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Research Note

Studies on genetic variability, heritability and genetic advance for quantitative traits and nutritional traits in rice (*Oryza sativa* L.)

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Abstract
Fifty selected rice genotypes including two checks were evaluated during *Kharif,* 2022-23 for genetic variability, heritability and genetic advance as per cent of mean for 16 yield and its attributing traits along with six nutritional parameters in Ranadevi Post Graduate Research Farm, M. S. Swaminathan school of Agriculture, Centurion University of Technology and Management. Analysis of variance indicated highly significant differences among the 50 genotypes studied indicating that substantial variability is present among the genotypes. Total grains panicle^{-1}, filled grains panicle^{-1}, test weight, grain yield plant^{-1}, straw yield plant^{-1}, biological yield plant^{-1}, protein content and mineral contents of Fe, Zn, Cu and Mn exhibited high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) suggesting that there is considerable genetic variability among the genotypes studied for the evaluated traits. All 22 traits showed a high heritability (broad sense) coupled with high genetic advance as percent of mean except panicle length, spikelet fertility, harvest index and carbohydrate content, which recorded moderate genetic advance as percent of mean, indicating that additive gene action operates for these traits and has potential for improvement through direct selection methods.

Keywords: Rice, Variability, Heritability, Genetic Advance

The slogan “Rice is life” accurately captures the significance of rice in ensuring food and nutritional security (Ashok *et al.*, 2017). With its status as the world’s second most crucial cereal crop and a staple food for over 60% of the global population, Rice (*Oryza sativa* L.) plays a vital role and contributes approximately 75% of the calories and 55% of the protein required in the daily diets of people. The demand for rice is on the increase, both at the state level and national level. Due to rapidly growing population, the estimated demand for rice is projected to reach 121.2 million metric tonnes by 2030, 129.6 million metric tonnes by 2040 and 137.3 million metric tonnes by 2050 (CRRI VISION 2050). To meet this escalating demand for rice in the future, it will be necessary to increase the production per unit area to 3.4 tonnes per hectare, up from the current 2.4 tonnes per hectare. This increase is assumed to occur while maintaining the existing rice cultivation area (CRRI VISION 2050). Therefore, it becomes imperative to increase rice production in accordance with the expanding population.

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The essential step in enhancing yields is to recognize genotypes with significant variations. High yielding rice stands out as a remarkably suitable and feasible breeding option among the array of inventive approaches aimed at supporting rice production and productivity in India and other rice growing nations. (Ahmed and Siddiq, 1998). The primary emphasis in the segregating generation is on attaining a more productive plant. The key elements to concentrate on during selection are the variations in yield and its associated characters.

The yield is the outcome arising from a combination of different morphological and biological factors. To improve the yield, one has to utilize diverse cultivars with broader genetic diversity in hybridization efforts. Sufficient genetic variability is considered a crucial requirement to initiate any crop improvement programme and the extent of this variability plays a pivotal role in determining the success of such programs. The genotypic coefficient of variation is a metric that quantifies the level of genetic diversity as it represents the heritable component of variability.

The fundamental factors that underpin the enhancement of a trait through genetic means are variability, genetic diversity, genetic advance and the heritability of the traits. Heritability represents the proportion of variation in a trait within a population that is attributed to genetic differences among individuals and it reveals the portion of a characteristic that is passed on to future generations. Genetic advance, on the other hand, quantifies the disparity between the average genotypic values of the chosen population and the original population from which they were selected. When heritability estimates are combined with genetic advance, the prediction of genetic gain through selection becomes more accurate compared to relying solely on heritability. (Aditya and Bhartiya, 2013). Keeping this in view, the present investigation was undertaken to study the genetic variability, heritability and genetic advance among the rice genotypes.

Fifty rice genotypes including two check varieties obtained from different research stations located in Andhra Pradesh, Odisha and West Bengal were evaluated in the present study. The research work was carried out in experimental plot located at the Ranadevi, Post Graduate Research Farm, M. S. Swaminathan School of Agriculture, Centurion University of Technology and Management. The cultivation was conducted during the *Kharif* season, 2022-23 to evaluate grain yield and its attributing characters along with biochemical traits in a Randomized Block Design (RBD) with three replications. The crop was raised following recommended set of package of practices. Phonological data on days to 50% flowering and days to maturity was recorded on plot basis for each genotypes. Data on quantitative traits was recorded on ten randomly selected plants from each replication for individual genotypes. Observation for test weight, quality and nutritional traits were recorded from randomly drawn grain samples from each plot and replication.

The biochemical traits like carbohydrate content (%), total protein content (%) and micronutrient such as Fe, Zn, Cu and Mn using grain sample of different rice genotypes. The estimation of carbohydrate was performed using anthrone method proposed by Dreywood (1946). The estimation of total protein content in each sample was given by Lowry *et al.* (1951). The micronutrient contents *viz.,* Fe, Zn, Cu and Mn were estimated in the studied genotypes using Atomic Absorption Spectrophotometer using the method given by Jones (1992). The data recorded for 22 parameters was subjected to statistical analysis using analysis of variance as per Panse and Sukhatme (1978). The genotypic and phenotypic coefficients of variation were determined using the formulae given by Burton and Devane (1953). Heritability in broad sense and genetic advance as percent of mean were estimated using the formulae provided by Lush (1940) and Johnson *et al.* (1955), respectively.

The results of analysis of variance are presented in **Table 1**. ANOVA revealed highly significant differences among the genotypes studied for all the 22 characters studied demonstrating the presence of significant variability and intrinsic genetic variation among the genotypes studied.

Mean, range, GCV, PCV, heritability and genetic advance for morphological yield, yield component traits and biochemical traits are presented in **Table 2 and Fig. 1 & 2**.

Table 1. Analysis of variance for yield and yield contributing characters along with biochemical traits for 50 genotypes including checks.

Source of variance	Degree of freedom	Days to 50% flowering	Days to maturity	Plant height	Productive tillers plant^{-1}	Panicle length	Total grains panicle^{-1}	Filled grains panicle^{-1}	Spikelet fertility (%)
		Mean sum of squares							
Replication	2	0.73	3.12	16.68	1.78	0.44	5.55	5.40	8.52
Genotype	49	775.21**	753.27**	646.80**	9.42**	11.14**	5188.30**	3819.47**	88.57**
Error	98	4.94	7.91	10.70	0.52	1.63	18.23	15.31	8.66

Table 1.Continued..

Source of variance	Degree of freedom	Test weight (1000 seeds)	Grain yield plant^{-1}	Straw yield plant^{-1}	Grain length	Grain breadth	Grain L/B Ratio	Biological yield plant^{-1}	Harvest index (%)
		Mean of sum squares							
Replication	2	1.34	8.30	1.68	0.03	0.03	0.10	14.74	5.96
Genotypes	49	56.41**	99.35**	136.81**	2.68**	0.27**	1.11**	405.01**	56.97**
Error	98	0.77	3.34	2.49	0.06	0.02	0.05	9.02	2.62

Source of variance	Degree of Freedom	Protein (%)	Carbohydrate (%)	Iron (mg/kg)	Zinc (mg/kg)	Copper (mg/kg)	Manganese (mg/kg)
		Mean of sum squares					
Replication	2	0.01	0.40	7.61	0.56	0.95	0.01
Genotypes	49	5.18**	144.14**	286.64**	45.61**	288.07**	55.61**
Error	98	0.04	1.45	1.76	0.86	1.53	0.49

* Significance at 5% level; ** Significance at 1% level.

Table 2. Mean, range, variability, heritability and genetic advance as per cent of mean for yield, yield components and biochemical traits in rice (*Oryza sativa* L.)

S. No.	Characters	Grand Mean	Range		Coefficient of variation		Heritability (Broad sense) (%)	Genetic advance as percent of mean
			Minimum	Maximum	GCV (%)	PCV (%)		
1.	Days to 50% flowering	104.49	77.33	150.67	15.34	15.48	98.11	31.29
2.	Days to maturity	134.78	108.33	180.67	11.69	11.88	96.91	23.72
3.	Plant height (cm)	117.38	94.83	164.77	12.41	12.71	95.20	24.93
4.	Productive tillers per plant	10.87	8.53	20.33	15.84	17.18	85.07	30.10
5.	Panicle length (cm)	23.24	19.27	27.60	7.66	9.43	66.00	12.82
6.	Total grains per panicle	167.57	80.03	270.43	24.77	24.90	98.95	50.77
7.	Filled grains per panicle	142.06	65.50	224.80	25.07	25.22	98.81	51.33
8.	Spikelet fertility (%)	84.85	74.33	94.70	6.08	7.00	75.44	10.88
9.	Test weight (g)	21.22	13.65	33.13	20.30	20.72	96.00	40.97
10.	Grain yield per plant (g)	25.98	14.45	43.29	21.78	22.89	90.55	42.69
11.	Straw yield per plant (g)	25.42	14.87	53.50	26.32	27.04	94.73	52.78
12.	Grain length (mm)	8.25	6.03	11.09	11.35	11.71	93.85	22.65
13.	Grain breadth (mm)	2.35	1.53	3.27	12.22	13.50	81.94	22.78
14.	Grain L/B ratio	3.57	2.45	5.02	16.64	17.77	87.72	32.11
15.	Biological yield per plant	51.40	29.32	96.79	22.35	23.11	93.60	44.55
16.	Harvest index (%)	50.63	42.06	58.97	8.41	8.99	87.35	16.18
17.	Protein (%)	3.92	2.13	8.20	33.38	33.74	97.91	68.05
18.	Carbohydrate (%)	74.11	61.77	87.70	9.31	9.45	97.04	18.88
19.	Iron (mg/kg)	48.58	34.60	75.50	20.06	20.25	98.18	40.95
20.	Zinc (mg/kg)	18.41	11.00	26.10	20.98	21.57	94.55	42.02
21.	Copper (mg/kg)	35.90	21.10	56.30	27.23	27.44	98.42	55.64
22.	Manganese (mg/kg)	13.23	6.20	23.30	32.41	32.84	97.41	65.89

PCV: Phenotypic coefficient of variation; **GCV:** Genotypic coefficient of variation.

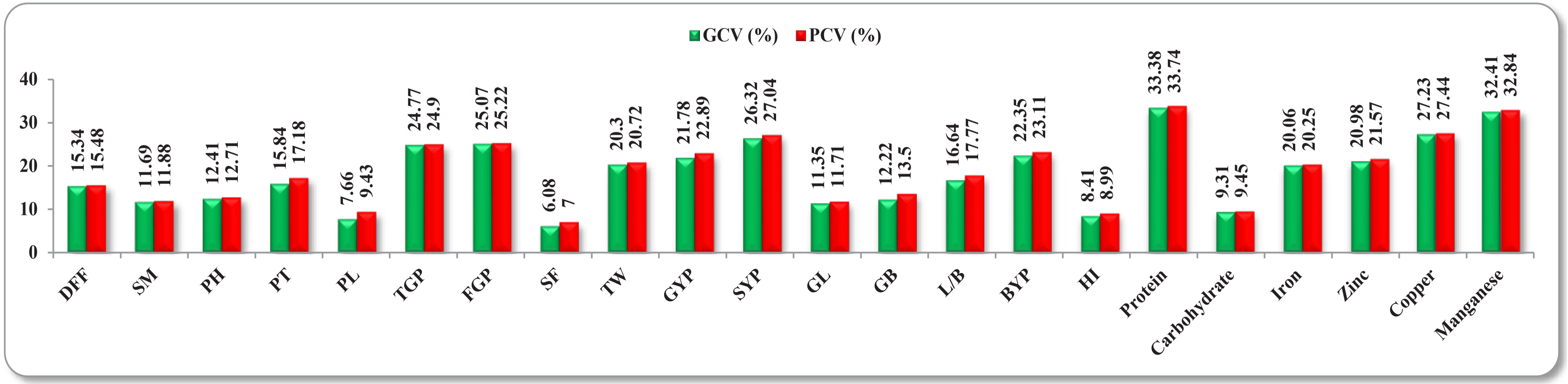

Fig. 1. GCV and PCV for yield, its components and biochemical traits studied

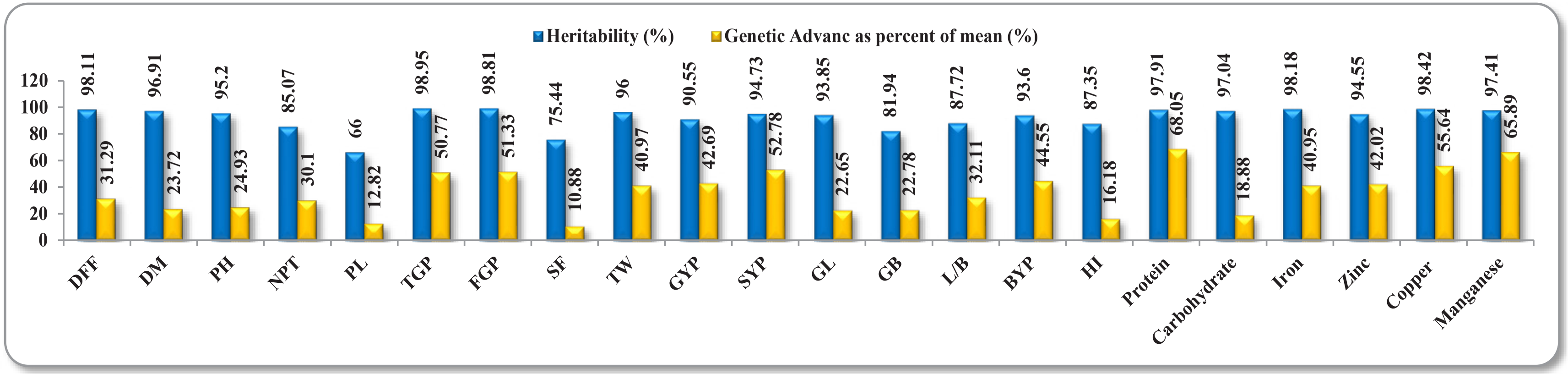

Fig. 2. Heritability and genetic advance as percent of mean for yield, its components and biochemical traits studied

DFF - Days to 50% flowering, DM - Days to maturity, PH - Plant height (cm), NPT - Number of productive tillers plant^{-1}, PL - Panicle length (cm), TGP - Total grains panicle^{-1}, FGP - Filled grains panicle^{-1}, SF - Spikelet fertility (%), TW - Test weight (g), GYP - Grain yield plant^{-1} (g), SYP - Straw yield plant^{-1} (g), GL - Grain length (mm), GB - Grain breadth (mm), L/B - Grain length/breadth ratio, BYP - Biological yield plant^{-1} (g), HI - Harvest index (%).

Mean performance for 22 morphological and biochemical traits among 50 genotypes is presented in **Table 3 and 4**. *Per se* performances of various genotypes revealed that NLR 9674 (180 days) followed by NLR 28523 (176 days), NLR 33892 (170 days), Barsha (162 days), Ranjit (153 days) and Gopalbhog (151 days) matured late when compared to both the checks. The entries Khandagiri (94.8 cm) followed by NLR 34449 (96 cm) NLR 4001 (96.2 cm), Rajendra Sweta (96.8 cm) and NLR 40065 (98.5 cm) recorded shorter height.

NLR 28523 exhibited high values for total (270.4) and filled (224.8) grains panicle^{-1} along with high grain yield plant^{-1} (43.3 g) and biological yield plant^{-1} (96.8 g). Tulaipanji (20.3) showed a higher number of productive tillers plant^{-1}. Maximum test weight was recorded in Rajlaxmi (33.1 g). Gopalbhog (27.6 cm) observed longest panicle leng

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Table 3. Mean performance for yield and yield attributing traits for 50 genotypes of rice (*Oryza sativa* L.) including check varieties

S.No.	Genotypes	DFF	DM	PH	NPT	PL	TGP	FGP	SF	TW	GYP	SYP	GL	GB	L/B	BYP	HI
1.	Barsha	134.3	162.7	158.3	9.6	22.5	162.4	122.4	75.4	27.0	25.4	29.3	9.2	2.7	3.4	54.7	46.5
2.	BB 11	110.7	142.7	110.1	10.0	21.3	155.2	135.7	87.8	21.5	27.1	23.0	7.1	2.5	2.8	50.1	54.1
3.	Bina 11	92.3	123.3	110.5	10.6	22.4	143.3	116.5	81.4	26.8	24.6	21.1	9.5	2.3	4.2	45.6	53.8
4.	Black Rice	110.3	139.3	153.5	10.0	21.7	160.9	125.5	78.3	24.8	24.2	22.5	8.3	3.3	2.5	46.6	51.9
5.	Bullet	92.0	122.7	112.3	9.9	23.0	183.6	154.2	84.0	18.9	21.8	17.8	7.8	2.5	3.1	39.6	55.1
6.	CR 1017	112.3	145.3	123.5	11.6	23.5	187.8	152.0	81.0	21.6	30.6	28.1	7.3	3.0	2.5	58.6	52.2
7.	Damini	97.3	126.7	124.4	10.3	21.8	234.3	216.6	92.5	21.5	26.1	30.4	8.1	2.1	3.8	56.5	46.1
8.	Dhiren	115.7	146.3	116.2	10.2	23.1	184.2	165.8	90.0	23.7	25.4	26.6	7.4	2.8	2.6	52.0	48.8
9.	GB 1	84.7	114.7	118.1	10.2	22.2	186.7	165.5	88.7	20.2	26.6	18.7	7.6	2.4	3.2	45.3	58.7
10.	GB 3	84.7	114.3	113.0	9.7	20.4	166.0	155.0	93.4	24.3	26.3	18.1	7.7	2.3	3.4	44.4	59.0
11.	Gopalbhog	120.7	151.7	164.8	10.5	27.6	215.5	185.4	86.1	13.7	25.0	31.1	6.0	2.1	2.9	56.1	44.5
12.	IET 5656	107.7	137.3	123.8	11.3	25.2	175.9	164.8	93.7	24.5	32.4	30.4	8.2	2.8	2.9	62.8	51.7
13.	IR 64	91.7	123.3	111.4	12.7	24.5	86.6	75.6	87.2	27.4	27.2	25.2	9.5	2.3	4.2	52.4	52.0
14.	Jaya	92.7	123.3	115.9	10.2	23.2	148.4	136.5	92.0	24.6	20.5	18.8	8.1	2.4	3.4	39.3	52.2
15.	Khandagiri	77.3	108.3	94.8	9.0	20.5	80.0	65.5	81.9	15.8	14.5	14.9	8.6	2.1	4.2	29.3	49.2
16.	Lalsita	93.7	122.7	112.1	13.6	19.4	93.1	76.7	82.6	21.5	32.7	24.5	10.3	2.3	4.4	57.2	57.1
17.	Lalat	91.7	121.3	122.5	13.7	24.8	116.2	93.4	80.4	16.9	27.7	26.7	9.0	2.2	4.1	54.4	50.9
18.	Lalgarh	108.7	139.7	121.7	10.3	26.4	168.0	146.3	87.1	22.4	29.4	25.7	7.9	2.8	2.9	55.2	53.3
19.	Lathisal	91.0	120.7	106.5	10.7	22.1	110.3	96.3	87.3	24.3	21.8	18.9	8.2	2.3	3.6	40.7	53.5
20.	Maharaj	105.0	136.7	108.5	12.0	23.4	104.8	86.0	82.1	26.8	26.5	24.8	9.2	2.4	3.8	51.3	51.8
21.	MTU 1001	103.0	133.3	119.5	11.4	22.2	155.3	134.3	86.5	24.0	28.1	25.9	8.8	2.6	3.4	53.9	52.1
22.	MTU 1010 (check)	82.3	112.3	99.6	10.5	22.4	108.4	86.5	79.8	23.4	18.7	20.6	9.0	2.1	4.3	39.2	47.6
23.	MTU 1075	99.7	129.7	116.9	12.1	24.0	226.2	192.8	85.3	20.7	33.2	26.5	8.9	2.2	4.0	59.6	55.6
24.	MTU 1153	85.3	118.3	113.2	10.4	24.6	194.3	174.5	89.8	23.9	25.6	22.4	8.9	2.3	3.8	48.0	53.2
25.	MTU 1156	83.3	116.0	112.3	11.2	23.9	182.5	156.1	85.5	23.6	30.4	25.4	8.5	2.3	3.7	55.8	54.5
26.	MTU 7029	114.7	144.3	103.8	9.6	22.2	155.8	135.1	86.7	20.2	23.4	19.5	7.5	2.4	3.2	42.9	54.6
27.	Nilanjana	111.3	141.0	125.1	11.5	23.8	175.6	145.1	82.6	22.8	30.8	26.9	8.0	2.7	3.0	57.8	53.4
28.	NLR 145	101.3	132.3	118.0	10.5	21.5	224.5	184.1	82.0	18.7	23.4	24.1	8.3	2.1	4.0	47.6	49.2
29.	NLR 28523	146.0	176.3	124.0	10.2	23.1	270.4	224.8	83.1	19.3	43.3	53.5	7.0	2.7	2.6	96.8	44.7
30.	NLR 3041	105.3	135.3	103.0	11.5	20.6	168.2	134.9	80.2	14.2	23.9	26.0	7.4	2.0	3.8	49.9	47.9

Table 3. Continued..

S.No.	Genotypes	DFF	DM	PH	NPT	PL	TGP	FGP	SF	TW	GYP	SYP	GL	GB	L/B	BYP	HI
31.	NLR 33359	93.3	122.7	110.6	8.5	25.5	192.5	168.6	87.6	19.3	19.0	23.0	8.1	2.4	3.4	42.0	45.3
32.	NLR 33892	141.0	170.7	129.7	10.2	23.7	235.9	175.3	74.3	15.8	34.8	41.9	7.0	2.3	3.0	76.7	45.4
33.	NLR 34449	98.0	127.0	96.0	9.9	22.0	152.4	115.6	75.9	14.7	17.3	23.9	7.6	1.9	4.0	41.2	42.1
34.	NLR 4001	110.7	140.3	96.2	9.9	21.0	195.5	165.1	84.5	15.5	22.9	20.7	8.3	2.4	3.6	43.6	52.6
35.	NLR 40054	94.7	126.3	103.3	9.3	20.1	155.3	143.1	92.2	14.9	18.6	20.4	7.2	2.3	3.2	39.0	47.6
36.	NLR 40058	95.3	125.3	112.6	10.1	25.0	193.7	157.1	81.1	17.6	21.5	24.3	7.9	2.3	3.5	45.7	46.9
37.	NLR 40065	98.0	127.3	98.5	9.9	25.0	195.9	177.2	90.4	20.8	19.6	20.0	8.5	2.0	4.2	39.6	49.5
38.	NLR 9674	150.7	180.7	126.9	10.9	24.0	149.0	129.0	86.6	17.1	36.3	45.4	6.9	2.5	2.8	81.7	44.5
39.	Pooja	107.7	138.7	121.6	11.2	24.3	154.3	146.1	94.7	22.9	24.5	25.9	8.2	2.4	3.4	50.4	48.7
40.	Pratikshya	110.3	136.7	110.0	9.7	25.0	257.2	204.9	79.7	21.5	26.1	21.7	8.5	2.3	3.7	47.8	54.5
41.	Rajendra Mahsuri	107.7	138.0	114.4	9.9	24.6	185.4	165.5	89.3	21.3	24.5	21.0	8.1	2.3	3.6	45.5	53.8
42.	Rajendra Sweta	99.3	130.7	96.8	9.1	19.3	175.7	145.0	82.6	13.7	16.7	19.4	7.6	1.9	4.1	36.2	46.3
43.	Rajlaxmi	121.7	151.0	119.2	11.3	25.6	125.4	107.3	85.6	33.1	27.4	25.7	11.1	2.2	5.0	53.1	51.7
44.	Ranjit	124.3	153.0	126.9	11.1	24.9	144.7	115.6	79.8	20.8	27.6	31.2	8.1	2.4	3.4	58.9	46.9
45.	RNR 15048 (check)	91.3	119.7	112.1	9.8	23.1	154.6	116.0	75.1	14.3	19.3	26.4	4.6	1.6	2.9	45.7	42.2
46.	Santoshi	118.3	148.7	122.8	10.5	22.3	134.2	123.2	91.8	26.7	29.5	28.2	9.3	2.4	3.9	57.7	51.2
47.	Sita	101.3	130.3	115.0	11.1	21.5	125.6	115.7	92.1	23.2	24.6	24.9	9.2	2.4	3.8	49.5	49.7
48.	Sonamukhi	98.3	132.7	121.9	12.9	25.2	204.8	164.5	80.4	21.6	34.7	24.9	7.7	2.6	3.0	59.6	58.2
49.	Super Shyamali	119.3	149.7	134.9	12.9	25.7	155.0	139.5	90.0	28.7	37.1	28.5	10.3	2.3	4.5	65.6	56.6
50.	Tulaipanji	96.3	127.7	142.5	20.3	27.0	166.9	124.7	74.7	18.5	20.1	26.5	8.1	1.9	4.2	46.6	43.2
	MEAN	104.49	134.78	117.38	10.87	23.24	167.57	142.06	84.85	21.22	25.98	25.42	8.25	2.35	3.57	51.40	50.63
	C. V.	2.13	2.09	2.79	6.64	5.50	2.55	2.75	3.47	4.14	7.04	6.21	2.90	5.74	6.22	5.84	3.20
	C.D. at 5%	3.60	4.56	5.30	1.17	2.07	6.92	6.34	4.77	1.42	2.96	2.56	0.39	0.22	0.36	4.87	2.62
	C. D. at 1%	4.77	6.03	7.01	1.55	2.74	9.16	8.39	6.31	1.88	3.92	3.39	0.51	0.29	0.48	6.44	3.47

DFF - Days to 50% flowering, DM - Days to maturity, PH - Plant height (cm), NPT - Number of productive tillers plant^{-1}, PL - Panicle length (cm), TGP - Total grains panicle^{-1}, FGP - Filled grains panicle^{-1}, SF - Spikelet fertility (%), TW - Test weight (g), GYP - Grain yield plant^{-1} (g), SYP - Straw yield plant^{-1} (g), GL - Grain length (mm), GB - Grain breadth (mm), L/B - Grain length/breadth ratio, BYP - Biological yield plant^{-1} (g), HI - Harvest index (%).

cm) and NLR 40065 (98.5 cm) recorded shorter height. The among selected genotypes. Maximum variation was recorded for plant height (94.83 cm to 164.77 cm), number of productive tillers plant^{-1} (8.53 to 20.33), test weight (13.65 g to 33.13 g), grain length (6.03 mm to 11.09 mm), biological yield plant^{-1} (29.32 g to 96.79 g), protein content (2.13% to 8.20 %), iron content (34.60 mg/kg to 75.50 mg/kg), grain breadth (1.53 mm to 3.27 mm) and spikelet fertility (74.33% to 94.70 %).

Study of coefficient of variation indicated that estimates of GCV for all characters studied are slightly less than PCV estimates thus indicating slight influence of the environment on the performance of genotypes. Similar results were earlier reported by Sudeepthi *et al.* (2020) and Akshay *et al.* (2022).

Estimates of PCV ranged from 33.74% (protein %) to 7.00% (spikelet fertility %) while GCV estimates ranged from 33.38% (protein %) to 6.08% (spikelet fertility %). High PCV and GCV were recorded for protein % (33.74%, 33.38%), grain manganese content (32.84%, 32.41%), grain copper content (27.44%, 27.23%), straw yield plant^{-1} (27.04%, 26.32%), filled grains panicle^{-1} (25.27%, 25.07%), total grains panicle^{-1} (24.90%, 24.77%), biological yield plant^{-1} (23.11%, 22.35%), grain yield plant^{-1} (22.89%, 21.78%), grain zinc content (21.57%, 20.98%), test weight (20.72%, 20.30%) and grain iron content (20.25%, 20.06%). High PCV and GCV observed indicated the presence of high variability present in the experimental material used. These findings are in agreement with the results reported earlier by Rao *et al.* (2020) for protein content;

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Table 4. Mean performance for biochemical traits for 50 genotypes of rice (*Oryza sativa* L.) including check varieties.

S. No.	Genotypes	Protein (%)	Carbohydrate (%)	Iron (mg/kg)	Zinc (mg/kg)	Copper (mg/kg)	Manganese (mg/kg)
1.	Barsha	4.3	71.3	58.5	15.1	51.8	19.4
2.	BB 11	3.7	74.1	49.3	18.3	36.3	6.2
3.	Bina 11	4.9	76.2	51.5	16.8	48.2	17.0
4.	Black Rice	5.4	69.6	48.7	12.3	49.7	8.0
5.	Bullet	3.7	75.7	41.5	11.0	49.1	8.6
6.	CR 1017	3.1	73.9	38.6	14.8	22.3	14.2
7.	Damini	6.5	70.2	41.3	13.6	26.8	11.3
8.	Dhiren	2.8	85.6	40.9	11.3	28.9	10.3
9.	GB 1	4.1	68.9	38.6	14.0	25.3	10.9
10.	GB 3	2.8	75.2	36.4	12.8	31.4	7.9
11.	Gopalbhog	5.3	63.1	42.5	14.5	42.6	7.8
12.	IET 5656	2.1	74.5	53.1	14.3	38.9	8.3
13.	IR 64	3.3	84.9	49.6	15.6	24.6	9.6
14.	Jaya	3.9	69.9	36.3	16.5	32.9	8.0
15.	Khandagiri	2.9	67.0	40.6	19.2	28.4	14.2
16.	Lalsita	3.5	69.0	34.6	22.5	21.6	11.6
17.	Lalat	5.3	87.5	36.2	19.6	27.1	8.6
18.	Lalgarh	2.6	69.6	41.3	18.7	42.3	10.3
19.	Lathisal	4.5	65.1	37.4	16.5	38.6	9.4
20.	Maharaj	2.8	67.7	38.6	18.7	29.3	13.0
21.	MTU 1001	4.8	85.6	40.2	15.6	32.2	13.8
22.	MTU 1010 (check)	3.5	62.6	42.4	20.4	21.1	9.9
23.	MTU 1075	6.9	66.6	44.6	21.7	24.7	10.7
24.	MTU 1153	2.5	79.1	38.6	23.2	32.3	8.4
25.	MTU 1156	2.5	72.2	43.2	26.0	28.2	10.3
26.	MTU 7029	3.2	82.2	45.0	24.1	26.5	8.8
27.	Nilanjana	3.3	73.6	42.7	22.4	31.0	12.9
28.	NLR 145	4.8	85.8	54.6	18.6	26.9	16.3
29.	NLR 28523	5.6	78.3	52.0	17.4	27.3	17.3
30.	NLR 3041	3.6	72.7	48.8	16.9	26.4	14.2
31.	NLR 33359	6.6	64.9	75.5	19.2	31.8	21.3
32.	NLR 33892	4.8	67.2	54.6	18.5	29.4	17.4
33.	NLR 34449	5.1	82.5	62.2	20.4	34.6	16.9
34.	NLR 4001	3.7	61.8	45.3	19.3	52.8	15.8
35.	NLR 40054	3.7	73.2	40.9	17.6	49.6	9.5
36.	NLR 40058	8.2	86.2	51.2	18.9	56.3	12.6
37.	NLR 40065	2.2	72.8	63.7	21.3	46.1	14.3
38.	NLR 9674	3.8	76.4	54.8	17.4	54.0	10.8
39.	Pooja	3.2	73.2	42.9	24.2	36.6	18.6
40.	Pratikshya	3.0	75.1	63.7	25.2	31.2	20.9
41.	Rajendra Mahsuri	3.7	83.6	58.5	17.7	25.4	17.2
42.	Rajendra Sweta	2.7	74.9	60.9	19.6	32.7	15.7

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Table 4. Continued ...

S. No.	Genotypes	Protein (%)	Carbohydrate (%)	Iron (mg/kg)	Zinc (mg/kg)	Copper (mg/kg)	Manganese (mg/kg)
43.	Rajlaxmi	3.3	87.7	42.6	22.4	40.6	16.3
44.	Ranjit	3.2	67.1	51.8	25.7	43.1	11.8
45.	RNR 15048 (check)	2.8	69.0	62.3	16.5	52.7	10.6
46.	Santoshi	2.8	71.4	58.6	12.0	35.8	12.8
47.	Sita	5.1	73.2	71.8	26.1	46.5	23.3
48.	Sonamukhi	4.1	70.9	60.3	18.3	41.9	18.4
49.	Super Shyamali	2.5	78.8	48.9	21.1	42.3	20.7
50.	Tulaipanji	3.3	78.0	50.7	16.7	38.7	19.2
	GRAND MEAN	3.92	74.11	48.58	18.41	35.90	13.23
	C. V.	4.88	1.62	2.73	5.04	3..45	5.28
	C. D. at 5%	0.31	1.95	2.15	1.50	2.00	1.13
	C. D. at 1%	0.41	2.58	2.85	1.99	2.66	1.50

Samak *et al.* (2011) for manganese and copper content; Jadhav *et al.* (2020) for straw yield plant^{-1}; Acharya *et al.* (2018), Dhakal *et al.* (2020), Pratap *et al.* (2018) and Shivani *et al.* (2018) for filled grains panicle^{-1}; Acharya *et al.* (2018), Edukondalu *et al.* (2017), Srujana *et al.* (2017) for total grains panicle^{-1}; Bagudam *et al.* (2018), Laxmi and Chaudhari (2019), Yadav *et al.* (2017) for biological yield plant^{-1}; Rao *et al.* (2021), Sreelakshmi and Babu (2020), Kurmanchali *et al.* (2019) for grain yield plant^{-1}; Rao *et al.* (2020), Samak *et al.* (2011), Akshay *et al.* (2022) for grain zinc content; Rao *et al.* (2020), Bagudam *et al.* (2018), Kurmanchali *et al.* (2019) for test weight and Rao *et al.* (2020) and Samak *et al.* (2011) for grain iron content.

Moderate PCV and GCV were recorded for days to 50% flowering (15.48%, 15.34%), days to maturity (11.88%, 11.69%), plant height (12.71%, 12.41%), number of productive tillers plant^{-1} (17.18%, 15.84%), grain length (11.71%, 11.35%), grain breadth (13.50%, 12.22%) and grain L/B ratio (17.70%, 16.64%). These findings are in agreement with the results reported earlier by Rao *et al.* (2021), Nithya *et al.* (2020) and Kurmanchali *et al.* (2019) for days to 50% flowering; Pratap *et al.* (2018), Kumar *et al.* (2018) and Jadhav *et al.* (2020) for days to maturity; Rao *et al.* (2020), Nithya *et al.* (2020) and Pratap *et al.* (2018) for plant height; Sreelakshmi and Babu (2020), Acharya *et al.* (2018) for number of productive tillers plant^{-1}; Dhakal *et al.* (2020) and Edukondalu *et al.* (2017) for grain length and grain breadth; Rao *et al.* (2021) and Singh and Verma (2018) for grain L/B ratio. While low PCV and GCV were recorded for panicle length (9.43%, 7.66%), spikelet fertility (7.00%, 6.08%), harvest index (8.99%, 8.41%) and carbohydrate content (9.45%, 9.31%). Similar findings are in agreement with the results reported earlier by Sreelakshmi and Babu (2020), Shivani *et al.* (2018), Kurmanchali *et al.* (2019) for panicle length; Singh and Verma (2018), Rao *et al.* (2021), Nithya *et al.* (2020) for spikelet fertility; Sreelakshmi and Babu (2020), Sumanth *et al.* (2017) for harvest index; Rao *et al.* (2020) for carbohydrate content.

Heritability for different traits varied from 75.44% (spikelet fertility %) to 98.95 % (total grains panicle^{-1}) and genetic advance as percent of mean ranged from 10.88% (spikelet fertility %) to 68.05% (protein %). For formulating selection criterion, estimates of heritability and genetic advance are highly useful for predicting the genetic gain derived through selection than heritability alone. The estimates of heritability are more advantageous where expressed in terms of genetic advance. Johnson *et al.* (1955) suggested that without genetic advance the estimates of heritability will not be of practical value and emphasize the concurrent use of genetic advance along with heritability (Rajesh *et al.,* 2019).

High heritability along with high genetic advance as percent of mean was observed for days to 50% flowering, days to maturity, plant height, number of productive tillers plant^{-1}, total grains panicle^{-1}, filled grains panicle^{-1}, test weight, grain yield plant^{-1}, straw yield plant^{-1}, grain length, grain breadth, grain L/B ratio, biological yield plant^{-1}, protein content, iron content, zinc content, copper content and manganese content indicating that all these traits are governed by additive gene action. Hence, for these characters better response can be obtained by selection. These results are in accordance with the findings of Rao *et al.* (2021), Nayak *et al.* (2016), Demeke *et al.* (2023), Loitongbam *et al.* (2020), Saidon *et al.* (2020), Tuhina *et al.* (2015), Singh *et al.* (2021), Akshay *et al.* (2022) and Samak *et al.* (2011).

High heritability estimates coupled with moderate genetic advance as percent of mean were recorded for the traits panicle length, spikelet fertility percentage, harvest index and grain carbohydrate content indicating that both additive and non-additive gene actions are involved and heritability exhibited and may be due to environment rather than genotype alone. Similar results are earlier reported by Demeke *et al.* (2023), Rao *et al.* (2021), Loitongbam *et al.* (2020) for panicle length; Singh *et al.* (2021) and Kumar *et al.* (2018) for spikelet fertility percentage; Sreelakshmi and Babu (2020) and Sumanth *et al.* (2017) for harvest index; Rao *et al.* (2020) for grain carbohydrate content.

From the present study, it can be inferred that morphological traits like days to 50% flowering and days to maturity, yield and yield attributing traits like plant height, number of productive tillers plant^{-1}, total grains panicle^{-1}, filled grains panicle^{-1}, test weight, grain yield plant^{-1}, straw yield plant^{-1}, grain length, grain breadth, grain L/B ratio, biological yield plant^{-1} all characters recorded moderate to high variability, high heritability coupled with high genetic advance indicating that additive gene action is operating in control of these traits. Thus, it can be inferred that substantial improvement in the expression above traits can be expected through simple selection. Further, the genotypes NLR 40058 for high protein content, NLR 4001 for low carbohydrate content, NLR 33359 and Sita for high iron content, Sita and MTU 1075 for high zinc content, Lalsita and MTU 1010 for low copper content and BB 11 and Gopalbhog for low manganese content. These entries can be utilized in breeding programme aimed at enhanced nutritional quality in grain.

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