

Original Research Article

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Genetic Parameters Study for Yield and Yield Contributing Characters in Rice (*Oryza sativa* L.) Genotypes with High Grain Zinc Content

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ABSTRACT

The present investigation for genetic variability was made based on the data recorded for sixteen yield and yield contributing quantitative and qualitative characters in twenty one rice genotypes using statistical tool. There are significant differences among the genotypes for all the characters under study showed by analysis of variance. Among the characters, higher estimates of phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV) were observed for the traits number of spikelet per panicle, no of filled grains per panicle, grain weight per panicle (g) and grain yield/ha (kg). This indicates the existence of wide genetic base among the genotypes taken for study and higher possibility of genetic improvement through selection for these traits. Heritability was higher for all the characters except tillers per plant, spikelet fertility per cent and panicle length (cm). Thus, selection based on phenotypic values would be effective for these traits. High heritability coupled with high genetic advance as per cent of mean was recorded for the characters; days to first flowering, days to 50 per cent flowering, number of filled grains per panicle, number of spikelet per panicle, grain yield per plot (kg), grain weight per panicle (g), grain yield per plant (g), 1000 grains weight (g), grain zinc content (ppm) and grain yield/ha (kg). These characters indicate the predominance of additive gene effects in their expression and would respond to selection effectively as they are least influenced by environment which can be improved through simple selection.

Keywords

Genetic variability,
GCV, PCV,
Heritability,
Genetic advance,
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Introduction

Rice (*Oryza sativa* L.) is a short day monocotyledonous self-pollinated angiosperm within the genus *Oryza* of family Poaceae. It is the principal nourishment for 33% of the total population and involves very closely one-fifth of the aggregate land territory occupied under cereals (Ren *et al.*, 2006). Rice is produced in 114 countries across the globe estimating production of 753mt (499mt milled rice, 2016) and forecasting 758mt (503.6mt milled rice, 2017) with world rice acreage of 161.1 mha (FAO, 2017). Among the rice growing countries in the world, India occupied the largest area under rice crop (about 45 million ha.) having the second position in production next to China, (IRRI 2016, standard evaluation system for rice.). As world's population is growing in exponential rate and maintain the food security as per the need is a challenging task for us as it is faced by so many constraints due to climate change. Variability is a vital factor which determines the amount of progress expected from selection. As phenotypic variation does not directly show its effectiveness for selection to obtain genetic improvement unless the genetic fraction of variation is known. Hence, an insight into the magnitude of genetic variability available is of paramount importance to a plant breeder for starting a prudent breeding programme. It becomes necessary to partition the phenotypic variability into heritable and non-heritable components with the help of genetic parameters such as genotypic and phenotypic co-efficient, heritability and genetic advance to facilitate selection. The variances were expressed as coefficient of variation so as to facilitate their comparison amongst different characters. The phenotypic co-efficient of variation was in general, higher than the genotypic co-efficient of variation. But the differences between PCV and GCV for many traits were less, suggesting the less impact of

environment for the traits. An estimate of heritability and genetic advance for different characters ultimately provides an appropriate guideline for selection and also the expected genetic gain. A quantitative measure which delivers information about the correspondence between genotypic variance and phenotypic variance is heritability. Achievement of a breeder in changing the characteristics of a population is subjected to heritability that is, the degree of correspondence between genotypic and phenotypic variance. Heritable improvement in yield is the ultimate object of plant breeder which calls for selection on the basis of yield components which are heritable. It becomes very important for breeders to go for selection of elite genotype from diverse population which helped by estimates of heritability. However, high heritability estimates coupled with high genetic advance render the selection most effective (Johnson *et al.*, 1955).

Materials and Methods

This experiment was conducted to study the genetic variability for yield and yield contributing traits among twenty-one diverse rice genotypes with high grain Zinc content collected from IRRI South Asia Hub, Hyderabad (Table.1) over five different locations i.e. (I) Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, UP, (II) Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, UP (III) Bhikaripur, Varanasi, UP (IV) Karsada, Varanasi, UP (V) Rampur, Mirzapur, UP during *Kharif* 2017. Net Plot size was 2.4 m×2.4m, twelve rows were grown having inter and intra row spacing was 20cm and 15cm respectively for each location under study. They were grown in a randomized block design with three replications and observations were recorded on randomly selected five plants for the

sixteen quantitative and qualitative traits i.e days to first flowering, days to 50% flowering, days to maturity, number of effective tillers per plant, plant height (cm), panicle length (cm), number of spikelet per panicle, number of filled grains per panicle, spikelet fertility per cent, grain weight per panicle (g) , grain yield per plant (g), 1000-grain weight (g), Grain yield per plot (kg), Grain yield per ha (kg), L/B ratio, and grain zinc content(mg/kg) were considered. Zinc content of rice grains was estimated in the aliquot of seed extract by using Atomic Absorption Spectrophotometer (AAS) at 213.86 nm for Zinc. The genotypic and phenotypic variances, genotypic (GCV) and phenotypic (PCV) coefficient of variation were estimated according to formula given by Burton (1952). Heritability in broad sense [$h^2_{(b)}$] was estimated according to formula given by Lush (1940) and genetic advance and Genetic advance as per cent of mean were estimated as formula suggested by Johnson *et al.*, (1955) by using suitable statistical tool.

Results and Discussion

Based on the Pooled analysis of variance (ANOVA) (Table 2) revealed that there is significant variation exists among the twenty one genotypes for all the sixteen characters over the five locations which will favourable for efficient selection. Among the characters, higher estimates of PCV and GCV were observed respectively for the traits, number of spikelet per panicle (PCV=32.85%, GCV=29.99%), number of filled grains per panicle (32.19%, 29.07%) and grain weight per panicle(g) (30.66%, 27.01%) (Table 3). This indicates the existence of wide genetic base among the genotypes taken for study and possibility of genetic improvement through selection for these traits. This was in conformity with the findings of Reddy De *et al.*, (1998) who reported higher PCV and GCV in rice for no of spikelet per panicle,

grain weight per panicle and number of filled grains per panicle. Mahto *et al.*, (2003), Satyanarayana *et al.*, (2005) and Singh *et al.*, (2007) also reported similar findings in upland rice for the grains per panicle. Moderate estimates of PCV and GCV were observed for the traits, days to first flowering (10.67%, 10.58%), number of effective tillers per plant (17.45%, 12.40%), 1000 grain weight(g) (16.71%, 15.62%) and grain zinc content (ppm) (18.08%, 15.5%) respectively. This suggests that the genetic improvement through selection for these traits may not be always effective. Similar results were also obtained by Dhurai *et al.*, (2014) and Dhanwani *et al.*, (2013) in rice reported for panicle length and other yield attributes. Low estimates of PCV and GCV were observed respectively for the characters days to 50% flowering (10.05%, 9.99%), days to maturity (8.41%, 8.36%) and spikelet fertility percent (7.95%, 5.26%), pant height (8.94%, 7.26%), panicle length (8.61%, 6.55%) and LB ratio (9.37%, 8.73%) suggesting that the direct selection for these traits may not be rewarding. The similar results were also reported by Kaw *et al.*, (1995), Muthuramu *et al.*, (2016) for days to maturity in cold stress environment. The estimate of heritability ranged from 46.4% (spikelet fertility percent) to 98.8% (Days to 50 % Flowering). Percentage of heritability was higher for all the characters except spikelet fertility percent (46.4%), panicle length (58.16%) and number of effective tillers per Plant (50.41%) (Table 3), similar study conducted by Satyanarayana *et al.*, (2005) in rice for panicle lengths and number of effective tillers per plant found to be not effective for selection due to low heritability. Thus, selection based on phenotypic values would be effective for these traits. These findings are in agreement with those of Kundu *et al.*, (2008) for number of filled grains per panicle and 1000-grain weight in tall indicaaman rice and Kole and Hasib (2008) for plant height, days to 50%

flowering, panicle length, kernel length and kernel L/B ratio in scented rice. In the present study most of the characters recorded high heritability estimates and selection would be effective if based on phenotypic values. High heritability coupled with high genetic advance as per cent of mean was recorded respectively for the characters, days to first flowering [$h^2(\text{broad sense})=98.34\%$ and $GA(\% \text{ per mean}) =21.62\%$], days to 50% percent flowering (98.8%, 20.46%), spikelet per panicle (83.38%, 56.44%), filled grains per panicle (81.48%, 54.13%), grain weight per panicle(g) (77.66%, 49.05%), grain yield per plant (g) (64.57%, 30.35%), grain yield per plot (kg) (64.52%, 30.33%), grain zinc content(mg/kg) (75.67%, 27.73%) and yield/ha rainfed (kg) (64.59%, 30.35%)

(Table.3). These results are similar with the results obtained by Gyanendrapal *et al.*, (2011) for grain yield per plant, spikelet per panicle, effective tillers per plant and days to 50% flowering, Krishna *et al.*, (2010) for number of total spikelets per panicle and number of filled grains per panicle, Anjaneyulu *et al.*, (2010), Bhinda *et al.*, (2017) for number of filled grains per panicle, Kundu *et al.*, (2008) for grain yield per plant and 1000-grain weight in tall *indica* rice and Singh *et al.*, (2007) for days to 50% flowering and grains per panicle. These characters indicate the predominance of additive gene effects in their expression and would respond to selection effectively as they are least influenced by environment.

Table.1 List of 21 genotypes collected from IRRI South Asia Hub, Hyderabad

<i>SL.No</i>	<i>Name of Genotype</i>	<i>Grain Zinc Content (ppm)</i>	<i>SL.No</i>	<i>Name of Genotype</i>	<i>Grain Zinc Content (ppm)</i>
1	IR 95044:8-B-5-22-19-GBS	20.6	12	BRRIdhan 64	24.97
2	IR 84847-RIL 195-1-1-1-1	21.8	13	BRRIdhan 72	20.7
3	IR 99704-24-2-1	14.67	14	DRR Dhan 45	18.13
4	IR 99647-109-1-1	23.7	15	DRR Dhan 48	19.2
5	IR 97443-11-2-1-1-1-1 -B	14.45	16	DRR Dhan 49	17.63
6	IR 97443-11-2-1-1-1-3 -B	23.47	17	IR 64	23.57
7	IR 82475-110-2-2-1-2	24.73	18	MTU1010	21.70
8	IR 96248-16-3-3-2-B	27.18	19	Sambamahsuri	24.47
9	R-RHZ-7	26.61	20	Swarna	18.89
10	CGZR-1	24.43	21	Local check	16.9
11	<i>BRRIdhan 62</i>	23.33			

Table.2 Pooled ANOVA of twenty one rice genotypes for sixteen characters over the five different locations

Entry No	Days to 1st flowering	Days to 50 % Flowering	Days to Maturity	Tillers Per Plant	Plant Height (cm)	Panicle Length (cm)	Spikelets Per Panicle	Filled grains Per Panicle	Spikelet s Fertility%	Grain Weight Per Panicle (g)	Grain Yield Per Plant (g)	1000-grain Weight (g)	Grain Yield Per Plot (kg)	Grain Yield/ha (kg)	L/B Ratio	Grain Zinc content (ppm)
Mean	93.746	98.181	126.800	7.873	106.7	26.013	109.300	83.121	76.374	1.507	11.618	18.258	0.941	3920.880	4.000	22.158
C.V.	1.361	1.094	0.932	12.206	5.000	5.551	13.281	13.684	5.818	14.420	13.086	5.844	13.106	13.086	3.288	8.476
F ratio	186.887	253.998	249.311	4.185	9.848	5.434	17.245	15.323	4.230	12.128	7.114	24.481	7.092	7.116	27.359	24.727
F Prob.	0.00E+00	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
S.E.	1.036	0.872	0.960	0.784	4.321	1.175	11.923	9.307	3.647	0.173	1.168	0.864	0.095	394.053	0.107	1.470
C.D. 5%	2.094	1.763	1.939	1.584	8.732	2.374	24.098	18.810	7.370	0.350	2.360	1.745	0.191	796.415	0.217	2.971
C.D. 1%	2.802	2.359	2.595	2.120	11.685	3.177	32.246	25.171	9.863	0.468	3.158	2.335	0.256	1065.700	0.290	3.976
Range Lowest	80.267	85.000	111.800	6.06	98.43	23.41	70.4	54.13	71.6	1.023	8.97	13.82	0.726	3027.49	3.2	16.64
Range Highest	114.800	119.000	148.333	9.733	128.08	30.30	185	136.6	81.67	2.182	14.57	21.76	1.18	4919.43	4.45	26.64

Table.3 Heritability (broad-sense), GCV, PCV and Genetic advance as per cent of mean of twenty one rice genotypes for sixteen characters over the five different locations

	Days to first flowering	Days to 50 % Flowering	Days to Maturity	Effective Tillers Per Plant	Plant Height (cm)	Panicle Length (cm)	Spikelets Per Panicle	Filled grains Per Panicle	Spikelets Fertility %	Grain Weight Per Panicle(g)	Grain Yield Per Plant (g)	1000-grain Weight (g)	Grain Yield Per Plot (kg)	Yield/ ha (kg)	L/B Ratio	Grain Zinc content (ppm)
Var Environmental	1.63746	1.155397	1.405397	0.9254	29.7057	2.08942	233.6224	139.858	21.66341	0.0484183	2.157278	1.128295	0.01418	245718	0.018	3.987831
ECV	1.360573	1.09444	0.932205	12.2055	5.000082	5.55101	13.28061	13.6836	5.818053	14.420084	13.08637	5.843566	13.1052	13.086	3.288	8.476248
VarGenotypical	98.11333	95.99508	112.4733	1.00349	61.52866	2.96129	1127.157	590.055	16.85615	0.1685124	3.80825	8.531916	0.02499	433942	0.123	12.0755
GCV	10.58295	9.994176	8.364306	12.4047	7.265034	6.55156	29.99571	29.0729	5.266001	27.01118	18.13647	15.62485	18.1344	18.14	8.73	15.50079
VarPhenotypical	99.75079	97.15048	113.8787	1.92889	91.23436	5.05071	1360.78	729.913	38.51956	0.2169307	5.965528	9.660211	0.03917	679661	0.141	16.06333
PCV	10.67104	10.05414	8.416493	17.451	8.945215	8.61475	32.85638	32.1909	7.957148	30.663744	22.5036	16.71846	22.5114	22.506	9.371	18.08228
h² (Broad Sense)	0.983438	0.988084	0.987613	0.50414	0.669151	0.5816	0.833896	0.81481	0.464045	0.7766145	0.645785	0.870445	0.6452	0.6459	0.867	0.756761
Gen.Adv as % of Mean 5%	21.621	20.46522	17.12366	18.2631	12.33268	10.3125	56.4474	54.1333	7.41412	49.05292	30.35108	30.1008	30.3314	30.358	16.78	27.73214
General Mean	93.74603	98.18095	126.8095	7.87302	106.7231	26.0127	109.2857	83.1206	76.37397	1.5067016	11.61752	18.25813	0.94109	3920.9	4	22.15819

In conclusion, there are significant differences among the genotypes for all the characters under study showed by analysis of variance. This indicated that there is ample scope for selection of promising genotypes from present set of genotypes for yield improvement. Among the characters, higher estimates of PCV and GCV were observed for the traits number of spikelet per panicle, no of filled grains per panicle, grain weight per panicle(g) and grain yield/ha (kg). This indicates the existence of wide genetic base among the genotypes taken for study and higher possibility of genetic improvement through selection for these traits. Heritability was higher for all the characters except tillers per plant, spikelet fertility percent and panicle length (cm). Thus, selection based on phenotypic values would be effective for these traits. High heritability coupled with high genetic advance as per cent of mean was recorded for the characters; days to first flowering, days to 50 percent flowering, number of filled grains per panicle, number of spikelet per panicle, grain yield per plot (kg), grain weight per panicle(g), grain yield per plant (g), 1000 grains weight (g), grain zinc content (ppm) and grain yield/ha (kg). These characters indicate the predominance of additive gene effects in their expression and would respond to selection effectively as they are least influenced by environment which can be improved through simple selection. Pedigree method of breeding can be used for improving the characters influenced by additive gene action, whereas the characters influenced by additive and non-additive and only by non-additive gene actions can be improved through population improvement methods like recurrent selection or by employing biparental mating in the early generations followed by selection.

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