

## Genetic analysis of grain yield and its associated traits in diverse salt-tolerant rice genotypes under coastal salinity condition

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### Abstract

A set of eighty-two salt-tolerant rice genotypes were evaluated under coastal salinity conditions for estimating genetic variability, correlation, and PCA in ten quantitative traits. Among the traits, grains per panicle recorded the highest Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) values, while days to maturity had the lowest PCV and GCV values. Heritability in broad sense was highest for grain yield followed by panicle length, per cent fertility, days to 50 per cent flowering and days to maturity. High heritability coupled with high genetic advance as percent of mean was observed for grains per panicle, per cent fertility and grain yield. Characters viz. panicle length, grains per panicle, per cent fertility and test weight showed positive and significant correlation with grain yield, whereas days to 50 per cent flowering and maturity days showed a significant and negative correlation with grain yield. Principal Component Analysis (PCA) of ten characters presented 3 principal components with eigen values greater than one, which accounted for 68.44% of the total variation. PCA revealed that five quantitative characters viz., per cent fertility, number of tillers, number of productive tillers, plant height and grain yield significantly influenced the variation in these cultivars. The present work identified the presence of sufficient amount of genetic variability for all the traits in the studied genotypes.

**Keywords:** Advanced breeding lines, correlation, heritability, principal component analysis, salinity

## 1. Introduction

Soil salinity is a major abiotic stress affecting the production and productivity of rice crop worldwide. In India, salinity is the most prevalent problem in the areas along the coastal lines. Nearly 30 per cent of the total salt-affected land is in the coastal regions of the country (Yadava *et al.* 1983). The area under salt-affected soil is increasing every year due to several factors like change in climate, sea-level rise, and excessive irrigation without proper drainage etc. (Hazra *et al.* 2002). Salt affected soils in Goa state are called locally *Khazan* lands. They are low lying areas, often inundated with seawater, prone to frequent floods, and have a poor drainage system. Rice is the only crop cultivated during the monsoon season and after the harvest of the rice crop, the same fields are

utilized for prawn culture. Farmers prefer to grow mostly local salt-tolerant landraces like *Korgut*, *Asgo* and *Shidde* due to their inbuilt tolerance to salinity and adaptation to waterlogged conditions (Manohara *et al.* 2013). These local varieties are very poor yielders and need to be replaced by the high-yielding varieties with combined tolerance to salinity, submergence and water stagnation.

Genetic variability is a prerequisite for initiating selection in any crop breeding program. Selection will be effective when there is sufficient variability among the breeding materials. Besides, information on the association between grain yield and its component traits, and association among different component traits are important for the selection of traits contributing to grain

yield (Ogunbaya *et al.* 2014). The present study was hence carried out with the objectives of estimating the genetic variability, correlation, and PCA in a set of 82 diverse salt-tolerant rice genotypes.

## 2. Material and methods

The study was carried out during the wet season of 2018 in the experimental site (15°33' N and 73°53' E 3M MSL) located in Chorao Island, North Goa district, Goa State. The trial comprised of 82 rice genotypes (Table 1) of which 75 were test entries and seven were check varieties (CSR 10, CSR 27, CSR 36, CST 7-1, Pusa 44, NSICR 222 and local check variety Goa Dhan 2). All these genotypes were received as part of the Salinity Tolerant Breeding Network (STBN) component of the Stress Tolerant Rice for Africa and South Asia (STRASA) project (IRRI-ICAR collaborative project). The salinity of the soil measured as  $EC_{(1:2.5)}$  (1 part of soil and 2.5 parts of distilled water) was varied from 0.70  $dSm^{-1}$  in the month of July (planting) to 9.64  $dSm^{-1}$  during October month. Soil pH ranged from 6.77 to 7.01. The trial was laid out in an augmented block design in three blocks accommodating 32 entries (25 test entries + 7 check entries) in each of the blocks. The genotypes were planted at 20 cm x 15 cm spacing in 8 rows of 3-meter length with a plot size of 4.8 m<sup>2</sup>. Recommended practices were followed to raise a good crop. The observations were recorded on five randomly selected plants per genotype for the traits viz., plant height, number of tillers, number of productive tillers, panicle length, grains per panicle, per cent fertility, and 1000 grain weight. For days to 50% flowering, days to maturity, and grain yield observation was recorded as per plot basis. The data of 82 genotypes was statistically analyzed using Window stat (Genetic variability and correlation) and SPSS (Principal Component Analysis) software.

## 3. Results and discussion

### 3.1. Genetic variability

The analysis of variance (ANOVA) indicates significant differences among the tested genotypes for all the ten traits. This suggests the presence of an ample amount of variability in the material used in the present investigation.

The amount of genetic variability present was measured in terms of genetic parameters such as coefficient of variation (CV), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in

broad sense ( $h^2$ ), and genetic advance as percent of mean (GA) (Table 2). CV which measures the dispersion of the variable ranged from 4.7% for days to maturity to 33.37% for grains per panicle. PCV ranged from 4.14% to 30.62% and GCV from 3.66% to 24.36%. High PCV and GCV was observed only for grains per panicle. Higher PCV and GCV for grains per panicle has earlier been reported by Fiyaz *et al.* (2011) in their study on 33 rice genotypes under alkaline soil conditions. Manohara *et al.* (2015) however reported moderate PCV and GCV values for grains per panicle in a set of 31 diverse salt-tolerant rice genotypes grown under coastal saline soils. Characters viz., number of tillers, number of productive tillers, and per cent fertility showed high PCV and moderate GCV. Grain yield and panicle length recorded moderate PCV and GCV values. Similar reports for grain yield were earlier reported by Girma *et al.* (2018) in 64 rice genotype set. PCV and GCV for days to 50% flowering, days to maturity, and plant height were low, which was in agreement with the findings of Ogunbayo *et al.* (2014). The low variability indicates little scope for improvement of these traits.

Johnson *et al.* (1955) classified broad sense heritability as low (<30%), medium (30% to 60%), and high (>60%). In this study, heritability varied from 23.19% for plant height to 85.06% for grain yield. Heritability was low to medium for characters plant height (23.19%), number of tillers (23.58%), number of productive tillers (42.21%), and test weight (59.36%) indicating the influence of environment on these traits. Therefore, direct selection for these traits may not be effective. The rest of the characters viz., grain yield (85.06%), panicle length (79.55%), per cent fertility (78.60%), days to 50% flowering (74.76%), and days to maturity (78.27%) showed high heritability indicating that these traits can easily be improved through selection. Since heritability alone does not always indicate genetic gain, heritability coupled with genetic advance is more effective for selection (Johnson *et al.* 1955). Genetic advance as percent of mean in this study ranges from 4.32 for plant height to 39.91 for grains per panicle. High heritability coupled with high genetic advance as per cent mean was recorded for grains per panicle, per cent fertility, and grain yield. This suggests these traits are less influenced by the environment, governed by additive gene action and therefore selection can be practiced based on phenotypic performance. Similar findings were reported by several workers viz., Girish *et al.* (2006), Girma *et al.*

**Table 1.** Details of the 82 rice genotypes used in the study and their source.

Sno.	Genotype	Source	Sno.	Genotype	Source	Sno.	Genotype	Source
1	CSR2016-IR18-12	CSSRI, Karnal	29	CR3882-7-1-6-2-2-1	NRRI, Cuttack	57	NDRK 11-29	NDUAT, Faizabad
2	CSR2016-IR18-15	CSSRI, Karnal	30	CR3881-4-1-3-7-2-3	NRRI, Cuttack	58	NDRK 11-30	NDUAT, Faizabad
3	CSR2016-IR18-17	CSSRI, Karnal	31	CR3881-M-3-1-5-1-1-1	NRRI, Cuttack	59	CR3882-7-1-6-2-1-3	NRRI, Cuttack
4	CSR-2748-4441-193	CSSRI, Karnal	32	CR3903-161-1-3-2	NRRI, Cuttack	60	CR3884-244-87-4-1-3	NRRI, Cuttack
5	CSR2016-IR18-1	CSSRI, Karnal	33	IR84649-81-4-13B/CR3397-S-B-4B-1	NRRI, Cuttack	61	CR2851-S-1-62B-4-1	NRRI, Cuttack
6	CSR2016-IR18-8	CSSRI, Karnal	34	IR83421-6-B-3-1-1/CR3364-S2B-14-2B	NRRI, Cuttack	62	RAU1397-18-3-7-9-4-7	Pusa, Bihar
7	CSR2016-IR18-2	CSSRI, Karnal	35	CR2851-S-B-1-2B-1	NRRI, Cuttack	63	RAU1525-1-2	Pusa, Bihar
8	CSR2016-IR18-6	CSSRI, Karnal	36	CR3437-1*S-200-83-1	NRRI, Cuttack	64	PAU5563-23-1-2	PAU, Ludhiana
9	CSR-2748-197	CSSRI, Karnal	37	PAU3835-36-6-3-3-4	PAU, Ludhiana	65	PAU5564-18-1-2	PAU, Ludhiana
10	CSR2016-IR18-3	CSSRI, Karnal	38	PAU5563-23-1-1	PAU, Ludhiana	66	CSAR17135	CSA, Kanpur
11	CSR2016-IR18-18	CSSRI, Karnal	39	PAU7114-3480-1-1-10	PAU, Ludhiana	67	CSAR17817	CSA, Kanpur
12	CSR2016-IR18-7	CSSRI, Karnal	40	CSAR1604	CSA, Kanpur	68	CSR TPB2	CSSRI, Karnal
13	CSR2016-IR18 - 5	CSSRI, Karnal	41	CSAR1620	CSA, Kanpur	69	CSR11-121	CSSRI, Karnal
14	CSR-2748-4441-195	CSSRI, Karnal	42	CSAR1610	CSA, Kanpur	70	IRLON-GSR5	IRRI, Philippines
15	CSRRIL-01-IR75	CSSRI, Karnal	43	KS-12	CCARI, Goa	71	IRLON-GSR9	IRRI, Philippines
16	CSR2016-IR18-9	CSSRI, Karnal	44	JK 58	CCARI, Goa	72	CSR89-IR15	CSSRI, Karnal
17	CSRRIL-01-IR165	CSSRI, Karnal	45	JK 238	CCARI, Goa	73	CSR2711-143	CSSRI, Karnal
18	CSR-C27SM-117	CSSRI, Karnal	46	CARI Dhana 6	CIARI, Portblair	74	CSR11-143	CSSRI, Karnal
19	CSR2016-IR18-10	CSSRI, Karnal	47	CARI Dhan7	CIARI, Portblair	75	CSR11-192	CSSRI, Karnal
20	CSR2016-IR18-11	CSSRI, Karnal	48	RP5706-120-7-2-2	IIRR, Hyderabad	76	CSR 10 (check 1)	Early salinity check
21	CSR2016-IR18-14	CSSRI, Karnal	49	RP5680-110-52-4-3	IIRR, Hyderabad	77	CSR 27 (check 2)	Inland saline check
22	RP5683-101-30-2-3-1	IIRR, Hyderabad	50	KRI5075	PAJANCOA, Karaikal	78	CSR 36 (check 3)	Alkaline check
23	RP5694-36-9-5-1-1	IIRR, Hyderabad	51	KRI5100	PAJANCOA, Karaikal	79	CST 7-1 (check 4)	Coastal saline check
24	CR3878-245-4-1	NRRI, Cuttack	52	KRI5103	PAJANCOA, Karaikal	80	Pusa 44 (check 5)	Sensitive check
25	CR3890-35-1-3-4	NRRI, Cuttack	53	NDRK 11-20	NDUAT, Faizabad	81	NSIRC 222 (check 6)	Sensitive check
26	CR3887-15-1-2-1	NRRI, Cuttack	54	NDRK 11-26	NDUAT, Faizabad	82	Goa dhan 2 (check 7)	Locally adapted variety
27	CR3883-3-1-5-2-1-2	NRRI, Cuttack	55	NDRK 11-27	NDUAT, Faizabad			
28	CR3884-244-8-5-6-1-1	NRRI, Cuttack	56	NDRK11-28	NDUAT, Faizabad			

(2018), Kishore *et al.* (2015) and Manohara *et al.* (2015) for grain yield and Akhtar *et al.* (2010), Girish *et al.* (2006) and Fiyaz *et al.* (2011) for grains per panicle. On contrary, high heritability coupled with moderate genetic advance in percent of mean was observed for panicle length indicating the role of both additive and non-additive gene effects for control of the characters. The results are in agreement with the findings of Singh *et al.* (2013). High heritability and low genetic advance shows the non-additive type of gene action and was observed in traits days to 50 per cent flowering and days to maturity. Similar findings were observed for days to maturity by Akhter *et al.* (2010) in their study of genetic variability in 29 F<sub>4</sub> rice lines screened for reproductive stage salt tolerance.

### 3.2 Correlation

The correlation analysis among the ten characters studied is presented in Table 3. Grain yield recorded a significant and positive association with per cent fertility (0.584\*\*), grains per panicle (0.483\*\*), test weight (0.455\*\*), and panicle length (0.252\*). This suggested an increase in grain yield is associated with an increase in these characters. Therefore, priority should be given to these traits while making the selection for yield improvement. Similar findings were earlier reported by Mohanty *et al.* (2012) for panicle length and grains per panicle in a set of 40 diverse rice genotypes. Girish *et al.* (2006) found a positive and significant correlation of grain yield with grains per panicle, test weight, and panicle length in an indica × japonica Recombinant Inbred Line (RIL) population under aerobic conditions. Krishnamurthy *et al.* (2014) also found similar findings in their study on 34 rice genotypes under salinity conditions. Gopikannan and Ganesh (2013) observed a similar significant positive correlation of grain yield with the number of filled grains per panicle, panicle length, spikelet fertility, and number of tillers under sodic conditions. On the contrary, an association of grain yield with days to 50 per cent flowering (-0.464\*\*) and days to maturity (-0.566\*\*) was significant and negative indicating a decrease in grain yield in the late-maturing genotypes. This has resulted from the increased levels of salinity during the end of the cropping season due to a decline in rainfall, which in turn affected important grain yield component traits like panicle length, grains per panicle, per cent fertility, and test weight in the late-maturing

genotypes. This is evident from the significant negative correlation of panicle length (-0.291\*\*, -0.171), grains per panicle (-0.397\*\*, -0.437\*\*), per cent fertility (-0.434\*\*, -0.523\*\*) and test weight (-0.301\*\*, -0.309\*\*) with days to maturity and days to 50% flowering. Characters like plant height, the number of tillers, and the number of productive tillers did not show any significant correlation with grain yield under saline conditions. Abdullah *et al.* (2001) reported that test weight, number of tillers, plant height, panicle length, and quantity of grains start to rapidly decrease with an increase in salinity levels.

### 3.3 Principal component analysis

PCA identifies traits that contribute to most of the variation within a group of genotypes. In this study, the first three components recorded an eigenvalue greater than one (Table 4). They together contributed 68.44% of the total variation. Principal component 1 (PC1), with an eigenvalue of 3.62, contributed 36.17% of the total variation, while PC2 with an eigenvalue of 1.90 accounted for 18.99% of the total variation. PC3 had an eigenvalue of 1.33 and contributed 13.28% to the observed variability. In the first principal component, traits such as days to maturity, per cent fertility, and grain yield contributed greater for total variation due to their high loading. The number of tillers and number of productive tillers per hill are the important traits in the second principal component. In the third principal component, plant height is the greatest contributor to the observed variation. Similarly, Sanni *et al.* (2012) explained 72.24% of the total variability using the first three principal components among 430 rice accessions from Africa. Similar results were found in the work of Girma *et al.* (2018) and Manohara *et al.* (2019) where 64% and 80.43% of total variation explained by the first three and four principal components, respectively. Their results also revealed that days to heading, days to maturity, and productive tillers per hill are the major factors contributing to the maximum variability among the studied genotypes.

## 4. Conclusion

The results indicate the presence of adequate genetic variability in the studied genotypes. Characters viz., grains per panicle, per cent fertility, panicle length, and test weight showed a strong and positive correlation with

**Table 2.** Estimates of mean, variability, heritability and genetic advance for ten characters in 82 rice genotypes

Characters	Mean ( $\mu$ )	SEm	Lowest	Highest	Range	SD	CV (%)	PCV (%)	GCV (%)	h <sup>2</sup> (%)	GAM
DFF	108.8	0.9	92	126	34	7.81	7.18	6.30	5.45	74.76	9.71
DM	134.8	0.7	114.5	149	34.5	6.34	4.7	4.14	3.66	78.27	6.68
PHT	85.8	1.1	59	128.9	69.9	10.06	11.72	9.06	4.36	23.19	4.32
NOT	4.8	0.1	1.9	8.3	6.4	1.25	26.16	22.58	10.96	23.58	10.97
NPT	4.4	0.1	1.92	8.6	6.68	1.21	27.36	22.60	14.68	42.21	19.65
PL	21.9	0.3	16.5	32.5	16	2.74	12.52	11.45	10.22	79.55	18.77
G/P	72	2.7	26.6	136.1	109.5	24.04	33.37	30.62	24.36	63.26	39.91
%F	63.5	1.6	32.8	91.6	58.8	14.29	22.51	20.08	17.80	78.60	32.52
TW	19.4	0.3	15	26.7	11.7	2.7	13.94	12.10	9.32	59.36	14.79
GY	973.4	25.7	661.6	1627	965.4	233	23.93	16.91	15.59	85.06	29.63

SEM: Standard error of mean; SD: Standard deviation; CV: Coefficient of variation; PCV: Phenotypic coefficient of variation; GCV: Genotypic coefficient of variation; h<sup>2</sup>: Heritability in broad sense; GAM: Genetic advancement as percent of mean.

DFF: Days to 50% flowering; DM: Days to maturity; PHT: Plant height; NOT: Number of tillers; NPT: Number of productive tillers; PL: Panicle length; GPP: Grains per panicle; %F: Per

**Table 3.** Phenotypic correlation coefficients among ten yield components in 82 rice genotypes under coastal salinity condition

	DM	PHT	NOT	NPT	PL	G/P	%F	TW	GY
DFF	0.611**	-0.06	0.074	0.088	-0.291**	-0.397**	-0.434**	-0.301**	-0.464**
DM		0.178	0.162	0.156	-0.171	-0.437**	-0.523**	-0.309**	-0.566**
PHT			-0.076	-0.057	0.261*	0.101	-0.019	0.186	0.014
NOT				0.968**	-0.005	-0.197	-0.217	-0.004	-0.062
NPT					-0.049	-0.201	-0.199	-0.022	-0.08
PL						0.311**	0.129	0.309**	0.252*
GPP							0.727**	0.240*	0.483**
%F								0.447**	0.584**
TW									0.455**

\*Significant at 5%; \*\* Significant at 1%

Abbreviations are same as in table 1.

**Table 4.** Eigen value of three major principal components and factor loadings (eigen vectors) for different yield attributing traits

	Principal components						
	PC1	PC2	PC3				
Eigen values	3.62	1.9	1.33	NOT	-0.09	0.984	-0.009
% of Variance	36.17	18.99	13.28	NPT	-0.097	0.978	-0.026
Cumulative % variance	36.17	55.16	68.44	PL	0.279	0.035	0.686
Characters	Eigen vectors			GPP	0.707	-0.191	0.191
DFF	-0.712	-0.002	-0.129	%F	0.818	-0.169	0.033
DM	-0.819	0.078	0.164	TW	0.521	0.09	0.445
PHT	-0.141	-0.1	0.836	GY	0.795	0.025	0.119

Abbreviations are same as in table 1.

grain yield. Further, PCA revealed characters viz., per cent fertility, number of tillers, number of productive tillers, plant height, and grain yield contributed for most of the variation in the studied genotypes. Therefore, emphasis may be given for selecting such traits under coastal salinity conditions to bring genetic improvement in rice.

## 6. References

1. Abdullah Z, MA Khan and TJ Flowers. 2001. Causes of sterility in seed set of rice under salinity stress. *Journal of Agronomy and Crop Science* **167**: 25-32.
2. Akhtar S, MM Islam, SN Begum, J Halder, MK Alam and AC Manidas. 2010. Genetic analysis of F4 rice lines for salt tolerance at the reproductive stage. *Progressive Agriculture* **21(1 & 2)**, 31-38.
3. Fiyaz AR, KT Ramya, BC Chikkalingaiah, BC Ajay, C Girish and RS Kulkarni. 2011. Genetic variability, correlation and path coefficient analysis studies in rice (*Oryza sativa* L.) under alkaline soil condition. *Electronic Journal of Plant Breeding* **2(4)**: 531-537.
4. Girish TN, TM Girisha, MG Vaishali, BG Hanamareddy and S Hittalmani. 2006. Response of a new IR50/Moroberekan recombinant inbred population of rice (*Oryza sativa* L.) from an indica x japonica cross for growth and yield traits under aerobic conditions. *Euphytica* **152**: 149-161.
5. Girma BT, MA Kitil, DG Banje, HM Biru and TB Serbessa. 2018. Genetic variability study of yield and yield related traits in rice (*Oryza sativa* L.) Genotypes. *Advances in Crop Science and Technology* **6**: 381. doi:10.4172/2329-8863.1000381.
6. Gopikannan M and SK Ganesh. 2013. Genetic analysis of sodicity tolerance in rice (*Oryza sativa* L.) *International Journal of Agriculture Environment and Biotechnology* **8(12)**: 1571-1578.
7. Hazra S, T Ghosh, R Dasgupta and G Sen. 2002. Sea level and associated changes in the Sundarbans. *Science & Culture* **68**: 309-332.
8. Johnson HW, HF Robinson and RE Comstock. 1955. Estimates of genetic and environmental variability in soybeans. *Agronomy Journal* **47**: 314-318.
9. Kishore NS, T Srinivas, U Nagabhusanam, M Pallavi and SK Sameera. 2015. Genetic variability, correlation and path analysis for yield and yield components in promising rice (*Oryza sativa* l.) genotypes. *SAARC Journal of Agriculture* **13(1)**: 99-108.
10. Krishnamurthy SL, SK Sharma, RK Gautam and V Kumar. 2014. Path and association analysis and stress indices for salinity tolerance traits in promising rice (*Oryza sativa* L.) genotypes. *Cereal Research Communications* **42**: 474-483.
11. Manohara KK and NP Singh 2013. Genetic divergence among rice landraces of Goa. *Oryza*, **50(2)**: 100-104.
12. Manohara KK and NP Singh. 2015. Genetic variability, correlation and path analysis in rice (*Oryza sativa* L.) under coastal salinity conditions of Goa. *Journal of the Indian Society of Coastal Agricultural Research* **33(1)**: 34-39.
13. Manohara KK, SP Bhosle and NP Singh. 2019. Phenotypic diversity of rice landraces collected from Goa state for salinity and agro-morphological traits. *Agricultural Research* **8(1)**:1-8. <https://doi.org/10.1007/s40003-018-0354-2>.
14. Mohanty N, MR Sekhar, DM Reddy and P Sudhakar. 2012. Genetic variability and character association of agro-morphological and quality characters in rice. *Oryza* **49(2)**: 88-92.
15. Ogunbayo SA, M Sie, DK Ojo, KA Sanni, MG Akinwale, B Toulou, A Shittu, EO Idehen, AR Popoola, IO Daniel and GB Gregorio. 2014. Genetic variation and heritability of yield and related traits in promising rice genotypes (*Oryza sativa* L.). *Journal of Plant Breeding and Crop Science* **6**: 153-159. doi: 10.5897/jpbs2014.0457.
16. Sanni KA, I Fawole, SA Ogunbayo, DD Tia, EA Somado, K Futakuchi, M Sie, FE Nwilene, RG Guie. 2012. Multivariate analysis of diversity of landrace rice germplasm. *Crop Science* **52**:494-504.

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17. Singh CM, GS Babu, K Binod and S Mehandi. 2013. Analysis of quantitative variation and selection criteria for yield improvement in exotic germplasm of upland rice (*Oryza sativa* L.). *Bioscan* **8(2)**: 485-492.
18. Yadav JSP, AK Bandopadhyay and BK Bandyopadhyay. 1983. Extent of coastal saline soils of India. *Journal of Indian Society of Coastal Agricultural Research* **1(1)**: 1-6.