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Estimates of genetic variability, heritability and genetic advance for grain yield and other yield attributing traits in rice (*Oryza sativa* L.)

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Abstract

Fifty two rice genotypes were evaluated in randomized block design for twelve metric traits to estimate the extent of genetic variability, heritability (broad sense) and genetic advance as per cent of mean. The analysis of variance revealed significant variability for all the characters studied. Among the 12 characters studied, high phenotypic and genotypic coefficients of variation were recorded for the traits viz., panicle number per plant, weight of 1000 fully developed grains and grain yield plant⁻¹ indicating that large amount of variation is present among the genotypes. High heritability coupled with high genetic advance as per cent of mean was recorded for time of heading (50% of plants with panicles), stem length (excluding panicle), panicle number per plant, weight of 1000 fully developed grains, decorticated grain width and grain yield plant⁻¹ indicating that these traits were governed by additive gene effects and may be chosen as selection criteria for formulating breeding strategies in rice.

Keywords: Rice, genetic advance, heritability, variability

Introduction

Rice (*Oryza sativa* L.) (2n=24) is the most important cereal crop which serves as a staple food for over 60% of the world's population (Singh and Singh, 2008) [24]. Approximately 90% of rice grown on the planet is produced and consumed in Asia (Singh *et al.*, 2015) [23]. The cultivation of rice is more than any other crop in the world with cultivated area of 162.57 million hectares with production of 499.07 million metric tonnes in 2018-19 (USDA, 2020) [28]. India is the second largest producer of rice after China occupying 43.8 million hectare area with an average grain yield of 3.99 metric tonnes per hectare while the total production is 116.48 million metric tonnes in 2018-19 (USDA, 2020) [28].

The success of any crop improvement programme relies upon the nature and magnitude of genetic variability. The efficiency of selection relies upon the degree of genetic variability present in the plant population. Characters like yield and its components being polygenic in nature, the breeder has to isolate desired genotypes from the knowledge of components of variation. The basic element is the partitioning of total variation into phenotypic and genotypic components and the extent of these components for various traits is a measure of the type of gene action, which helps in deciding a breeding procedure for the genetic improvement of a trait. High heritability values alone provides no indication of the amount of genetic progress that would result from selection of the better individuals. Heritability values coupled with genetic advance are more reliable and useful genetic parameters in predicting the genetic gain under selection than heritability estimates alone (Kundu *et al.*, 2008) [14]. Therefore, the objective of this study was to assess the genetic variability, heritability and genetic advance of grain yield and other associated traits in some rice genotypes to assist the future breeding programs for yield improvement.

Material and Methods

The present investigation was carried out using 52 rice genotypes grown in randomized block design with three replications during *kharif*, 2019 at Wetland farm, Sri Venkateswara Agricultural College, Tirupati. Each genotype was grown in a single row of 1.5 m length with a spacing of 20 cm between rows and 15 cm between plants within the row. The data was recorded on five competitive plants taken from each replication for time of heading (50% of plants with panicles) (days), stem length (excluding panicle) (cm), panicle length of main axis

(cm), panicle number per plant, time of maturity (days), weight of 1000 fully developed grains (g), grain length (mm), grain width (mm), decorticated grain length (mm), decorticated grain width (mm), length/breadth ratio and grain yield plant⁻¹ (g).

Statistical Analysis

Analysis of variance was worked out by the method suggested by Panse and Sukhatme (1961) [15] and the genotypic and phenotypic coefficient of variations were estimated by the method suggested by Burton (1952) [6] and heritability (broad sense) as the ratio of genotypic to phenotypic variance. The procedure of Johnson *et al.*, (1955) [13] was followed for calculating the expected genetic advance and genetic advance as per cent of mean. The data analysis was carried out with INDOSTAT software.

The GCV and PCV are classified as low (< 10%), moderate (10-20%) and high (> 20%) as suggested by Sivasubramanian and Madhavamenon (1973) [25]. Heritability was estimated by the formula given by Johnson *et al.* (1955) [13] and they classified the heritability as low (below 30%), moderate (30-60%) and high (above 60%). The range of genetic advance as per cent of mean was classified as low (< 10%), moderate (10-20%) and high (> 20%) as suggested by Johnson *et al.* (1955) [13].

Results and Discussion

Analysis of variance for 12 characters, revealed significant differences among the genotypes for all the characters included under study indicating the presence of greater variability among the genotypes. The details pertaining to ANOVA are furnished in Table 1.

The PCV estimates were slightly higher than the corresponding GCV estimates for the characters studied (Table 2 and Figure 1) indicating that the characters were less influenced by the environment. Therefore, phenotypic selection would be effective for the improvement of these traits. Low GCV and PCV values were recorded for the traits *viz.*, grain length (7.76% and 8.26%), decorticated grain length (8.16% and 8.47%) and length/breadth ratio (6.09% and 7.01%) indicating that the variability for these characters among the genotypes was meagre. Similar findings were reported by Islam *et al.* (2015) [12] and Senapati and Kumar (2015) [20] and Bhinda *et al.* (2017) [5] for grain length, Babu *et al.* (2012) [4], Pratap *et al.* (2012) [16], Dhurai *et al.* (2014) [9] and Aravind *et al.* (2019) [3] for decorticated grain length and Subbaiah *et al.* (2011) [26] and Dhurai *et al.* (2014) [9] for length/breadth ratio. The traits *viz.*, panicle length of main axis, time of maturity and grain width showed low GCV (9.73%, 9.83% and 9.95%) and moderate PCV (10.94%, 10.00% and 10.40%) estimates respectively. These results were in accordance with the findings of Chuchert *et al.* (2018) [7], Ranjith *et al.* (2018) [18] and Aravind *et al.* (2019) [3] for panicle length of main axis, Abebe *et al.* (2017) [1] for time of maturity and Bhinda *et al.* (2017) [5] for grain width. Moderate

GCV and PCV values were observed for the traits *viz.*, time of heading (50% of plants with panicles) (13.29% and 13.54%), stem length (excluding panicle) (11.36% and 12.85%) and decorticated grain width (10.00% and 10.29%). These observations are in agreement with the earlier reports of Veni *et al.* (2013) [29], Gyawali *et al.* (2018) [11], Ranjith *et al.* (2018) [18] for time of heading (50% of plants with panicles), Sao *et al.* (2019) [19] for stem length (excluding panicle) and Umarani *et al.* (2017) [27] for decorticated grain width. The traits, panicle number per plant (21.95% and 24.26%), weight of 1000 fully developed grains (20.30% and 20.70%) and grain yield plant⁻¹ (32.97% and 36.81%) registered higher GCV and PCV values respectively indicating that large amount of variation is present among the genotypes. Similar results were obtained by Chuchert *et al.* (2018) [7] and Aravind *et al.* (2019) [3] for panicle number per plant, Gangashetty *et al.* (2013) [10] and Veni *et al.* (2013) [29] for weight of 1000 fully developed grains, and Gangashetty *et al.* (2013) [10], Veni *et al.* (2013) [29], Dhurai *et al.* (2014) [9], Gyawali *et al.* (2018) [11] for grain yield plant⁻¹.

High heritability coupled with high genetic advance as per cent of mean (Table 2 and Figure 2) was reported for time of heading (50% of plants with panicles), stem length (excluding panicle), panicle number per plant, weight of 1000 fully developed grains, decorticated grain width and grain yield plant⁻¹ indicating that these traits were mostly under the control of additive gene action and direct selection of these traits would be effective for crop improvement. Similar works were reported by Gyawali *et al.* (2018) [11] and Ranjith *et al.* (2018) [18] for time of heading (50% of plants with panicles), Sao *et al.* (2019) [19] for stem length (excluding panicle) and decorticated grain width, Chuchert *et al.* (2018) [7] and Sao *et al.* (2019) [19] for panicle number per plant, Dhurai *et al.* (2014) [9], Devi *et al.* (2016) [8], Chuchert *et al.* (2018) [7] and Aravind *et al.* (2019) [3] for weight of 1000 fully developed grains, Shanthi and Singh (2001) [21], Gangashetty *et al.* (2013) [10], Dhurai *et al.* (2014) [9] and Rahangdale *et al.* (2019) [17] for grain yield plant⁻¹.

High heritability coupled with moderate genetic advance as per cent of mean was observed for the traits *viz.*, panicle length of main axis, time of maturity, grain length, grain width, decorticated grain length and length/breadth ratio indicating the presence of both additive and non-additive genetic effects and genetic improvement of these characters can be exploited through heterosis breeding. Similar reports were published by Shanthi and Singh (2001) [21], Abebe *et al.* (2017) [1], Singh and Verma (2018) [22] and Ranjith *et al.* (2018) [18] for panicle length of main axis, Islam *et al.* (2015) [12] and Dhurai *et al.* (2015) for time of maturity, Islam *et al.* (2015) [12] and Bindha *et al.* (2017) [5] for grain length and grain width, Babu *et al.* (2012) [4], Aditya and Bhartiya (2013) [2], Singh and Verma (2018) [22] for decorticated grain length, Aditya and Bhartiya (2013) [2] and Dhurai *et al.* (2015) for length/breadth ratio.

Table 1: Analysis of variance for grain yield and its component traits in 52 rice genotypes

S. No.	Character	Mean sum of squares for		
		Replications (df: 2)	Genotypes (df: 51)	Error (df: 102)
1.	Time of heading (50% of plants with panicles) (days)	4.410	529.497**	6.783
2.	Stem length (excluding panicle) (cm)	2.438	462.845**	39.382
3.	Panicle length of main axis(cm)	0.517	17.692**	1.434
4.	Panicle number per plant	3.000	21.860**	1.503
5.	Time of maturity (days)	2.673	479.659**	5.549

6.	Weight of 1000 fully developed grains (g)	0.458	54.707**	0.715
7.	Grain length (mm)	0.003	1.316**	0.056
8.	Grain width (mm)	0.007	0.202**	0.006
9.	Decorticated grain length (mm)	0.002	0.783**	0.020
10.	Decorticated grain width (mm)	0.001	0.139**	0.003
11.	Length/Breadth Ratio	0.002	0.180**	0.018
12.	Grain yield plant ⁻¹ (g)	155.579	735.304**	55.868

** Significant at 1 per cent level

Table 2: Mean, Range, Coefficients of variation, Heritability (broad sense) and Genetic advance as per cent of mean for grain yield and its component traits in 52 rice varieties

S. No.	Character	Mean	Range		Coefficient of variation (%)		Heritability (%) (broad sense)	Genetic Advance	Genetic advance as per cent of mean (5% level)
			Minimum	Maximum	Genotypic	Phenotypic			
1.	Time of heading (50% of plants with panicles) (days)	99.34	63.67	118.33	13.29	13.54	96.25	26.68	26.86
2.	Stem length (excluding panicle) (cm)	104.59	75.93	124.73	11.36	12.85	78.19	21.64	20.69
3.	Panicle length of main axis (cm)	23.93	18.73	28.60	9.73	10.94	79.07	4.26	17.82
4.	Panicle number per plant	11.87	6.67	17.67	21.95	24.26	81.86	4.85	40.92
5.	Time of maturity (days)	127.88	97.00	150.67	9.83	10.00	96.61	25.45	19.90
6.	Weight of 1000 fully developed grains (g)	20.89	13.00	29.77	20.30	20.70	96.18	8.57	41.02
7.	Grain length (mm)	8.35	7.27	9.67	7.76	8.26	88.20	1.25	15.01
8.	Grain width (mm)	2.57	2.13	3.17	9.95	10.40	91.40	0.50	19.59
9.	Decorticated grain length (mm)	6.18	5.30	7.40	8.16	8.47	92.81	1.00	16.19
10.	Decorticated grain width (mm)	2.13	1.80	2.67	10.00	10.29	94.41	0.43	20.02
11.	Length/Breadth Ratio	3.82	3.31	4.37	6.09	7.01	75.49	0.42	10.90
12.	Grain yield plant ⁻¹ (g)	45.65	22.35	98.50	32.97	36.81	80.21	27.76	60.82

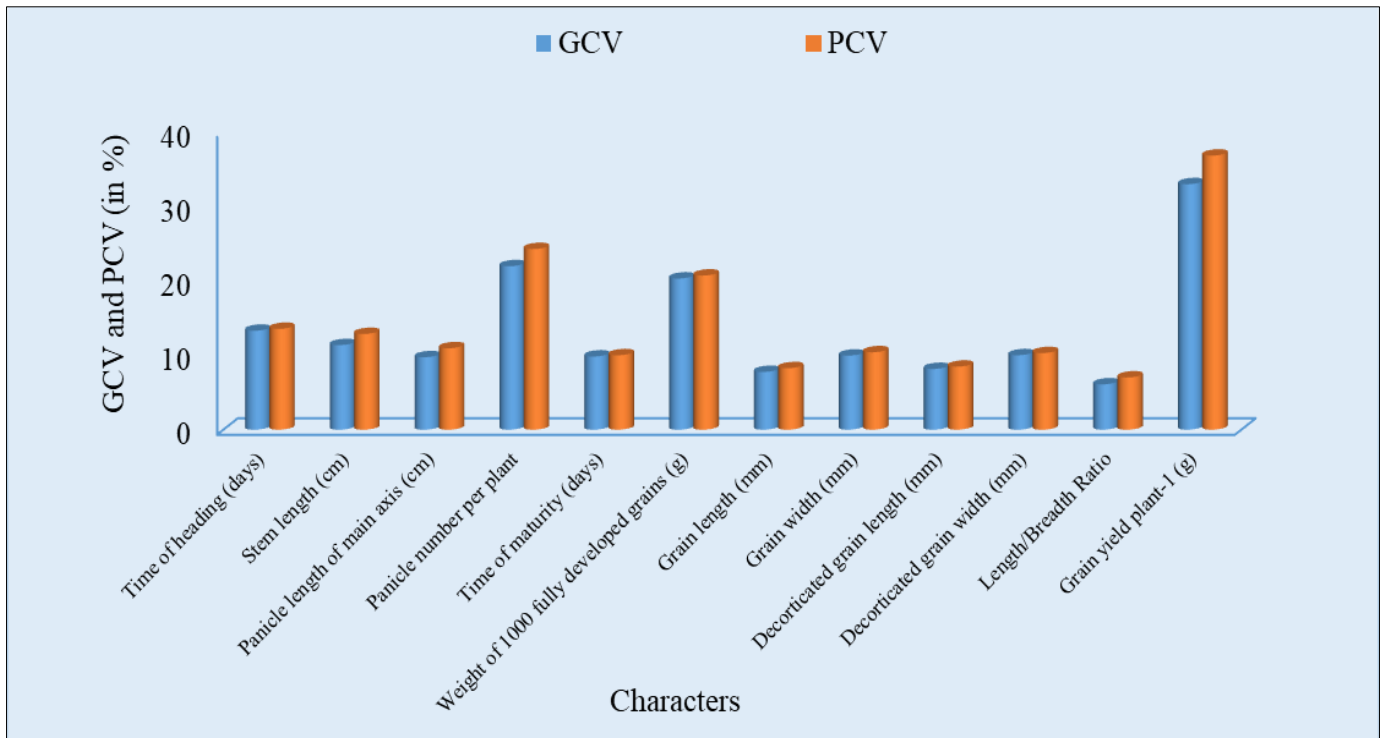


Fig 1: Genotypic and Phenotypic coefficients of variation of various traits

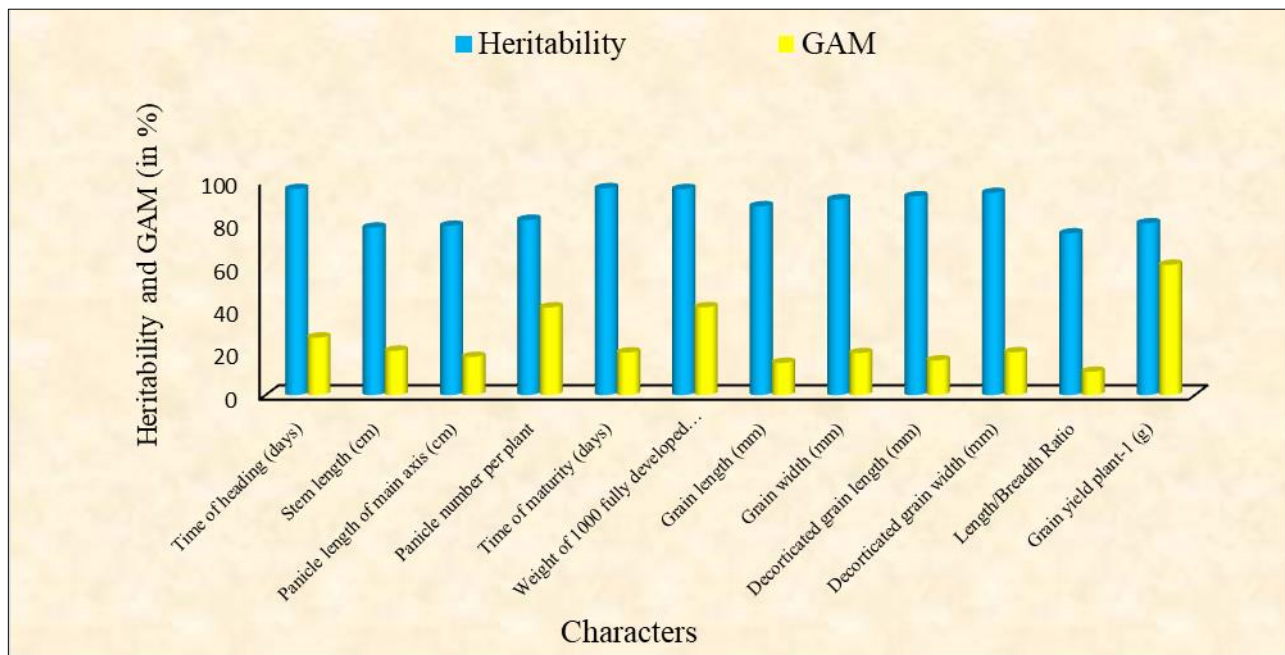


Fig 2: Heritability and Genetic advance as per cent (GAM) of mean for various traits in rice genotypes

Conclusion

The analysis of variance demonstrated significant differences among 52 genotypes for all the traits studied. High PCV and GCV were recorded for the traits *viz.*, panicle number per plant, weight of 1000 fully developed grains and grain yield plant⁻¹ indicating that large amount of variation is present among the genotypes. High heritability coupled with high genetic advance as per cent of mean was recorded for time of heading (50% of plants with panicles), stem length (excluding panicle), panicle number per plant, weight of 1000 fully developed grains, decorticated grain width and grain yield plant⁻¹ indicating that these traits were mostly under the control of additive gene action and direct selection of these traits would be effective for crop improvement.

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