Variability and divergence studies on rice genotypes for micronutrient potential and its utility in biofortification

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ARTICLE INFO	ABSTRACT
	Rice is the staple food crop for more than half of the world population. Thus, rice varieties enriched with various micronutrients qualifies as a better alternative to combat micronutrient deficiency. The present investigation was undertaken to study the variability, heritability and genetic divergence for grain characters especially grain Zinc (Zn) content and grain Iron (Fe) content in 30 genotypes of rice. Among the 30 genotypes that were under investigation, the Phenotypic Coefficient of Variation (PCV) values were found to be higher than that of Genotypic Coefficient of Variation (GCV) values for all the traits. High heritability (>60%) was observed for all the studied traits. Days to 50% flowering showed highest heritability (99.1%) followed by test weight (94.8%) and grain Fe content (94.8%). The genetic advance as percent of mean ranged between medium (10%-20%) to high (>20%) with grain yield per plant showing the highest GAM (40.84%) followed by test weight (38.56%) and grain Zn content (33.73%). These 30 genotypes were assigned into groups of 11 clusters using Tocher's method. Cluster I comprised of the most number of genotypes with 18 genotypes followed by Cluster V with 3 genotypes while the remaining 9 clusters were monogenotypic. Days to 50% flowering was found to have the highest contribution towards genetic divergence. These findings indicated that the genotypes under study have sufficient trait variability and varietal diversity which could be exploited in crop improvement programmes aimed at developing Zinc (Zn) and Iron (Fe) biofortified varieties.

Introduction

Rice (*Oryza sativa L.*) is the single most important staple crop of the world. Asia is second to none in terms of production and constitutes 90% of the global rice cultivation area (Singh *et al.*, 2018).India produced an estimated 117.94 Mt of grain with a productivity of 2.7 t/ha during the 2019-2020 season. Although rice production is high in India, productivity is meagre compared to other major producers such as China (6.5 t/ha) and Indonesia (5.2 t/ha) (MoA and FW, 2019-2020).Though the progress in rice production has moved forward by leaps and bounds, there is still a necessity to increase production and productivity to meet the needs of the growing population. However, feeding the ever growing population is not the only concern; we should also ensure the

nutritional security especially with respect to essential micronutrients, vitamins and proteins as micronutrient deficiency is a major issue plaguing developing countries like India (Bain *et al.*, 2013). According to a survey by the WHO (2002), more than two billion people are afflicted with micronutrient deficiencies. Development of rice cultivars that possess substantial yield with ample amount of micronutrients could create an avenue for solving two problems with a single solution. In view of these various hurdles and predicaments, this present research was undertaken to study variability, heritability and genetic divergence in 30 genotypes of rice to explore their potential for utility in crop improvement programmes aimed at yield increments along with biofortification.

Material and Methods

The present investigation was undertaken at Research farm, RPCAU, Pusa, Bihar during *Kharif* 2019-2020. The experimental materials comprised of 30 rice genotypes, of which 29 were test entries and one check entry. The test entries were acquired from Harvest Plus programme, ICRISAT, Hyderabad while the local check entry was taken from Rice breeding section, Department of Plant Breeding and Genetics, RPCAU, Pusa, Samastipur, Bihar. 21 days old seedlings were transplanted in an experimental unit of $5m^2$ atspacing of 20cm apart between rows and 15cm apart between plants. Randomized Complete Block Design was followed with three replications. Standard agronomic practices along with plant protection measures were followed to raise healthy crop stand. Eleven quantitative traits were taken into consideration for the present study. The observations on traits like plant height, number of panicles per plants, panicle length and grain yield per plant were taken by selecting 5 random plants from each plot while number of days to 50% flowering was recorded on a plot basis. Observation on test weight, kernel length, kernel breadth, kernel L/B ratio, grain Iron content and grain Zinc content was recorded from seeds taken from bulk harvest of individual plot. An instrument known as Energy Dispersive X-Ray Fluorescence(ED-XRF) was used for estimation of the grain Iron and Zinc content. The computed mean data for each character was subjected to analysis for variance following methods illustrated by Panse and Sukhatme (1985), genotypic (GCV) and Phenotypic (PCV) coefficients of variation according to the formula as illustrated by Burton (1952), Broad sense heritability as per the formula given by Lush (1940) and Genetic Advance as per cent of mean according to Johnson *et al.* (1955). Genetic Divergence among the thirty genotypes was estimated using D^2 analysis proposed by Mahalanobis (1936). The genotypes were grouped into several clusters in accordance with Tocher's method (Rao, 1952).

Results and Discussion

The results obtained from the analysis of variance (Table 1) indicated that the genotypes under investigation varied significantly for all 11 quantitative traits that were studied ($p < 0.01$). Similar findings were reported by Singh *et al.* (2017) for traits like kernel length and kernel breadth. The perusal of the data on coefficients of variation revealed that for all of the traits examined, GCV and PCV estimates were greater than their corresponding GCV estimates in the current study. GCV and PCV values for kernel breadth (6.82%and 8.41%), kernel length (7.06%and 7.32%), kernel L/B ratio (8.26%and 9.48%), plant height (9.41% and 9.7%) and panicle length (9.66%and 10.63%) were found to be low, ranging from 10% to 20%. Similar findings were reported by Singh *et al.* (2020). Moderate values of GCV and PCV were observed for test weight (19.22% and 19.74%), number of panicles per plant (15% and 18.94%), days to 50% flowering (12.39 and 12.45%), grain Fe content (15.80% and 16.22%) and grain Zn content (17.52% and 18.76%). A similar finding for panicle length, test weight and days to 50% flowering was documented by Khan *et al.* (2009). These findings were also in concordance with the findings of Raza *et al.* (2019) as they reported ample amount of variability in grain Iron and Zinc content.The resultant GCV and PCV value for grain yield per plant (20.71% and 21. 65%) was determined to be high with a value greater than 20%. Similar findings of high GCV and PCV values had been previously reported by Bekele *et al.* (2013) for grain yield. It was observed that the values of PCV and GCV were in a close range for almost all of the traits studied during the investigation inferring that environment had little impact on the expression of these traits. The greatest ECV value was observed in number of panicles suggesting that of all the traits studied, it is the most influenced by the environment.

Table 1: Analysis of variance (ANOVA) for 11 quantitative traits in Rice

Traits	Mean sum of squares		
	Replication (df=1)	Treatment (df=29)	Error (df=29)
Plant height (cm)	16.69	161.44**	4.74
Days to 50% flowering	4.81	285.56**	1.26
Number of panicles per plant	0.41	7.08**	1.62
Panicle length (cm)	1.32	12.13**	1.16
Test weight (g.)	0.50	25.53**	0.68
Kernel length (mm)	0.03	0.36**	0.01
Kernel breadth (mm)	0.00	0.05**	0.01
Kernel L/B ratio	0.012	0.11**	0.01
Grain Fe content (ppm)	0.59	12.81**	0.33
Grain Zn content (ppm)	1.10	30.42**	2.06
Grain yield per plant (g.)	0.73	30.13**	1.32

Table 2: Genetic parameters for 11 quantitative traits in Rice.

Traits	Mean	Min	Max	GCV (%)	PCV (%)	h^2 (%)	GA as % of Mean
Plant height (cm)	93.97	79.36	124.80	9.41	9.70	94.3	18.42
Days to 50% flowering	96.18	80.50	124.	12.39	12.45	99.1	25.42
Number of panicles per plant	11.01	9.00	17.50	15.00	18.94	62.7	24.47
Panicle length (cm)	24.24	20.00	30.93	9.66	10.63	82.5	18.07
Test weight ((g.)	18.33	11.91	24.59	19.22	19.74	94.8	38.56
Kernel length(mm)	5.95	5.22	6.79	7.06	7.32	93.2	14.04
Kernel breadth(mm)	2.18	1.80	2.45	6.82	8.41	65.7	11.38
Kernel L/B ratio	2.74	2.25	3.14	8.26	9.48	75.9	14.83
Grain Fe content (ppm)	15.80	10.85	19.5	15.80	16.22	94.8	31.70
Grain Zn content (ppm)	21.48	11.15	30.61	17.52	18.76	87.3	33.73
Grain yield per plant (g.)	18.31	14.05	28.75	20.71	21.65	91.6	40.84

Table 3: Clustering pattern of 30 genotypes of Rice for 11 quantitative traits.

Cluster number	No. of genotypes	Genotypes in cluster
I	18	R-RHZ-MB-119, DRR Dhan 48, R-RHZ-IR-142, RRHP-MI 30, IR 64, R-RGY-IS-110, R-RHZ-SM-14, DRR Dhan 49, CGZR-1, R-RHZ-IB-80, R-RHZ-IR-132, DRR Dhan 45, IET 25470, R-56, R-RH2-M1-93, R-RHZ-IR-131, R-RHZ-SK-128, R-RHZ-IH-82, R-RHZ-IR-140
II	1	RajendraBhagwati
III	1	R-RGY-MH-113
IV	1	CGZR-2
V	3	CR Dhan 310, CR 2818-1-11-1-B-1-1-2-B-1, MI 127
VI	1	Zinco Rice
VII	1	CR Dhan48
VIII	1	Samba Mahsuri
IX	1	CR 2819-1-5-3-2B-12-1
X	1	IET 26383
XI	1	MI 156

Table 4: Intra and Inter cluster distance between 30 genotypes of Rice for 11 quantitative traits.

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	146.14										
II	189.56	0.00									
III	211.57	68.24	0.00								
IV	255.93	149.73	128.68	0.00							
V	530.75	199.34	164.16	404.66	138.20						
VI	309.14	77.09	94.48	123.99	226.94	0.00					
VII	232.69	153.69	173.31	198.71	318.47	231.87	0.00				
VIII	212.87	332.92	423.84	277.73	856.62	534.53	318.37	0.00			
IX	194.37	183.78	154.20	204.11	433.99	224.85	344.15	315.10	0.00		
X	265.32	418.25	406.15	607.16	791.68	613.60	595.54	393.92	191.52	0.00	
XI	405.72	256.69	220.24	564.19	256.98	492.95	372.56	635.02	390.06	441.94	0.00

Table 5: Cluster mean and per cent contribution of 11 quantitative traits of Rice.

Traits / Clusters	PH	DFF	NPP	PL	1000-GW	KL	KB	L/B	FeC	ZnC	YPP
I	94.12	90.67	10.56	24.33	18.83	5.86	2.14	2.76	15.71	21.05	17.04
II	94.42	105.00	10.00	24.50	20.24	5.80	2.22	2.62	18.65	26.60	17.06
III	91.01	105.50	13.50	25.00	15.29	5.80	2.28	2.54	14.25	19.20	18.39
IV	79.37	100.00	13.00	25.50	13.47	6.35	2.27	2.81	18.40	21.45	17.34
V	92.15	120.67	14.17	23.66	19.95	6.04	2.30	2.64	14.77	19.98	22.34
VI	90.01	110.00	9.00	20.00	14.84	5.99	2.23	2.69	18.10	22.10	14.05
VII	79.45	101.50	13.50	20.10	21.10	6.30	2.22	2.84	17.10	11.85	28.75
VIII	86.71	80.50	11.50	26.24	18.09	6.14	2.10	2.93	19.55	30.61	22.85
IX	103.96	98.00	9.50	22.80	11.91	6.80	2.17	3.14	14.65	26.45	14.99
X	124.83	84.50	9.00	23.24	14.14	5.98	2.25	2.66	13.90	23.90	14.10
XI	98.91	106.50	9.00	30.94	22.23	5.95	2.40	2.50	12.45	23.45	28.27
% contribution towards divergence	6.21	51.03	0.00	0.00	6.90	9.66	2.53	0.23	15.40	1.15	6.90
No. of times ranked 1st	27	222	0	0	30	42	11	1	67	5	30

Most of the traits in the current study had high heritability of *i.e.* > 60% which was coupled with large values of Genetic Advance as per cent of mean (Table 2), suggesting that selection for enhancement of these traits could be performed with relative ease. Grain Fe content (94.8% and 31.70%), test weight (94.8% and 38.56%), grain yield per plant (91.6% and 40.84%), grain Zn content (87.3% and 33.73%), days to 50% flowering (99.1% and 25.42%) and number of panicles per plant (62.7% and 24.47%) demonstrated high heritability percent in tandem with high values for Genetic Advance as per cent of mean. Agrawal (2003) and Girma *et al.* (2018) documented similar findings for these traits. However, non-additive gene action in the traits *viz.,* panicle length (82.5% and 18.07%), kernel length (93.2% and 14.04%), plant height (94.3 % and 18.42%), kernel breadth (65.7% and 11.38%) and kernel L/B ratio (75.9% and 14.83%) is likely to be present due high heritability coupled with poor genetic advance as a percent of mean exhibited by these traits. These results were similar with the findings of Parihar *et al.* (2017).

The existence of significant variation in the collection of thirty genotypes was shown by D^2 analysis in the current study. The genotypes were divided into eleven groups based on their degree of

divergence (Table 3). Clusters II, III, IV, VI, VII, VIII, IX, X, and XI had 0 intra cluster distance since each cluster had just one genotype. Cluster I (146.14), with 18 genotypes, demonstrated largest intra cluster distance closely followed by Cluster V (138.20) which had three genotypes. Cluster V and Cluster VIII (856.62)exhibited the largest inter cluster distance between each other followed by Cluster V and Cluster IX (433.99) suggesting that crosses between these different clusters would produce desirable segregates with the accumulation of beneficial genes in successive generations (Table 4). Days to 50% flowering, grain Fe content, kernel length, test weight, grain yield per plant, plant height, kernel breadth, grain Zn content, and kernel L/B ratio, all made contribution towards total divergence (Table 5). These findings are similar to those of Nachimuthu *et al.* (2014), Ranjith *et al.* (2018) and Rathan *et al.* (2020) who also reported that days to 50% contributed greatly towards total divergence. Based on the results obtained from D^2 statistics, the genotypes located at more diverse clusters with high mean values for desirable traits could be used in breeding programmes to accumulate favourable alleles and desirable traits into a single background, and thus could be effectively used in developing improved cultivars.

Furthermore, since 9 out of the 11 clusters were monogenotypic, the cluster mean of the 9 clusters could be used to find genotypes appropriate for crossing.

Conclusion

The Analysis of Variance (ANOVA) revealed that significant variation exists among the genotypes for all the traits. The traits like days to 50% flowering, panicle length, number of panicles per plant, test weight, grain Fe content, grain Zn content and grain yield per plant exhibited high values of GCV and PCV and high heritability in conjunction with high Genetic advance as percent of mean inferring the possibility for efficient selection of these traits and their modification towards the desired direction of selection. Clustering of genotypes grouped all the 30 genotypes into eleven clusters. Inter cluster distances showed high values suggesting the genotypes possessed a lot of variability indicating that selection of diverse parents for hybrid production could be done in the genotypes that were under investigation.

Conflict of interest

The authors declare that they have no conflict of interest.

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