



Estimation of Genetic Variability, Heritability and Genetic Advance in Hybrid RICE (*Oryza sativa* L.)

G. Prasanna^{a*}, K. B. Eswari^a, P. Senguttuvel^a and S. Narender Reddy^a

^a *Department of Genetics and Plant Breeding, College of Agriculture, Professor Jayashankar Telangana State Agricultural University, Rajendranagar, Hyderabad-030, Telangana, India.*

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Article Information

DOI: 10.9734/IJECC/2022/v12i630695

Open Peer Review History:

This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: <https://www.sdiarticle5.com/review-history/85093>

Original Research Article

Received 18 January 2022

Accepted 23 March 2022

Published 28 March 2022

ABSTRACT

The current study was conducted at the Indian Institute of Rice Research (IIRR) to look at the genetic characteristics for quantitative characters in 64 hybrid rice genotypes (*Oryza sativa* L.). For all of the characters, the analysis of variance indicated significant differences. The characters with the highest phenotypic and genotypic coefficients of variation were productive tillers per plant, filled grains per panicle, and single plant yield (GCV). Plant height, number of productive tillers per plant, number of filled grains per panicle, grain yield per plant, and test weight all had high heritability and genetic advance as a percent of mean, indicating the influence of additive gene action. As a result, simple selection could likely be effective for improving these traits.

Keywords: Genetic advance; GCV; PCV; heritability; hybrid rice.

1. INTRODUCTION

Rice (*Oryza sativa* L.) is the world's most important cereal crop, providing 60% of the world's dietary needs, 20% of calories, and 14% of protein. Rice will be consumed by 5 billion people, with a 38 percent increase in demand by

2030. Rice varieties with higher yield potential and greater stability must be developed to address this challenge [1]. One method for dealing with the enormous challenge given by ever-increasing populations is to use hybrid rice technology. Hybrid rice types outperform traditionally grown current kinds by 1.0 to 1.5

*Corresponding author: E-mail: prasannagricos@gmail.com, praveen6650@gmail.com;

tonnes per hectare (20 to 30%). China was the first to develop, followed by India, which released the first rice hybrid in 1994 [2]. In order to breed hybrid rice, top parental lines must be developed in either a three-line or two-line system. To generate high-yielding, high-quality varieties, information on the variability and genetic factors of grain quality traits, as well as their relationships with one another, including grain yield, is needed to establish appropriate breeding techniques for grain quality improvement. An attempt has been made in this study to elucidate information on the type and magnitude of genetic variation identified in certain parents and rice hybrids for yield and yield components.

The phenomena of heterosis is used to create hybrid rice. Heterosis, often known as hybrid vigour, is a phenomenon in which an F1 hybrid outperforms its parents. The value of heterosis in rice for yield and its component features has been reported by Reddy et al., [3] and Gnanamalar and Vivekanandan [4]. The effectiveness of any breeding programme is determined by the selection of appropriate parents for hybridization. The most deserving parental lines are chosen as part of the hybrid rice breeding effort.

2. MATERIALS AND METHODS

The experiment was carried out at the Indian Institute of Rice Research (IIRR) Farm in Rajendranagar, Hyderabad, over two seasons in 2018. The experiment site is 543 metres above mean sea level (MSL), with a geographic bearing of 780231 E longitude and 170191 N latitude. A total of 64 hybrid rice parental lines were included in the materials. The experimental material was planted in a two replications in randomised block design. Twenty-one-day-old seedlings were transplanted at a distance of 20 centimetres between rows and 15 centimetres inside each row. Urea, single superphosphate, and muriate of potash were used to deliver a recommended nutritional dose (120:60:40 kg NPK ha⁻¹). Throughout the crop's growing phase, proper soil moisture was maintained. The study included observations such as days to 50% flowering, plant height, panicle length, pollen fertility, number of productive tillers per plant, number of filled grains per panicle, spikelet fertility percentage, 1000 grain weight and grain yield per plant, and per day productivity from five randomly selected plants from each row. The analysis of variance was carried out with the aid of computer software Version 9.2 of the

WINDOWS STAT PACKAGE. Falconer's method was used to compute the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) (1981). Allard's formula was used to calculate heritability (h^2) in a broad sense (1960). Burton's formula was used to determine estimates of genetic advance (GA) based on heritability (1952). Productive tillers per plant, spikelet fertility, single plant yield and number of filled grains per panicle are important for hybrid rice development.

2.1 Genotypic and Phenotypic Coefficients of Variance

The genotypic and phenotypic coefficients of variation were calculated according to the formula given by Falconer [5].

$$\text{Genotypic coefficient of variation (GCV)} = \frac{\text{Genotypic standard deviation}}{\text{Mean}} \times 100$$

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{\text{Phenotypic standard deviation}}{\text{Mean}} \times 100$$

Categorization of range of variation was done by Sivasubramanian and Madhava menon [6] as low (<10%), moderate (10-20%) and high (>20%).

2.2 Heritability and Genetic Advance

Heritability in the broad sense refers to the proportion of genotypic variance to the total observed variance in the total population. Heritability (h^2) in the broad sense was calculated according to the formula given by Allard [7]

$$h^2_{(bs)} = \frac{\sigma^2_g}{\sigma^2_p}$$

Where,

h^2 = heritability in broad sense

σ^2_g = genotypic variance

σ^2_p = phenotypic variance ($\sigma^2_g + \sigma^2_e$)

σ^2_e = environmental variance

As suggested by Johnson et al. [8] heritability (h^2) estimates were categorized as low (0-30%), Medium (30-60%) and High (above 60%).

2.3 Genetic Advance (Expected)

Genetic advance refers to the expected gain or improvement in the next generation by selecting

the superior individuals under certain amount of selection pressure. From the heritability estimates the genetic advance was estimated by the following formula given by Burton [9].

$$GA = K \cdot h^2 (b) \cdot \sigma_p$$

Where,

GA = expected genetic advance
 K = Selection differential, the value of which is 2.06 at 5 per cent selection intensity
 σ_p = phenotypic standard deviation
 $h^2 (b)$ = heritability in broad sense

In order to visualize the relative utility of genetic advance among the characters, genetic advance as per cent for mean was computed.

$$\text{Genetic advance as per cent of mean} = \frac{GA}{\text{Grand mean}} \times 100$$

The range of genetic advance as per cent of mean was classified as low (< 10%), moderate (10-20%) and high (>20%) by Johnson et al. [8].

3. RESULTS AND DISCUSSION

For all of the characters, the analysis of variance indicated significant differences (Table 1). According to Sivasubramanian and Madhava menon, the range of variation estimations were classified as low (less than 10%), moderate (10-20%), and high (more than 20%) [6]. The characters productive tillers per plant (26.31 and 27.76), filled grains per panicle (41.30 and 41.67), and single plant yield (38.29 and 38.82) had high genotypic and phenotypic coefficients of variation (Table 2 and Fig. 1), while plant height (18.78 and 19.19), panicle length (10.05 and 11.50), and test weight (16.18 and 16.33) had moderate genotypic and phenotypic coefficients of variation (5.96 and 8.04). Johnson et al. [8] suggested categorising heritability (h^2) estimates as low (0-30 percent), medium (30-60 percent), and high (>60 percent) in a broad sense.

The present findings of low GCV and PCV for days to 50% blooming were consistent with Padmaja et al. [10] and Rita et al. [11] findings, as well as Rohit et al. [12] findings on spikelet fertility and pollen fertility (2017). In line with Prasad et al. [13] and Padmaja et al. [10], similar results for high GCV and PCV were seen for

productive tillers per plant, full grains per panicle, and single plant yield (2008). For panicle length, there was moderate GCV and PCV, and the test weight results were consistent with Venkatesan et al. [14].

Days to 50 percent flowering (96.2 percent), plant height (95.8%), productive tillers per plant (89.9%), panicle length (76.3 percent), pollen fertility (97.9%), filled grains per panicle (98.2%), test weight (98.1 percent), and grain yield per plant had the highest heritability (Table 2 and Fig. 2). (97.3 percent). The heritability of spikelet fertility (55%) was moderate. Johnson et al. defined the range of genetic advance as a percentage of the mean as low (less than 10%), moderate (10-20%), and high (more than 20%) [8]. Plant height (37.89), productive tillers per plant (51.38), full grains per panicle (84.33), test weight (33.01), and grain yield per plant had the highest genetic gain as a percentage of the mean (Table 2 and Fig. 2). (77.80). Days to 50% blooming (14.48), panicle length (18.09), and pollen fertility all showed moderate genetic progress as a percentage of the mean (15.23). Spikelet fertility (9.10) was low in terms of genetic progress as a percentage of the mean.

Plant height, number of productive tillers per plant, number of filled grains per panicle, grain yield per plant, and test weight all had high heritability and genetic advance as a percent of mean, indicating the influence of additive gene action. As a result, simple selection would likely be effective for improving these traits. Pollen fertility, Days to 50% flowering and panicle length showed high heritability with moderate genetic advance as percent of mean, whereas spikelet fertility showed medium heritability with low genetic advance as percent of mean, indicating the influence of non-additive gene action and selection may be ineffective.

Prasad et al. [13] and Padmaja et al. [10] found similar results for high heritability combined with high genetic advance as percent of mean for productive tillers per plant, full grains per panicle, test weight and grain yield per plant, and plant height (2008). Seyoum et al. found high heritability with moderate genetic progress as a percent of mean for days to 50% flowering and panicle length [15]. Seyoum et al. [15] and Rohit et al. [12] found moderate heritability with low genetic progress as a percent of mean for spikelet fertility (2012).

Table 1. Analysis of variance for yield and its component traits in hybrid rice

Source of variation	df	Days to 50% Flowering	Plant height	Productive tillers	Panicle length	Pollen fertility	Spikelet fertility	Filled grains	Test weight	Single plant yield
Replication	1	0.031	42.51	3.92	0.54	0.002	82.35	1.59	0.72	6.47
Treatments	63	92.63***	758.96***	19.55***	12.16***	87.16***	74.87***	4994.19***	22.91***	153.61***
Error	63	1.78	16.13	1.04	1.64	0.94	21.75	44.47	0.220	2.12
Total	127	46.83	384.83	10.24	6.87	43.70	48.58	2499.51	11.48	77.30
General mean		94.04	102.57	11.56	22.87	87.80	86.42	120.43	20.81	22.73
CV (%)		1.46	3.91	8.83	5.66	1.10	5.39	5.53	2.25	6.41

Table 2. Genotypic and phenotypic coefficient of variance (GCV and PCV), Heritability (h^2) and genetic advance as percent of mean for different character

Characters	Coefficient of variability		Heritability (%) broad sense	Gen. Advance as percent of mean (at 5%)
	GCV%	PCV%		
Days to 50% Flowering	7.16	7.30	96.2	14.48
Plant Height (cm)	18.78	19.19	95.8	37.89
No. of productive tillers per plant	26.31	27.76	89.9	51.38
Panicle Length (cm)	10.05	11.50	76.3	18.09
Pollen Fertility (%)	7.47	7.55	97.9	15.23
Spikelet Fertility (%)	5.96	8.04	55	9.10
Number of filled grains per panicle	41.30	41.67	98.2	84.33
1000 grain weight (g)	16.18	16.33	98.1	33.01
Single plant yield (g)	38.29	38.82	97.3	77.80

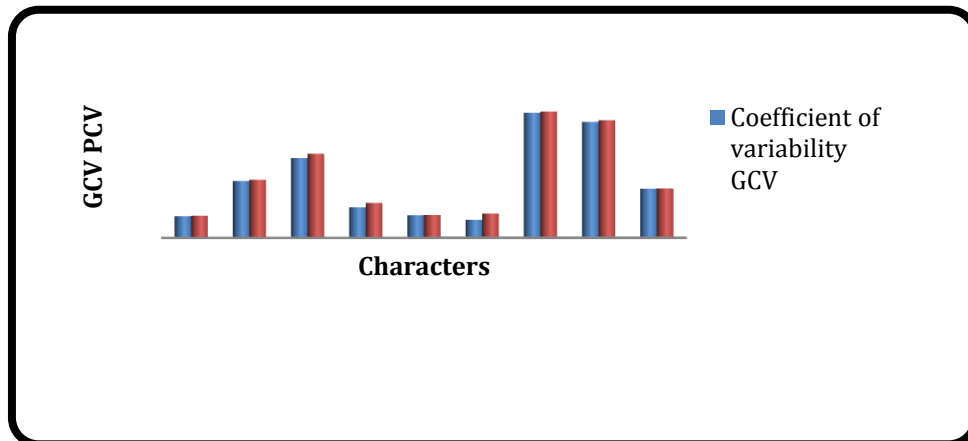


Fig. 1. Graphical representation of GCV and PCV for yield and attributing traits in hybrid rice

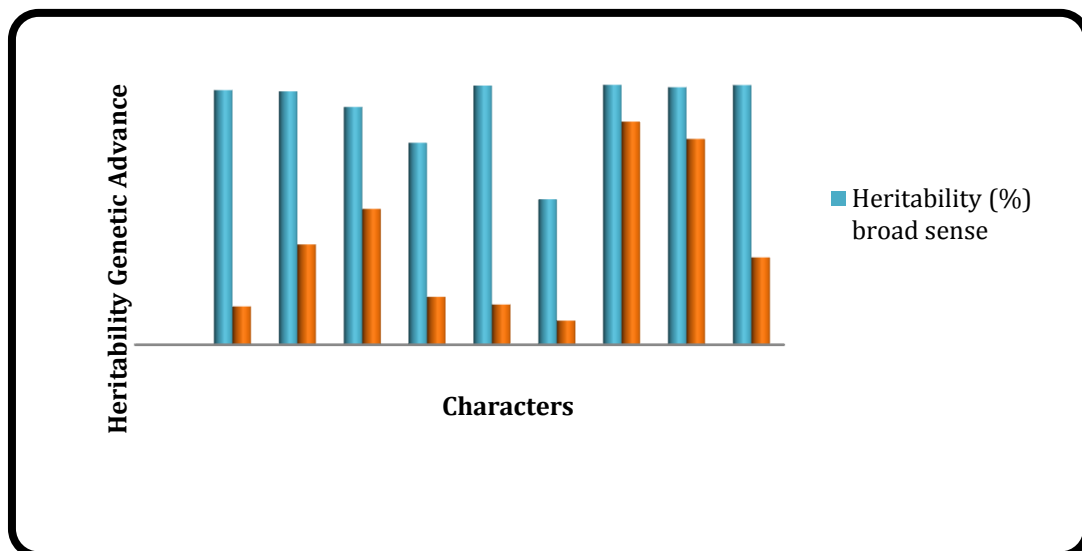


Fig. 2. Graphical representation of heritability and genetic advance for yield and yield attributing traits in hybrid rice

4. CONCLUSIONS

High heritability coupled with high genetic advance as percent of mean were observed for plant height, number of productive tillers per plant, number of filled grains per panicle, grain yield per plant and test weight indicating the influence of additive gene action, as such simple selection would likely be effective for improvement of these traits. High heritability with moderate genetic advance as percent of mean were observed for pollen fertility, Days to 50% flowering and panicle length, whereas spikelet fertility showing medium heritability with low genetic advance as percent of mean indicating the influence of non-additive gene action hence selection is ineffective. High GCV and PCV were seen for productive tillers per plant, full grains per

panicle, and single plant yield. Characters with high GCV, PCV, heritability and genetic advance (productive tillers per plant, full grains per panicle, and single plant yield) would be effective for development of hybrid rice. As a result, these characters should be selected for direct selection.

DISCLAIMER

The products used for this research are commonly and predominantly use products in our area of research and country. There is absolutely no conflict of interest between the authors and producers of the products because we do not intend to use these products as an avenue for any litigation but for the advancement of knowledge. Also, the research was not funded by

the producing company rather it was funded by personal efforts of the authors.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Khush GS. Rice research challenge for the 21st century. *Journal of Rice Research*. 2006;1(1).
2. Janaiah A, Hussain M. Can hybrid rice technology help productivity growth in asian tropics farmers experiences. *Economic and Political Weekly*. 2003; 38(25):2492–2501.
3. Reddy GE, Suresh BG, Sravan T, Reddy PA. Interrelationship and cause-effect analysis of rice genotypes in North East plain zone. *The Bioscan*. 2012;8(4):1141-1144.
4. Gnanamalar RP, Vivekanandan P. Heterosis for grain yield and grain quality traits in rice (*Oryza sativa* L.). *Asian Journal of Plant Science and Research*. 2013;3(3):100-106.
5. Falconer DS. *Introduction to quantitative genetics*. Oliver and Boyd, London; 1981.
6. Sivasubramanian S, Madhavamenon P. Combining ability in rice. *Madras Agricultural Journal*. 1973;60:419-421.
7. Allard RW. *Principles of Plant Breeding*. John Wiley and Sons Inc., New York, USA. 1960;485.
8. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybean. *Agronomy Journal*. 1955;47(7):314-318.
9. Burton GW. Quantitative inheritance in grasses. *Proceedings on 6th International Grassland Congress*. 1952;1:277-283.
10. Padmaja D, Radhika K, Rao LVS, Padma V. Studies on variability, heritability and genetic advance for quantitative Characters in Rice (*Oryza sativa* L.). *Journal of Plant Genetic Resources*. 2008; 21(3).
11. Rita B, Sarawgi AK, Verulkar SB. Study of heritability, genetic advance and variability for yield contributing characters in rice. *Bangladesh Journal of Agricultural Research*. 2009;34(2):175-179.
12. Rohit Y, Rajpoot P, Verma OP, Singh PK, Singh P, Pathak V. Genetic variability, heritability and genetic advance in Rice (*Oryza sativa* L.) for grain yield and it's contributing attributes under sodic soil. *Journal of Pharmacognosy and Phytochemistry*. 2017;6(5):1294-1296.
13. Prasad B, Patwary AK, Biswas PS. Genetic variability and selection criteria in fine rice (*Oryza sativa* L.). *Pakistan Journal of Biological Sciences*. 2001; 4(10):1188-1190.
14. Venkatesan M, Sowmiya CA, Anbarasi B. Studies on variability, heritability and genetic advance analysis in rice (*Oryza sativa* L.) under submergence. *International Journal of Agricultural Sciences*. 2017;13(1):49.
15. Seyoum M, Alamerew S, Bantte K. Genetic variability, heritability, correlation coefficient and path analysis for yield and yield related traits in upland rice (*Oryza sativa* L.). *Journal of plant sciences*; 2012.

© 2022 Prasanna et al.; This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Peer-review history:

The peer review history for this paper can be accessed here:
<https://www.sdiarticle5.com/review-history/85093>