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Bapsila Loitongbam

Department of Genetics and Plant breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, Uttar Pradesh, India

PK Singh

Department of Genetics and Plant breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, Uttar Pradesh, India

Prashant Bisen

Department of Genetics and Plant breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, Uttar Pradesh, India

Sandhya

Genetics and Plant Breeding, Agriculture Research Station, AU, Kota, Rajasthan, India

SR Rathi

Department of Genetics and Plant breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, Uttar Pradesh, India

Sameer Upadhayay

Department of Genetics and Plant breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, Uttar Pradesh, India

Dipika Singh

Department of Genetics and Plant breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, Uttar Pradesh, India

Anuj Kumar

Department of PMB & GE, NDUAT Kumarganj, Ayodhya, Uttar Pradesh, India

Correspondence

Bapsila Loitongbam Department of Vegetable Science, Narendra Deva University of Agriculture & Technology, Kumarganj, Faizabad, Uttar Pradesh, India

Genetic variability and correlation analysis for zinc deficiency tolerance in RIL population of rice (Oryza sativa L.)

Bapsila Loitongbam, PK Singh, Prashant Bisen, Sandhya, SR Rathi, Sameer Upadhayay, Dipika Singh and Anuj Kumar

Abstract

Genetic variability is the fundamental requirement of any crop breeding program to develop superior cultivars. The objective of this study was to estimate the genetic variability, heritability and correlation among the fourteen quantitative traits of two hundred and thirty eight Recombinant Inbred Lines (RILs) under zinc deficient condition. The analysis of variance revealed significant differences for all the traits under study, indicating the presence of high genetic variability among the lines. Phenotypic coefficients of variances (PCV) were higher than genotypic coefficients of variances (GCV) in all the traits across the two locations of BHU and Faizabad. Broad sense heritability (h²) of Days to 50 % flowering was highest in both the locations suggesting that the traits were primarily under genetic control. The highest GA% was observed in Zn Scoring followed by Plant Mortality. Grain Yield per Plant is highly correlated in all the traits except Thousand Grain Weight and Panicle Length in BHU.

Keywords: Genetic variability, Oryza sativa L. RIL

Introduction

Rice is an important cereal, belonging to the family Graminae with a genome consisting of 430Mb. It is the major staple food for more than half of the world population and 90% of it is being produced and consumed in Asia. According to the recent estimates, world's food production will have to be increased by 70 % in 2050 to meet the demand of growing population (FAO, 2011). Rice is highly sensitive to zinc (Zn) deficiency and Zn is the most important micronutrient, limiting rice growth and yield. Grain yield losses due to Zn have been reported in rice as high as 80%, along with reduced grain Zn level (Refuerzo et al., 2009)^[16]. The demand for food will be double by the year 2025 with the current trends of population growth and agricultural production, nearly triple by 2050. The development of new genotypes requires knowledge of genetic variability presents in the crop to build efficient breeding programme. The knowledge about genetic variability helps to know the variations are heritable or non-heritable. However, variability for yield in crop species will get exhausted this in turn, limits the prospects of further improvements in the crop species since variability is the prerequisite for any improvement in the crop species. Thus, selection for high yield requires knowledge about genetic variability and good understanding of correlation present in a crop species for the character under improvement for the success of any crop breeding programme (Konate *et al.*, 2016)^[9]. Heritability is a good index of the transmission of character from parents to their offspring. The estimates of heritability provide authentic information about a particular genetic attribute which will be transmitted to the successive generations and constitute an efficient guide for breeders in the choice of parents for crop improvement in selection of elite genotypes from diverse genetic populations (Rashmi et al., 2017)^[15].

Correlation among yield trait and its components provide the information about their performance and association with one another. Information on correlation coefficients between grain yield and its component characters is essential since grain yield in rice is a complex character and is highly influenced by several component characters (Hossain *et al.*, 2015) ^[3]. Positive correlation between yield and yield components are requires for effective yield component breeding programme in rice (Ogunbayo *et al.*, 2014) ^[13]. So, it is important for plant breeders to understand the degree of correlation between yield and its components. Therefore, on the background of this information, the objective of the present study was to assess and evaluate genetic variability and correlation of rice recombinant inbred lines.

Materials and Methods

The research work was carried out at the research farm of the Institute of Agricultural Sciences, Banaras Hindu University, Varanasi and NDUAT, Faizabad in the *kharif* 2018-19 seasons in Zinc deficient field condition. The field experiment was conducted in an alpha lattice design with a spacing of 15 cm and 20 cm between plants and rows respectively. The study consists of 238 F₇ Recombinant Inbred Lines derived from the crosses between the two parents Kinandang Patong and A69-1 by single seed descent method. Kinandang Patong is a high yielding Tropical Japonica variety but sensitive to zinc deficiency and A69-1 is an Indica variety tolerant to zinc deficiency.

Data collection and analysis

Observations were recorded on fourteen quantitative traits at appropriate growth stage of rice plant. The traits that were evaluated include Leaf Bronzing Score (1-9), Plant Mortality (%), Days to 50 % Flowering, Days to Maturity, Plant height (cm), Panicle Length (cm), Effective Tillers per plant, Straw Yield per plant (g), Biological Yield (g), Harvest Index (%), Filled Grain per panicle (g), Spikelet Fertility Percent (%), Thousand Grain Weight (g) and Grain Yield per plant (g),

Statistical Analysis

The analysis of variance was performed at 1 % level of significance using Alpha Latice design to derive variance components using the software SAS. Various genetic parameters such as genetic variance, phenotypic variance, genetic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h²), genetic advance (GA) and genetic advance as percentage of mean (GAM) were computed by using the formula given by Burton and De Vane (1953) ^[2]; and Johnson *et al.* (1955) ^[5] and applied by Tuhina-Khatun *et al.* (2015) ^[18]. The correlation analysis was performed using the software packages ADEL-R and META-R developed by CIMMYT, Mexico.

Results and Discussion

The RIL mapping populations along with parent were evaluated in Kharif 2019 for zinc deficiency and other morphological traits. The results of ANOVA in BHU and Faizabad (FZD) are presented in table 1. The analysis of variance exhibited the presence of highly significant differences at (P<0.01) among the tested Recombinant Inbred Lines for all the characters indicating the existence of variability in both the locations. The results are in accordance to those found by (Pallavi *et al.*, 2017) ^[14].

Estimate of genetic parameters

Estimates of genotypic (Vg) and phenotypic variances (Vp), genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), broad sense heritability (h²), genetic advance (GA) and genetic advance as percentage of the mean (GAM) are shown in Table 2.

High genotypic and phenotypic variances were recorded with Plant Mortality in both the locations, BHU (290.33, 597.35) and FZD (291.09, 657.44) respectively followed by filled grain in BHU (221.14, 405.12) and FZD (303.43, 466.87) respectively. In general, the phenotypic variances were higher than genotypic variances for all the traits studied. This is highly consistent with the result obtained by (Sandhya *et al.*, 2018; Maurya *et al.*, 2018; Meena *et al.*, 2018) ^[17, 10, 11] which illustrated phenotypic variances were higher than genotypic variances. In this study, high heritability and genetic advance was observed in grain yield, days to heading and maturity indicated presence of additive genetic control also in agreement with (Islam *et al.*, 2016, Bekele *et al.*, 2013) ^[4, 1] during their study in aromatic and fine rice germplasm. Similar finding was reported by (Konate *et al.*, 2016) ^[9] which is fully in agreement with the present finding.

Genotypic coefficients of variance (GCV) were ranged from (1.59, 4.82) for Harvest Index to (44.71, 46.03) for Zn Scoring in BHU and FZD respectively, whereas phenotypic coefficients of variance (PCV) were ranged from 6.59 for Harvest Index to 59.05 for Zn Scoring in BHU and the highest PCV in FZD was observed by Zn Scoring (59.47) and lowest by Days to Maturity. PCV and GCV values more than 20% are regarded as high, whereas values less than 10% are considered to be low and values between 10 and 20% to be moderate. Based on this delineation, GCV and PCV values were low for Day to 50% flowering, Days to Maturity and Harvest Index and high for Zn Scoring, Plant Morality and Filled Grain in both the locations. In addition, PCV values were higher than theirs corresponding GCV values for all the characters considered. Similar finding was reported by (Konate et al., 2016)^[9] which is fully in agreement with the present finding.

Heritability analyses estimate the relative contributions of differences in genetic and non-genetic factors to the total phenotypic variance in a population. It is an important concept in quantitative genetics, particularly in selective breeding. Broad sense heritability of Days to 50 % Flowering (87.18, 88.14) was highest and lowest heritability was observed in Harvest Index (24.19, 46.74) in BHU and FZD respectively. All the characters studied had high heritability (>60%) except the Harvest index. This result indicates that this trait could be easily improved by selection.

Genetic advance (GA) under selection refers to the improvement of characters in genotypic value compared with the base population under one cycle of selection at a given selection intensity (Wolie *et al.*, 2013) ^[19]. High value of GA was observed in Plant Mortality (35.10, 35.15) in both the locations whereas lowest GA was exhibited by Harvest Index (1.43) in BHU and Effective tiller (3.48) for FZD.

The genetic advance as percentage of mean (GA%) showed that the highest GA% was observed in Zn Scoring (92.10, 94.84) followed by Plant Mortality (83.08 and 81.42) whereas GA% was found very low in Harvest Index (3.28, 9.93) (Table 2).

Correlation

Correlation coefficient analysis is widely used to measure the degree and direction of relationships between various traits including grain yield. Leaf Bronzing Score possessed positive and highly significant correlation between Plant Mortality (r = 0.87, r = 0.82), Days to 50 % Flowering (r = 0.22, r = 0.18) and Days to Maturity (r = 0.17, r = 0.18) and negatively correlated to Effective Tillers per plant (r = -0.73, r = -0.59), Grain Yield per plant (r = -0.83, r = 0.68), Straw Yield (r = -0.81, r = -0.64), Biological Yield (r = -0.83, r = -0.68), Filled grain per panicle (r = -0.86, r = 0.78) and Spikelet Fertility Percent (r = -0.85, r= 0.73) in both the locations. Plant Mortality had positive correlation with Days to 50 % Flowering (r = 0.20, r = 0.21) and negatively correlated to Days to Maturity, Effective Tillers per plant, Grain Yield per plant, Straw Yield per plant, Biological yield, Filled Grain per Panicle and Spikelet Fertility Percent. However, Days to 50 % Flowering had highly significant correlation with Days to

Maturity (r = 0.89, r = 0.98). On the contrary, it revealed negative correlation with Plant Height, Biological yield, Filled Grain per Panicle and Spikelet Fertility Percent. Days to Maturity had negatively correlated with all the traits. Plant Height possessed positive correlation with Panicle Length (r = 0.58) and Effective Tillers per Plant (r = 0.19) only in FZD. The trait Effective tillers per plant is positively and significantly correlated with Grain Yield per plant, Straw Yield, Biological Yield and Filled Grain per panicle in both the locations. Biological yield showed positive and highly significant correlation with Filled Grain per panicle (r = 0.87, r = 0.79) and Spikelet Fertility Percent (r = 0.78, r = 0.62) but negatively correlated with Harvest Index and Thousand grain weight) in both the locations. Filled grain had positive correlation with Spikelet Fertility Percent (r = 0.86, r = 0.80). The correlation of Grain Yield per Plant had positive and highly correlated with all the traits except Thousand Grain Weight in both the locations and Panicle length in BHU Table 3. However, this is in contrast with the previous study of Khan *et al.* (2014) ^[7] and Moosavi *et al.* (2015) ^[12] that presented the negative correlation between plant height and yield per plant but similar observation was reported by Karad and Pol (2008) ^[6] and Khare *et al.* (2014) ^[8] showing strong inherent association among themselves and with grain yield per plant.

 Table 1: Analysis of Variance (ANOVA) of 14 quantitative traits for zinc deficiency tolerance across the environment in parents and RIL population

Source of		Mean														
variation	d.f	Location	LB	PM%	DFF	DM	PH	PL	ETP	SYP	BY	HI%	FGP	SFP	TGW	GYP
Treatment		BHU	8.33**	887.68**	126.09**	152.89**	148.82**	4.75**	4.58**	15.37**	59.34**	8.76**	626.27**	289.20**	36.86**	15.35**
	239	FZD	8.428**	948.53**	125.13**	105.42**	244.35**	9.39 **	8.27**	14.36**	53.83**	24.46**	770.30**	366.57**	37.72**	14.47**
Replication		BHU	0.03	213.33	3.68	39.11	6939.87	375.41	62.81	33.63	69.93	9.77	2036.62	399.61	121.40	6.57
	1	FZD	0.918	3.33	1.41	24.30	155.17	1.596	3.882	6.599	30.28	4.89	6.55	872.69	57.44	9.49
Block(Rep)		BHU	5.58	644.11	29.39	62.97	127.54	3.57	4.21	12.40	39.07	6.79	323.78	116.69	3.37	8.42
	38	FZD	6.239	883.24	29.66	28.15	111.88	5.66	7.643	13.80	44.287	14.92	343.96	156.67	6.71	9.537
Error		BHU	2.26	307.02	17.18	47.49	52.47	1.94	1.94	5.08	18.14	7.79	183.98	112.21	2.61	5.12
	201	FZD	2.111	366.34	17.08	16.25	48.12	3.18	2.55	5.768	16.58	15.68	163.44	155.44	6.13	4.063

Note: ** - Significant at P < 0.01, BHU: Banaras Hindu University; FZD: Faizabad d.f (degree of freedom), LB (Leaf Bronzing), PM (Plant Mortality), DFF (Days to 50 % Flowering), DM (Days to Maturity), PH (Plant Height), PL (Panicle Length), ETP (Effective Tillers per Plant), SYP (Straw Yield per Plant), BY (Biological Yield), HI (Harvest Index), FGP (Filled Grain per Panicle), SFP (Spikelet Fertility Percent), TGW (Thousand Grain Weight), GYP (Grain Yield per Plant).

Table 2: Phenotypic performance	for 14 quantitative traits
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Parameters	Location	Kinandang Patong (sensitive)	A69-1 (tolerant) Range		nge	Mean	$\mathbf{V}_{\mathbf{g}}$	Vp	h ² (%)	GCV	PCV	GA	GA%
				Min	Max								
LB	BHU	9	1	1	9	3.89	3.03	5.29	75.71	44.71	59.05	3.50	92.10
	FZD	9	1	1	9	3.86	3.16	5.27	77.41	46.03	59.47	3.66	94.84
PM%	BHU	80	0.00	0	90	42.25	290.33	597.35	69.72	40.33	57.85	35.10	83.08
	FZD	80.00	0.00	0	100	43.17	291.09	657.44	66.54	39.52	59.39	35.15	81.42
DEE	BHU	115.50	105.00	73.5	128	93.11	54.45	71.63	87.18	7.93	9.09	15.20	16.33
DFF	FZD	125	118	83.5	133.5	103.11	59.50	76.58	88.14	7.48	8.49	15.89	15.41
DM	BHU	145.50	136.00	105.5	160.5	123.58	52.71	100.19	72.52	5.87	8.09	14.95	12.10
DM	FZD	152	144	115	163	132.92	44.58	60.84	85.60	5.02	5.87	13.75	10.35
DLL (am)	BHU	75.66	68.95	62.16	110.11	82.306	48.18	100.64	69.18	8.43	12.18	14.29	17.37
r m (cm)	FZD	74.99	63.79	45.13	110.79	75.85	98.12	146.23	81.91	13.05	15.94	20.40	26.90
DL (am)	BHU	18.17	18.33	14.94	25.41	19.20	1.40	3.35	64.75	6.17	9.53	2.44	12.71
PL (CIII)	FZD	18.16	19.54	12.12	25.63	19.03	3.11	6.29	70.28	9.26	13.18	3.63	19.07
ETD	BHU	5.00	11.00	4.50	12.00	7.46	1.32	3.26	63.61	15.40	24.22	2.37	31.74
LIF	FZD	5.5	11.00	2.50	14.5	7.69	2.86	5.41	72.66	21.97	30.24	3.48	45.27
	BHU	11.39	19.77	9.51	23.59	16.39	5.15	10.22	70.95	13.84	19.50	4.67	28.50
51F(g)	FZD	12.12	19.37	5.23	22.04	14.17	4.29	10.06	65.34	14.62	22.38	4.27	30.12
DV	BHU	20.49	36.53	16.66	42.64	29.25	20.59	38.74	72.92	15.52	21.28	9.35	31.97
DI	FZD	20.22	33.55	8.84	40.32	25.23	18.62	35.21	72.73	17.11	23.52	8.89	35.24
1110/	BHU	44.40	45.64	36.85	49.56	43.65	0.48	8.28	24.19	1.59	6.59	1.43	3.28
FI1%	FZD	40.35	42.14	20.45	50.42	43.45	4.39	20.08	46.74	4.82	10.31	4.31	9.93
ECD	BHU	20.50	84.50	13.18	101.5	46.04	221.14	405.12	73.89	32.30	43.72	30.63	66.54
FOF	FZD	15.57	104.50	7.00	99.50	42.51	303.43	466.87	80.62	40.98	50.83	35.88	84.41
SED	BHU	38.73	75.10	24.49	82.69	57.58	88.49	200.71	66.40	16.34	24.61	19.38	33.66
SFP	FZD	28.91	81.99	16.91	84.94	54.13	105.56	261.01	63.59	18.98	29.85	21.17	39.10
	BHU	20.45	19.55	12.45	37.53	22.53	15.60	18.21	66.40	16.34	24.61	19.38	33.66
1Gw(g)	FZD	20.95	20.20	12.35	38.38	23.11	14.43	20.57	83.77	16.44	19.62	7.83	33.86
	BHU	9.10	16.77	6.72	21.14	12.85	5.12	10.23	70.72	17.60	24.89	4.66	36.27
GYP(g)	FZD	8.10	14.18	3.62	18.68	11.06	5.20	9.27	74.94	20.63	27.53	4.69	42.51

Vg (Genotypic variance), Vp (Phenotypic variance), h² (Heritability), GCV (Genotypic coefficient of variance), PCV (Phenotypic coefficient of variance), GA (Genetic Advance), GA% Mean (Genetic Advance% as mean)

Table 3: Correlation Co-efficient among phenotypic traits studied in RIL population

Traits	Locati On	LB	PM%	DFF	DM	PH (cm)	PL (cm)	ET	SYP	BY	HI%	FGP	SFP	TGW	GYP
LB	BHU	1.00	0.87***	0.22***	0.17**	-0.38***	-0.10	-0.73***	-0.81***	-0.83***	-0.41	-0.86***	-0.85***	0.00	-0.83***
	FZB	1.00	0.82***	0.18***	0.18***	-0.38***	-0.37***	-0.59***	-0.64***	-0.68***	-0.17**	-0.78***	-0.73***	-0.02	-0.68***
PM%	BHU		1.00	0.20**	0.16*	-0.37***	-0.12	-0.73***	-0.81***	-0.82***	-0.38***	-0.87***	-0.79***	0.03	-0.81***
	FZB		1.00	0.21***	0.20***	-0.29**	-0.29	-0.53***	-0.62***	-0.67***	-0.19**	-0.79***	-0.67***	0.03	-0.68***
DFF	BHU			1.00	0.89***	-0.18**	-0.02	-0.16*	-0.17**	-0.19**	-0.14*	-0.22***	-0.23***	-0.05	-0.20**
	FZB			1.00	0.98***	-0.19***	-0.01	-0.08	-0.10	-0.18**	-0.26**	-0.20**	-0.22***	-0.03	-0.25**
DM	BHU				1.00	-0.22***	-0.02	-0.12	-0.12	-0.13*	-0.09	-0.17**	-0.18**	-0.12	-0.14*
	FZB				1.00	-0.18***	-0.01	-0.07	-0.09	-0.16**	-0.26**	-0.19**	-0.21***	-0.02	-0.24***
PH	BHU					1.00	0.27**	0.30**	0.40***	0.40***	0.10	0.44***	0.36***	0.11	0.38***
	FZB					1.00	0.58***	0.19**	0.44***	0.43***	-0.01	0.44***	0.39***	0.11	0.39***
PL	BHU						1.00	0.07	0.12	0.12	0.02	0.16*	0.08	0.02	0.12
	FZB						1.00	0.36***	0.39***	0.41***	0.07	0.39***	0.31***	0.03	0.39***
ET	BHU							1.00	0.72***	0.73***	0.32***	0.72***	0.67***	-0.07	0.73***
	FZB							1.00	0.61***	0.65***	0.12	0.58***	0.50***	-0.07	0.64***
SYP	BHU								1.00	0.99***	0.34***	0.85***	0.76***	0.00	0.95***
	FZB								1.00	0.96***	-0.13*	0.73***	0.54***	0.01	0.84***
BY	BHU									1.00	0.44	0.87***	0.78***	0.01	0.98***
	FZB									1.00	0.10	0.79***	0.62***	0.00	0.95***
HI%	BHU										1.00	0.42***	0.49***	0.11	0.55***
	FZB										1.00	0.21***	0.34***	0.04	0.37***
FGP	BHU											1.00	0.86***	-0.07	0.87***
	FZB											1.00	0.80***	-0.07	0.80***
SFP	BHU												1.00	0.04	0.79***
	FZB												1.00	0.04	0.65***
TGW	BHU													1.00	0.02
	FZB													1.00	0.01
GYP	BHU														1.00
	FZB														1.00

Note: ***Significant at P<0.001, ** Significant at P<0.01, * Significant at P<0.05

Conclusion

Among the two hundred and thirty eight rice lines, highest mean performance for the grain yield per Plant was range from 6.72 to 21.14 in BHU and 3.62 to 18.68 in Faizabad respectively. The lines which show highest mean performance would be more suitable for the direct selection and hybridization in order to make the desirable rice improvement programme.

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