International Journal of Advanced Biochemistry Research
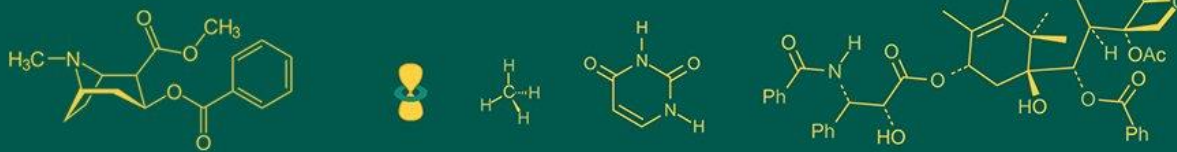
Jambhulkar Rohit Kashinath
Mahatma Phule Krishi
Vidyapeeth, Rahuri, College of
Agriculture, Pune,
Maharashtra, India

C Banu Teja
Mahatma Phule Krishi
Vidyapeeth, Rahuri, College of
Agriculture, Pune,
Maharashtra, India

Dr. TJ Bhor
Assistant Professor of
Agriculture Botany,
Agriculture Research Station,
Vadgaon, Maval, Pune,
Maharashtra, India

Genetic variability, heritability, and correlation analysis of rice (*Oryza sativa*) for iron and zinc content: Implications for biofortification and yield improvement

Jambhulkar Rohit Kashinath, C Banu Teja and Dr. TJ Bhor

Abstract
Rice (*Oryza sativa* L.) is a vital cereal crop, serving as the staple food for over half of the global population, particularly in Asia. However, widespread malnutrition persists, primarily due to the consumption of milled rice lacking in essential micronutrients such as iron and zinc. This study aimed to assess the genetic variability of 41 rice genotypes for 11 key traits, focusing on grain yield and nutritional content, particularly iron and zinc. Conducted during the *kharif* season of 2022 at the Agricultural Research Station, Vadgaon (Maval), Pune, the investigation evaluated variability, heritability, character associations, and path analysis. Results revealed significant variability among genotypes for all studied traits. Both genotypic and phenotypic coefficient of variation were notably high for grain yield per plant, grain iron content, grain zinc content, fertile spikelet's per panicle, and total spikelet's per panicle. Path analysis highlighted direct positive effects of total spikelet's per panicle on grain yield per plant, indicating its importance in yield improvement. Additionally, days to 50% flowering exhibited positive correlations with grain yield per plant, mediated by indirect positive effects through test weight. Conversely, plant height demonstrated a negative direct correlation with grain yield per plant but had positive indirect effects through productive tillers per plant and grain yield per plant. Productive tillers per plant showed significant positive correlations with grain yield via indirect effects through various traits, underlining its role in enhancing yield.

Keywords: Rice, genetic variability, heritability, path analysis, iron, zinc, grain yield

Introduction
Rice (*Oryza sativa* L.) is a vital crop worldwide, serving as the staple food for more than half of the global population (Verma *et al*., 2006) [28]. More than 90 percent of the world's rice is produced and consumed in Asia, which is known as the "rice bowl of the world." China is the world's biggest producer of rice, while India is the country that grows the largest quantity of it. Total production of Rice for the year 2021- 2022 stood at 130.29 million tonnes covering the area of 463.79 lakh hectare with productivity of 2809 kg per hectare. (Directorate of Economics and Statistics, Department of Agriculture and Farmers Welfare, Ministry of Agriculture and Farmers Welfare, Government of India, 2022)
However, despite its widespread consumption, rice-based diets are plagued by nutritional deficiencies, notably in essential micronutrients like iron and zinc, leading to what is commonly termed as "hidden hunger" or micronutrient malnutrition (Verma *et al*., 2006) [28]. This issue is exacerbated by the prevalent consumption of milled rice, which removes vital nutrients, leaving grains with inadequate nutritional value (Bandumula, 2018) [6].
To combat malnutrition, especially in regions heavily reliant on rice, biofortification has emerged as a promising strategy. Biofortification, employing advanced breeding techniques, aims to enhance the nutritional content of crops like rice, addressing hidden hunger and improving the health of vulnerable populations globally (Cakmak, 2008; Wissuwa *et al.,* 2008) [9, 31]. Iron (Fe) and zinc (Zn) are crucial micronutrients vital for various cellular functions. Efforts have been directed towards improving the content of these essential nutrients in rice grains, given the wide genetic variability in rice germplasm. Plant breeding-based biofortification has been identified as a sustainable approach to enhancing grain micronutrient content and curbing malnutrition.

Corresponding Author:
C Banu Teja
Mahatma Phule Krishi
Vidyapeeth, Rahuri, College of
Agriculture, Pune,
Maharashtra, India

Understanding the genetic variability and relationships between genotypes are crucial for effective plant breeding. High heritability coupled with significant genetic advance suggests favourable conditions for trait improvement through selection. Analysing the correlation and path coefficients among yield and quality-related traits aids in effective yield improvement and breeding strategy design.

This paper aims to explore the significance of variability, heritability, genetic advance, character associations, and path coefficients in high zinc and iron rice varieties. Through the evaluation of potential rice cultivars derived from advanced breeding techniques, this study seeks to provide valuable insights into addressing hidden hunger and enhancing the nutritional security of rice-dependent populations.

Materials and Methods
The study aimed to assess variability in 11 agronomic and yield-related traits among 41 rice genotypes sourced from diverse regions. Conducted at the Agricultural Research Station, Vadgaon (Maval), Pune, during the kharif season of 2022, the experiment utilized a randomized block design (RBD) with two replications. Seedlings, aged 28 days, were transplanted in the main field with a spacing of 20 × 15 cm, following recommended agricultural practices.

Observations were recorded for 11 quantitative traits, including days to 50% flowering, plant height, productive tillers per plant, panicle length, fertile spikelet's per panicle, total spikelet's per panicle, spikelet fertility %, test weight (1000 grain weight), grain yield per plant, grain iron (Fe) content, and grain zinc (Zn) content. Quantitative trait data were collected from five randomly selected plants in each plot per replication, except for days to 50% flowering, which was recorded on a plot basis. Grain iron and zinc contents were determined using Atomic Absorption Spectrophotometry (Perkin Elmer AAnalyst 200) at the College of Agriculture, Pune.

Genotypic differences were assessed through analysis of variance following the format prescribed by Panse and Sukhatme (1995) [4]. Genotypic and phenotypic coefficients of variation, heritability, and genetic advance were calculated using Burton's (1952) [8] and Johnson et al.'s (1955) [16] formulas. Genotypic correlation coefficients were calculated according to the method described by Singh and Chaudhary (1977) [27]. Path coefficient analysis, following Dewey and Lu's (1959) [10] procedure, was conducted to explore cause-and-effect relationships among traits.

These statistical analyses provided comprehensive insights into genetic variability, heritability, trait associations, and causal relationships, enhancing understanding of the experimental data.

Results and Discussion
The analysis of variance (ANOVA) for yield, yield contributing and quality traits are presented in Table 2. The results revealed highly significant differences among the genotypes for all the traits under study, indicating the existence of adequate variation in experimental material. Thus, there is a good opportunity to select better parental types to improve grain yield and quality.

For each of the traits examined in the current analysis a significant range of variance was observed. In forty-one (41) genotypes, overall high significant differences were identified in total spikelet's per panicle (109.00-221.50)

followed by fertile spikelet's per panicle (89.00-201.00), and minimum for panicle length (17.05-28.75) and productive tillers per plant (6.25-9.85).This observed that there was a large amount of space for these features to be exploited as reported earlier for total spikelet's and plant height by Maurya et al. (2022) [19] and for total spikelet's per panicle, productive tillers per plant, seed yield per plant and 1000 grain weight Divya et al. (2018) [13].

Variability is very essential for any character for improvement through plant breeding. The genotypic coefficient variation (GCV) phenotypic coefficient variation (PCV), heritability and genetic advance as percent of mean were computed and analysed for all characters studied in the present investigation. The results are presented in Table 3.

PCV was noticed to be higher than GCV value for all the traits studied indicating the role of environment. These results are supported by the findings of earlier workers he findings of Panigrahi et al. (2018) [21], Roy et al. (2021) [24] and Maurya et al. (2022) [19]. For spikelet fertility % exhibited the lowest GCV (4.474) as well as PCV (4.935), whereas grain yield per plant exhibited the highest GCV (32.111) and PCV (32.618). The highest GCV and PCV difference was recorded for productive tillers per plant. However lowest GCV and PCV difference was recorded for days to 50% flowering followed by spikelet fertility % and grain yield per plant. The larger difference between GCV and PCV showed by the characters were influenced due to the environment. Genetic advance and heritability are recognised as important selection parameter. According to Burton (1952) [8], combining genetic variation with heritability estimates, would provide a better idea of the effectiveness of selection. Heritability is a reliable indicator of how parental values are transmitted in to their offspring. The plant breeder can pick superior traits from a variety of genetic groups with the use of heritability estimations.

Days to 50% flowering (95.60%). Grain iron (Fe) content showed heritability (94.60%) followed by fertile spikelet's per panicle (92.90%), grain zinc (Zn) content (92.30%), total spikelet's per panicle (91.30%), panicle length (91.20%), plant height (90.70%), followed by high heritability in some characters like such as 1000 grain weight (90.40%), spikelet fertility % (82.20%) and productive tillers per plant (74.10%) character. High heritability estimates suggest that these characters were least influenced by the environment. These findings were in agreement with the findings by Asante et al. (2019) [4] for days to 50% flowering and plant height, Anbanadan (2018) [3] for grain yield, days to 50% flowering and plant height, Divya et al. (2018) [13] for characters number of productive tillers per plant, 1000 grain weight, number of grains per panicle and grain yield per plant, Akshaya et al. (2020) [1] for plant height, Shaili et al. (2022) [25] for grain yield per plant, number of panicles, test weight and plant height. High heritability (h2) with moderate genetic advance as percent of mean showed for the characters fertile spikelet's per panicle, total spikelet's per panicle, 1000 grain weight and plant height suggested that both additive and non-additive gene effects were involved in the genetic regulation of these traits. These results supported prior findings by Mustafa and Elsheikh (2007) [30] regarding plant height and 1000 grain weight.

In current study, high heritability (h2) along with higher genetic advance (GA) as per-cent of mean was recorded for the characters viz., grain yield per plant, grain iron (Fe)

content, grain zinc (Zn) content, fertile spikelet's per panicle, 1000 grain weight, total spikelet's per panicle, plant height and days to 50% flowering indicated that these traits were under control of additive gene action. The selection could be practised in all these traits for higher magnitude of genotype. Similar result was reported by Anbanadan (2018) [3] for grain yield. The results were agreement with Panigrahi et al. (2018) [21] for 1000 grain weight and Shaili et al. (2022) [25] for test weight, grain yield and plant height. Similar result was reported by Lalitha et al. (2019) [18] reported for grain yield per plant.

The genotypic correlation between various yield and yield contributing characters showed that grain yield per plant was positively and significantly correlated with days to 50 percent flowering, productive tillers per plant, panicle length, fertile spikelet's per panicle, total spikelet's per panicle, spikelet fertility percent, test weight and positively but non-significantly correlated with plant height. The character productive tillers per plant had highest positively significant correlation with grain yield per plant. And it is found that there is no character which is negatively correlated with the grain yield per plant. Days to 50 percent flowering indicated positive and significant correlation with plant height, fertile spikelet's per panicle, total spikelet's per panicle, spikelet fertility percent and grain yield per plant. Similarly plant height observed positive significant correlated with panicle length, fertile spikelet's per panicle, panicle length with test weight and grain yield per plant, productive tillers per plant with grain yield per plant. Fertile spikelet's per panicle with total spikelet's per panicle, spikelet fertility percent and grain yield per plant. Total spikelet's per panicle with spikelet fertility percent and grain yield per plant. Spikelet fertility percent with grain yield per plant. 1000 grain weight (test weight) with grain yield per plant. Number of productive tillers per plant exhibit positive association with grain yield per plant, panicle length and number of productive tillers per plant, also exhibited high direct effect on yield. This result was in conformity with the earlier findings of Babu et al. (2012) [5], Amit et al. (2014) [2] and Ramanjaneyulu et al. (2014) [23]. Correlation analysis of yield contributing characters shows that all the characters under study were significantly and positively correlated with grain yield per plant except, plant height. These results were agreement with Dhakal et al. (2017) [11], Iqbal et al. (2018) [15]. Similarly, grain yield was significantly positively correlated with panicle length. This result was in conformity with the findings of Kamana et al. (2019) [17]. Spikelet fertility percentage, days to 50% flowering, plant height and 1000 grain weight had positive direct effect on grain yield. Similar kind of association was also revealed by Nithya et al. (2020) [20].

In present experiment, the character total spikelet per panicle observed highest direct positive effect on grain yield per plant and followed by spikelet fertility percent, test weight, productive tillers per plant and panicle length. Hence direct selection for these characters will be beneficial for yield improvement programme. The characters days to 50 percent flowering, plant height and fertile spikelet per panicle showed negative but non-significant direct effect on grain yield per plant. These findings was similar with reports of Babu et al. (2012) [5] for panicle length and number of productive tillers per plant which had shown higher positive direct effects on grain yield. Bhadru et al. (2012) [7] reported panicle length and productive tillers per plant recorded maximum positive direct effect to yield. Similar types of findings were reported by Singh and Ekka (2019) [27] for percentage of spikelet fertility also, findings were reported by Nithya et al. (2020) [20] for spikelet fertility percentage. The residual effect determines how well the causal factors account for the variability of the dependent factors, in this case, the grain yield. The residual effect in the current study was relatively low (0.1035), indicating that the characters selected were sufficient for explaining variability in rice grain yield.

Table 1: Genotypes and their pedigree

Sr. No.	Entry No.	IET No.	Designation	Cross Combination	Grain Type	Source
				AVT2/1 Biofort 2021		
1	4501	28701 (R)	GNV 1905	Selection from IR 95097:3-B-16-11-4-GBS	LS	AICRP Trial -2021
2	4503	--	BPT 5204	GEB24xTN1xMahsuri	MS	AICRP Trial -2021
3	4504	28694 (R)	GNV 1906	Selection from IR 99290-11-2-2	LB	AICRP Trial -2021
4	4506	28703 (R)	RP 6362-IR15M1298 (GID:4289666)	IR 91145-AC 26 / IRRI 123 // OM 4498 /// IR 58 /4/ IR 69428-6-1-1-3-3 / IR 69807-13-2-1 // IR 58	LS	AICRP Trial -2021
5	4507	--	DRR Dhan 45	IR 73707-*45*-3-2-3x IR 77080-B-34-3	LS	AICRP Trial -2021
6	4509	--	IR-64	IR5657-33-2-1/IR2061-465-1-5-5	LS	AICRP Trial -2021
7	4510	--	Chittimutyalu	Local landrace	SS	AICRP Trial -2021
8	4511	27984	HURS 17-6-IR 82475-110-2-2-1-2	IR 68144-2B-2-2-3-1-120/IR64	LS	AICRP Trial -2021
			IVT- Biofort 2021			
9	4601	29460 (R)	NVSR 522	NVSR-303 / IRRI-AMT-301	SB	AICRP Trial -2021
10	4602	29482 (R)	RP 6211-PR/RIL-Q181	PR116/Ranbir Basmati	MB	AICRP Trial -2021
11	4603	29469 (R)	CSR HZR 17-42	Fedearroz 50/IR07F287 // IR 45427-2B-2-2B-1-1 / NSIC RC 158 /// Sanhuangzhan No 2 / IR 4630-22-2-5-1-3 // IRRI 123 / IR 77298-14-1-2-10 / 4 / Fedearroz 50 / IR 4630-22-2-5-1-3 /// IRRI 123 / Sanhuangzhan No 2 /// IR 77298-14-1-2-10 / NSIC RC 158 // IR 45427-2B-2-2B-1-1 / IR07F287 / 5 / FED	LS	AICRP Trial -2021
12	4605	30118	HURS 21-7-IR 105696-1-2-3-1-1-1-B	IR 102831/SARO 5	LS	AICRP Trial -2021
13	4606	30119	NVSR 526	NVSR 303 / IET 22121	MS	AICRP Trial -2021
14	4611	30124	RP 6195-MC/RIL-A147	MTU 1010 / Chittimuthyalu	SB	AICRP Trial -2021
15	4614	30125	HURS21-6-IR 08195-3-1-1-2	IR 106293 / IR 106294	LS	AICRP Trial -2021

16	4615	29484 (R)	RP 6204-MB/RIL-J159	MTU 1010 / BR 2655	SS	AICRP Trial -2021
17	4619	30129	R-RHZ-IA-99	IBD / Abhaya	SB	AICRP Trial -2021
18	4622	30132	CSR HZR 23-1	IR 68144-2B-2-2-3-1-166 / Joryeongbyeo // BR 802-118-4-2 (BRRI Dhan 29) /// Basmati 370 (ACC 6426) / 4 / IR 72967-12-2-3 / 5 / IR05A193 / IR 75862-206-2-8-3-B // II 69428-6-1-1-3-3 /// IR 05A199 / Joryeongbyeo // IR 69428-6-1-1-3-3 / 4 / IR 00A117 / 6 /IR 07F289 / 29 IR 69428-6-1-1-3-3 // IR 09	LS	AICRP Trial -2021
19	4626	29465 (R)	CSR HZR 17-8	Fedearroz 50 / IR 77298-14-1-2-10 // IRRI123 / IR07F287 /// Sanhuangzhan No 2 / NSIC RC 158 // IR 45427-2B-2-2B-1-1 / IR 4630-22-2-5-1-3 / 4 / IRRI 123 / Sanhuangzhan No 2 // IR 77298-14-1-2-10 / IR07F287 /// NDIC RC 158 / IR 4630-22-2-5-1-3 // Fedearroz 50 / IR 45427-2B-2-2B-1-1 / 5 / FED	MS	AICRP Trial -2021
20	4628	30136	HURS-21-3-IR128773-4-4-2-3-B	IR 69428-6-1-1-3-3 / Rajendra Mahsuri	LB	AICRP Trial -2021
21	4630	30138	BRR-0184-1-IR 108194-9-1-2-1	IR 106292 / IR 106295	LS	AICRP Trial -2021
22	4633	30141	NVSR 3148	IR 28 / Lal Kada	SB	AICRP Trial -2021
23	4635	30143	RP5401-JBB-B-622-3-1-1-1-1	Swarna / IRGC 63248 // DSB 3	MS	AICRP Trial -2021
24	4639	30146	CR 4365-1-IR 128768-7-2-2-5	IR 68144-2B-2-2-3-1-166 / Sambha Mahsuri	MS	AICRP Trial -2021
25	4641	30148	RP 6204-MB/RIL-J65	MTU 1010 / BR 2655	SS	AICRP Trial -2021
26	4649	30156	RP 6196-PC/RIL-B162	PR 116 / Chittimuthyalu	SB	AICRP Trial -2021
27	4651	30158	RP 6253-MV/RIL-MV 208	MTU 1010 / Varadhan	SB	AICRP Trial -2021
28	4652	30159	RP6514-IR128768-7-2-2-4	IR 68144-2B-2-2-3-1-166 / Samba Mahsuri	SS	AICRP Trial -2021
29	4653	30160	RP 4993-BC/RIL-Z102	BPT 5204 / Chittimuthyalu	MS	AICRP Trial -2021
30	--	--	Karjat-4	IR 22 x Zinia 63	SS	RARS, Karjat
31	--	--	PDKV Red Rice-1	Selection from local Ludaka	SS	ARS, Sakoli
32	--	--	Phule Samruddhi	Indrayani x Sonsali	LS	ARS, Vadgaon
33	--	--	Indrayani	Ambemohar-157 x IR-8	LS	ARS, Vadgaon
34	--	--	Pawana	Pusa 33 x IR-28	LS	ARS, Vadgaon
35	--	--	Phule Maval	Pawana x Indrayani	LB	ARS, Vadgaon
36	--	--	Kundalika	Ratnagiri-24 x IET 3228	SS	ARS, Vadgaon
37	--	--	Bhogawati	RPSP328(Introduction)	LS	ARS, Radhanagari
38	--	--	VDN-1832	VDN-1206 x CB 06-555	SS	ARS, Vadgaon
39	--	--	Phule Radha	TN-1 x Kolamba-540	SS	ARS, Radhanagari
40	--	--	Ambemohar-157	Selection from Ambemohar	SB	ARS, Vadgaon
41	--	--	IGP-13-12-19	Mutant of Pawana	LS	ZARS, Igatpuri

Table 2: Analysis of variance for 11 different characters

Sr. No.	Characters	Mean sum of square		
		Replication	Treatments	Error
		(d.f.1)	(d.f.40)	(d.f.40)
1.	Days to 50% flowering	18.56	114.97**	2.57
2.	Plant height	1.97	525.29**	25.56
3.	Panicle length	2.74	13.87**	0.64
4.	Productive tillers/plant	1.19	2.09**	0.31
5.	Fertile spikelets/panicle	1705.80	1612.29**	59.50
6.	Total spikelets/panicle	1615.80	1798.75**	82.25
7.	Spikelet fertility %	16.70	33.83**	3.31
8.	1000 grain weight	1.01	28.53**	1.44
9.	Grain yield/plant	0.66	66.23**	1.04
10.	Grain iron (Fe) content	15.28	280.38**	7.84
11.	Grain zinc (Zn) content	2.70	326.48**	13.10

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

Table 3: Estimates of genetic variability parameters for 11 different characters of rice genotypes

Sr. No.	Name of the Character	Range	Mean	G.C.V. (%)	P.C.V. (%)	Heritability (h2) (bs) %	Genetic Advance (at 5% K)	GA as % of mean (at 5% K)
1.	Days to 50% flowering	82.00 – 116.50	96.50	7.76	7.94	95.60	15.10	15.64
2.	Plant height	75.70 – 172.60	100.02	15.80	16.59	90.70	31.01	31.00
3.	Panicle length	17.05 – 28.75	22.64	11.35	11.89	91.20	5.05	22.34
4.	Productive tillers/plant	6.25 – 9.85	7.69	12.28	14.26	74.10	1.67	21.78
5.	Fertile spikelets/panicle	89.00 – 201.00	136.17	20.46	21.23	92.90	55.31	40.62
6.	Total spikelets/panicle	109.00 – 221.50	155.59	18.82	19.71	91.30	57.65	37.05
7.	Spikelet fertility %	80.10 – 95.85	87.32	4.47	4.93	82.20	7.29	8.35
8.	1000 grain weight	11.25 – 23.65	19.26	19.10	20.09	90.40	7.20	37.41
9.	Grain yield/plant	9.95 – 33.50	17.78	32.11	32.61	96.90	11.57	65.12
10.	Grain iron(Fe) content	20.70 – 66.35	37.49	31.13	32.02	94.60	23.38	62.37
11.	Grain zinc(Zn) content	22.45 – 68.40	46.29	27.03	28.14	92.30	24.77	53.50

Table 4: Genotypic correlation coefficients of 8 characters of 41 genotypes of rice on grain yield

Sr. No.	Days to 50% flowering	Plant Height	Panicle Length	Productive tillers per plant	Fertile spikelets per panicle	Total spikelets per panicle	Spikelet Fertility %	Test weight	Grain yield per plant
	1	2	3	4	5	6	7	8	9
1.	1.0000	0.3488**	0.1818	0.0555	0.5392**	0.4892**	0.4603**	-0.1501	0.3171**
2.		1.0000	0.4913**	-0.0603	0.2235*	0.2067	0.1771	0.0583	0.1903
3.			1.0000	-0.0471	-0.0523	-0.0697	0.0003	0.4095**	0.2974**
4.				1.0000	0.1982	0.1770	0.1280	-0.0642	0.5732**
5.					1.0000	0.9811**	0.4734**	-0.4045	0.5101**
6.						1.0000	0.2974**	-0.4441	0.4519**
7.							1.0000	0.0336	0.4570**
8.								1.0000	0.4378**

Table 5: Direct (diagonal) and indirect (above and below diagonal) path effects of different characters towards grain yield at genotypic level in rice

Sr. No.	Days to 50% flowering	Plant Height	Panicle Length	Productive tillers per plant	Fertile spikelet per panicle	Total spikelet per panicle	Fertility %	Test weight	Grain Yield per plant
	1	2	3	4	5	6	7	8	9
1.	-0.0340	-0.0119	-0.0062	-0.0019	-0.0183	-0.0166	-0.0157	0.0051	0.3171**
2.	-0.0196	-0.0563	-0.0277	0.0034	-0.0126	-0.0116	-0.0100	-0.0033	0.1903
3.	0.0276	0.0745	0.1516	-0.0071	-0.0079	-0.0106	0.0001	0.0621	0.2974**
4.	0.0281	-0.0306	-0.0239	0.5068**	0.1004	0.0897	0.0649	-0.0326	0.5732**
5.	-1.3752	-0.5701	0.1334	-0.5054	-2.5506	-2.5024	-1.2075	1.0318	0.5101**
6.	1.4646**	0.6189**	-0.2087	0.5300**	2.9374**	2.9940**	0.8905**	-1.3297	0.4519**
7.	0.3277**	0.1261	0.0002	0.0911	0.3370**	0.2117	0.7118**	0.0239	0.4570**
8.	-0.1021	0.0397	0.2787*	-0.0437	-0.2753	-0.3022	0.0229	0.6805**	0.4378**

(Residual effect = 0.1035) *, ** Significant at 5 and 1 percent, respectively

Conclusion

In the current study grain yield per plant and grain iron (Fe) content observed high magnitude of GCV and PCV this indicates that there is opportunity for improvement through selection. There was a high heritability (h2) (b. s.) with a high genetic advance (GA) as percent of mean for the traits grain yield per plant, grain iron (Fe) content, grain zinc (Zn) content, fertile spikelet's per panicle, 1000 grain weight, total spikelet's per panicle, plant height and days to 50 percent flowering showed that these characters were primarily governed by additive gene action, and selecting for these traits would be more effective in achieving desired genetic improvement. Grain yield per plant was observed significant and positive correlation with days to 50 percent flowering, panicle length, fertile spikelet's per panicle, total spikelet's per panicle, spikelet fertility, test weight and highly significant with productive tillers per plant. Plant Height showed non-significant positive correlation with grain yield per plant. There is no character which is negatively correlated with the grain yield per plant character and total spikelet's per panicle has significant direct effect on grain yield and positive indirect effect through days to 50 percent flowering, plant height, productive tillers per plant, fertile spikelet's per panicle, spikelet fertility percent and grain yield per plant. In the path analysis, highest and significant positive direct effect on grain yield per plant was showed through total spikelet per panicle followed by spikelet fertility percent, test weight, productive tillers per plant and panicle length. The trait panicle length also showed positive but non-significant direct effect on grain yield per plant. The direct selection to these traits will be beneficial for yield improvement programmes. Taking into consideration, overall indirect effect all the studied characters contributed indirectly towards grain yield per plant.

The study indicated high heritability and genetic advance as percent of mean for grain yield plant[-1], zinc content, iron content, plant height and days to 50 percent flowering indicating the effectiveness of direct selection for improvement of these traits. Among these, grains panicle[-1] and zinc content were recorded high positive direct effect coupled with significant and positive correlation with grain yield plant[-1]. Hence, these traits are identified as effective selection criterion for effecting grain yield improvement in the zinc and iron rich landraces of rice.

Conflict of interest
All authors declare that they have no conflict of interest.

References
1. Akshaya M, Thirumurugan T, Chitra S, Nithila S, Jeyaprakash P. Genetic variability in rice (*Oryza sativa* L.) landraces for seedling vigour traits. Electron J Plant Breed. 2020;11(1):91-96.
2. Amit PR, Ashish Singh G, Suresh Babu GR, Lavanya, Yuvraj Yadav. Diversity analysis of local land races and improved germplasm of rice (*Oryza sativa* L.). Ind J Applied Res. 2014;4:2249-555.
3. Anbanandan V. Yield and its component traits association in diverse genotypes of rice (*Oryza sativa* L.). J Pharmacogn Phytochem. 2018;7(1S):75-77.
4. Asante MD, Adjah KL, Afful EA. Assessment of genetic diversity for grain yield and yield component traits in some genotypes of rice (*Oryza sativa* L.). J Crop Sci Biotech. 2019;22(2):123-130.
5. Babu VR, Shreya K, Dangi KS, Usharani G, Shankar AS. Correlation and path analysis studies in popular rice hybrids of India. Int J Sci Res Publ. 2012;2(3):1-5.
6. Bandumula N. Rice production in Asia: key to global food security. Proc Natl Acad Sci India Sect B Biol Sci. 2018;88:1323-1328.
7. Bhadru D, Rao VT, Mohan YC, Bharathi D. Genetic variability and diversity studies in yield and its

component traits in rice (*Oryza sativa* L.). SABRAO J Breed Genet. 2012;44(1).

8. Burton GW. Quantitative inheritance in grasses. Proc Sixth Int Grassl Congr. 1952;1;2:277-283.

9. Cakmak I. Enrichment of cereal grains with zinc: agronomic or genetic biofortification. Plant Soil. 2008;302:1-17.

10. Dewey DR, Lu K. A correlation and path-coefficient analysis of components of crested wheatgrass seed production. Agron J. 1959;51(9):515-518.

11. Dhakal R, Yadav RK, Paudel DP, Deosarkar DB. Studies on genetic divergence and reaction to iron chlorosis in aerobic rice on vertisols in Maharashtra. J Plant Stress Physiol. 2017;3:12-21.

12. Directorate of Economics and Statistics, Department of Agriculture and Farmers Welfare, Ministry of Agriculture and Farmers Welfare, Government of India. [Internet] Available from: https://eands.dacnet.nic.in/Advance_Estimates.htm.

13. Divya J, Raju CD, Rao LS, Aparna K. Genetic variability studies in genetically diverse rice genotypes. Int J Curr Microbiol Appl Sci. 2018;7(4):1169-1172.

14. Genotypes of Rice (*Oryza sativa* L.). Int J Curr Microbiol Appl Sci. 2019;8(4):1832-1837.

15. Iqbal T, Hussain I, Ahmad N, Nauman M, Ali M, Saeed S, Ali F. Genetic variability, correlation and cluster analysis in elite lines of rice. J Sci Agric. 2018;2:85-91.

16. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. Agron J. 1955;47(7):314-318.

17. Kamana B, Ankur P, Subarna S, Prasad KB, Koshraj U. Genetic variability, correlation and path analysis of rice genotypes in rainfed condition at Lamjung, Nepal. Russ J Agric Soc Econ Sci. 2019;92(8):274-280.

18. Lalitha R, Mothilal A, Arunachalam P, Senthil N, Hemalatha G. Genetic variability, correlation and path analysis of grain yield, grain quality and its associated traits in EMS derived M4 generation mutants of rice (*Oryza sativa* L.). Electron J Plant Breed. 2019;10(3):1140-1147.

19. Maurya RK, Dwivedi DK, Khan NA, Giri SP, Dixit S. Genetic variability studies for qualitative and quantitative traits in rice (*Oryza sativa* L.). Pharma Innov J. 2022;11(5):1140-1143.

20. Nithya N, Beena R, Abida PS, Sreekumar J, Stephen R, Jayalekshmi VG, *et al*. Genetic diversity and population structure analysis of bold type rice collection from southern India. 2021 Jun;49:311-328.

21. Panigrahi AK, Bharathi M, Kumaravadivel N. Genetic variability and character association studies in advanced backcross generation of rice (*Oryza sativa* L.). J Pharmacogn Phytochem. 2018;7(1):2397-2400.

22. Panse VG, Sukhatme PV. Statistical methods for agricultural workers. ICAR, New Delhi. 1995.

23. Ramanjaneyulu AV, Shankar GV, Neelima T, Shashibhusahn D. Genetic analysis of rice (*Oryza sativa* L.) genotypes in aerobic conditions on alfisols. SABRAO J Breed Genet. 2014;46(1):99-111.

24. Roy A, Hijam L, Roy SK. Genetic variability and character association studies for quality attributing traits in rice (*Oryza sativa* L.). Electron J Plant Breed. 2021;12(4):1201-1208.

25. Shaili MR, Kumar GV, Lal GM, Lavanya GR. Assessment of genetic diversity in rice (*Oryza sativa* L.) genotypes for grain yield characters. Int J Environ Clim Change. 2022;12(11):1113-1122.

26. Singh A, Ekka RE. Correlation and path analysis in aromatic and pigmented rice. 2019;8:1832-7

27. Singh RK, Chaudhary BD. Biometrical methods in quantitative genetic analysis. Biometrical; c1977.

28. Verma DD, Hota M, Randhawa GJ, Bhalla S, Chalam VC, Tyagi V. Document on biology of rice (*Oryza sativa* L.) in India. National Bureau of Plant Genetic Resources. Indian Council of Agricultural Research, New Delhi. Alpha Lithographics Inc. 2006.

29. Wissuwa M, Ismail AM, Graham RD. Rice grain zinc concentrations as affected by genotype, native soil-zinc availability, and zinc fertilization. Plant Soil. 2008;306:37-48.

30. Mustafa MA, Elsheikh MY. Variability, correlation and path co-eeficient analysis for yield and its components in rice. African Crop Science Journal. 2007;15(4): 183-189.