasil persilangan padi lokal bangka x varietas unggul. J. Kultivasi. 21(1): 60-68.

Muthuramu S, Sakthivel S. 2018. Correlation and path analysis for yield traits in upland rice (*Oryza sativa*). Res. J. Agric. Sci. 7(5): 763-765.

Nithya N, Beena R, Sthephen R, Adiba PS, Jayalekshmi VG, Viji MM, *et al.* 2020. Genetic variability, heritability, correlation coefficient and path analysis of morphophysiological and yield related traits of rice under drought stress. Chem. Sci. Rev. Lett. 9(33): 48-54.

Oladosu Y, Raffi MY, Magaji U, Abdullah N, Miah G, Chukwu SC, *et al.* 2018. Genotypic and phenotypic relationship among yield components in rice under tropical conditions. BioMed Res. Int. 23(3): 1-10.

Priyanto SB, Azrai M, Syakir M. 2018. Analisis ragam genetik, heritabilitas, dan sidik lintas karakter agronomik jagung hibrida silang tunggal. Informatika Pertanian 27(1): 1-8.

Rahman MA, Haque ME, Sikdar B, Islam MA, Matin MN. 2013. Correlation analysis of flag leaf with yield in several rice cultivars. J. Life & Earth Sci. 8: 49-54.

Rashid K, Kahliq I, Farooq O, Ahsan MZ. 2014. Correlation and cluster analysis of some yield and yield related traits in rice (*Oryza sativa*). J. Recent. Adv. Agr. 2(6): 271-276.

Sheoran OP, Tonk DS, Kaushik LS, Hasija RC, Pannu RS. 1998. Statistical software package for agricultural research workers. Recent advances in information theory, statistics & computer applications by DS Hooda & RC Hasija. Department of Mathematics Statistics, CCS HAU, Hisar 139-143.

Shrestha J, Subedi S, Subedi NR, Subedi S, Kushwaha UKS, Maharjan B, *et al.* 2021. Assessment of variability, heritability and correlation in rice (*Oryza Sativa* L.) genotypes. Nat. Resour. & Sustain. Dev. 11(2): 181-192.

Singh RK, Chaudhary BD. 1979. Biometrical methods in quantitative genetics analysis. Kalyani Publishers, New Delhi.

Singh R, Yadav V, Mishra DN, Yadav A. 2018. Correlation and path analysis studies in rice (*Oryza sativa* L.). J. Pharmacogn. Phytochem. 1: 2084-2090.

Stansfield WD, Elrod SL. 2002. Schaum's outline of theory and problems of genetics. 4th ed. Mc Graw-Hill, New York.

UPOV. 2017. Guidelines for the conduct of tests for distincness, uniformity and stability of rice (*Oryza sativa* L.). Switzerland. Ganeva.

Vasquez-Kool J. 2019. Coheritability and coenvironmen-

tability as concepts for partitioning the phenotypic corre-
lation. BioRxiv.

Yulina N, Ezward C, Haitami A. 2021. Karakter high tanaman, umur panen, jumlah anakan dan bobot panen pada 14 genotipe padi lokal. J. Agrosains dan Teknologi. 6(1): 15-24.

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