Estimation of Genetic variability and Association Studies for Quantitative Traits in Rice (*Oryza sativa* L.)

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ABSTRACT: An experiment was conducted during *kharif* (July–November), 2021 at ARS, Kampasagar, Telanagana, India to estimate variability, genetic parameters and association among yield and its contributing traits in 270 rice genotypes. ANOVA by REML method showed significant variation among the genotypes for all the traits i.e., days to 50% flowering, plant height (cm), number of effective tillers plant[-1], number of tillers plant[-1], panicle length (cm) and grain yield (kgha[-1]). The phenotypic variance was higher than the corresponding genotypic variance for all the traits indicating profound influence of environment in the expression of the traits. The magnitude of difference between phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV) was more for all the traits revealing the environmental effect. GCV was moderate for grain yield and low for the remaining traits and PCV was moderate for plant height, low for days to 50% flowering and high for the remaining traits. Low PCV and GCV values indicate the need for creation of variability through hybridization followed by selection. Moderate heritability coupled with high genetic advance as percent of mean was found for grain yield indicating the preponderance of additive type of gene action in governing the trait and selection may be done in early generations. Heritability was moderate for days to 50% flowering and low for the remaining traits coupled with low genetic advance as percent of mean revealing non-additive gene action in governing these traits hence, direct selection is not effective. Improvement is possible by creating variation and selection. Days to 50% flowering, plant height, number of effective tillers plant[-1] and number of tillers plant[-1] had positive and highly significant correlation with grain yield indicating selection of these traits can increase grain yield.

Keywords: Rice, GCV, PCV, heritability, genetic advance, correlation.

INTRODUCTION

Rice occupies second place after wheat in the world and first place followed by wheat in India. Half of the world's human population rely on rice crop for nutritional requirement and had high economic impact (Lopez 2008). It is the major part of a meal in everyday diet and majority of the Asian countries achieved food security through rice yields (Kumar and Kumar 2020). Worldwide rice occupies 165.25 mha area with 502.98 mt milled rice production and 4.55 t ha^{-1} productivity in the year 2022-23 (Anonymous, 2022). At global level, India ranks first in area with 47.7 mha, second in production with 130.83 mt and 2.8 t ha^{-1} productivity in rice next to wheat. At Global level, projected demand for rice will be about 580 mt (Samal *et al.,* 2022) and in India 197.40 mt *i.e.,* 80% more over the present demand for 1.65 billion population.

In India, rice share is 40.5% and 44.4% of total food grain and cereal production, respectively (Anonymous 2022). Low rice productivity levels are challenging food and nutritional security in India as 60% of population depends mainly on rice. Rice occupies a pivotalplace in Indian agriculture and rice trade contributes roughly 6.2 percent of the BIN GDP. It

provides 43 percent calorie requirement to nearly 70% of Indian population.

Cultivation of high yielding semi dwarf varieties under high input management resulted in increased rice production. Crop improvement is mainly dependant on nature and magnitude of genetic variability, heritability and introgression of desirable traits into new cultivars targeting yield and yield components (Ramachary *et al.,* 2022; Dhanuja *et al.,* 2021; Singh *et al.,* 2021; Shrestha *et al.,* 2021; Sudeepthi *et al.,* 2020). The success of breeding programmes rely on enriched variability in the existing germplasm so that plant breeder exercise effective selection for producing new varieties or improving existing ones. Genetic variability is measured through genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance (GA) (Gupta *et al.,* 2020; Nithya *et al.,* 2020; Srilakshmi *et al.,* 2018; Singh and Verma 2018; Manjunatha *et al.,* 2017; Umarani *et al.,* 2017). Genetic gain under selection can be predicted through heritability estimates coupled with genetic advance (Singh and Narayanan 2006) and high values offer the most effective selection of a specific character (Devi *et al.,* 2022). Hence, characterization of rice germplasm is very important in obtaining breeding

values prior to crop improvement. Yield is controlled by polygenes and is the resultant of interaction of multiple yield components. Correlation studies reveal magnitude and direction of association among yield and its components (Lingaiah *et al.,* 2020; Tejaswini *et al.,* 2018; Tiwari *et al.,* 2019; Umarani *et al.,* 2019; Sreedhar and Reddy 2019; Pratap *et al.,* 2018; Panigrahi *et al.,* 2018; Mani and Kumar 2018; Maurya *et al.,* 2019). Hence, an experiment was conducted to estimate genetic variability, heritability of yield and its components and association between them to enhance yield potential.

MATERIALS AND METHODS

The present investigation comprised of two hundred and seventy genotypes received under OneIRRI-Network-2021WS-Medium maturity segment-IN from IRRI South Asia hub located at ICRISAT campus, Patancheru, Hyderabad including three local checks *viz.,* KPS-2874, KPS-6262 and WGL-14. KPS-2874 is a medium maturing high yielding, fine grain, saline tolerant and BPH resistant variety released through SVRC in the name of Kampasagar Vari-1 from ARS, Kampasagar in 2021 and WGL-14, a medium maturing and high yielding variety moderately resistant to gall midge and rice tungro virus coupled with high head rice recovery and good cooking quality released through CVRC in the name of Warangal Samba in the year 2005. KPS-6262 is an early duration, fine grain, high yielding pre-release variety resistant to gall midge and BPH. These entries were evaluated at Agricultural Research Station, Kampasagar during *kharif*, 2021 (July–November) located in southern zone of Telangana at 16.85°N latitude and 79.56°E longitude and at an altitude of 152 m from sea level. Experimental design was alpha lattice design replicated twice and each entry was sown in a single row of 3 m length. Nursery rising was done on 2nd July, 2021 and transplanting was done after thirty days on 3rd August, 2021 and 20 cm × 15 cm row-row and plant-plant spacing was followed and two seedlings were kept per hill. The fertilizers NPK were applied @ 120:60:40 kg ha^{-1}, respectively and the recommended agronomic practices were taken up for a good crop.

Data was taken on five randomly selected plants for each genotype in each replication for plant height, number of effective tillers plant[-1], number of total tillers plant[-1], and panicle length while the data on days to 50% flowering was taken on plot basis and grain yield plot[-1] (g) was converted into grain yield (kg ha^{-1}).

For all the traits, treatment means were subjected to Restricted Maximum Likelihood (REML) analysis using GenStat (Fifteenth Edition). REML is an appropriate analysis for a general model of alpha lattice design developed by Patterson and Williams (1976). Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were calculated as per Burton and Devane (1953). Heritability in broad sense (h^2) and genetic advance as percent of mean were estimated according to Allard (1960). The correlation coefficient among pairs of characters was calculated as per the formula suggested by Searle (1961). To test the significance of correlation

coefficients, the estimated values were compared with the table value (statistical table by Fisher and Yates, 1963) at n-2 degrees of freedom (where n denotes the number of genotypes tested) at 5% and 1% level of significance.

RESULTS AND DISCUSSION

A. Analysis of variance

Restricted Maximum Likelihood method (REML) indicated significant differences among the 270 genotypes for all the six quantitative traits (Table 1). Saha *et al.* (2019); Devi *et al.* (2022) also reported variation among the genotypes for days to 50% flowering, plant height, number of effective tillers plant[-1], panicle length and grain yield plant[-1].

B. Genetic variability

The amount of genetic variability present in breeding material is very important for trait improvement in any crop. Phenotypic variance was higher than genotypic variance for all the studied traits indicating the profound influence of environment in the phenotypic expression of the traits (Table 2). The highest variability (Vg & Vp) was found in grain yield followed by plant height and days to 50% flowering.

For trait improvement, wide range of genetic variation is highly essential and the heritability estimates are presented in Table 2. Difference between the genotypic and phenotypic coefficient of variation of a particular trait indicates environmental influence on it. Large difference shows high environmental influence while small difference reflects high genetic influence.

Coefficient of variation indicated that the PCV estimates were higher than the corresponding GCV (Table 2) indicating the influence of environment. Greater difference between PCV and GCV indicates high environmental influence while smaller difference indicates high genetic influence. Chandra *et al.* (2022); Devi *et al.* (2022); Srinivas *et al.* (2016) also reported similar findings. Sivasubramanian and Madhava Menon (1973) categorized the genotypic and phenotypic coefficients of variation as low (< 10%), moderate (10–20%) and high (> 20%). PCV ranged from 5.23 (Days to 50% flowering) to 28.21(Number of effective tillers plant[-1]) while GCV ranged from 3.74 (Days to 50% flowering) to 17.91 (Grain yield kg ha^{-1}). GCV was moderate for grain yield (kg ha^{-1}) (17.91) (Kavyashree *et al.,* 2022; Salman *et al.,* 2022; Krishnamrutha *et al.,* 2023) and low for the remaining traits (Chandra *et al.,* 2022) and moderate variability indicated that improvement of grain yield could be possible through selection in advanced generations. PCV was highest for number of productive tillers plant[-1] (28.21) followed by grain yield (kg ha^{-1}) (25.61) (Devi *et al.,* 2017), number of total tillers plant[-1] (19.32) and panicle length (19.24), moderate for plant height (15.64) and low for days to 50% flowering (5.23) (Chandra *et al.,* 2022; Singh *et al.,* 2021; Devi *et al.,* 2020). Low PCV and GCV values indicate narrow genetic base for these traits and the variability can be achieved through hybridization or induced mutagenesis followed by pedigree selection.

C. Heritability

Heritability estimates the relative contribution of genetic and non-genetic factors to the total phenotypic

variance in a population. In quantitative genetics, it is an important concept particularly in selective breeding. Broad sense heritability selects elite genotypes from homozygous lines and narrow sense heritability selects elite lines from segregating populations. The heritability estimation varied from -5.14%–51.07% for panicle length and days to 50% flowering, respectively (Table 2). Johnson et al., (1955) categorized heritability estimates as low (< 30%), moderate (30–60%) and high (> 60%). Heritability was moderate for days to 50% flowering and grain yield indicating a moderate response to selection in these two traits and low for plant height, number of productive tillers plant[-1], number of total tillers plant[-1] and panicle length. These results were in concurrent with that of Chandra et al. (2022) for grain yield, Chandra et al. (2022) and Nithya et al., (2020) for number of productive tillers plant[-1]. Contrary to this, high heritability for days to 50% flowering, plant height and grain yield and medium heritability for number of productive tillers plant[-1] and panicle length was reported by Devi et al. (2022) and Kumari et al. (2022). In quantitative genetics, heritability indicates the reliability of the phenotypic value as a guide to breeding value (Falconer and Mackay 1996). The breeder should be more cautious during selection based on heritability as it indicates both additive and non-additive gene action. Hence, heritability coupled with genetic advance would be more reliable and useful while formulating breeding programmes.

D. Genetic advance

Genetic advance as percent of mean (5%) was highest for grain yield (25.80) and lowest for panicle length (-0.46) and low for the other traits. Johnson et al. (1955) classified genetic advance as percent of mean as low (< 10%), moderate (10–20%) and high (> 20%). Grain yield had moderate heritability coupled with high genetic advance as percent of mean indicating the preponderance of additive type of gene action in governing the trait and early generation selections may be effective. Low heritability coupled with low genetic

advance as percent of mean was found for number of productive tillers plant[-1] and number of total tillers plant[-1] indicating high environmental influence on these traits and selection would be ineffective. Moderate heritability coupled with low genetic advance as percent of mean were observed for days to 50% flowering and panicle length and low heritability coupled with high genetic advance as percent of mean was observed for plant height indicating non-additive gene action in governing these traits (Table 2) and recurrent selection could improve these traits. These results were in agreement with that of Devi et al. (2017) for grain yield. Days to 50% flowering and grain yield exhibited moderate heritability due to favorable environment rather than genotype hence, selection for such traits could not bring satisfactory improvement over the population mean.

E. Correlation

Correlation coefficient measures the mutual relationship between various plant characters and its components on which selection can be based for genetic improvement in yield. For a plant breeder, a positive correlation between desirable characters is favorable as it helps in simultaneous improvement of both the characters. The results on correlation analysis showed that all the traits had positive and highly significant correlation with grain yield except panicle length which had negative and significant correlation (Table 3) and this could be due to more number of unfilled/ chaffy grains in long panicles and low test weight. Devi et al. (2022) found the same result. Correlation between days to 50% flowering and plant height (Aswin et al., 2021; Manivelan et al., 2022) and number of productive tillers plant[-1] and number of total tillers plant[-1] were positive and highly significant. Negative and significant correlations were found for days to 50% flowering, plant height and number of productive tillers plant[-1] with panicle length and between plant height and number of productive tillers plant[-1]. Contrary to this, Aswin et al. (2021) found positive and significant correlations among these traits.

Table 1: REML variance component analysis for quantitative traits in rice.

Parameter	DF	PH	NET	NTT	PL	GY
Treatment	16.65	62.7	1.02	0.56	-0.95	381140
Residual	31.90	323.4	19.67	14.95	38.88	796701
Wald statistic						
Rep	6.48[*]	17.44[**]	14.81[**]	0.10	10.17[**]	147.64[**]
Rep/Block	54.60[*]	53.15[*]	75.68[**]	99.41[**]	54.15[*]	111.51[**]

**, *- significant at 1% and 5% level, respectively

Table 2: Variability parameters for six quantitative traits in rice genotypes.

Trait	DF	PH	NET	NTT	PL	GY
Vg	16.65	62.7	1.02	0.56	-0.95	381140
Vp	32.60	224.4	10.86	8.04	18.49	779491
GCV	3.74	8.27	8.65	5.1	-	17.91
PCV	5.23	15.64	28.21	19.32	19.24	25.61
h^2%(B.S.)	51.07	27.94	9.4	6.97	-5.14	48.9
GA	6.01	8.62	0.64	0.41	-0.46	889.3
GA as % of mean	5.50	9.01	5.46	2.77	-2.04	25.8

Vg: Genotypic variance; Vp: Phenotypic variance; GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation; h^2% (B.S.): Heritability (broad sense); GA: Genetic advance.

Table 3: Estimates of phenotypic correlation between yield and yield contributing traits in rice.

Trait	DF	PH	NET	NTT	PL	GY
DF	1	0.22**	0.11*	0.10	-0.12*	0.31**
PH		1	0.17**	0.09	-0.34**	0.16**
NET			1	0.49**	-0.13*	0.31**
NTT				1	-0.03	0.14*
PL					1	-0.17**
GY						1

Note: Abbreviations used in Tables 1, 2 & 3

DF: Days to 50% flowering; PH: Plant height (cm); NET: Number of effective tillers plant^{-1}; NTT: Number of tillers plant^{-1};
PL: Panicle length (cm); GY: Grain yield (kg ha^{-1})
**, *- significant at 1% and 5% level, respectively

CONCLUSIONS

Phenotypic variance was higher than genotypic variance for all the studied traits indicating the profound influence of environment in the phenotypic expression of the traits. Except grain yield, all the traits had low PCV and GCV values indicating narrow genetic base for these traits and variability could be created either through hybridization or induced mutagenesis followed by pedigree selection. Moderate heritability coupled with high genetic advance as percent of mean was found for grain yield indicating the preponderance of additive type of gene action in governing the trait and early generation selection is effective and for the remaining traits recurrent selection could be followed to improve the traits.

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