

The performance of agronomic traits, genetic variability, and correlation studies for yield and its components in some red rice (*Oryza sativa*) promising lines

GUSTI RAY SADIMANTARA¹, DEWI NURHAYATI YUSUF^{2,*}, EKA FEBRIANTI¹, SITTI LEOMO², MUHIDIN¹

¹Department of Agrotechnology, Faculty of Agriculture, Universitas Halu Oleo. Jl. HEA Mokodompit, Kendari 93212, Southeast Sulawesi, Indonesia

²Department of Soil Sciences, Faculty of Agriculture, Universitas Halu Oleo. Jl. HEA Mokodompit, Kendari 93212, Southeast Sulawesi, Indonesia.

*email: dewi.yusuf@uho.ac.id

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Abstract. Sadimantara GR, Yusuf DN, Febrianti E, Leomo S, Muhidin. 2021. The performance of agronomic traits, genetic variability, and correlation studies for yield and its components in some red rice (*Oryza sativa*) promising lines. *Biodiversitas* 22: 3994-4001. Improving a new variety commonly depends on the nature and magnitude of genetic variability and its utilization, followed by selection and evaluation before being released into new superior types. The present study aims to estimate the genetic variability and relation between yield and its related traits of the red rice promising lines. The experiment was arranged based on a randomized complete block design (RCBD) with three replications. Analysis of variance revealed significant differences among rice lines for 12 quantitative traits. The phenotypic coefficient of variation (PCV) value was higher than the genotypic coefficient of variation (GCV), indicating a negligible environmental influence in the phenotypic expression of traits. High heritability estimates coupled with high genetic advance were recorded for grain total per panicle and grain yield per hill. Grain yield observed a highly significant positive correlation with panicle length (0.63), percentage of filled grains (0.53), grain weight per panicle (0.54), and thousand-grain weight (0.52). It correlated negatively with days to 50% flowering (-0.61) and days to maturity (-0.48). The study indicated that panicle length, percentage of filled grains, grain weight per panicle, and thousand-grain weight are important yield-related traits and could be used for selection to improve the genetic potential of rice yield.

Keywords: Correlation, genetic variability, paddy field, promising lines, red rice, yield-related characters

INTRODUCTION

Rice is a staple food and still the primary source of carbohydrate intake (Priyanka and Jaiswal 2017). It consumes 90% in Asia and mainly in Southeast Asia, including Indonesia (Manzanilla et al. 2011; Panuju et al. 2013). The rice demand in Indonesia continues to increase with population growth, while the rice production capacity to increase is minimal (Sutariati et al. 2017; Muhidin et al. 2018). The population increased, and the wetland conversion, causes rice supply cannot be fulfilled sustainably (Muhidin et al. 2013; Sutariati et al. 2016; Kadidaa et al. 2017).

Besides being a source of carbohydrates, rice also contains proteins, fats, fiber, minerals, and anthocyanins (Sivamaruthi et al. 2018; Thanuja and Parimalavalli 2018), mainly for red rice. Red rice is a *functional food* with a high health value (Ravichanthiran et al. 2018). Anthocyanin is a phenolic compound that is included in the flavonoid group and functions as an antioxidant (Goufo and Trindade, 2014). Thus, it plays an essential role for the plant itself and human health.

Rice demand is expected to rise in the future as the world's population grows. Rice self-sufficiency has been the subject of numerous efforts (Sutariati et al. 2017; Kadidaa et al. 2017). Several programs have been created

to increase rice production in Indonesia, including increasing productivity (Sutariati et al. 2018), breeding program (Suliantini et al. 2018; Sadimantara et al. 2019), and also trying to decrease rice level consumption and promote local food as a carbohydrate source (Muhidin et al. 2016). One of the promises programs to achieve this target is upland rice development to increase rice production (Kadidaa et al. 2017; Sadimantara et al. 2018) planted on dry land (Sutariati et al. 2018). Common problems in upland rice cultivation are mostly because of low-level production and length of harvest time. One of the solutions is through the breeding program to increase upland rice production and shorten harvest time. The productivity of rice plants can be increased through the development of superior varieties in plant breeding programs.

Rice breeding is critical for food production to meet the needs of a growing population (Osei et al. 2014; Lenaerts et al. 2018). To date, improved rice varieties must be developed to increase rice production to meet rising demand (Osei et al. 2014).

In the country where rice consumption has increased, the high-yielding cultivar with broad adaptation capabilities to diverse environments needs to be developed (Hyoda et al. 2015; Bailey-Serres et al. 2019; Takai et al. 2019). According to Akter et al. (2014), the development of improved varieties can increase the productivity of red rice

through plant breeding programs. Several upland rice lines have assembled through crossbreeding between superior lowland rice and local upland rice cultivars. Via crossbreeding between local upland rice and paddy rice cultivars, Sadimantara et al. (2014) have assembled many promising red rice lines. Furthermore, these red rice crossbreed lines must be evaluated in the rice field to determine the potential yield and adaptability. The crossing-derived lines have been tested on dry land through yield ability and multilocation tests.

A character's appearance within a population is determined by genetic variation, environment, genetic and environmental interactions (Griffiths et al. 2005). The selection of parents solely based on the yield is often deceptive. As a result, understanding the relationship between yield and its related traits is needed for plant breeders to develop an economically viable variety (Khan et al. 2015; Li et al. 2019; Qaim 2020). Genetic diversity for the agronomic trait is a vital component of breeding programs to expand rice and other crops' gene pool (da Silva Dias 2015; Xu et al. 2017; Bailey-Serres et al. 2019). When combined with the heritability calculation, the genetic coefficient of variation would provide the best reference for the amount of advance predicted from the selection (Kumar et al. 2017). Plant selection can be aided by correlation studies between yield and its contributing characters (Pratap et al. 2020). The correlation coefficient may also be used to distinguish characters with little or no effect on rice yield.

Any crop improvement program's success is determined by genetic variability, heritability, genetic advance, character interaction, direct and indirect effects on yield, and its attributes, all of which are influenced by the genotypes' genetic diversity (Rashmi et al. 2017; Adhikari et al. 2018; Saha et al. 2019). The evaluation and analysis of genetic diversity are critical for crop enhancement and the efficient management and conservation of germplasm resources (Govindaraj et al. 2015; Yan et al. 2016; Bhandari et al. 2017). The breeding program to increase the economic value of rice focused on breeding for high yield and pest resistance and introducing favored quality characteristics (Khan et al. 2015; Kaiser et al. 2020). The study aimed to quantify the diversity indices, variability, and heritability of various traits to aid effective selection in a rice breeding program.

MATERIALS AND METHODS

Experimental materials and design

The research was conducted at the Extended Experimental Garden, Department of Agrotechnology, Faculty of Agriculture, Halu Oleo University Kendari Southeast Sulawesi Indonesia, during the growing season in 2019 from July to November 2019. The experimental material in this study comprised eight new upland rice lines derived from **Inpari-33** x Wagamba crosses, and the name of the cultivar are GS11-1, GS11-2, GS12-1, GS12-2, GS44-1, GS44-2, GS16-1, GS16-2, developed from the

cross between paddy rice and local upland rice, and one local upland rice as a check variety.

The red rice promising lines were planted in a randomized complete block design with three replications. Twenty-eight days old seedlings were transplanted in the experimental site with a spacing of 25 cm between plant to plant and 25 between the rows, keeping a single seedling per hill. The standard agronomic practices had applied for average plant growth. Five plants were randomly chosen from each replication in each line for yield-related traits. Twelve traits were observed, i.e., plant height, leaf area, flag leaf angle, flag leaf area, panicle length, filled grain percentage, grain total per panicle, grain weight per panicle, thousand-grain weight, days to 50% flowering, days to maturity, and grain yield per hill. The observations were recorded and subjected to statistical analysis using the mean values of five randomly selected plants.

Statistical analysis

The analysis of variance was done using SPSS 23.0 software. Parameters of genetic variability include mean, range, genotypic and phenotypic coefficient of variation were calculated according to the method suggested by Burton (1952), and the estimate of GCV and PCV were classified as low (0-10%), moderate (10-20%) and high (20% and above) according to Sivasubramanian and Madhavamenon (1973). The broad-sense heritability and genetic advance in percent of mean were calculated as suggested by Jonson et al. (1955). Normal Pearson's correlation was calculated using SPSS 20.0 software. The Heritability estimates were categorized as low (0-30%), moderate (30-60%), and high (60% and above) as given by Robinson et al. (1949). Genetic advance as percent of mean was categorized as low (0-10%), moderate (10-20%), and high (20% and above) as given by Johnson et al. (1955) and Falconer (1996). The value of genetic and phenotypic diversity is derived from analysis of variance, such as presented in Table 1.

Based on variance analysis, phenotype and genotype variations can be predicted as follows:

$$\begin{aligned}\sigma_g^2 &= \frac{M2-M1}{r} \\ \sigma_e^2 &= M1 \\ \sigma_p^2 &= \sigma_g^2 + \sigma_e^2\end{aligned}$$

Where:

σ_g^2 = Genotype Variance,

σ_p^2 = Phenotype Variance

Table 1. Analysis of variance and genetic parameters

SV	DF	MS	E (MS)
Block	(r-1)	M3	$\sigma_e^2 + g \sigma_r^2$
Genotype	(g-1)	M2	$\sigma_e^2 + r \sigma_g^2$
Error (a)	(r-1)(g-1)	M1	σ_e^2
Total	rg-1		

Note: SV: source of variation; DF: Degree of Freedom, MS: Mean Square; EMS: Expected Mean Square; r: block; g: genotype

Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are calculated according to the formula:

$$KKF = \frac{\sqrt{\sigma_p^2}}{\bar{Y}} \times 100\% \quad KKG = \frac{\sqrt{\sigma_g^2}}{\bar{Y}} \times 100\%$$

Where:

\bar{Y} : population mean

GCV: Genotypic Coefficient of Variation

PCV : Phenotypic Coefficient of Variation

RESULTS AND DISCUSSION

Field performance

The results of the phenotypic study of eight promising rice lines showed in Table 2. There is a large variability among observed genotypes, which can be used for further breeding programs. The DMRT was carried out to determine the differences between genotypes in all characters. The findings revealed that among the promising rice lines, except for the filled grain percentage, almost all yield-related attributes of red rice promising lines were higher than the check variety based on phenotypic results.

The highest value for plant height, leaf area, and flag leaf angle was observed in GS16-2, and the lowest value for plant height was exhibited in GS12-2, for leaf area and flag leaf angle in GS44-2. The highest Flag leaf area was observed in GS16-1, and the lowest value was exhibited in GS11-1. The generative character found that the highest value for panicle length was observed in GS16-1 while the lowest value was exhibited GS11-2. The highest filled grain percentage was found in GS12-2 and the lowest found in GS44-2. The highest grain total panicle⁻¹ was found in GS12-1, and the lowest was found in GS11-2. The highest grain weight panicle⁻¹ was found in GS16-1, and the lowest was found in GS11-1. The GS44-1 lines were recorded as the highest weight of 1000 grains and days to 50% flowering. The lowest thousand-grain weight and the fastest day to 50% flowering found in GS12-1.

The longest day to maturity was 104.00 days found in GS12-1, GS12-2, GS44-1 and GS44-2. The shortest day to maturity was 100.00 days found in GS11-1, GS11-2, GS16-1 and GS16-2. Furthermore, the GS16-1 recorded as red rice promising lines with the highest grain yield, which was statistically different from other varieties, and the lowest was in GS11-1.

Genetic variability

The degree of variability for a given trait is required to improve the breeding of field crops. The estimates of genotypic variation (σ_g), phenotypic variation (σ_p), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2_b), genetic advance (GA), and genetic advance as percentage of the mean (GAM) for different characters have been presented in Table 3.

The genetic analysis revealed significant substantial variations among all the promising lines for all the traits examined. The PCV and GCV values of the characters analyzed in this study were low, moderate, and strong. Days to 50% flowering had the highest PCV and GCV values among the yield characters, followed by grain total per panicle and grain weight per panicle.

The parameter of days to 50% flowering (53.82) had the highest genotypic coefficient of variation (GCV), followed by grain total per panicle (33.85), grain weight per panicle (26.26), flag leaf area (22.58), and leaf area (21.52), suggesting a higher degree of genetic heterogeneity among the red rice lines tested for these traits. Ansari et al. (2010) found similar findings with different hybrid rice maintainer lines. The GCV and PCV values (Table 2) were recorded high for leaf area, flag leaf area, grain total per panicle, grain weight per panicle, and days to 50% flowering. This result was in agreement with the finding reported by Shrivastava et al. (2015), Gautam et al. (2016), Devi et al. (2017), Srujana et al. (2017), and Choudhary et al. (2018).

Table 2. Mean performance of eight red rice promising lines and a check variety

Traits	Rice promising lines								Check variety
	GS11-1	GS11-2	GS12-1	GS12-2	GS44-1	GS44-2	GS16-1	GS16-2	
PH	43.83b	44.20b	50.56a	44.23b	44.43b	47.11b	46.05b	51.17a	39.98c
LA	12.76ab	12.14ab	14.71a	11.38ab	12.01ab	11.27ab	12.40ab	15.11a	10.46b
FLA	12.42ab	12.11ab	12.64a	12.09ab	11.93ab	11.57ab	12.84ab	12.97a	10.24b
FLW	21.48c	20.98c	25.66b	23.37bc	21.68c	25.53b	30.85a	27.78a	22.64bc
PL	23.83b	23.53b	25.27a	24.17ab	24.83ab	25.10a	25.60a	23.93b	20.37c
FG/P	76.02bc	73.54bc	79.06ab	79.32ab	76.34bc	68.49c	74.26bc	77.19bc	86.93a
GT/P	128.18b	126.53b	166.69a	144.75ab	141.17ab	146.64ab	163.91a	145.29ab	75.08c
GW/P	2.53b	2.60ab	2.80ab	2.83ab	2.93a	2.60ab	2.95a	2.77ab	1.73c
TGW	28.55ab	26.92b	26.05b	26.77b	30.74a	28.58ab	29.92ab	28.16ab	26.50b
DTF	69.00ab	69.67a	67.67b	70.57a	70.67a	70.00a	69.00ab	69.33ab	54.00c
DTM	100.00b	100.00b	104.00a	104.00a	104.00a	104.00a	100.00b	100.00b	84.00c
GY	26.63c	28.62b	26.88bc	28.16b	27.51bc	29.51b	35.88a	29.20b	34.94a

Note: Means followed by the same letter in the same row are not significantly different. PH: Plant height, LA: Leaf area, FLA: Flag leaf angle, FLW: Flag leaf area, PL: Panicle length, FG/P: Filled grain percentage, GT/P: Grain total per panicle, GW/P: Grain weight per panicle, TGW: Thousand-grain weight, DTF: Days to 50% flowering, DTM: Days to maturity, GY: Grain yield per hill.

Moderate estimates of phenotypic and genotypic coefficients of variation were recorded for panicle length, filled grain percentage, days to maturity, and grain yield per hill. In the present study, moderate GCV and PCV were obtained for plant height, flag leaf angle, panicle length, filled grain percentage, days to maturity, and grain yield per hill; this was in agreement with Choudhary et al. (2018) and partial agreement with Devi et al. (2017). Thousand-grain weight showed low GCV and PCV (<10%), which was in accord with Hossain et al. (2016), and Sohgaure et al. (2014). The lowest PCV and GCV values were recorded thousand-grain weight parameter.

According to the analysis of variability parameters, the phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all of the characters analyzed in this research, which could be due to the environment's role in the phenotypic expression of the characteristics to some extent. This conformed with earlier (Ravishanker et al. 2013; Akter et al. 2020). The limited variations in genotypic and phenotypic coefficients of variance suggested that environmental factors had little effect on the speech of these characters. These findings are consistent with those reported previously (Adhikari et al. 2018; Tiwari et al. 2019).

Heritability and genetic advance are essential parameters in the selection of rice traits. The genetic advance helps quantify the amount of improvement that might be expected with selection in a character, while heritability measures the relative amount of the heritable portion of variance (Bello et al. 2012; Khan et al. 2016; Keerthana et al. 2019). Genetic advance is a valuable measure of the progress that can be expected from selecting the relevant population (Reddy et al. 2013; Islam et al. 2015; Ajmera et al. 2017; Terfa and Gurmu 2020). Heritability combined with genetic advance would provide

a more accurate index of selection value (Senapati et al. 2013; Oladosu et al. 2014; Huda et al. 2018).

Heritability estimates in a broad sense (h^2_{bs}) were recorded high for all the traits evaluated. High heritability estimates help make the selection of superior genotypes based on phenotypic performance. The estimates of heritability and genetic advance as percent of mean were high for plant height, leaf area, flag leaf angle, flag leaf area, panicle length, filled grain percentage, grain total per panicle, grain weight per panicle, thousand-grain weight, and yield per hill. It indicates the predominance of additive gene action, and hence the direct selection is useful for these traits. In general, the characters that recorded high heritability with high genetic advances are controlled by additive gene action and can be improved through simple or progeny selection methods (Sravan et al. 2014; Roy and Shil 2020).

High heritability combined with moderate genetic advance as percent of mean was recorded only for days to maturity. High heritability combined with low genetic advance as percent of mean was recorded for days to 50% flowering parameter. For selecting the best individual, heritability estimates and genetic gain would be more useful (Singh et al. 2011). Similar results were also recorded by Adhikari et al. (2018) on lowland irrigated rice. Broad-sense heritability helps estimate the inheritance of a character by explaining both fixable (additive) and non-fixable (dominant and epistatic) variances (Nirmaladevi et al. 2015).

In this study, most of the traits exhibited high broad-sense heritability. High heritability coupled with high genetic advance showed by grain total per panicle and grain yield per hill, indicating the role of the additive gene expression of these traits.

Table 3. Variances, Coefficient of variation (%), broad-sense heritability (h^2_{bs}), genetic advance, and genetic advance as percent of the mean for 12 traits of eight red rice lines evaluated

Traits	\bar{x}	Variance		Coefficient of variance (%)		h2bs (%)	GA	GAM
		$\sigma^2_{\bar{x}}$	σ^2_p	GCV	PCV			
PH	45.73	33.69	36.73	12.69	13.25	91.72	11.45	25.03
LA	12.74	7.51	8.01	21.52	22.22	93.76	5.47	42.93
FLA	12.41	4.83	5.11	17.70	18.21	94.52	4.40	35.46
FLW	24.45	30.48	32.83	22.58	23.44	92.84	10.96	44.83
PL	23.96	6.34	6.50	10.51	10.64	97.54	5.12	21.37
FG/P	77.31	72.50	75.93	11.01	11.27	95.48	17.14	22.17
GT/P	137.59	2169.51	2198.41	33.85	34.08	98.68	95.31	69.27
GW/P	2.67	0.49	0.51	26.26	26.70	96.08	1.41	52.81
TGW	28.02	7.25	7.72	9.61	9.91	93.91	5.38	19.20
DTF	67.78	1.78	1.90	53.82	55.68	93.68	2.66	3.92
DTM	100.07	82.51	82.67	13.40	13.41	99.81	18.69	18.68
GY	26.71	119.74	112.15	10.47	10.58	97.85	21.35	79.93

Note: Phenotypic variance ($\sigma^2_{\bar{x}}$), genotypic variance (σ^2_p), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad-sense heritability (h^2_{bs}), genetic advance (GA), and genetic advance as percent of mean (GAM). PH: Plant height, LA: Leaf area, FLA: Flag leaf angle, FLW: Flag leaf area, PL: Panicle length, FG/P: Filled grain percentage, GT/P: Grain total per panicle, GW/P: Grain weight per panicle, TGW: Thousand-grain weight, DTF: Days to 50% flowering, DTM: Days to maturity, GY: Grain yield per hill

Table 4. Coefficient correlation for yield-related traits of eight promising lines of red rice evaluated

Traits	PH	LA	FLA	FLW	PL	FG/P	GT/P	GW/P	TGW	DTF	DTM	GY
PH	1	0.70**	0.33	0.53**	0.52**	-0.36	0.67**	0.43*	-0.03	0.36	0.45*	-0.12
LA		1	0.58**	0.43*	0.57**	-0.48*	0.70**	0.63**	0.13	0.61**	0.53**	-0.33
FLA			1	0.46*	0.40*	-0.11	0.55**	0.57**	0.23	0.48*	0.37	-0.34
FLW				1	0.37	-0.04	0.55**	0.50**	0.19	0.05	0.10	-0.02
PL					1	-0.51**	0.88**	0.82**	0.34	0.80**	0.89**	0.63**
FG/P						1	-0.41*	-0.29	-0.13	-0.62**	-0.60**	0.53**
GT/P							1	0.89**	0.23	0.71**	0.82**	-0.28
GW/P								1	0.41*	0.71**	0.73**	0.54**
TGW									1	0.34	0.25	0.52**
DTF										1	0.94**	-0.61**
DTM											1	-0.48*
GY												1

Note: *Significance at the 5% level, and **Significance at the 1% level. PH: Plant height, LA: Leaf area, FLA: Flag leaf angle, FLW: Flag leaf area, PL: Panicle length, FG/P: Filled grain percentage, GT/P: Grain total per panicle, GW/P: Grain weight per panicle, TGW: Thousand-grain weight, DTF: Days to 50% flowering, DTM: Days to maturity, GY: Grain yield per hill.

The effectiveness of selection in any crop depends on the nature and magnitude of phenotypic and genotypic variability present in different agronomic traits of the population (Bahadur et al. 2016). Genetic parameters such as genotypic coefficient of variation, heritability, and genetic advance are needed to improve crops. The knowledge of genetic parameters for desirable traits is a prerequisite for the success of crop improvement programs (Roychowdhury et al. 2012).

Genetic diversity is the basis for the survival of plants in nature and crop improvement (Bhandari et al. 2017). A high genotypic coefficient of variation indicates the availability of high genetic variation (Ene et al. 2016; Gebregergs and Mekbib, 2020). On the other hand, a low genotypic coefficient of variation also indicates the narrow genetic variability, and the selection is not effective for a particular character. The PCV and GCV are not only useful for comparing the relative amounts of phenotypic and genotypic variations among different traits but are very useful for estimating the scope of improvement through selection (Bello et al. 2012).

The heritability information, genetic advance of yield attributing traits, and their association will help plant breeders identify the characters that are effective for selection (Bello et al. 2012; Dabalo et al. 2020). Heritability is an essential factor in determining the response of selection and breeding programs. Its estimations are important aspect of the inheritance of quantitative traits as they indicate the genetic gains that may be gained through selection (Schmidt et al. 2019). Heritability estimates and genetic advances are usually more helpful in predicting the gain under selection than heritability estimates alone (Cooper et al. 2021).

Correlation coefficient analysis

Pearson correlation analysis among traits, yield, and its related traits are shown in Table 4. The results revealed that panicle length, filled grain percentage, grain weight per panicle, and thousand-grain weight were highly positive significant correlations present with yield. These results agreed with the previous research result (Sadimantara et al. 2018).

Correlation coefficient analysis measures the mutual relationship between various plant characters and determines the component characters on which selection can be based for genetic improvement in yield. Correlation among traits is generally due to the presence of linkage and pleiotropic effect of different genes (Deep et al. 2017). Correlation coefficient analysis is also widely used to measure the degree and direction of relationships between various traits, including grain yield (Tiwari et al. 2019; Rachana et al. 2021).

Panicle length showed a significant positive correlation with plant height, leaf area, grain weight per panicle, grain total per panicle, filled grains per panicle, days to 50% flowering, days to maturity, and grain yield per hill. Earlier researchers, Patel et al. (2014), Ketan and Sarkar (2014), Ramanjaneyulu et al. (2014), Liu et al. (2016), Shamim et al. (2017), Onyia et al. (2017), and Pratap et al. (2018) reported similar results. The grain weight per panicle and panicle length is considered an essential component for achieving high yield because it showed a significant and positive association with grain total per panicle, 1000 grain weight, days to 50% flowering, days to maturity, and grain yield per hill. Similar results were also reported by Gopikannan and Ganesh (2013), Thippiani et al. (2017), and Venkanna et al. (2014). The panicle length and grain weight per panicle trait would be effective in the direct selection process. On the other hand, days to 50% flowering showed a strong negative association with yield, so this trait must be excluded from direct selection. Similarly, plant height and leaf area showed a non-significant negative correlation with yield and met with the findings of Rawte and Saxena (2017).

The difference of 1000 grains weight of each treatment is genetically derived from each rice lines trait. The studies of Aghamolki et al. (2015) found that the grain yield had a positive and significant correlation with the number of grains per panicle, the number of filled grains per panicle, and 1000-grain weight. However, a negative and significant correlation of grain yield per hill was observed with days to maturity, days to 50% flowering followed by leaf area, and flag leaf angle. This finding was in confirmation with the results of Lingaiah et al. (2014),

Sohgaura et al. (2014), Onyia et al. (2017), and Hosagoudar and Kovi (2018).

In conclusion, The character with high PCV, GCV, and heritability are days to 50% flowering, grain total per panicle, and grain weight per panicle. High heritability coupled with high genetic advance was observed for grain total per panicle and grain yield per hill. A high percentage of the genetic advance of the mean value was found in the characters GTP, GWP, and GY. The panicle length, the percentage of filled grains, grain weight per panicle, and thousand-grain weight were found a significantly positive correlation with the yield of red rice promising lines. Based on the value of heritability, genetic variability, and genetic advance, the character used as selection criteria in this study are grains total per panicle and grain weight per panicle. Both GTP and GWP are considered important yield-related traits and could be used for selection to improve the genetic potential of rice yield.

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