RESEARCH PAPER

Genetic variability study for yield and its attributing traits in rice (*Oryza sativa* L.)

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Abstract: A study on genetic variation and its understanding in cultivated rice (*Oryza sativa* L.) can help in improving the crop yield. The present investigation was undertaken with twenty-three rice genotypes to assess the variability parameters for yield and its component traits. The experiment was conducted in a randomized complete block design with two replications during *kharif* 2022 at three locations *viz.*, AICRIP (Vol. Centre), ARS (Paddy) Sirsi, ARS Malagi and ARS Mugad. The investigation revealed that the estimates of GCV for all the characters studied were slightly less than PCV estimates indicating influence of environment on the genotype performance. PCV and GCV were high for trait like straw yield per plot (kg). Moderate GCV and PCV showed by number of panicles hill[-1], number of panicles sqm[-1], grain yield per plot (kg), grain length/breadth (L/B) ratio and kernel length/breadth (kl/kb) ratio. High heritability coupled with high genetic advance over mean were recorded for number of panicles hill[-1], number of panicles sqm[-1], grain yield per plot (kg), straw yield per plot (kg) and kernel length/breadth (kl/kb) ratio indicating that most likely the heritability was due to additive gene effects.

Key words: GCV, Genetic advance over mean, PCV, Rice, Variability

Introduction

Rice is referred as "Global Grain" as it is the staple food crop for more than 50% population across the world contributing about 20% of the global calorie supply. Across the world, rice is cultivated in an area of 165.25 million hectares with the production of 787.29 million tonnes during 2022-23 (Indiastat 2022-23). Approximately, 90% of the world's rice is produced and consumed in Asia (Singh *et al.*, 2015). India stands second to China with the production of 129.47 million metric tonnes (Indiastat, 2022-23). Owing to a burgeoning population, it is estimated that the demand for rice will be 129.6 million metric tonnes by the year 2040 and 137.3 million metric tonnes by the year 2050. In view of the increasing demand of rice foreseen for the future, the production per unit area needs to be increased to the level of 3.4 tonnes per ha from the present 2.4 tonnes per ha assuming the rice area under plough remains at existing level (CRRI-VISION 2050). The presence of adequate genetic variability is regarded as the fundamental pre-requisite to conduct any crop improvement programme. Sometimes phenotypic selection based on their performance may not be effective because these genotypes may perform poor in further segregating generations, so it is essential to select the genotypes based on heritability and genetic advance. The genotypic coefficient of variation measures the magnitude of genetic variability and reflects the heritable portion of variability. Genetic variability along with heritability estimates would provide the amount of genetic gain expected out of selection (Burton, 1952). Therefore, assessment of variability for grain yield and its attributesin rice genotypes is essential to formulate selection criteria for the constructive yield augmentation through breeding. The present investigation was undertaken in this context to elucidate information on variability, heritability and genetic advance in 23 rice genotypes to identify effective selection criteria for grain yield improvement of rice genotypes.

Material and methods

The present investigation was carried out during *kharif*, 2022 at three locations *viz.*, AICRIP (Vol. Centre), ARS (Paddy) Sirsi, ARS Malagi and ARS Mugad. In the present study twenty-three genotypes were evaluated to assessed the variability and genetic parameters for yield and its components traits. Each genotype was sown in five rows of 5 m length following a spacing of 20 cm between the rows and 15 cm between the plants in a randomised block design (RBD) with two replications.The observations were recorded on five randomly selected competitive plants for characters *viz.* days to 50 per cent flowering, plant height (cm), panicle length (cm), number of panicles hill[-1], number of panicles sqm[-1], grain length (mm), grain breadth (mm), grain length/breadth (L/B) ratio (mm), kernel length (mm), kernel breadth (mm), kernel length/breadth (kl/kb) ratio (mm), straw yield per plot (kg) and grain yield per plot (kg). The data were subjected to the analysis of phenotypic and the genotypic coefficients of variation as per the method suggested by Burton (1952) and heritability and genetic advance following the method of Johnson *et al.* (1955).

Experimental material

Genotypes	Parents/Checks	Genotypes
BA – 01	A-67	BD -01
BA – 02	BPT–5204	BD – 02
BA – 03	D6-2-2	BD – 03
BA – 04		BD – 04
BA – 05		BD – 05
BA – 06		BD – 06
BA – 07		BD – 07
BA – 08		BD – 08
BA – 09		BD – 09
BA – 10		BD – 10

(BD = BPT-5204/DODDIGA and BA = BPT-5204/ANTHRASALI)

Table 1. Pooled analysis of variance for 13 yield and yield component characters over three environments in rice (*Oryza sativa* L.) genotypes

Source of variation	df	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	Number of panicles hill^{-1}	Number of panicles sqm^{-1}	Grain length (mm)	Grain breadth (mm)	Grain L/B ratio (mm)	Kernel length (mm)	Kernel breadth (mm)	Kernel L/B ratio (mm)	Straw yield per plot (kg)	Grain yield per plot (kg)
Genotypes	22	161.726**	261.679**	9.340*	2.529*	5146.173**	0.622**	0.184**	0.258**	0.386**	0.129**	0.226**	4.486**	0.109*
Environments	2	2.098	8255.475**	5.442	67.707**	784.574**	0.266	0.030	0.038	0.243*	0.005	0..019	269.240**	0.581*
Genotype x Environment	44	8.367**	58.018	2.692	2.290	696.697*	0.095	0.049	0.044	0.044	0.025	0.031	3.474**	0.106**
Pooled Error	66	2.939	8.380	0.432	0.246	91.675	0.013	0.005	0.005	0.009	0.004	0.002	0.105	0.010

*, ** Significant at 5 % and 1 % levels, respectively

Table 2. Estimates of variability and genetic parameters for thirteen yield and yield contributing characters in twenty-three rice (*Oryza sativa* L.) genotypes over three locations

Character	Mean	Range		Coefficient of variation (%)		Heritability in broad sense($h^2_{(bs)}$)	Genetic advance as per cent of mean (GAM)
		Min.	Max.	Genotypic (GCV)	Phenotypic (PCV)		
Days to 50% flowering	112.18	96.00	128.00	6.38	6.88	86.00	12.20
Plant height (cm)	95.17	63.03	109.23	9.55	10.39	84.63	17.23
Panicle length (cm)	22.21	18.53	24.93	7.55	8.38	81.16	14.01
Number of panicles hill^{-1}	8.14	6.77	10.43	10.93	12.02	82.68	20.47
Number of panicles sqm^{-1}	301.07	238.67	389.17	13.46	14.35	88.04	26.02
Grain length (mm)	7.89	6.89	8.60	5.57	6.26	78.95	10.19
Grain breadth (mm)	2.88	2.31	3.22	7.89	9.91	63.35	12.93
Grain L/B ratio (mm)	2.78	2.38	3.48	10.01	11.32	78.27	18.25
Kernel length (mm)	5.65	4.86	6.31	5.92	7.15	68.50	10.09
Kernel breadth (mm)	2.47	2.06	2.84	7.67	9.73	62.08	12.45
Kernel L/B ratio (mm)	2.31	1.88	2.79	11.39	13.33	72.91	20.43
Straw yield per plot (kg)	4.07	2.40	6.40	28.77	32.37	78.99	52.66
Grain yield per plot (kg)	1.12	0.58	1.38	17.92	19.32	86.03	34.24

Results and discussion

The combined analysis of variance was revealed significant differences among rice genotypes for all traits studied (P<0.05) (Table 1). The results showed that the presence of acceptable amount of variability among the genotypes. This gives an opportunity for rice breeders to improve those traits through selection and hybridization to improve the desired traits.

The estimates of co-efficient of variation, heritability and genetic advance observed for yield and yield components are presented in Table 2. Further PCV and GCV were high for trait like straw yield per plot (kg). Moderate GCV and PCV showed by number of panicles hill^{-1}, number of panicles sqm^{-1}, grain yield per plot (kg), grain length/breadth (L/B) ratio and kernel length/breadth (kl/kb) ratio.The earlier reports of Singh *et al.* (2021) Prajapati *et al.* (2011) and Manjunatha *et al.* (2019), Behera *et al.* (2020), Gangashetty *et al.* (2013) and Patil *et al.* (2003).

In the present study majority of the yield and yield components showed higher level of broad sense heritability. The selection for these traits would be sufficient to increase the overall yield in rice. Earlier reports of Akshay *et al.* (2022) also recorded high heritability for majority of the yield and its traits in rice.The traits *viz.*, number of panicles hill^{-1}, number of panicles sqm^{-1}, kernel length/breadth (kl/kb) ratio, straw yield per plot (kg) and grain yield per plot (kg) exhibited high genetic advance over mean. while the traits *viz.*, days to 50 per cent flowering, plant height (cm),panicle length (cm), number of panicles hill^{-1}, number of panicles sqm^{-1},grain length (mm), grain breadth (mm), grain length/breadth (L/B) ratio (mm), kernel length (mm), kernel breadth (mm) showed moderate genetic advance over mean.

The effectiveness of selection depends upon the high GAM coupled with high heritability. The traits having high heritability coupled with high genetic advance as per cent of mean were recorded for number of panicles hill^{-1}, number of panicles sqm^{-1},grain yield per plot (kg), straw yield per plot (kg) and kernel length/breadth (kl/kb) ratio indicates the traits are controlled by additive gene action and early selection is effective for these traits. Similar reports are found by Patil *et al.* (2003), Manjunatha *et al.* (2019) and Singh *et al.* (2021).

Narrow difference was observed between GCV and PCV for most of the traits indicated that less influence by environment indicated high or moderate heritability for all the traits. High value of genetic advance as per cent of mean coupled with high value of heritability is indicative of high

breeding value and practicing selection for such traits is reliable. In addition to this, all those traits possessed wide range of variability which was controlled by additive gene action. Hence, selection for these traits is reliable. From this study it was concluded that advanced breeding lines which were evaluated in three locations contained considerable genetic variability for yield attributing traits.

Conclusion

The outcome of present study revealed that the presence of variability among the advanced breeding lines and provides more opportunity for selection. Additionally, most of the yield related traits showed moderate to high variability. Considering the grain yield the genotypes BA-01 and BA-08 were found superior hence, these genotypes are selected through simples selection procedure.

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