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Original Research Article

Estimation of Genetic Variability, Heritability and Genetic Advance of Thirty Rice (*Oryza sativa* L.) Genotypes in Saline and Normal Condition

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A B S T R A C T

The present investigation consists of thirty rice genotypes and the experiment was conducted during *Kharif*-2016 in Randomized Block Design with three replications. The data were recorded for fourteen quantitative characters to study genetic variability, heritability, genetic advance, correlation coefficient analysis and path analysis. Analysis of variance among thirty genotypes showed significant difference for all characters studied. Highest genotypic coefficient of variation (GCV) and phenotypic coefficient variation (PCV) was observed for panicle bearing tillers per plant followed by grains per panicle and spikelet per panicle in controlled condition whereas in saline condition for grains per panicle followed by spikelet per panicle and panicle bearing tillers per plant indicating that these characters could be used as selection parameters for crop improvement. High estimates of heritability were observed for spikelet per panicle followed by grains per panicle, plant height, days to 50% flowering and test weight in controlled condition, whereas, in saline condition highest broad sense heritability was recorded in the case of spikelet per panicle followed by grains per panicle, grain yield per plant, days to 50% flowering and plant height. In controlled condition high genetic advance were observed for grains per panicle followed by spikelet per panicle, whereas, in saline condition maximum genetic advances was recorded is same as in controlled condition, indicating predominance of additive gene effects and possibilities of effective selection for the improvement of these characters.

Keywords

Rice, Salinity, Genetic variability, Heritability and Genetic Advance

Introduction

Rice (*Oryza sativa* L.) belongs to the family Poaceae. The haploid chromosome number of rice is n=12. The species can be either diploid or tetraploid. In this respect, *Oryza sativa* L. and *Oryza glaberrima* L. both are diploid species (2n= 24) (Brar and Khush 2003). The Asian cultivated rice (*Oryza sativa* L.) is the first fully sequenced crop genome and is a model crop species. Rice is considered as a major food crop across major countries worldwide. As a food crop, it forms the staple food of more than three billion people accounting for about 50-80% of their daily calorie intake (Khush 2005). Rice protein is biologically richest as its digestibility is very high (88%). It is the 2nd most important crop in the world after wheat, covering almost 90% of area across Asia alone. The use of the crop varies widely ranging from its use as food in cereals, snacks, brewed beverages, flour, rice bran oil to its use in religious events across India. The medicinal value of the crop adds on more to the list. Rice cultivation has been predominant in India across ages. Rice covers a global area of 156 million hectares of land producing about 650 million tons of crops (FAO 2008). Globally covering an area of 149.15 million ha area yielding about 550.19 million tones, this food crop is being cultivated across an area of 44.6 million ha in India. India ranks first in area and second in production following China, the largest producer of rice. As an economically and industrially important crop of India, rice provides about 23% of total world rice production and 45% of the total Indian food grain production. However, with the expanding population, the increase in production of the crop is the urgent need of the hour in order to keep in accord to the national food and livelihood security system. India is one of the leading exporters of rice, in specific, basmati rice. However, abiotic stress, which includes salinity, drought, heat and cold, critically threatens crop production and causes significant yield loss in large areas (Pareek *et al.*, 2010; Mantri *et.al.*, 2012).

Salinity as an abiotic stress widely limit the crop production severely (Shannon, 1998). A saline soil is usually the reservoir of a number of soluble salts such as $Ca2^{+}$, $Mg2^{+}$, Na^{+} and anions SO42-, Cl-, $HCO3^{-}$ with exceptional amounts of K^{+}, $CO32^{-}$, and $NO3^{-}$. A soil can be termed as saline if its EC is 4 dS/m or more (USDA-ARS 2008), (equivalent to approximately 40 mM NaCl) with an osmotic pressure of approximately 0.2 MPa. Salinity is the condition when the EC is sufficient to cause yield reduction of most crops. The pH of saline soils generally ranges from 7- 8.5 (Mengel *et al.* 2001). The arid and semi-arid zones, characterized by low precipitation and high evaporation are the most affected due to minimum lixiviation of salt from the soil profile resulting in increased salt accumulation. Salinity prone areas found in the arid and semiarid zones are usually accounted to the accumulation of salts over ages**.** The effect of salinity on rice is many fold, leading to inhibition of germination, difficulties in crop area establishment, leaf area development, decrease in dry matter production, delay in seed set and also even sterility can occur (Khatun *et al.* ,1995; Asch *et al.*, 2001). It has been well documented that the effect of salinity on seedling growth, seedling establishment, grain yield components such as spikelet number, tiller number has successively lead to a reduction in grain yield (Khatun *et al.*, 1995; and Zeng *et al.*, 2003).

Materials and Methods

Plant materials

A total of 30 traditional and improved rice genotypes were used in the study *viz*., IR91167-31-3-1-33, IR91167-99-1-1-1-3, IR91167-133-1-1-2-3, IR91171-66-3-2-1-3, IR91175-27-1-3-1-3, IR91158-85-3-2-3-3, IR92953-49-1-3, IR92960-75-1-3, IR92966-95-1-3, IR92971-70-3-3, IR68144-2B-2-2-3-1-166, IR82475-110-2-2-1-2, IR83294-66-2-2-3-2, IR83668-35-2-2-2, IR84722-82-2-3-3-3, RP-BIO-5478-185M, RP4993-55-14-3-5-1, R-RHZ-2, R-RHZSM-4, R-RHZIH-7, IR68144-2B-2-2-3-1-120, IR68144-2B-2-2-3-1-127, TARAMON, SWARNA, IR-64, NUD-3, NDR-359, AYAAR, SAMBHA MANSSURI and MTU-1010.

Screening of rice genotypes at the reproductive stage

The genotypes were evaluated for their tolerance to salinity under net house of PMB and GE dept. of N. D. U. A. T. Kumarganj, Faizabad using standard protocol (Gregorio *et al.*, 1997). The experimental design was completely randomized design with three replications. Two setups were maintained: normal and salinized. Pregerminated seeds of rice genotypes were sown in earthen pots. After 2 weeks, seedlings were thinned and the water level was raised to about 1 cm. The pots were salinized at EC 6 dS /m three weeks after sowing and EC was monitored in every week. Data were recorded for days to 50% flowering, Plant height (cm), Panicle bearing tillers per plant, Panicle length(cm), Number of spikelets per panicle, Number of grains per panicle, Spikelet fertility (%), Test weight(g), Biological yield/plant (g), Harvest index (%), Na^+ / K^+ ratio and Grain yield/plant (g) and data was subjected to statistical analysis. The variability was estimated as per procedure for analysis of variance suggested by Panse and Sukhatme (1967) PCV and GCV were calculated by the formula given by Burton (1952), heritability in broad sense (h2) by Burton and De Vane (1953) and genetic advance i.e. the expected genetic gain were calculated by using the procedure given by Johnson *et al.* (1955) .

Results and Discussion

Genetic variability in any crop is pre-requisite for selection of superior genotypes over the existing cultivars. The analysis of variance for different characters indicated the existence of highly significant differences for all fourteen characters under study at 1% level of significance suggesting each and every genotype are genetically divergent from each other and there is ample scope for selection of characters from these diverse sources for yield and its components for both the conditions (normal and treated) (Table 1a, 1b). These findings were in accordance with the findings of Bekele *et al.*, (2013) and Sandhya *et al.* (2015) . A wide range of variance was observed for all the characters. Phenotypic variance was higher than genotypic variance for all the yield and its contributing characters indicate the ninfluence of environmental factors on these traits. The highest variability (Vg & Vp) was recorded for spikelets per panicle (1280.97 and 1292.66) followed by grains per panicle (1222.50 and 1244.26) and plant height (284.25 and 299.56) in controlled condition whereas in saline condition the highest variability (Vg & Vp) was recorded for spikelets per panicle (1247.39 and 1250.47) followed by grains per panicle (1196.75 and 1210.98) and plant height (155.83 and 181.47) Similar results were also reported by Anjaneyulu *et al.*, (2010), Idris *et al.* (2012) and Sandhya (2014). Coefficients of variation studies indicated that the estimates of PCV were slightly higher than the corresponding GCV (table 2a,b) among the all traits panicle bearing tillers per plant (33.30 and 29.69), exhibited high estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) followed by grains per panicle (31.05 and 30.77), Na^+/K^+ (20.11and 14.95) in controlled condition whereas in saline condition grains per panicle (32.63 and 32.44) exhibited high estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) followed by spikelets per panicle(31.17 and 31.12) , panicle bearing tillers per plant (27.60 and 25.03) , high values of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for these traits suggested the possibility of yield improvement through selection of these traits. Close relationship between GCV and PCV was found in all the characters and PCV values were slightly greater than GCV, revealing very little influence of environment for their expression. The amount of genetic variation considered alone will not be of much use to the breeder unless supplemented with the information on heritability estimate, which gives a measure of the heritable portion of the total variation. It has been suggested by Burton and Devane (1953) that the GCV along with heritability estimate could provide a better picture of the amount of advance to be expected by phenotypic selection. Since genetic advance is dependent on phenotypic variability and heritability in addition to selection intensity, the heritability estimates in conjunction with genetic advance will be more effective and reliable in predicting the response to selection (Johnson *et al*., 1955). Heritability in broad sense includes both additive and non-additive gene effects. While, narrow sense heritability includes only additive components (Johnson *et al*., 1955). In the present study, heritability in broad sense was estimated. In controlled condition highest broad sense heritability was recorded in the case of spikelets per panicle (99.10) followed by grains per panicle (98.25), plant height (94.86), days to 50% flowering (94.84) and test weight (89.47) Table 2a whereas in saline condition highest broad sense heritability was recorded in the case of spikelets per panicle (99.67) followed by grains per panicle(98.82), grain yield per plant (91.03), days to 50% flowering (88.99) and plant height (85.87) Table 2b Fiyaz *et al.* (2011), Dhanwani *et al*., (2013). Maximum genetic advance was recorded for grains per panicle (62.84) followed by spikelets per panicle (60.04) showed in Table 2a in controlled condition whereas in saline condition maximum genetic advances was recorded is same as in controlled condition only the numerical value is decreased i.e grains per panicle (66.43) followed by spikelets per panicle (64.01) (Table 2b) Tiwari *et al.* (2011).

Table.1(a) Analysis of variance for randomized block design for 14 characters in rice under normal condition

Characters	**Sources of variation**		
	Replication	**Treatments**	**Error**
d.f	**2**	**29**	**58**
Days to 50 % Flowering	1.01	97.16**	1.72
Plant Height (cm)	5.99	868.07**	15.31
Panicle Bearing Tillers/ Plant	0.71	40.65**	3.21
Panicle Length (cm)	0.87	29.69**	1.29
Spikelets / Panicle	36.61	3854.61**	11.69
Grains Per Panicle	12.75	3689.27**	21.76
Spikelet Fertility (%)	13.13	34.28**	10.04
Test Weight (g)	1.97	28.49**	1.07
Biological Yield/ Plant (g)	10.89	118.12**	6.29
harvest Index (%)	13.33	119.28**	16.18
Grain Yield/ Plant (g)	1.10	6.19**	1.56
Na+	0.50	0.50**	0.17
K+	1.71	41.45**	2.37
Na+/K+	0.0004	0.0018**	0.0005

Table.2(a) Estimates of variance, phenotypic (PCV), genotypic (GCV), heritability in broad sense (h^2b) and genetic advance in per mean for 14 character in rice under normal condition

Characters	σ^2g	σ^2p	Coefficient of variation(%)		Heritability in broad sense(%)	Genetic advance as % of mean
			PCV	GCV		
Days to 50 % Flowering	31.81	33.59	5.32	5.18	94.86	10.40
Plant Height (cm)	284.25	299.56	20.09	19.57	94.89	39.28
Panicle Bearing Tillers/ Plant	12.47	15.69	33.30	29.69	79.50	54.53
Panicle Length (cm)	9.46	10.76	13.54	12.70	87.94	24.54
Spikelets/ Panicle	1280.97	1292.66	29.41	29.28	99.10	60.04
Grains Per Panicle	1222.50	1244.26	31.05	30.77	98.25	62.84
Spikelet Fertility (%)	8.07	18.12	4.60	3.07	44.59	4.22
Test Weight (g)	9.13	10.21	15.64	14.80	89.47	28.83
Biological Yield/ Plant (g)	37.27	43.57	20.74	19.18	85.56	36.55
harvest Index (%)	34.36	50.55	17.36	14.31	67.98	24.31
Grain Yield/ Plant (g)	1.54	3.11	13.88	9.78	49.64	14.20
Na+	0.11	0.28	15.80	9.91	39.39	12.82
K+	13.02	15.39	15.71	14.45	84.60	27.38
Na+/K+	0.0004	0.0008	20.11	14.95	55.29	22.90

σ^2g = Genotypic variance. σ^2p = Phenotypic variance, GCV = Genotypic coefficient of variation. PCV = Phenotypic coefficient of variation.

Table.1(b) Analysis of variance for randomized block design for 14 characters in rice under saline condition

Characters	Sources of variation		
d.f	Replication	Treatments	Error
	2	29	58
Days to 50 % Flowering	1.66	129.42**	5.12
Plant Height (cm)	4.28	493.15**	25.63
Panicle Bearing Tillers/ Plant	1.49	22.55**	1.51
Panicle Length (cm)	1.93	25.63**	1.63
Spikelets/ Panicle	4.49	3743.26**	4.08
Grains Per Panicle	3.61	3604.49**	14.23
Spikelet Fertility (%)	0.44	13.506**	1.75
Test Weight (g)	2.76	28.17**	1.08
Biological Yield/ Plant (g)	0.88	86.24**	0.95
harvest Index (%)	7.98	27.73**	4.99
Grain Yield/ Plant (g)	0.03	11.15**	0.35
Na+	0.17	0.45**	0.09
K+	4.85	36.67**	6.74
Na+/K+	0.0010	0.0016**	0.0003

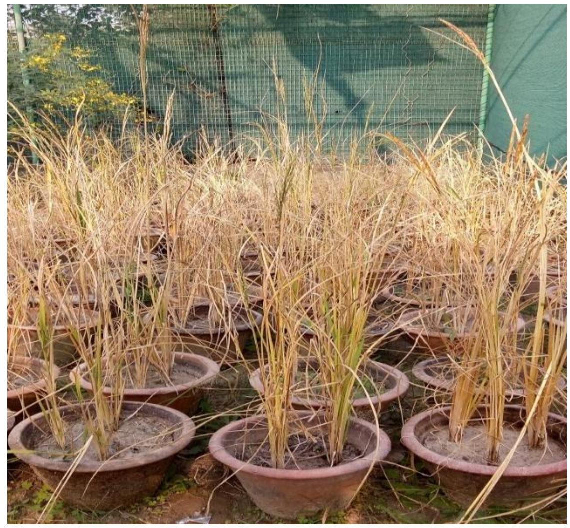
** Significant at 1% level of significance

Table.2(b) Estimates of variance, phenotypic (PCV), genotypic (GCV), heritability in broad sense (h^2b) and genetic advance in per mean for 14 character in rice under saline condition

Characters	σ^2g	σ^2p	Coefficient of variation (%)		Heritability in broad sense (%)	Genetic advance as % of mean
			PCV	GCV		
Days to 50 % Flowering	41.43	46.56	6.71	6.33	88.99	12.30
Plant Height (cm)	155.83	181.47	17.45	16.17	85.87	30.87
Panicle Bearing Tillers/ Plant	7.01	8.52	27.60	25.03	82.29	46.78
Panicle Length (cm)	7.99	9.63	14.55	13.26	82.99	24.88
Spikelets/ Panicle	1247.39	1250.47	31.17	31.12	99.67	64.01
Grains Per Panicle	1196.75	1210.98	32.63	32.44	98.82	66.43
Spikelet Fertility (%)	3.91	5.67	2.55	2.12	69.04	3.63
Test Weight (g)	9.02	10.11	16.63	15.71	89.24	30.58
Biological Yield/ Plant (g)	28.43	29.38	19.04	18.72	96.76	37.94
harvest Index (%)	7.75	12.57	8.87	6.88	60.25	11.01
Grain Yield/ Plant (g)	3.59	3.95	17.59	16.78	91.03	32.98
Na+	0.11	0.21	11.84	8.77	54.86	13.38
K+	9.97	16.71	15.49	11.96	59.67	19.04
Na+/K+	0.0005	0.0009	19.39	14.45	55.52	22.18

Fig.1 The figure showing the view at (a) Control condition and (b) Saline stress condition

(a)



(b)

In general heritability along with genetic advance can be useful in selection programmes. High heritability with high genetic advance as percent of mean indicates that these characters are largely controlled by additive gene action, which indicates that improvement in these characters is possible through mass selection and progeny selection.

In conclusion, the present investigation included 30 genotypes of rice was carried out in order to study the nature and amount of variability, heritability and genetic advance for 14 quantitative characters. Analysis of variance among 30 genotypes showed significant difference for all characters studied. Highest genotypic coefficient of variation (GCV) & phenotypic coefficient variation (PCV) was observed for panicle bearing tillers per plant followed by grains per panicle and spikelets per panicle in controlled condition whereas in saline condition highest genotypic coefficient of variation (GCV) & phenotypic coefficient variation (PCV) was observed for grains per panicle followed by spikelets per panicle and panicle bearing tillers per plant indicating that these characters could be used as selection for crop improvement. High estimates of heritability were observed for spikelets per panicle followed by grains per panicle, plant height, days to 50% flowering and test weight in controlled condition whereas in saline condition highest broad sense heritability was recorded in the case of spikelets per panicle followed by grains per panicle, grain yield per plant, days to 50% flowering and plant height. In controlled condition high genetic advance were observed for grains per panicle followed by spikelets per panicle whereas in saline condition maximum genetic advances was recorded is same as in controlled condition indicating predominance of additive gene effects and possibilities of effective selection for the improvement of these characters.

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