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## Genetic variability studies for yield and its attributes, quality and nutritional traits in rice (*Oryza sativa* L.)

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### Abstract

The studies 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 forty-four rice genotypes to study the variability and genetic parameters for yield and its components, quality and nutritional traits. 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. The traits plant height, number of productive tillers per plant, panicle length, number of grains per panicle, 1000 grain weight, grain yield per plant, head rice recovery percentage, grain length, grain width, length/breadth ratio, protein content, iron and zinc content all showed moderate to high variability, high heritability coupled with high genetic advance as per cent of mean revealing the role of additive gene effect and simple selection procedures may be effective for improving these traits. Low PCV and GCV were recorded for the traits viz., days to 50% flowering, hulling percentage and milling percentage. High heritability coupled with moderate genetic advance as per cent of mean was observed for days to 50% flowering, hulling percentage and milling percentage indicating that role of both additive and non-additive gene effects in the inheritance of these traits.

**Keywords:** Genetic advance, GCV, PCV, heritability, grain yield, quality traits

### 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 162.57 million hectares with a production of 499.0 million metric tonnes during 2018-19 (United States Department of Agriculture, 2020). Approximately, 90% of the world’s rice is produced and consumed in Asia (Singh *et al.*, 2015) [23]. India stands second to China with the production of 118.87 million metric tonnes (Indiastat, 2019-20) [10]. Owing to a burgeoning population, it is estimated that the demand for rice will be 121.2 million metric tonnes by the year 2030, 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) [3]. The present deceleration drift in production and yield is a cause of concern and has to be upturned to meet the growing demand. It is, therefore necessary to harness the available rice knowledge and exploit genetic resources to maximize production to ensure food security and prosperity for the country.

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) [2]. Therefore, assessment of variability for grain yield and its attributes, quality and nutritional parameters in 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 44 rice genotypes to identify effective selection criteria for grain yield and quality improvement of rice genotypes.

## Materials and Methods

The present investigation was carried out during *Rabi*, 2020-2021 at Regional Agricultural Research Station, Warangal. In the present study forty-four genotypes were assessed to study the variability and genetic parameters for yield and its components, quality and nutritional traits. List of genotypes used in the present study is presented in Table 1. Each genotype was sown in three rows of 4 m length following a spacing of 20 cm between the rows and 15 cm between the plants in randomised block design (RBD) with three replications. Standard agronomic practices were performed uniformly for all the experimental units. Crop was raised following recommended package of practices. Phenological data on days to 50% flowering was recorded for plots of each genotype. At maturity five plants from each accession were selected randomly for recording data on grain yield per plant; yield component traits, namely, plant height, productive tillers per plant, panicle length, grains per panicle and test weight; and quality characters, namely, hulling per cent, milling per cent, head rice recovery per cent, kernel length, kernel breadth, length/breadth (L/B) ratio. In contrast, observations for test weight and all the quality and nutritional traits studied were obtained from a random grain sample drawn from each plot and replication using standard procedures. Mean performance of the genotypes were calculated and the genotypic (GCV) and phenotypic (PCV) coefficients of variation were estimated by using the formula given by Burton (1952) [2]. The estimates of PCV and GCV were classified as low (0-10%), moderate (10-20%) and high (>20%) according to Sivasubramanian and Madhavamenon (1973) [24]. Heritability in broad sense ( $h^2_b$ ) was estimated according to the formula suggested by Johnson *et al.* (1955) [11] and Hanson *et al.* (1956) [9]. Estimation of genetic advance was carried out following the formula given by Johnson *et al.* (1955) [11].

## Results and Discussion

The analysis of variance (ANOVA) revealed significant differences among the genotypes for all characters, demonstrating the presence of significant amount of variability and intrinsic genetic variation in the genotypes studied. Coefficient of variation studies implied that the estimates of GCV for all the characters studied were slightly less than PCV estimates indicating slight influence of environment on the genotype performance. Similar finding was reported earlier by Sudeepthi *et al.* (2020) [25]. The results of analysis of variance are presented in Table 2. The results of mean, variability, heritability and genetic advance of each trait in the present study are presented in Table 3. Maximum variation was observed for grain yield per plant (24.23 – 49.90 g), no. of productive tillers per plant (10.13–16.67), no. of grains per panicle (118.73 – 320.87) while minimum was observed for hulling percentage (75.19 – 86.40 %) followed by grain width (1.39 – 2.85mm).

The PCV ranged from 2.69 (Hulling percentage) to 26.74 (no. of grains per panicle); whereas, GCV ranged from 2.46 (Hulling percentage) to 26.46 (no. of grains per panicle). High PCV and GCV were recorded for no. of grains per panicle (26.74, 26.46), 1000 grain weight (24.55, 24.46) and zinc content (21.07, 21.04). Similar results were reported by Devi *et al.* (2020) [4] and Saha *et al.* (2019) [18] for no. of grains per panicle; Parimala *et al.* (2020) [16] and Amegan *et al.* (2020) [1] for 1000 grain weight; Suman *et al.* (2020) [26], Umarani *et al.*

(2017) [29] and Ravindrababu *et al.* (2012) for zinc content. Moderate PCV and GCV was observed for the traits plant height (16.56, 16.44), productive tillers per plant (14.40, 13.21), panicle length (11.01,10.83), grain yield per plant (14.41, 12.65), head rice recovery percent (12.83, 12.27), grain length (11.38, 11.27), grain width (19.10, 19.05), L/B ratio (17.98, 17.86), protein content (19.06, 15.01) and iron content (19.47, 19.36). The results are in consonance with the findings of Devi *et al.* (2020) [4] and Mani and Kumar (2018) for plant height; Nithya *et al.* (2020) [15] and Girma *et al.* (2018) [7] for productive tillers per plant; Singh *et al.* (2020) [22] and Umarani *et al.* (2017) [29] for panicle length; Nithya *et al.* (2020) [15] for grain yield per plant; Suman *et al.* (2020) [26] and Devi *et al.* (2020) [4] for head rice recovery and grain length; Shivani *et al.* (2018) [21] and Gangashetty *et al.* (2013) [6] for iron content and grain width respectively; Singh *et al.* (2020) [22] and Maurya *et al.* (2019) [13] for protein content and L/B ratio respectively. Low PCV and GCV were recorded for the days to 50% flowering (10.0, 9.85); hulling percent (2.69, 2.46) and milling percent (6.06, 5.49). Similar findings were reported by Saha *et al.* (2019) [18] for days to 50% flowering; Nirmaladevi *et al.* (2015) [14] for hulling percentage; Hari *et al.* (2018) [8] and Dhanwani *et al.* (2013) [5] for milling percentage. In the present study values of PCV are higher for all characters than corresponding GCV indicating the influence of environment over the expression of these characters.

The estimates of heritability ranged from 62.0 (protein content) to 99.72% (zinc content) whereas, genetic advance as per cent of mean ranged from 4.61 (hulling percentage) to 53.88% (no. of grains per panicle). Heritability and genetic advance are two important selection parameters. Heritability estimates along with genetic advance are more useful in predicting genetic gain under selection than heritability estimates alone. High heritability coupled with high genetic advance as per cent of mean was observed for the characters plant height, panicle length, no. of productive tillers per plant, no. of grains per panicle, 1000 grain weight, grain yield per plant, head rice recovery percent, grain length, grain width, L/B ratio, protein content, iron and zinc content indicating that these characters are governed by additive gene action. Hence, better response to selection can be attained for improvement of these traits. The results are in accordance with the reports of Saha *et al.* (2019) [18] for no. of grains per panicle; Nithya *et al.* (2020) [15] for grain yield per plant and productive tillers per plant; Umarani *et al.* (2017) [29] and Sundaram *et al.* (2019) [7] for zinc and iron content; Sandeep *et al.* (2018) [19] for panicle length; Amegan *et al.* (2020) [1] for 1000 grain weight; Maurya *et al.* (2019) [13] and Supriya *et al.* (2017) for L/B ratio and Singh *et al.* (2020) [22] and Sangamithra *et al.* (2018) for protein content. High heritability estimates coupled with moderate genetic advance was manifested by the traits *viz.*, days to 50 per cent flowering and milling percentage indicating involvement of both additive and non-additive gene action in the inheritance of these traits and the heritability exhibited may be due to influence of the environment rather than genotype alone. The results are in accordance with the findings of Saha *et al.* (2019) [18] for days to 50 per cent flowering; Hari *et al.* (2018) [8] for milling percentage. Further, hulling percentage exhibited high heritability coupled with low genetic advance suggesting non-additive gene action in inheritance of this trait. Hence, simple selection may not be rewarding in

improving this trait. The finding is in accordance with the reports of Nirmaladevi *et al.* (2015) [14].

### Conclusion

The study concluded that important yield attributing characters like plant height, number of productive tillers per plant, panicle length, number of grains per panicle, 1000 grain weight, grain yield per plant, head rice recovery percentage, grain length, grain width, L/B ratio, protein, iron and zinc content all showed moderate to high variability, high heritability coupled with high genetic advance as per cent of mean, indicating the predominant role of additive gene action. As a result, our study concludes that substantial improvement

in the expression of these characters over base population can be expected through simple selection. Further, the genotypes Yellava samba (19.5 ppm) for iron content and Kakirekkalu (24.4 ppm) for zinc content might be useful as donors in future breeding programmes for their potential commercial exploitation in development of nutritionally rich rice varieties.

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**Table 1:** List of rice genotypes used in the present study

Treatment	Entry Name	Treatment	Entry Name
1	Njavara	23	Jeeraga samba
2	Kasyam sannalu	24	Kamarsambra
3	Ramsree	25	Kandasagar
4	Manipuri black	26	Gani
5	Kalabunt	27	Chitthloori sannalu
6	Bahurupi	28	Didianga
7	Sammela bogulu	29	Kareja jawal
8	Laicha	30	WGL 1245
9	Kudel	31	WGL 1246
10	Kistappa sannalu	32	WGL 1252
11	Ranikanda	33	WGL 1261
12	Chattisgarh local	34	JGL 27356
13	Ramyagali	35	JGL 28545
14	Asthothal	36	KNM 1638
15	Burma black	37	WGL 962
16	Narayana kamini	38	KPS 2874
17	Ambe mohar	39	KNM 6871
18	Yellava samba	40	KNM 6869
19	Kakirekkalu	41	WGL 1413
20	Ratnachodi	42	KNM 7715
21	Nico	43	RNR 21278
22	Kasmikanda	44	WGL 1262

**Table 2:** Mean performance of 44 rice (*Oryza sativa* L.) genotypes for all the characters under study

S. No.	Genotype	Days to 50 per cent flowering	Productive tillers/plant	Plant height (cm)	Panicle length (cm)	No. of Grains/panicle	1000 grain weight (g)	Grain yield/plant (g)	Hulling%	Milling %	Head rice recovery %	Grain length (mm)	Grain width (mm)	L/ B ratio	Protein content (%)	Iron content (ppm)	Zinc content (ppm)
1.	Njavara	101.67	12.07	116.60	23.12	137.47	22.23	38.10	80.14	62.55	36.49	5.73	2.43	2.36	7.45	11.7	18.0
2.	Kasyam sannalu	97.00	13.93	128.13	24.37	153.07	21.76	40.90	81.46	68.60	61.45	5.26	2.63	2.00	5.64	13.4	12.8
3.	Ramsree	102.33	13.90	129.33	27.02	161.40	20.89	39.70	82.53	68.80	57.31	5.57	2.26	2.46	5.49	12.1	15.0
4.	Manipuri black	117.33	14.07	90.33	25.92	146.87	22.89	39.23	78.04	64.57	56.27	7.11	2.16	3.29	7.69	17.0	13.0
5.	Kalabunt	114.00	10.50	138.87	28.89	165.00	23.53	40.57	75.41	67.92	60.84	6.31	2.41	2.61	6.47	17.1	17.3
6.	Bahurupi	120.67	10.50	132.87	24.74	225.00	18.10	37.37	81.15	73.82	70.67	4.53	2.44	1.86	5.03	8.8	9.0
7.	Sammela bogulu	93.33	10.90	131.20	26.35	249.60	19.98	45.67	81.18	65.13	52.46	5.62	2.27	2.48	5.14	9.2	9.0
8.	Laicha	100.33	12.53	129.07	22.76	153.13	24.09	38.07	81.02	67.69	61.24	5.60	2.50	2.24	5.06	16.6	14.4
9.	Kudel	103.00	11.97	147.80	29.35	166.00	24.69	43.37	83.88	66.72	55.12	5.67	2.60	2.18	6.24	11.8	13.7
10.	Kistappa sannalu	115.00	10.90	133.80	29.66	214.93	17.11	34.88	78.74	72.92	61.32	5.68	1.94	2.92	6.96	12.3	20.1
11.	Ranikanda	92.67	13.07	106.93	21.87	218.93	10.32	24.23	82.34	73.82	67.81	4.01	1.67	2.40	7.70	11.0	13.5
12.	Chattisgarh local	94.67	12.30	119.27	26.26	132.40	24.57	37.67	81.07	71.50	59.34	5.75	2.35	2.45	6.78	14.2	12.4
13.	Ramyagali	84.33	11.50	115.53	24.53	142.80	24.87	41.22	77.76	64.63	58.87	6.06	2.44	2.48	6.48	11.4	15.3
14.	Asthothal	93.67	13.27	129.53	23.14	151.87	21.55	35.33	81.44	69.79	55.25	6.23	2.17	2.87	6.39	14.2	13.2
15.	Burma black	103.00	10.43	133.20	29.77	156.27	25.33	34.50	75.19	54.85	38.16	5.84	2.59	2.26	7.06	16.4	19.1
16.	Narayana kamini	94.67	10.63	141.13	26.30	223.20	19.06	41.73	81.89	72.59	69.49	6.07	1.91	3.18	5.70	14.3	18.7
17.	Ambe mohar	116.67	10.30	137.60	28.07	289.47	15.61	42.03	82.48	67.33	65.84	4.19	2.24	1.87	3.76	13.3	12.9
18.	Yellava samba	93.33	16.37	140.93	28.81	118.73	13.17	30.23	82.02	72.34	56.71	4.34	1.94	2.23	6.55	19.5	17.1

19.	Kaki rekkalu	100.00	13.87	127.40	32.31	173.93	18.15	37.97	80.82	67.07	50.79	6.01	1.93	3.11	5.91	16.3	24.4
20.	Ratnachodi	103.33	13.33	131.73	25.49	214.33	15.79	38.40	82.03	72.43	61.18	5.17	1.55	3.34	7.18	11.9	12.6
21.	Nico	94.33	12.03	135.73	26.75	166.60	25.87	49.27	82.06	69.81	66.95	5.38	2.85	1.88	6.53	14.2	13.8
22.	Kasmikanda	81.00	12.27	135.00	31.31	185.87	17.24	38.80	82.96	67.89	47.95	5.59	1.97	2.85	7.00	16.6	15.2
23.	Jeeraga samba	121.33	14.33	137.27	28.61	163.53	22.63	40.00	79.30	65.19	56.58	5.61	2.34	2.39	7.78	19.4	16.2
24.	Kamarsambra	111.67	15.17	121.00	23.43	161.40	22.21	49.90	81.05	69.54	66.28	5.25	2.68	1.96	5.37	12.4	13.7
25.	Kandasagar	117.33	16.67	133.67	27.87	152.00	22.35	41.33	80.49	63.57	53.23	5.64	2.51	2.24	7.07	13.8	13.4
26.	Gani	85.00	13.50	122.47	25.90	214.67	13.84	41.79	81.61	72.63	61.57	4.49	1.54	2.92	7.51	16.2	14.7
27.	Chithloori sannalu	84.67	10.20	123.13	24.33	234.40	18.17	36.95	81.74	70.96	59.51	5.64	2.15	2.62	6.35	14.1	11.2
28.	Didianga	93.00	10.30	137.73	24.85	179.93	21.74	33.97	80.93	71.34	59.92	5.52	2.32	2.38	9.46	15.6	21.0
29.	Kareja jawal	95.33	12.70	129.87	27.36	180.40	18.21	37.67	81.16	70.58	52.39	5.00	1.93	2.60	7.54	11.0	12.3
30.	WGL 1245	103.67	10.43	95.53	23.87	294.20	18.15	46.29	81.21	72.78	67.26	5.33	1.96	2.72	6.02	11.1	11.8
31.	WGL 1246	105.67	11.03	106.13	24.94	273.13	18.20	46.83	82.08	72.29	66.24	5.54	1.86	2.98	5.86	10.3	11.9
32.	WGL 1252	106.33	10.33	112.27	26.21	305.87	17.60	47.65	83.66	73.00	58.70	5.20	1.98	2.62	5.50	15.3	14.4
33.	WGL 1261	104.00	10.93	96.67	24.32	279.87	14.80	42.21	81.25	71.86	63.04	4.84	1.79	2.70	5.36	11.4	13.5
34.	JGL 27356	104.33	13.60	92.80	20.51	278.33	12.16	40.50	82.31	67.67	63.87	5.16	1.39	3.72	7.22	13.3	13.7
35.	JGL 28545	104.33	12.97	84.80	23.88	278.13	13.83	42.80	83.86	74.80	66.16	5.52	1.72	3.22	7.57	9.7	13.3
36.	KNM 1638	94.00	10.13	91.67	24.19	245.80	14.50	32.45	82.76	72.22	64.46	5.34	1.71	3.12	5.74	11.3	11.1
37.	WGL 962	107.67	13.00	85.80	21.05	243.20	13.58	39.90	82.75	72.80	64.40	5.52	1.56	3.54	5.76	12.2	10.8
38.	KPS 2874	109.00	11.93	91.13	25.52	262.47	13.80	44.47	86.40	73.84	55.57	5.20	1.71	3.04	5.89	9.6	12.4
39.	KNM 6871	99.00	11.17	88.40	22.30	289.33	10.94	33.13	84.02	66.55	58.76	4.69	1.44	3.26	7.41	11.2	11.5
40.	KNM 6869	98.33	11.93	89.60	22.54	320.87	11.28	43.33	83.11	74.77	68.95	4.62	1.54	3.01	5.31	11.7	11.7
41.	WGL 1413	104.00	10.27	118.40	29.29	185.00	21.33	49.01	80.99	70.40	57.80	6.33	2.09	3.04	5.30	12.4	12.6
42.	KNM 7715	118.33	12.70	92.73	26.07	257.53	11.73	33.70	82.87	72.59	68.17	5.12	1.42	3.60	6.40	14.0	14.0
43.	RNR 21278	107.00	11.33	86.40	20.55	246.87	13.13	33.87	83.12	73.28	63.67	4.98	1.62	3.08	5.01	11.6	12.1
44.	WGL 1262	113.33	11.20	98.60	25.11	251.47	15.47	39.50	81.69	71.32	50.81	4.90	1.71	2.87	5.90	11.1	13.5
	Mean	102.36	12.19	117.46	25.67	210.12	18.33	39.69	81.45	69.70	59.52	5.39	2.05	2.70	6.35	13.38	14.22
	Maximum	121.33	16.67	147.80	32.31	320.87	25.87	49.90	86.40	74.80	70.67	7.11	2.85	3.72	3.76	8.8	9.0
	Minimum	81.00	10.13	84.80	20.51	118.73	10.32	24.23	75.19	54.85	36.49	4.01	1.39	1.86	9.46	19.5	24.4
	SEM	1.17	0.4	1.31	0.29	4.79	0.22	1.58	0.52	1.03	1.29	0.05	0.02	0.03	0.43	0.2	0.4
	C.V %	1.98	5.74	1.94	1.98	3.95	2.07	6.91	1.11	2.55	3.75	1.56	1.44	2.05	1.17	2.04	1.12
	C.D at 5%	3.29	1.14	3.69	0.83	13.47	0.62	4.45	1.46	2.89	3.62	0.14	0.05	0.09	1.21	0.68	1.11

SEM = Standard error of mean; C.V = Coefficient of variation; C. D = Critical difference

**Table 3:** Analysis of variance for yield and its components, quality and nutritional traits in rice (*Oryza sativa* L.)

Source of Variation	d.f.	Days to 50 per cent flowering	Productive tillers/ plant	Plant height (cm)	Panicle length (cm)	No. of Grains/ panicle	1000 grain weight (g)	Grain yield/ plant (g)	Hulling %
Replications	2	8.553	0.218	12.046	0.375	118.904	0.036	21.527	2.412
Treatments	43	308.859**	8.273**	1124.48**	23.446**	9333.249**	60.453**	83.117**	12.821**
Error	86	4.119	0.489	5.172	0.259	68.844	0.144	7.533	0.812

Source of Variation	d.f.	Milling %	Head rice recovery %	Grain length (mm)	Grain width (mm)	L/ B ratio	Protein (%)	Iron content (ppm)	Zinc content (ppm)
Replications	2	8.122	1.283	0.022	0.003	0.007	0.056	0.093	0.052
Treatments	43	47.121**	164.933**	1.114**	0.459**	0.701**	3.285**	20.216**	26.884**
Error	86	3.134	4.973	0.007	0.001	0.003	0.557	0.077	0.024

d.f. = Degrees of freedom  
 \*\* = Significant at 1% level.

**Table 4:** Mean, coefficient of variation, heritability (broad sense), genetic advance as per cent of mean for different characters in rice.

Character	Mean	Range		Coefficient of variation		h <sup>2</sup> (b) (%)	Genetic advance	Genetic advance as % of mean (%)
		Minimum	Maximum	Phenotypic (%)	Genotypic (%)			
Days to 50 per cent flowering	102.36	81.00	121.33	10.04	9.85	96.1	20.35	19.88
No. of productive tillers/ plant	12.19	10.13	16.67	14.40	13.21	84.1	3.14	24.96
Plant height (cm)	117.46	84.80	147.80	16.56	16.44	98.6	39.52	33.64
Panicle length (cm)	25.67	20.51	32.31	11.01	10.83	96.8	5.63	21.95
No. of grains per panicle	210.12	118.73	320.87	26.74	26.46	97.8	113.22	53.88
Grain yield per plant (g)	39.69	24.23	49.90	14.41	12.65	77.0	9.07	22.86
1000 grain weight (g)	18.33	10.32	25.87	24.55	24.46	99.3	9.20	50.21
Hulling %	81.45	75.19	86.40	2.69	2.46	83.1	3.76	4.61
Milling %	69.70	54.85	74.80	6.06	5.49	82.2	7.15	10.26
Head rice recovery %	59.52	36.49	70.67	12.83	12.27	91.5	14.39	24.17
Grain length (mm)	5.39	4.01	7.11	11.38	11.27	98.1	1.24	22.99
Grain width (mm)	2.05	1.39	2.85	19.10	19.05	99.4	0.80	39.13
L/B ratio	2.70	1.85	3.72	17.98	17.86	98.7	0.99	36.56



Protein content %	6.35	3.76	9.46	19.06	15.01	62.0	1.55	24.34
Iron content ppm	13.38	8.80	19.50	19.47	19.36	98.8	5.30	39.65
Zinc content ppm	14.22	9.00	24.40	21.07	21.04	99.7	39.65	43.29

$h^2$  (b) = Heritability in broad sense

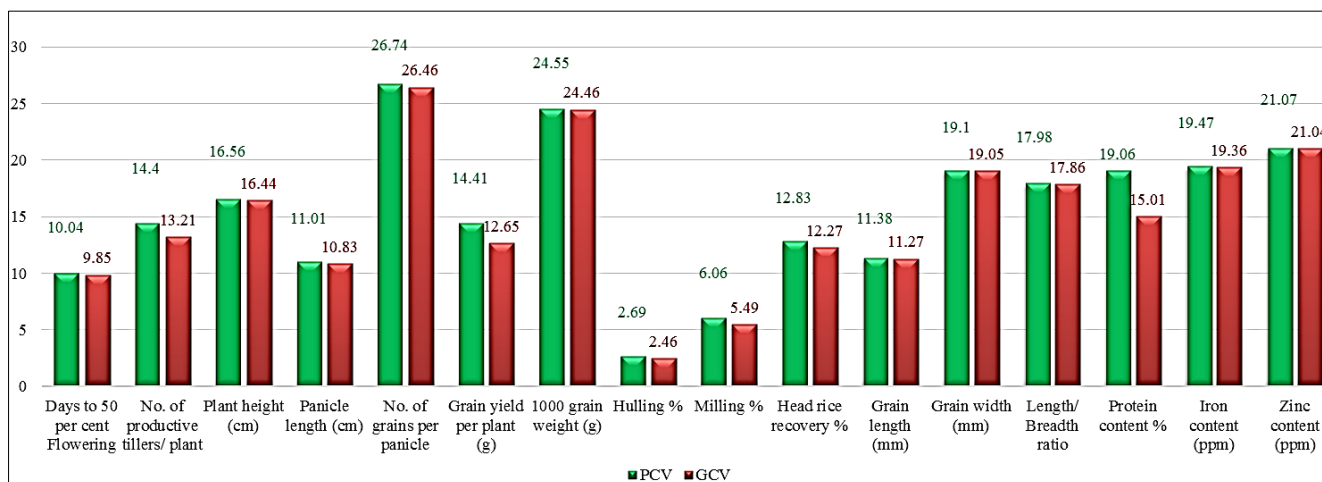


Fig 1: Variability parameters for yield and its components, quality and nutritional characters studied

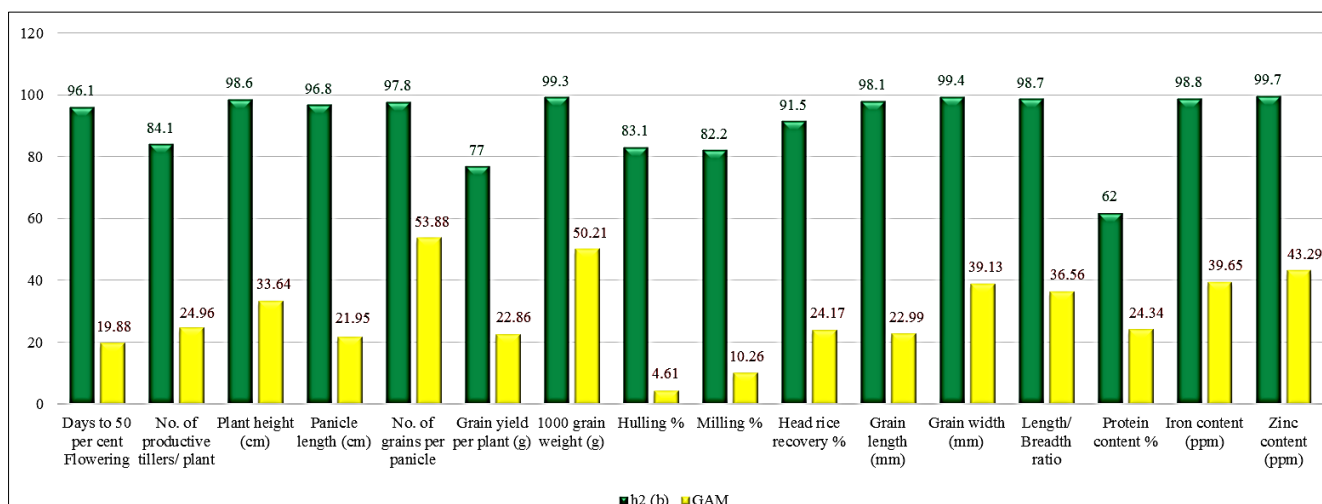


Fig 2: Heritability and genetic advance as per cent of mean for yield and its components, quality and nutritional characters studied

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