



Genetic Variability for Yield Components, Iron and Zinc contents in Rice (*Oryza sativa* L.) Genotypes

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Received: 15th July, 2024; Accepted: 12th October, 2024

Abstract

The experiment was carried out for 11 characters in 41 rice genotypes during *kharif* 2022 at Agricultural Research Station, Vadgaon Maval, Pune. The highest value of GCV (32.111) and PCV (32.618) observed for grain yield per plant and followed by grain iron (Fe) content, GCV (31.137) and PCV (32.021), grain zinc (Zn) content GCV (27.039) and PCV (28.147), fertile spikelets per panicle GCV (20.462) and PCV (21.232), 1000 grain weight GCV (19.104) and PCV (20.094). The grain yield per plant was observed as the highest broad sense heritability (96.90%) followed by days to 50% flowering (95.60%) and grain iron (Fe) content (94.60%). The highest genetic advance as per cent of mean was observed for the traits grain yield per plant (65.121), grain iron content (62.373), grain zinc content (53.509) and fertile spikelets per panicle (40.625). The significant positive correlation was observed among grain yield per plant and days to 50% flowering (0.3171), panicle length (0.2974), fertile spikelets per panicle (0.5101), total spikelets per panicle (0.4519), spikelet fertility (0.4570), test weight (0.4378) and productive tillers per plant (0.5732). High heritability with high genetic advance observed for the trait grain yield per plant, grain iron (Fe) content, grain zinc (Zn) content, fertile spikelets per panicle and total spikelets per panicle indicated additive gene actions. The total spikelet per panicle (2.9940) was observed that had highest direct positive effect on grain yield per plant and followed by spikelet fertility % (0.7118), test weight (0.6805), productive tillers per plant (0.5068) and panicle length (0.1516).

Key words: Variability, heritability, genetic advance, correlation, direct effect

Introduction

The *Oryza sativa* (rice) species are commonly divided into three subspecies namely; *Indica*, *Japonica* and *Javanica*. Rice (*Oryza sativa* L.) is one of the three leading cereals in the family Poaceae. It is cultivated during warm wet (*kharif*) and winter (*rabi*) seasons in the tropical and subtropical humid regions of the world. Rice is the staple food for a majority of the people of Asia, providing 50-60 per cent of the total calorie and 30 per cent of the total protein (Mackill *et al.*, 2012).

According to the FAO (2003) and ICMR (2009), the recommended daily allowance (RDA) for zinc and iron is 10 mg for children and 12-15 mg for adults. Due to their effects on growth and development, as

well as other physiological and neurophysiological processes, these micronutrients are important for health and medicine. According to estimates, 49 per cent of people worldwide fail to consume sufficient amounts of zinc. Micronutrients are necessary for both plants and animals to have a balanced diet. Additionally, micronutrients are essential for rice plants' ability to withstand abiotic stresses. From an agronomic perspective, zinc is important to rice for a number of reasons such as nitrogen assimilation and protein metabolism. Approximately 10% of proteins in plants require Zn for structural function and integrity. Low Zn supply limits the rice plant's ability to

convert amino acids to proteins. Iron (Fe) participates in several important metabolic processes such as photosynthesis, chloroplast development, chlorophyll biosynthesis, electron transport and redox reactions. The focus of the green revolution on increasing grain productivity resulted in a decrease in the amount of micronutrients available in a balanced diet. Most of the Iron and Zinc is found in rice bran-aleuronic layer and 80% of it gets removed in polishing. Hence it is essential to have genotypes with high Iron and Zinc content in endosperm.

The increase in rice production is crucial for providing food security. Understanding genetic variability in the experimental material offers a useful opportunity for selection (Singh *et al.*, 2020). Phenotypic variability is the differences between individuals in a population due to genetic composition and growing environment (Sumanth *et al.*, 2017). Planning and execution of any breeding program for improvement on quantitative traits depends on magnitude of genetic variability. Therefore, success on plant breeding activities entirely depends on the existence of genetic variability with respect to desired traits and selection skill of plant breeder (Adhikari *et al.*, 2018). Variability, genetic diversity, expected genetic advances and heritability of the traits are therefore key basis for genetic improvement of the trait.

The level of heritable variation in the traits studied is extremely useful in determining the genotype's potential for future breeding programs. Before planning an appropriate breeding strategy for genetic improvement, it is critical to assess variability for yield and its component characters (Singh *et al.*, 2011). For efficient crop development, understanding the nature and extent of genetic variation in quantitative traits such as yield and its components is critical. Heritability is the ratio of variation due to differences between genotypes to the total phenotypic variation for a trait in a population and shows the component of a character transmitted to future generations. Genetic

advance shows the difference between the mean genotypic values of selected population and the original population from which these were selected. Heritability estimates along with genetic advance is more precise in predicting the genetic gain under selection than heritability alone. In addition relationship between yield and yield attributing traits is prime important for direct and indirect selection of traits which contributes to yield (Aditya and Bhartiya, 2013). Although there are thousands of distinguished genotypes in cultivation, the diverse material available will give the scope to evolve the cultivars which are having potential for biotic and abiotic stresses along with good quality characters (Khan, 2018). The selected material from evaluations can be utilised for further hybridisation programme. Choosing high-yielding varieties purely on the basis of grain yield will be ineffective unless sufficient data on genetic characteristics is available to use them in hybridization programmes for the further improvement. In the selection process, information on character association, as well as the direct and indirect effects that each character has on yield, will be beneficial. The degree of the association between grain yield and its components, as well as the relative relevance of their direct and indirect effects, are revealed by correlation and path analysis, offering a comprehensive knowledge of their relationship with grain yield (Khan, 2018). About 176 million tons rice is required by 2035, which can be fulfilled by increasing yield potential from 10 to 12.3 tons per hectare (Khush, 2013).

Therefore, the present study was undertaken to know information on variability, heritability, genetic advance and traits correlation in promising rice genotypes to develop a high yielding rice genotype. Information on genetic variability is essential for selection, which is the ultimate tool in plant breeding. However, the selection is challenging due to the masking effect of non-heritable variation. Therefore, partitioning of the total variation to understand the



role of the heritable component is very important, which helps the breeder to formulate a sound breeding programme. Correlation is very important factor for any election program. Success in selection depends on the knowledge of the association of component traits with grain yield. However, partitioning the correlation coefficients through path analysis is very important to understand the cause-effect relationship. This helps in understanding the relative importance of component characters for improvement in seed yield of rice. Finally, this type of research could aid the breeder in developing selection strategies to improve grain yield. Given the above scenario, the current investigation is carried out with the objectives of studying the genetic variability, character association and path coefficients in rice genotypes for yield improvement.

Materials and Methods

The present investigation was carried out during *kharif* 2022 at Agricultural Research Station, Vadgaon Maval, Pune. In the present study, forty-one genotypes were assessed to study the variability and genetic parameters for yield and its components, iron and zinc content. 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 randomized 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

for days to 50% flowering was recorded on plots basis for each genotype in each replication. At maturity five plants from each accession were selected randomly for recording data on grain yield per plant and yield component traits, namely, plant height, productive tillers per plant, panicle length, grains per panicle and test weight. In contrast, observations for test weight and iron and zinc content traits were obtained from a random grain sample drawn from each plot and replication using standard procedures. The statistical analysis was done by standard statistical method suggested by Panse and Sukhatme (1995). 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). The estimates of PCV and GCV were classified as low (0-10%), moderate (10-20%) and high (>20%) according to Sivasubramanian and Madhavamenon (1973). Heritability in broad sense (h^2 b) was estimated according to the formula suggested by Johnson *et al.*, (1955) and Hanson *et al.*, (1956) and classified as low (0-30%), moderate (30-60%) and high (> 60%). Estimation of genetic advance was carried out following the formula given by Johnson *et al.*, (1955) and classified as low (< 10%), moderate (10-20%) and high (> 20%). The genotypic correlation coefficients were worked out by adopting the method described by Singh and Chaudhary (1977). Path coefficient analysis was done according to the procedure suggested by Dewey and Lu (1959).

Table 1: List of Rice genotypes used in the study

Sl. No	Entry	Source	Sl. No	Entry	Source	Sl. No	Entry	Source	Sl. No	Entry	Source
1	GNV 1905	AICRP Trial 2021	11	CSR HZR 17-42	AICRP Trial 2021	21	BRR-0184-1-IR 108194-9-1-2-1	AICRP Trial 2021	31	PDKV Red Rice-1	ARS, Sakoli
2	BPT 5204	AICRP Trial 2021	12	HURS 21-7-IR 105696-1-2-3-1-1-1-B	AICRP Trial 2021	22	NVSR 3148	AICRP Trial 2021	32	Phule Samruddhi	ARS, Vadgaon Maval
3	GNV 1906	AICRP Trial 2021	13	NVSR 526	AICRP Trial 2021	23	RP5401-JBB-B-622-3-1-1-1-1	AICRP Trial 2021	33	Indrayani	ARS, Vadgaon Maval
4	RP 6362-IR15M1298 (GID:4289666)	AICRP Trial 2021	14	RP 6195-MC/RIL-A147	AICRP Trial 2021	24	CR 4365-1-IR 128768-7-2-2-5	AICRP Trial 2021	34	Pawana	ARS, Vadgaon Maval

Sl. No	Entry	Source	Sl. No	Entry	Source	Sl. No	Entry	Source	Sl. No	Entry	Source
5	DRR Dhan 45	AICRP Trial 2021	15	HURS21-6-IR 08195-3-1-1-2	AICRP Trial 2021	25	RP 6204-MB/RIL-J65	AICRP Trial 2021	35	Phule Maval	ARS, Vadgaon Maval
6	IR-64	AICRP Trial 2021	16	RP 6204-MB/RIL-J159	AICRP Trial 2021	26	RP 6196-PC/RIL-B162	AICRP Trial 2021	36	Kundalika	ARS, Vadgaon Maval
7	Chittimutyalu	AICRP Trial 2021	17	R-RHZ-IA-99	AICRP Trial 2021	27	RP 6253-MV/RIL-MV 208	AICRP Trial 2021	37	Bhogawati	ARS, Radhanagari
8	HURS 17-6-IR 82475-110-2-2-1-2	AICRP Trial 2021	18	CSR HZR 23-1	AICRP Trial 2021	28	RP6514-IR128768-7-2-2-4	AICRP Trial 2021	38	VDN-1832	ARS, Vadgaon Maval
9	NVSR 522	AICRP Trial 2021	19	CSR HZR 17-8	AICRP Trial 2021	29	RP 4993-BC/RIL-Z102	AICRP Trial 2021	39	Phule Radha	ARS, Radhanagari
10	RP 6211-PR/RIL-Q181	AICRP Trial 2021	20	HURS-21-3-IR128773-4-4-2-3-B	AICRP Trial 2021	30	Karjat-4	RARS, Karjat	40	Ambemohar-157	ARS, Vadgaon
									41	IGP-13-12-19	ZARS, Igatpuri

Results and Discussions

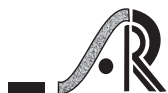
The amount of genetic diversity in the crop is measured by the genotypic coefficient of variation (GCV) as it represents the heritable component of variability. Additionally, the difference between genotypic and phenotypic expression gives the role of environmental in expression of that particular trait. The genotypic differences were significant for almost all the traits studied indicated that there was considerable amount of variability present in genotypes (**Table 2**). The estimates of genotypic coefficient of variation, range of variability and phenotypic coefficients of variation, the percentage of heritability in a broad sense and the genetic advance reported as a percentage of mean are given in

Table 3. For each of the traits examined in the current analysis a significant range of variance was observed. In forty-one (41) genotypes, the total spikelets per panicle ranged from 109.00-221.50 followed by fertile spikelets per panicle (89.00-201.00), plant height (75.70-172.60 cm), grain zinc content (22.45-68.40 ppm), grain iron content (20.70-66.35 ppm), days to 50% flowering (82.00-116.50), grain yield per plant (9.95-33.50 g), spikelet fertility % (80.10-95.85), 1000 grain weight (11.25-23.65 g), panicle length (17.05-28.75 cm) and productive tillers per plant (6.25-9.85). This indicated that there was a large amount of variation for these traits (Maurya *et al.*, 2022 and Divya *et al.*, 2018).

Table 2: Analysis of variance for eleven different characters

Sl. No.	Characters	Mean sum of square		
		Replication (d.f.1)	Treatments (d.f.40)	Error (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



For all characters, it was observed that the values for genotypic coefficients of variation (GCV) were lower than phenotypic coefficients of variation (PCV) (**Table 3**) indicated that these traits were considerably influenced by environments. The trait 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 broad difference between GCV and PCV were observed for productive tillers per plant indicated that the trait influenced more by environment whereas, days to 50% flowering, spikelet fertility and grain yield per plant recorded

narrow difference that indicated less influence of environment. High GCV and PCV were observed for grain yield per plant followed by grain iron content, grain zinc content and fertile spikelets per panicle. Moderate GCV and PCV were observed for 1000 grain weight, total spikelets per panicle, plant height, productive tillers per plant and panicle length. The trait days to 50% flowering recorded low GCV and PCV. Roy *et al.*, (2021) and Maurya *et al.*, (2022) also reported high GCV and PCV for grain yield per plant and moderate GCV and PCV for 1000 grain weight, total spikelets per panicle, plant height and productive tillers per plant.

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

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

Genetic advance and heritability are recognised as important selection parameters. According to Burton (1952), combining genetic advance with heritability estimates, would provide a better idea for effective selection. Heritability is a reliable indicator that shows the transmission of parental values to their offspring. The plant breeder can pick superior traits from diverse genetic groups using the heritability estimates. The high heritability values were recorded for grain yield per plant (96.90%) followed by days to 50% flowering (95.60%), grain iron (Fe) content (94.60%), fertile

spikelets per panicle (92.90%), grain zinc (Zn) content (92.30%), total spikelets per panicle (91.30%), panicle length (91.20%), plant height (90.70%), 1000 grain weight (90.40%), spikelet fertility % (82.20%) and productive tillers per plant (74.10%) character. High heritability estimates suggested that these characters were least influenced by the environment. Similar results were obtained by Divya *et al.*, (2018) for the characters number of productive tillers per plant, 1000 grain weight, number of grains per panicle and grain yield per plant and Shaili *et al.*, (2022) for grain

yield per plant, number of panicles, test weight and plant height.

The highest genetic advance (GA) as per cent of mean was observed for the trait grain yield per plant (65.121) followed by grain iron (Fe) content (62.373), grain zinc (Zn) content (53.509), fertile spikelets per panicle (40.625), 1000 grain weight (37.418), total spikelets per panicle (37.054) and plant height (31.009). The moderate genetic advance (GA) as per cent of mean was exhibited by the traits such as panicle length (22.342), productive tillers per plant (21.787) and days to 50% flowering (15.649). The low values were recorded by the trait spikelet fertility % (8.354). High heritability (h^2) with moderate genetic advance as per cent of mean showed for the characters fertile spikelets per panicle, total spikelets 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. High heritability (h^2) 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 spikelets per panicle, 1000 grain weight, total spikelets 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 for these traits for improvement of genotype. Panigrahi *et al.*, (2018) reported additive gene action for 1000 grain weight and Shaili *et al.*, (2022) for test weight, grain yield and plant height.

Correlation studies

The genotypic correlation coefficient values between yield and its related characters are presented in **Table 4**. The highest and significant positive correlation of grain yield per plant was found with productive tillers per plant (0.5732) followed by fertile spikelets per panicle (0.5101), spikelet fertility (0.4570), total spikelets per panicle (0.4519), test weight (0.4378), days to 50% flowering (0.3171) and panicle length (0.2974). Plant height (0.1903) showed non-significant positive correlation with grain yield per plant. When making selections to improve yield, it is recommended that these characters be given top priority. Similar type of associations were reported earlier by Pachauri *et al.*, (2017) for days to 50% flowering, panicle length and number of productive tillers per plant. All the studied characters had a positive correlation with grain yield per plant.

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

Sl. No.	Days to 50% flowering	Plant height (cm)	Panicle Length (cm)	Productive tillers per plant	Fertile spikelets per panicle	Total spikelets per panicle	Spikelet Fertility %	Test weight (g)	Grain yield per plant (g)
	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**
9.									1.0000

*, ** Significant at 5(0.2172) and 1(0.2829) per cent, respectively



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 Ramanjaneyulu *et al.*, (2014). 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 Iqbal *et al.*, (2018). Kamana *et al.*, (2019) reported positive direct effect of spikelet fertility, days to 50% flowering, plant height and 1000 grain weight on grain yield.

Path analysis: The path coefficient evaluation using genotypic correlation indicates the interrelationships between the characters, which are illustrated in **Table 5**. The character total spikelet per panicle (2.9940) showed highest direct positive effect on

grain yield per plant followed by spikelet fertility % (0.7118), test weight (0.6805), productive tillers per plant (0.5068) and panicle length (0.1516). Hence, direct selection for these characters will be beneficial for yield improvement programme. The characters days to 50% flowering (-0.0340), plant height (-0.0563) and fertile spikelet per panicle (-2.5506) observed negative direct effect on grain yield per plant. Similar types of findings were reported by Singh and Ekka (2019). Days to 50 per cent flowering showed positive correlation with grain yield per plant (0.3171) but it showed negative indirect effect with plant height (-0.0119), panicle length (-0.0062), productive tillers per plant (-0.0019), fertile spikelet per panicle (-0.0183), total spikelet per panicle (-0.0166) and spikelet fertility % (-0.0157). Days to 50% flowering showed positive indirect effect with test weight (0.0051).

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

Sl. No.	Days to 50% flowering	Plant Height (cm)	Panicle length (cm)	Productive tillers per plant	Fertile spikelet per panicle	Total spikelet per panicle	Spikelet Fertility %	Test Weight (g)	Grain Yield per plant (g)
	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 per cent, respectively

Productive tillers per plant showed significant positive correlation (0.5732) with grain yield, it also had the significantly positive direct effect (0.5068) on grain yield. The character influences the yield positively indirect effect with days to 50% flowering (0.0281), fertile spikelet per panicle (0.1004), total spikelet

per panicle (0.0897), spikelet fertility % (0.0649). It also had negative indirect effect on grain yield with plant height (-0.0306), panicle length (-0.0239) and test weight (-0.0326). Total spikelets per panicle had significant positive direct effect (2.9940) on grain yield per plant and indirect effect through days to

50% flowering (1.4646), plant height (0.6189), productive tillers per plant (0.5300), fertile spikelets per panicle (2.9374) and spikelet fertility (0.8905). It also observed that character had negative indirect effect like Panicle Length (- 0.2087) and Test weight (-1.3297). Test weight had positive direct effect (0.6805) on grain yield per plant and had positive significant correlation (0.4378) on grain yield. It had positive indirect effect through plant height (0.0397), panicle length (0.2787), spikelet fertility % (0.0229).

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. The productive tillers per plant, total spikelet per panicle, spikelet fertility % and test weight identified as important components of rice grain yield. Similar type of association was recorded by Akinwale *et al.*, (2011) for productive tillers per plant and test weight and, Hasan *et al.*, (2011) for productive tillers per plant, spikelet fertility % and test weight and,

Conclusion

The trait grain yield per plant and grain iron content observed high magnitude of GCV and PCV this indicates that there is opportunity for improvement through selection. There was a high heritability with a high genetic advance as per cent of mean for the traits grain yield per plant, grain iron content, grain zinc content, fertile spikelets per panicle, 1000 grain weight, total spikelets per panicle, plant height and days to 50 per cent flowering indicated 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 had significant and positive correlation with days to 50 per cent flowering, panicle length, fertile spikelets per panicle, total spikelets per panicle, spikelet fertility, test weight and productive

tillers per plant. In the path analysis, highest and significant positive direct effect on grain yield per plant was recorded through total spikelet per panicle followed by spikelet fertility per cent, test weight, productive tillers per plant and panicle length. The direct selection of these traits will be beneficial for yield improvement programmes.

Acknowledgements

The authors are thankful to the Director, ICAR-IIRR, Hyderabad, Rice Specialist, RARS, Karjat, Officer In-charge, ARS, Radhnagari, ZARS, Igatpuri, ARS, Sakoli and ARS, Vadgaon Maval for supply of seed material.

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