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## Genetic variability, heritability and genetic advance in Rice (*Oryza sativa* L.) for grain yield and its contributing attributes under sodic soil

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**Abstract**

Thirty five diverse genotypes of rice (*Oryza sativa* L.) with two checks were evaluated for twelve quantitative traits under sodic soil. The variability studies indicated that high PCV (phenotypic coefficient of variability) and GCV (genotypic coefficient of variability) was observed in case of biological yield/plant indicating greater scope of improvement through selection in the environment. Moderate PCV and GCV was observed in case of plant height (PCV =18.80%, GCV =18.52%), grain yield per plant (18.67%, 18.15%) effective tillers per plant and flag leaf area (PCV =17.47%, GCV = 14.07%). while spikelets per panicle followed by 1000 grain weight, days to 50% flowering, harvest index, days to maturity, panicle length and spikelet fertility (%) showed lower PCV and GCV. High heritability in broad sense was noted for plant height followed by days to 50% flowering, biological yield per plant, days to maturity, grain yield per plant 1000-grain weight and spikelet per panicle whereas, flag leaf area per plant, spikelet fertility and harvest index showed moderate heritability. Panicle length and effective tillers per plant recorded low heritability among all traits under study. while high genetic advance as % of mean was noted for biological yield per plant while panicle length had lowest value for this parameter. High heritability coupled with high genetic advance as per cent mean was observed for plant height and grain yield per plant indicating the involvement of additive gene action. Hence, emphasis should be given to select these quantitative traits to enhance the yield potential of rice in sodic soil.

**Keywords:** (*Oryza sativa* L.), genetic variability, heritability, genetic advance.

**Introduction**

Rice (*Oryza sativa* L.) is the world's largest food crop, providing the caloric needs of millions of people daily. It plays a pivotal role in Indian economy being the staple food for two third of the population (Singh *et al.*, 2008) [16]. It is vary paramount cereal for the people of South-East Asia where about 90 percent of the population consumers rice. The slogan- "Rice is life " because it is not only the staple food for more than 70 percent of the Indians but also a source of livelihood for about 120-150 million rural households. Utter Pradesh is also an important rice growing state in the country. In India, it is staple food for more than 65 percent of the people. It provides about 29.4 per cent of total calories/capita/day in Asian countries (FAO, 2006) [4]. In India it is grown on 43.4 million hectares of land and producing approximately 106.3 million tons rice grain with an average productivity of 2.42 tons per hectare (Anonymous, 2013-14) [2]. The presence and mangnitude of genetic variability in a gene pool is the pre-requisite of a breeding programme. Heritability estimates provide the information on the proportion of variation that is transmissible to the progenies in subsequent generations (Kumar *et al.*, 2014) [10]. Genetic advance provides information on expected genetic grain resulting from selection of superior individuals. The estimates of heritability and genetic advance are of great significance to plant breeders for developing suitable selection strategy. Sawant and patil (1995) [15] observed high values of heritability coupled with high expected genetic advance for plant height and grain yield per plant. The grain yield is a complex character, quantitative in nature and an integrated function of a number of component traits. The success of any breeding programme depends on the exploitation of existing variability and therefore, it is desirable to collect, evaluate and utilize the available diversity for crop improvement to suit specific need with regards to specific ecosystem.

**Materials and Methods**

The materials for present study comprised of thirty five genotypes along with two checks viz.

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Usar dhan- 3 and Sarjoo 52 in Rice under salt affected soil. The material comprising indigenous as well as exotic germplasm lines, exhibited wide spectrum of variation for various agronomic and morphological characters. The experiment was conducted at the Research Farm of Department of Genetics and Plant Breeding, Narendra Deva University of Agriculture & Technology, Narendra Nagar (Kumarganj), Faizabad, during *Kharif*, season of 2010 in salt affected soil (pH=9.2 and EC 1.61 dSm<sup>-1</sup>) under irrigated condition. The material was sown in Randomized complete Block Design with two replications. Each genotype was grown by transplanting single seedling per hill in single row plots of 3 meter length following inter-row and intra-row spacing of 20 cm and 15 cm, respectively. In each plot, five plants were randomly tagged and utilized to collect data on yield and its component characters viz., days to 50% flowering, days to maturity, flag leaf area (cm), plant height (cm), effective tillers per plant, panicle length (cm), spikelets per panicle, spikelet fertility (%), 1000-grain weight (g), biological yield per plant (g), harvest index (%) and grain yield per plant (g). The data were subjected to statistical analysis using genotypic and phenotypic coefficient of variation (Burton and de Vane, 1953)<sup>[3]</sup> heritability in broad sense (Hanson *et al.*, 1956)<sup>[5]</sup> genetic advance in per cent of mean (Johnson *et al.*, 1955)<sup>[8]</sup> was applied to carry out selection based on characters which would be more effective to meet higher grain yield.

### Results and Discussion

The analysis of variance revealed significant differences among treatments for all the characters under salt affected soil are presented in (Table 1). The genotypic and phenotypic coefficient of variability, heritability (%) in broad sense and genetic advance in per cent of mean are presented in (Table 2). Estimates of genetic variability revealed that the GCV and PCV were comparatively higher for biological yield/plant (PCV=21.65%, GCV=21.08%), the possibility of getting high response to selection in these mentioned traits in salt affected soil, similar findings were also reported by Suman *et al.*, (2005)<sup>[17]</sup>, Idris *et al.* (2012)<sup>[7]</sup> Sandhya (2015)<sup>[13]</sup>, Kumar *et al.* (2015)<sup>[11]</sup>. Moderate PCV and GCV was observed in case of plant height (PCV=18.80, GCV=18.52), grain yield per plant (PCV=18.67%, GCV= 18.15%), effective tillers per plant (PCV=17.97%, GCV=11.35%) and flag leaf area (PCV =17.47%, GCV=14.07%) these reports are in accordance with Hasib *et al.*, (2004)<sup>[6]</sup> while spikelets per panicle (PCV=9.78%, GCV=8.10%), followed by 1000 grain weight(PCV= 9.70%, GCV=9.30%), days to 50% flowering (PCV=8.87%, GCV=8.67%), harvest index(PCV=7.77%, GCV=5.90%), days to maturity (PCV=6.96%, GCV=6.77%), panicle length (PCV=6.13%, GCV=4.02%) and spikelet fertility (PCV=4.59%, GCV= 3.52%) showed lower PCV and GCV, indicated that these characters were highly influenced by environmental factors. The phenotypic coefficient of variation which measures total variation was found to be greater than genotypic coefficient of variation for all the characters indicating some degree of environmental influence on the traits. High heritability in broad sense was noted for plant height (97.13) followed by days to 50% flowering (95.39), biological yield per plant (94.82%), days to maturity (94.60), grain yield per plant (94.52%), 1000 grain weight

(91.26%) and spikelet per panicle (84.05%) whereas, flag leaf area per plant (64.91), spikelets fertility (59.97) (%) and harvest index (57.71 %) showed moderate heritability, these findings are in accordance Kumar and Ramesh (2008)<sup>[9]</sup> while high genetic advance as % of mean was noted for biological yield per plant (42.28%) while panicle length (5.44%) had lowest value for this parameter. High heritability coupled with high genetic advance as per cent mean was observed for Plant height and grain yield per plant, indicating the involvement of additive gene action (Sathya *et al.* (2013)<sup>[14]</sup>). Therefore, emphasis should be given to select these quantitative traits to enhance the yield potential of rice in salt affected soil. Hence, the improvement of these traits can be made through direct phenotypic selection. Heritability estimates along with genetic advance would be more useful in predicting yield under phenotypic selection than heritability estimates alone as suggested by Johnson *et al.* (1955)<sup>[8]</sup>. Days to 50% flowering, days to maturity, 1000-grain weight and spikelets per panicle showed in which high heritability accompanied by moderate genetic advance. Similar findings were also reported by Prasad *et al* 2017<sup>[12]</sup>. Moderate heritability coupled with high genetic advance was found for flag leaf area and biological yield per plant (g). Moderate heritability in broad sense coupled with low genetic advance were observed the characters viz., Spikelet fertility (%) and Harvest index (%). Effective tillers per plant showed low heritability and moderate genetic advance in per cent of mean whereas panicle length recorded low heritability and low genetic advance in per cent of mean. High heritability coupled with high genetic advance have additive gene action and may be directly utilized for rice improvement. On the other hand the character having low heritability and high genetic advance in percent of mean and high heritability and low genetic advance in percent of mean have non-additive gene action and hence heterosis breeding were rewarding for these traits. These findings are accordance with previous report of Ahmadikhan (2010)<sup>[1]</sup>, Veludandi *et al.* (2017)<sup>[18]</sup>. To break yield barrier and to attend yield plateau, the proper investigation on variability, heritability and genetic advance suggested those characters which would be taken into consideration for formulating selection breeding programme in order to bring out improvement in the studied population of rice (*Oryza sativa* L.) under sodic soil.

**Table 1:** Analysis of variance for 12 characters in rice (*Oryza sativa* L.)

Source of variation	Replications	Treatments	Error
d.f.	2	34	68
Days to 50 ( %) flowering	24.466*	226.320**	3.584
Days to maturity	26.314**	232.554**	4.343
Flag leaf area (cm <sup>2</sup> )	16.398	72.115**	11.012
Plant height (cm)	28.796*	937.041**	9.146
Effective tillers per plant	0.503	6.252**	2.092
Panicle length (cm)	1.415	4.153**	1.270
Spikelets per panicle	6.367	424.958**	25.288
Spikelet fertility (%)	11.353	33.058**	6.017
1000 grain weight (g)	0.163	16.982**	0.525
Biological yield per plant (g)	36.784	715.665**	12.803
Grain yield per plant (g)	16.595**	87.750**	1.665
Harvest index (%)	8.9506	21.897**	4.299

\*, \*\* Significant at 5 (%) and 1(%) probability level, respectively

**Table 2:** Estimates of general mean, range, coefficients of variation (%), heritability and genetic advance for 12 characters in rice (*Oryza sativa* L.)

S. No.	Characters	General mean± SE	Range		Coefficient of variation (%)		Heritability in broad sense (%)	Genetic advance in (%) of mean
			Lowest	highest	PCV	GCV		
1.	Days to 50 ( %) flowering	99.42 ± 1.09	91.33	129.67	8.87	8.67	95.391	17.44
2.	Days to maturity	128.86 ± 1.20	120.00	159.33	6.96	6.77	94.602	13.57
3.	Flag leaf area (cm <sup>2</sup> )	32.08 ± 1.92	22.30	40.12	17.47	14.07	64.91	23.35
4.	Plant height (cm)	94.97 ± 1.75	72.97	167.67	18.80	18.52	97.13	37.60
5.	Effective tillers per plant	10.38 ± 0.84	7.00	13.20	17.97	11.35	40.27	14.75
6.	Panicle length (cm)	24.41 ± 0.65	22.13	26.67	6.13	4.02	43.07	5.44
7.	Spikelets per panicle	129.09 ± 2.90	97.97	151.20	9.78	8.10	84.053	16.89
8.	Spikelet fertility (%)	85.45 ± 1.42	77.48	90.06	4.54	3.52	59.07	5.60
9.	1000 grain weight (g)	25.34 ± 0.42	18.99	28.67	9.70	9.30	91.264	18.19
10.	Biological yield per plant (g)	72.63± 2.07	34.00	95.93	21.65	21.08	64.82	42.28
11.	Grain yield per plant (g)	29.52± 0.74	15.50	37.59	18.67	18.15	94.52	36.35
12.	Harvest index (%)	41.07± 1.20	32.68	45.73	7.77	5.90	57.71	9.23

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