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## Heritability and genetic advance analysis using generation mean analysis in rice (*Oryza sativa* L.) under sodic soil

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**Abstract**

Heritability and genetic advance was estimated in rice for twenty quantitative traits in four cross combinations Swarna *Sub-1* x CSR-10, Sambha *Sub-1* x CSR-10, Pusa Sugandha -5 x CSR-10, and Pusa Sugandha -5 x NDR-2064 with respect to yield including quality attributes using generation mean analysis *viz.*, six generation (P1, P2, F1, F2, B1, B2) following Compact Family Block Design in three replications. The promising two crosses, first and second have been discussed. This experiment was conducted on Main Experimental Station of A.N.D. University of Agriculture & Technology, Narendra Nagar (Kumarganj), Ayodhya during *Kharif*, season 2019. The analysis of variance revealed that all the six generations in each cross combination were highly significant for majority of the yield contributing and quality traits indicating sufficient variability among the parents and their derivatives under study. High heritability coupled with high genetic advance were observed in the cross I for days to 50% flowering, carotene, plant height (cm), flag leaf area (cm<sup>2</sup>), number of spikelets/panicle, grains/panicle and protein content. In cross II for days to 50% flowering, chlorophyll a, carotene, total chlorophyll, plant height, number of effective tillers/plant, flag leaf area, number of spikelets/panicle, grains/panicle and protein content. which indicated better scope of their improvement through selection to enhance the yield potential of rice (*Oryza sativa* L.) under sodic soil, as these characters were predominantly governed by additive gene action possessing fixable in nature to sustain the production in target environment.

**Keywords:** Rice, Broad sense heritability, Narrow sense heritability, Genetic advance.

**Introduction**

Rice (*Oryza sativa* L.) is the most important food crop in the world and the prime staple food of Asia, for more than 2/3rd of its population. Rice is the oldest domesticated grain (~10,000 years) and most important primary source of food for more than three billion people in the world. It is grown under diverse agroclimatic conditions and over wide geographical range (Cheng *et al.*, 2005) [6]. Sodicity is the major constraints on crop production and food security and adversely impact the socioeconomic fabric of many developing countries. Rice is relatively tolerant of salt stress during germination, active tillering and grain filling and is sensitive during the early seedling and reproductive stages [panicle initiation (PI), anthesis and fertilization], (Zeng *et al.* 2001, Singh *et al.* 2008, Singh and Flowers 2010) [30, 25, 24]. It is estimated that 20% of all cultivated land and nearly half of the irrigated land is affected by salt which greatly reducing the yield of crops to well below their genetic potential. There is limited evidence at present that remediation of saline soils enhances crop yield stability (Tester and Devenport, 2003) [27]. Salinity-stress effects on crop grown are manifested by impairment of photosynthetic capacity. High amounts of sodium in the soil solution impair cell metabolism and photosynthesis by imposing an osmotic stress on cell water relations and by increasing the toxicity of sodium in the cytosol. Heritability is the proportion of observed differences on a trait among individuals of a population that are due to genetic differences. Factors including genetics, environment and random chance can all contribute to the variation between individuals in their observable characteristics. The variability of a trait describes how much that trait tends to vary in response to environmental and genetic influences. Burton (1952) [4] and Johnson *et al.*, (1955) [11] reported that to arrive at a reliable conclusion, genetic variability and heritability should jointly be considered in totality so as to bring an effective improvement in yield and in other yield related characters. Therefore, present investigation was under taken with the view to find out genetic variability in the study materials and their inheritance.

## Methods and Material

This experiment was conducted during *Kharif*, 2018 and 2019 at Student's Instructional Farm of Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya-224229 (U.P.), during *Rabi* 2018 ( off season) at Research Farm of ICAR-National Rice Research Institute (ICAR-NRRI), Cuttack, Odisha, India. Five genetically diverse genotypes are used in 4 cross combinations viz., (Swarna *Sub-1* x CSR-10), (Sambha *Sub-1* x CSR-10), (Pusa Sugandha -5 x CSR-10) and (Pusa Sugandha -5 x NDR2064) were crossed to generate six generations viz., parents (P<sub>1</sub>, P<sub>2</sub>), the F<sub>1</sub>, F<sub>2</sub>, and back crosses with both the parents (B<sub>1</sub> and B<sub>2</sub>) following generation mean analysis. The experiment was evaluated in Compact Family Block Design with three replications during *Kharif* 2019. Each plot was consisting of a double row of 3-meter-long beds with intra row spacing spaced 20 cm apart. Plant to plant distance within a row was kept 15 cm. Similar planting distance was maintained for P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub>, B<sub>1</sub> and B<sub>2</sub>. Only two crosses; first and second have been described. The desired observations were recorded on ten randomly selected plants of parents, 10 plants from F<sub>1</sub>s, 15 plants from B<sub>1</sub>, B<sub>2</sub> population and 30 plants from F<sub>2</sub> generation. The soil type of the experimental site was sandy loam, low in organic carbon, nitrogen, and phosphorus and rich in potash (pH-9.2; EC-3.2dSm-1 and ESP-45%). Data were collected on 20 characters viz., germination percentage, days to 50% flowering, chlorophyll a, chlorophyll b, carotene, total chlorophyll, days of maturity, plant height (cm), number of effective tillers/plant, panicle length (cm), flag leaf area (cm<sup>2</sup>), biological yield/plant(g), number of spikelet's/panicle, grains/panicle, spikelet fertility (%), grain size (l: b ratio), test weight (g), harvest index (%), protein content (%) and grain yield/plant (g). Heritability in broad sense (h<sup>2</sup>b) was calculated using the formula as suggested by Burton and de Vane (1953) [5]. Heritability in narrow sense (h<sup>2</sup><sub>n</sub>) was estimated following Warner (1952) [29]. pH-9.2. Genetic advance was calculated first in expected genetic advance and second in genetic advance as per cent of mean- (a) Expected genetic advance ( $\overline{Ga}$ ) was computed by using the formula of Johnson *et al.* (1955) [11]. (b) Genetic advance as per cent of mean ( $\overline{Ga}$  %)

## Results

The analysis of variance for four cross combinations have been depicted in Table-1. The analysis of variance was carried out for twenty characters of four cross families following Compact Family Block Design under sodic soil. Significance of data was tested by 'F' test. The analysis of variance of Compact Family Block design for differences between families (crosses) for twenty characters of four crosses (Swarna *Sub-1* x CSR-10), (Sambha *Sub-1* x CSR-10), (Pusa Sugandha -5 x CSR-10) and (Pusa Sugandha -5 x NDR2064) was calculated. The mean squares for differences between four crosses families were either significant or highly significant for all the twenty characters under study. The mean sum of squares due to replications were significant in case of chlorophyll content (cross II) and plant height (cross IV). The mean sum of squares due to replications were found non-significant for all the characters in all the crosses except chlorophyll content in cross II and plant height in cross IV. The mean sum of squares due to differences among generations or progenies within each cross family were significant or highly significant in all the characters except

germination percentage and chlorophyll b in cross I, chlorophyll a and chlorophyll b in cross III.

The estimates of heritability in broad sense (h<sup>2</sup>b %) for twenty characters of four crosses are given in Table-3. The broad sense heritability in cross I ranged from 19.41% (germination percentage) to 97.37% (grains/panicle). High heritability estimates (more than 60%) were noted for most of the traits, except total chlorophyll which had moderate heritability (> 40%) while chlorophyll a, chlorophyll b, biological yield/plant (g) and germination percentage having low (< 40%) heritability. (Kumar and Verma, 2016., Gyawali *et al.*, 2018 [10], Longjam and Singh, 2019) [13, 10, 16] In case of cross II, the h<sup>2</sup>b% varied between 39.01% (spikelet fertility) to 99.00 % (grains/panicle). High heritability (>60%) was observed for most of the traits, except chlorophyll b; germination percentage and spikelet fertility which had moderate heritability (> 40%). Dhanwani *et al.* 2013 [7], Lingaiah *et al.*, 2014 [15] Patel *et al.*, (2018) [22] Gyawali *et al.*, 2018 [10]; Parimala and Devi 2019 [21].

The estimates of heritability in narrow sense (h<sup>2</sup><sub>n</sub>) for twenty metric traits of four crosses are given in Table 4. In cross I, heritability in narrow sense was recorded for 50.63 % for germination percentage, 3.37% for days to 50% flowering, 2.54% for plant height, 23.93% for number of spikelets/panicle, 18.79% for grains/panicle, 36.02% for spikelet fertility (%), 32.76% for grain size (l: b ratio), 5.57% for protein content (%), 82.32% for grain yield/plant (g). For rest of the characters of cross I recorded negative values of the h<sup>2</sup><sub>n</sub>. In cross II, h<sup>2</sup><sub>n</sub> was found 65.93% for germination percentage, 92.46% for chlorophyll a, 17.01% for chlorophyll b, 56.10% for carotene, 77.69% for total chlorophyll, 2.03 for plant height, 30.29% for biological yield/plant, 5.37% for number of spikelets/panicle, 23.50% for grains/panicle, 55.89% for spikelet fertility (%), 37.38% for harvest index (%), 7.87% for protein content (%), 32.64% for grain yield/plant (g). Rest of the characters of cross II showed negative values of the h<sup>2</sup><sub>n</sub>. these results corroborates the findings of Akbar *et al.* 1986 [1], Mishra *et al.* 1990 [17], Narayanan and Sree Rangasamy 1990 [18].

Genetic advance refers to the improvement in the mean genotypic value of selected individuals over the parental population. It is influenced by the genetic variability, heritability and selection intensity. The estimates of genetic

advance in per cent of mean ( $\overline{Ga}$ ) for twenty metric traits of four crosses are given in Table 5. The estimates of genetic advance in case of cross I ranged from 0.83% (germination percentage) to 68.47% (grains/panicle). This cross exhibited high genetic advance (> 20%) for days to 50% flowering, carotene, plant height (cm), flag leaf area (cm<sup>2</sup>), number of spikelets/panicle, grains/panicle, protein content (%), Anjaneyulu *et al.*, 2010 [3] while moderate genetic advance (10% to 20%) for chlorophyll a, chlorophyll b, total chlorophyll, days of maturity, number of effective tillers/plant, panicle length (cm), harvest index (%), grain yield/plant (g) and low genetic advance (less than 10%) for germination percentage, biological yield/plant (g), spikelet fertility (%), grain size (l: b ratio), test weight (g), Parimala and Devi 2019 [21]. The genetic advance in case of cross II, ranged from 1.85% (germination percentage) to 65.51(grains/panicle) Rahman *et al.*, (2014). In this cross most of the traits show high genetic advance (> 20%) except days of maturity, panicle length (cm), biological yield/plant (g), grain size (l: b ratio), harvest index (%) had moderate level of genetic advance (10% to 20%) while germination percentage,

spikelet fertility (%) and test weight (g) showed low genetic advance (less than 10%). These results are similar to those of Kumari and Parmar (2020) [14].

## Discussion

Basic information on heritability and expected genetic advance is a prerequisite for effective improvement through selection. Genetic advance predicts the quantum gain expected by imposing a particular intensity of selection. Panse (1957) [19] emphasized the role of heritability coupled with genetic advance during selection of particular traits. In view of Panse (1957) [19] high magnitude of both the parameters is expected due to presence of additive gene action, which was further supported by Gandhi *et al.* (1964) [9]. For effective selection criteria, Dudley and Moll (1969) [8] had narrated the interpretation and use of estimate of heritability and genetic advance, since magnitude of genetic advance depends upon the heritability, intensity of the selection and phenotypic standard deviation. However, the degree of improvement attained through selection is not only dependent on heritability but also on the amount of genetic variation present in the breeding population and the extent of selection pressure applied by the breeder. High heritability ( $h^2b$ ) coupled with high genetic advance in percent of mean were recorded for days to 50% flowering, carotene, plant height (cm), flag leaf area (cm<sup>2</sup>), number of spikelets/panicle, grains/panicle, protein content in cross I; in cross II days to 50% flowering, chlorophyll a, carotene, total chlorophyll, plant height, number of effective tillers/plant, flag leaf area, number of spikelets/panicle, grains/panicle and protein content. These findings are similar to those of Akinwale *et al.*, (2011) [2] and Ketan and Sarkar (2014) [12], Tripathi *et al.*, (2018) [28].

## Conclusion

Considering the overall results, it may be concluded that

present study showed the importance of the additive as well as non-additive gene effects and thus such type of gene action can not be ignored in formulating consistent breeding programme. Genetic variability resulting from additive gene effects possessing fixable nature can be effectively utilized because of its retainment in subsequent generations by self-fertilization. It reflects that any selection procedure can be effectively utilized. For exploitation of non-additive component, which is not fixable, the breeding methodology like production of hybrids may be used depending upon biological and economic feasibility.

**Table 1:** Analysis of variance for differences between families (crosses)

Characters	D.F.	Replications	Families	Error
		2	3	6
Germination percentage		0.42	3.18**	0.11
Days to 50% flowering		0.12	12.22**	0.54
Chlorophyll a		0.095	0.176**	0.014
Chlorophyll b		0.006	0.023**	0.003
Carotene		0.009	0.022**	0.002
Total chlorophyll		0.14	0.32**	0.03
Days of Maturity		0.15	12.31**	0.15
Plant height (cm)		0.09	130.25**	0.42
Number of effective tillers/plant		0.08	0.89**	0.10
Panicle length (cm)		0.57	4.46**	0.06
Flag leaf area (cm <sup>2</sup> )		4.64	70.13**	0.35
Biological yield/plant (g)		1.79	9.47*	1.69
Number of spikelets/panicle		101.85	785.22**	8.82
Grains/panicle		33.92	873.82**	2.53
Spikelet fertility (%)		6.64	20.20**	2.25
Grain size (L: B ratio)		0.01	3.70**	0.00
Test weight (g)		0.06	2.84**	0.04
Harvest index (%)		1.83	0.36	0.23
Protein content (%)		0.00	2.58**	0.01
Grain yield/plant (g)		0.96	1.78**	0.43

**Table 2:** Analysis of variance for differences between progenies (generations) within families (crosses) for a cross I, II, III and IV in Saline sodic soil

Characters	Cross I			Cross II			Cross III			Cross IV		
	Replications	Progenies	Error	Replications	Progenies	Error	Replications	Progenies	Error	Replications	Progenies	Error
	D.F.	2	5	10	2	5	10	2	5	10	2	5
Germination percentage	2.06	3.66	2.12	2.39	3.96**	1.06	0.06	15.12**	3.59	0.06	23.02**	2.99
Days to 50% flowering	0.50	290.77**	3.17	1.72	379.12**	2.46	2.06	121.82**	2.19	6.22	36.46**	1.62
Chlorophyll a	0.020	0.399**	0.149	0.304	0.385**	0.048	0.473	0.230	0.104	0.029	0.411**	0.064
Chlorophyll b	0.005	0.055	0.026	0.004	0.068**	0.015	0.082	0.082	0.039	0.002	0.104**	0.011
Carotene	0.013	0.080**	0.013	0.026	0.059**	0.009	0.047	0.060**	0.015	0.012	0.123**	0.014
Total chlorophyll	0.05	0.66**	0.22	0.36	0.50**	0.08	0.92	0.52**	0.14	0.02	0.84**	0.10
Days of Maturity	0.50	270.50**	3.30	1.17	372.67**	2.03	1.56	111.56**	4.36	0.39	34.09**	2.32
Plant height(cm)	0.78	209.00**	2.47	0.85	199.66**	1.37	4.99	391.05**	2.88	1.42	102.83**	2.87
Number of effective tillers/plant	2.08	3.71**	0.60	0.11	3.59**	0.12	0.07	4.56**	0.13	0.08	1.33**	0.13
Panicle length (cm)	0.80	7.35**	0.24	0.18	6.04**	0.17	1.94	12.39**	0.34	1.62	1.85**	0.24
Flag leaf area (cm <sup>2</sup> )	2.04	25.19**	0.38	7.42	55.05**	0.88	18.78	96.41**	1.06	5.89	42.66**	2.15
Biological yield/plant (g)	20.24	9.98*	4.90	13.08	29.02**	3.81	6.21	45.15**	5.89	1.68	47.20**	7.81
Number of spikelets/panicle	87.35	4479.68**	53.34	128.75	5805.42**	27.41	68.20	947.25**	8.71	485.52	911.63**	310.44
Grains/panicle	94.06	4606.47**	41.16	43.57	5025.00**	16.88	48.84	740.77**	7.92	62.52	1129.02**	19.76
Spikelet fertility (%)	12.59	25.33**	2.91	6.17	17.40**	5.96	7.90	10.62**	2.67	53.73	143.26**	64.74
Grain size (L: B ratio)	0.009	0.047**	0.003	0.011	0.185**	0.011	0.129	3.679**	0.031	0.008	2.028**	0.011
Test weight (g)	0.26	1.04**	0.11	0.17	1.16**	0.12	0.04	9.34**	0.19	0.52	4.65**	0.44
Harvest index (%)	4.97	29.64**	1.22	2.94	45.66**	2.81	6.59	34.70**	1.24	0.65	16.01**	4.67
Protein content (%)	0.00	5.63**	0.07	0.05	5.23**	0.07	0.00	4.46**	0.07	0.20	0.55**	0.14
Grain yield/plant (g)	7.18	5.47**	0.76	4.57	13.60**	0.82	1.06	6.34**	0.77	0.67	10.88**	1.42



**Table 3:** Heritability in broad sense ( $h^2_b$ ) for 16 metric traits in cross I and II in sodic soil

Traits	Cross I	Cross II
Germination percentage	19.41	47.80
Days to 50% flowering	96.80	98.08
Chlorophyll a	35.95	70.20
Chlorophyll b	27.09	54.54
Carotene	62.50	65.71
Total chlorophyll	40.25	63.31
Days of Maturity	96.43	98.38
Plant height(cm)	96.54	97.97
Number of effective tillers/plant	63.57	90.60
Panicle length (cm)	90.72	92.11
Flag leaf area (cm <sup>2</sup> )	95.61	95.34
Biological yield/plant (g)	25.65	68.81
Number of spikelets/panicle	96.51	98.60
Grains/panicle	97.37	99.00
Spikelet fertility (%)	71.95	39.01
Grain size (L: B ratio)	85.06	83.64
Test weight (g)	74.54	73.92
Harvest index (%)	88.60	83.56
Protein percentage	96.25	96.24
Grain yield/plant (g)	67.23	83.90

@ indicates negative estimates

**Table 4:** Heritability in narrow sense ( $h^2_n$ ) for 20 metric traits in cross I-IV in sodic soil

Traits	Cross I	Cross II
Germination percentage	50.63	65.93
Days to 50% flowering	3.37	@
Chlorophyll a	@	92.46
Chlorophyll b	@	17.01
Carotene	@	56.10
Total chlorophyll	@	77.69
Date of Maturity	@	@
Plant height	2.54	2.03
Number of effective tillers/plant	@	@
Panicle length (cm)	@	@
Flag leaf area (cm <sup>2</sup> )	@	@
Biological yield/plant (g)	@	30.29
Number of spikelet's/panicle	23.93	5.37
Grains/panicle	18.79	5.25
Spikelet fertility (%)	36.02	55.89
Grain size (L: B ratio)	32.76	@
Test weight (g)	@	@
Harvest index (%)	@	37.38
Protein content (%)	5.57	7.87
Grain yield/plant (g)	82.32	32.64

**Table 5:** Genetic advance in per cent of mean (Ga%) for twenty traits in four crosses in F<sub>2</sub> generation under Saline sodic soil

Traits	Cross I	Cross II
Germination percentage	0.83	1.85
Days to 50% flowering	21.30	24.92
Chlorophyll a	16.78	26.49
Chlorophyll b	15.67	30.12
Carotene	38.06	32.39
Total chlorophyll	17.93	21.57
Days of Maturity	15.58	18.67
Plant height(cm)	21.00	20.59
Number of effective tillers/plant	17.76	21.05
Panicle length (cm)	14.20	13.07
Flag leaf area (cm <sup>2</sup> )	23.61	31.16
Biological yield/plant (g)	3.03	11.21
Number of spikelets/panicle	61.80	63.20
Grains/panicle	68.47	65.51
Spikelet fertility (%)	5.23	2.80
Grain size (L: B ratio)	8.79	15.43
Test weight (g)	4.48	4.62
Harvest index (%)	14.64	17.65
Protein percentage	30.50	29.31
Grain yield/plant (g)	11.60	21.85

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