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## Genetic variability, heritability and genetic advance for yield and related traits in rice (*Oryza sativa* L.)

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### Abstract

This research was carried out at Wetland Farm, Sri Venkateswara Agricultural College, Tirupati, during the *kharif* season of 2020, in order to determine genetic variability, heritability, and genetic advance in 42 variants (genotypes) of rice. The analysis of variance revealed substantial differences among the 42 genotypes for all of the attributes assessed. The number of filled grains per panicle was followed by grain yield per plant and 1000-grain weight, all of which reported high PCV, GCV, heritability (broad sense), and genetic advance as a percentage of the mean, showing that these traits were driven by additive gene action and that simple selection could be employed to improve them. Days to 50% flowering, plant height, panicle length, number of panicles per plant, and spikelet fertility, on the other hand, showed moderate to low GCV, PCV, strong heritability, and moderate to low genetic advance as a percentage of mean. As a result, intermating of chosen genotypes might be proposed to produce variability, followed by selection for superior segregants for the abovementioned traits in following generations.

**Keywords:** Variability, GCV, PCV, rice and genetic advance

### Introduction

Rice (*Oryza sativa* L.) is a significant staple food crop for two-thirds of the world's population. It offers 23% of the calories and contributes to around 20% of the world's grain output (Singh *et al.*, 2018) [16]. Asia is the world's rice-growing center, accounting for 90 percent of global output. Rice contributes to 30-75% of all calories consumed by almost three billion Asians (Pathak *et al.*, 2019) [14]. According to the Food and Agricultural Organization, world rice consumption is expected to rise by 50%. This entails feeding the world's rapidly growing population, which is predicted to exceed 9 billion by 2050 (Khush, 2018) [8]. Rice is an upland crop in Asia, where it is frequently cultivated by transplanting on puddled soils (heavy ploughing in ponded conditions) with periodic floods (Singh *et al.*, 2018; Kumar and Kar, 2020) [16, 10]. The crop is grown under a variety of agro-ecological conditions. Despite its widespread acceptance, the crop is vulnerable to extreme temperatures. It is cultivated on an average of 162.71 m<sup>2</sup>/ha worldwide, with an annual yield of 741.47 mt and a productivity of 4556 kg/ha. It is India's most significant food crop, ranking first in area (43.85 m<sup>2</sup>/ha) and second in production (to China). Rice is grown over an area of 43.49 m<sup>2</sup>/ha in India, with an annual yield of 104.40 mt and an average productivity of 2400 kg/ha. The tagline "Rice is Life" refers to rice's significance as a staple grain and a source of income for around 120-150 million rural families in the nation. Rice is essential to the lives of billions of people worldwide. With the world's population expected to reach 10 billion by 2050, demand for rice will outpace that for other grains. The effects of global warming on rice production are considerable. The global average temperature has risen by 0.6 °C in the last century and is expected to climb by another 0.5-2.8 °C by the end of the twenty-first century (Kumar and Kar, 2020) [10]. Because of the increased frequency of severe high-temperature occurrences and a projected worldwide average surface temperature rise of 1.5 to 4.8 °C by 2100, yield declines in the second half of the century are expected to be greater in the tropics than in temperate regions. The bulk of rice is now cultivated in places where temperatures are near to ideal for rice cultivation. Heat waves are predicted to become more strong and frequent in the future, putting more rice fields at risk. As a result, any further increases in mean temperatures or brief periods of high temperatures during sensitive phases may be excessive and reduce grain production. Despite the fact that rice evolved in the tropics, temperatures exceeding 35 °C during the flowering stage result in severe production losses, poor grain quality and a low harvest index. It has been proposed that spikelet fertility at high temperatures may be employed as a heat tolerance screening method during the flowering stage (Chuchert *et al.*,

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2018) [5]. Genetic variability is of particular interest to plant breeders because it plays a critical role in developing a successful breeding programme. The heritability of a metric character is important to breeders because it measures the degree of resemblance between parents and offspring and its magnitude indicates the heritability with which a genotype can be identified by its phenotypic expression, whereas genetic advance aids in applying the necessary selection pressure.

## Material and Methods

The current study used 42 rice genotypes planted in a

randomised block design with three replications at the Wetland Farm, Sri Venkateswara Agricultural College, Tirupati, during the *kharif* season of 2020. The genotype was cultivated in three rows of three metres each, with a 20 cm gap between rows and a 15 cm spacing between plants within each row. On five competing plants from each replication, 50% flowering, plant height (cm), panicle length (cm), number of panicles per plant, 1000-grain weight (g), number of filled grains per panicle, spikelet fertility (percent), and grain yield/plant were all measured. Table 1 contains a list of genotypes with pedigrees.

**Table 1:** List of 42 rice genotypes included in the study and their pedigree

S. No.	Designation	Pedigree	S. No.	Designation	Pedigree
1	54-3	BPT5204 x NLR33892	22	MDP6	MTU1010 x IR64 Drt1
2	150-3	BPT5204 x NLR33892	23	MTU1010	KRISHNAVENI x IR 64
3	187-1	BPT5204 x NLR33892	24	28C1	N22 x IR64
4	187-3	BPT5204 x NLR33892	25	46C2	N22 x IR64
5	239-3	BPT5204 x NLR33892	26	76C2	N22 x IR64
6	419-1	BPT5204 x NLR33892	27	81C	N22 x IR64
7	419-3	BPT5204 x NLR33892	28	130C	N22 x IR64
8	538-3	BPT5204 x NLR33892	29	153C1	N22 x IR64
9	BPT5204	(GEB24 x TN1) x MAHSURI	30	221C3	N22 x IR64
10	NLR33892	NLR 27999 x MTU 4870	31	273C2	N22 x IR64
11	NDP3	NLR34449 x IR64 Drt1	32	405C3	N22 x IR64
12	ND13	NLR34449 x IR64 Drt1	33	425C3	N22 x IR64
13	ND42	NLR34449 x IR64 Drt1	34	457C2	N22 x IR64
14	ND44	NLR34449 x IR64 Drt1	35	476C3	N22 x IR64
15	ND60	NLR34449 x IR64 Drt1	36	488C	N22 x IR64
16	NLR34449	IR 72 x BPT5204	37	NAGINA 22	LANDRACE
17	MDP2	MTU1010 x IR64 Drt1	38	IR64	IR5657-33-2-1 x IR2061-465-1-5-5
18	MDP3	MTU1010 x IR64 Drt1	39	SM227	SWARNA MUTANT
19	MDP4	MTU1010 x IR64 Drt1	40	MTU3626	IR B x MTU 3
20	MD4	MTU1010 x IR64 Drt1	41	MTU1121	BPT5204 x MTU BB 8-24-1
21	MD5	MTU1010 x IR64 Drt1	42	SMB3	SWARNA MUTANT

## Statistical analysis

The analysis of variance was performed using the method proposed by Panse and Sukhatme, 1961 [13] and the genotypic and phenotypic coefficients of variation were estimated using the method proposed by Burton, 1952 [3] and heritability (in the broad sense) was defined as the genotypic to phenotypic variance ratio. The Johnson *et al.*, 1955 [7] approach was used to calculate anticipated genetic advance and genetic advance as a percentage of the mean. The INDOSTAT programme was used to analyse the data.

According to Burton (1952) [3], the GCV and PCV are classed as low (10%), moderate (10-20%) and high (>20%). Heritability was calculated using the method proposed by Johnson *et al.*, 1955 [7] and it was classed as low (less than 30%), moderate (30-60%), or high (above 60 percent). According to Johnson *et al.*, 1955 [7], the range of genetic advance as a percentage of the mean was defined as low (10%), moderate (10-20%) and high (> 20%).

## Results and Discussion

The analysis of variance found significant differences in all nine traits investigated for 42 rice genotypes. Significant variations between genotypes justified the variability as demonstrated by ANOVA in the current investigation. ANOVA is discussed in detail in Table 2.

PCV estimates for the characters studied were slightly higher than GCV estimates (Table 3 and Figures 1 and 2 for PCV

and GCV, respectively), indicating that the characters were less influenced by the environment. As a result, phenotypic selection could help improve these characteristics.

Number of filled grains per panicle, number of grains per panicle, grain yield per plant, and 1000-grain weight all had high GCV and PCV values, which is consistent with previous findings by Priyanka *et al.*, 2020 [15] for 1000-grain weight and Koshle *et al.*, 2020 [9] for number of filled grains per panicle and number of grains per panicle. GCV and PCV were moderate when the number of panicles per plant, plant height, days to 50% flowering and panicle length were measured. Kumar and Parmar, 2020 [10], observed similar results for days to 50% flowering and panicle length; Pandey *et al.*, 2020 [12], reported similar findings for plant height and panicle number per plant. The GCV and PCV estimates for spikelet fertility were low. Identical spikelet fertility findings were reported by Koshle *et al.*, 2020 [9]. The phenotypic coefficient of variation was greater than the genotypic coefficient of variation for all of the characters, indicating that the environment has an impact on the expression of these traits. For 1000-grain weight, number of filled grains per panicle, number of grains per panicle, and grain production per plant, GCV and PCV values were high. As a result, simple selection might be a good way to improve these features further.

The number of filled grains per panicle, days to 50% blooming, 1000-grain weight, panicle length, panicle length

per plant, and spikelet fertility all had substantial heritability in this study.

As a result, these characteristics could be used as selection criteria in breeding programmes to maximize productivity. For improving these traits, simple selection based on per se performance is more successful. Direct selection for grain yield per plant may be advantageous due to the high heredity of grain yield per plant. The number of filled grains per panicle, number of grains per panicle, days to 50% flowering, 1000-grain weight, grain yield per plant, number of panicles per plant and spikelet fertility were all the similar, according to Farooq *et al.*, 2019 [6].

High heritability for a character implies the efficacy of phenotypic selection, but it cannot be regarded as the amount of genetic advance that may be accomplished by selecting the best individual in the population. A high heritability value for character does not always reflect a substantial genetic gain, according to Panse and Sukatme (1961) [13]. The predicted genetic gain is low, if heritability is mostly due to non-additive genetic effects (dominance and epistasis); the expected genetic gain is high if it is primarily due to additive effects. As a result, estimating genetic advance as a percentage mean can assist in this regard. (Johnson *et al.*, 1955) [7].

The genetic advance ranged from 10.01 percent to 72.47 percent, respectively, as a percentage of mean estimates. The number of filled grains per panicle (72.47 percent) had the greatest genetic advance as a percentage of the mean, followed by grain yield per plant (47.84 percent), number of panicles per plant (33.00 percent), plant height (32.10 percent), days to 50% flowering (30.63 percent), and panicle length (23.75 percent), with spikelet fertility (10.01 percent)

having a moderate genetic advance as a percentage of the mean.

The number of filled grains per panicle, number of grains per panicle, days to 50% flowering, 1000-grain weight, panicle length, plant height, grain yield per plant, and number of panicles per plant all had high heritability and genetic advance as a percentage of the mean (Table 2 and Figure 2). It showed that additive gene action is common in the inheritance of certain traits, and that the environment has a smaller impact on their expression. As a result, they are amenable to simple selection, resulting in enormous genetic gain. Singh *et al.*, 2019 [17] reported similar findings for days to 50% flowering; Umarani *et al.*, 2019 [19] and Bhor *et al.*, 2020 [2] for plant height; Kumar and Parmar, 2020 [10] and Thakur and Pandey, 2020 [12] for panicle length and number of panicles for the plant; Farooq *et al.*, 2019 [6] for number of filled grains per panicle, number of grains per panicle and 1000-grain weight; Kumar and Kar, 2020 [10] for grain yield.

For example, spikelet fertility had a high heritability and a moderate genetic advance as a percentage of the mean. It indicates non-additive gene action as well as the impact of the environment in the manifestation of these traits. As a result, traits with larger estimates of genetic advance as a percentage of the mean should be emphasized when deciding on selection tactics. These findings are consistent with those obtained by Amegan *et al.*, 2020 [1] and Bhor *et al.*, 2020 [2] for spikelet fertility, as well as Chaitanya *et al.*, 2018. Germination rates were discovered to have moderate heritability combined with low genetic advance as a percentage of the mean. It implies that the character is heavily influenced by environmental factors and that selection would be futile.

**Table 2:** Analysis of variance (ANOVA) for 9 quantitative characters in 42 genotypes of rice

Sr. No.	Character	Mean sum of squares		
		Replications	Genotypes	Error
		(df 2)	(df 41)	(df 82)
1.	Days to 50% flowering	2.45	610.75**	1.58
2.	Plant height (cm)	33.39	996.21**	18.87
3.	Panicle length (cm)	0.28	27.31**	0.51
4.	Number of panicles plant <sup>-1</sup>	0.88	19.42**	0.46
5.	1000-grain weight (g)	0.42	60.51**	0.34
6.	Number of filled grains panicle <sup>-1</sup>	14.21	19,354.81**	14.03
7.	Number of grains panicle <sup>-1</sup>	5.47	23,965.46**	22.19
8.	Spikelet fertility (%)	3.26	64.79**	2.742
9.	Grain yield plant <sup>-1</sup> (g)	0.20	137.02**	2.97

\*Significant at 5% level; \*\* Significant at 1% level.

**Table 3:** Variability and genetic parameters for yield, yield attributes and early seedling vigour related traits in 42 genotypes of rice

Sr. No.	Characters	Mean	Range		Variance		Coefficient of variation		Heritability (Broad sense) (%)	Genetic advance (%)	GA as percent of mean (%)
			Min.	Max.	Genotypic	Phenotypic	Genotypic (%)	Phenotypic (%)			
1.	Days to 50% flowering	95.48	75.00	140.67	213.47	215.13	14.93	14.98	99.23	29.24	30.63
2.	Plant height (cm)	112.63	85.40	158.4	342.49	362.32	16.03	16.48	94.53	36.15	32.10
3.	Panicle length (cm)	25.21	19.78	33	9.39	9.93	11.86	12.19	94.58	5.99	23.75
4.	Number of panicles plant <sup>-1</sup>	12.7	8.20	16.93	4.78	5.24	16.78	17.58	91.15	4.19	33.00
5.	1000 grain weight (g)	20.97	14.19	35.7	21.08	21.44	21.36	21.54	98.31	9.15	43.63
6.	Number of filled grains panicle <sup>-1</sup>	228	69	419.89	6740.8	6755.1	35.22	35.26	99.78	165.22	72.47
7.	Number of grains panicle <sup>-1</sup>	258.98	78.22	464.67	8457.7	8481.5	34.5	34.54	99.72	183.78	70.96
8.	Spikelet fertility (%)	87.95	77.08	96.51	21.74	24.62	5.17	5.5	88.29	8.8	10.01
9.	Grain yield plant <sup>-1</sup> (g)	27.87	14.79	43.23	46.97	50.09	23.98	24.77	93.77	13.33	47.84

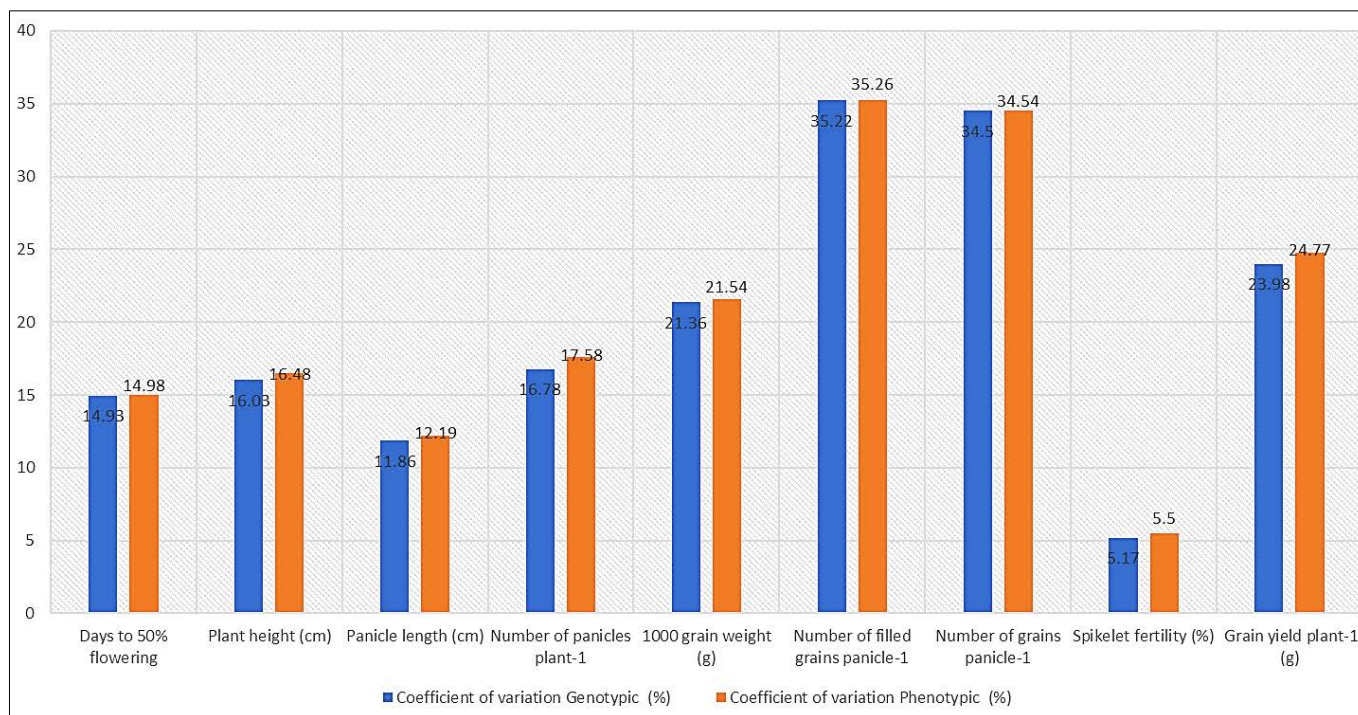


Fig 1: Phenotypic coefficient of variation for various characters in 42 genotypes of rice

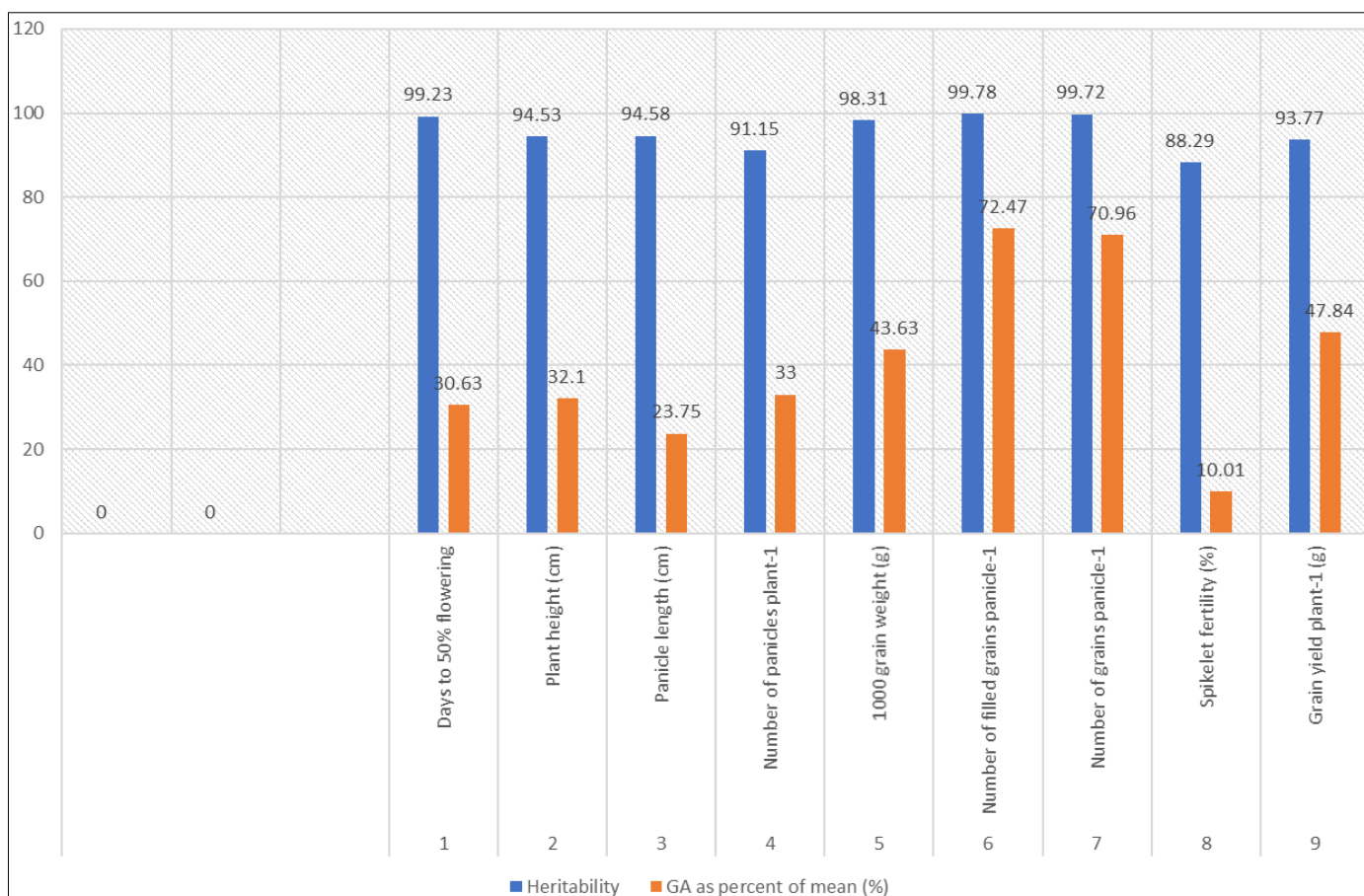


Fig 2: Heritability and genetic advance as percent of mean for 9 characters in 42 genotypes of rice

**Conclusion**

The analysis of variance found substantial differences across the 42 genotypes for all of the traits investigated. The number of filled grains per panicle was followed by grain yield per plant and 1000-grain weight, all of which demonstrated high

PCV, GCV, heritability (broad sense) and genetic advance as a percentage of the mean, indicating that additive gene action governed these characters and that simple selection could be used to improve them. On the other hand, GCV, PCV, high heritability, and moderate to low genetic advance as a

percentage of mean was found in days to 50% flowering, plant height, panicle length, number of panicles per plant and spikelet fertility. As a result, intermingling of selected genotypes could be proposed to generate variability, followed by selection for superior segregants for the aforementioned traits in later generations.

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