



RESEARCH ARTICLE

Assessment of genetic variability, character association and path analysis for yield and its contributing characters in rice (*Oryza sativa* L.) under saline conditions

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Abstract

The present investigation was conducted to access genetic variability, trait association and their contribution to grain yield in rice under saline condition. A total of 24 rice genotype including 4 check varieties CSR23, CSR36, CSR10 and NDR 2008 were evaluated during the kharif season of 2022 in a randomized block design (RBD) with 3 replications. Observation was recorded for 13 agronomic traits including flowering time, plant height, yield components and grain yield per plant. High phenotypic and genotypic coefficient of variation was observed for flag leaf area and grains per panicle indicating substantial variability among the genotype. High heritability coupled with high genetic advance was recorded for days to 50 % flowering, days to maturity, grains per panicle and number of fertile spikelets per panicle suggesting the predominance of additive gene action. Grain yield per plant showed a significant positive correlation with harvest index and productive tillers. Path coefficient analysis revealed that harvest index and biological yield per plant exerted the highest positive direct effects on grain yield. Cluster analysis based on Mahalanobis D² statistics, grouped the 24 genotypes into 5 distinct clusters indicating considerable genetic divergent. The results suggested that traits such as harvest index, biological yield and grain per panicle could be effective selection criteria for improving rice yield under saline environment.

Keywords: cluster analysis; correlation coefficient; genetic advance; heritability; salinity tolerance; variability

Introduction

As the primary source of calories for over half of the world's population, rice is the most significant staple food crop. In addition to serving as a basic good and the main source of nutrition for over half of the world's population, rice has a significant impact on global concerns including food security and development. Total cropped area under rice cultivation is 164.19 million hectares, while production is projected at 511.7 million tons (1). India had an approximately 45 million hectares of land for cultivation of rice. India is expected to produce a record 127.93 million tons of rice in 2021–22 (1, 2). Salinity is one of the major abiotic stresses that greatly affect growth and productivity of plants. As salt accumulates in the soil in some inland and coastal saline tracts, more and more land is becoming unusable every year. The effects of salinity are particularly noticeable on one-third of the world's irrigated land. The area under problem soil has increased from 220 lakh hectares to 243 lakh hectares, comprising of alkali soils- 37.0 lakh hectares, saline soil including coastal saline area account of 27.0 lakh hectares and acid soil 179.0 lakh hectares (3). As such, about 4 lakh hectares is annually increasing under such soil. Successful selection in crop breeding depends on a clear understanding of genetic variability and the association of morpho-agronomic traits with grain

yield, as direct selection for yield under complex environmental condition may be misleading. The correlation coefficient assists to determine the way of various traits relate to grain yield. Breeders can choose genotypes possessing sets of desired qualities by studying associations among various traits. Salinity is one of the serious abiotic stresses limiting rice productivity worldwide, rice is generally considered moderately sensitive to salinity particularly during the seedling and reproductive stages. Several studies have reported significant reduction in plant growth, spikelet fertility and grain yield under saline condition. Previous investigations have highlighted the importance of traits such as harvest index, biological yield and productive tillers in improving yield under salt stress. Genetic variability and trait association studies under saline environment provide useful information for identifying tolerant genotype and important selection criteria. Therefore, evaluation of rice germplasm under saline condition is essential to identify promising genotypes and traits for breeding salt tolerant varieties. Despite extensive research on salinity stress in rice, limited information is available regarding the combined evaluation of genetic variability, trait association and genetic divergent among rice genotype under saline conditions. Understanding the relationship among yield component and their direct and indirect contribution to grain yield

is essential for effective selection in breeding program targeting salinity tolerance. Therefore, the present study was undertaken to assess genetic variability, correlation and path coefficient analysis and genetic divergent among rice genotype grown under saline condition in order to identify important traits and promising genotypes for improving yield under saline stress.

The present investigation was undertaken with the following objectives:

1. To estimate genetic variability, heritability and genetic advance for yield and its contributing traits in rice under saline conditions.
2. To study the association among yield and yield component traits through correlation and path correlation analysis.
3. To assess genetic divergent among rice genotype using Mahalanobis D^2 cluster analysis for identification of suitable parents in breeding program.

Materials and Methods

The present investigation was evaluated with 24 genotypes including 4 check varieties viz., CSR23, CSR36, CSR10 and NDR 2008 in randomized block design (RBD) with 3 replications at Genetics and Plant Breeding Farm, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya (26.47° N latitude and 81.85° E longitude) during the kharif season 2022. The experimental soil was sandy loam with saline characteristics having an electrical conductivity of 4.3 dSm⁻¹ and ESP of 23 (4). Soil salinity was measured using a digital conductivity meter following the standard method (5). The salinity conditions were naturally occurring in the experimental field rather than artificially imposed, Rice is more sensitive to salinity during the seedling and reproductive stages and therefore the crop experienced natural salinity stress throughout the growing period under field conditions. Each salinity level is comparable to those commonly found in salt affected rice growing regions of Uttar Pradesh. The experimental material exhibited a wide spectrum of variation for agronomical and morphological characters with diverse genetic background and reported performance under saline environments. The checks used in the experiment were well adopted varieties of the saline region. The details of these genotypes/ lines presented in Table 1. Each genotype was planted with a spacing of 20 cm between rows and 15 cm between plants with plot size 3 × 2 m consisting of 10 rows per plot. The recommended cultural approaches will be used to develop a healthy normal crop. Recommended agronomic practices for rice cultivation in saline soil were followed fertiliser was applied at the recommended dose of 120:60:40 kg N: P₂O₅: K₂O per hectare and nitrogen (N) was applied in 3 splits: basal, tillering and panicle initiation stages. Standard irrigation and weed management practices were followed to maintain uniform crop growth. We omit the border rows to lessen the border impact and 5 randomly selected plants from each plot were tagged for recording observations on 13 traits. However, days to 50 % flowering and days to maturity were recorded on a plot basis as the plants within each plot were grown under uniform field conditions. The other observations, however, are made on a plant-by-plant basis viz., plant height (cm), number of productive tillers/plants, panicle length (cm), grains/ panicle, flag leaf area (cm²), number of fertile spikelets/panicle, spikelets fertility (%), biological yield/plant (g), harvest index (%), 1000-grain weight (g) and grain yield/plant (g).

The mean data were subjected to analysis of variance (ANOVA) following the RBD (6). Heritability (7), genetic advance (8), correlation coefficients (9), path-coefficient analysis (10), genetic divergence analysis (11) were estimated. All statistical analysis were carried out using R statistical software (version 4.2.2).

The variability for different characters was estimated (12), the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was computed as,

$$PCV = \frac{\text{Phenotypic standard deviation } (\sigma_p)}{\text{Mean } (X)} \times 100$$

$$GCV = \frac{\text{Genotypic standard deviation } (\sigma_g)}{\text{Mean } (X)} \times 100$$

Heritability in broad sense (h^2) was calculated using the formula (13),

$$h^2b = \frac{\sigma^2g}{\sigma^2g + \sigma^2e} \text{ or } \frac{\sigma^2g}{\sigma^2p} \times 100$$

where,

σ^2g = Genotypic variance

σ^2p = Phenotypic variance

σ^2e = Environmental variance

Genetic advance (GA) was estimated (14),

$$GA (\%) = \frac{\sigma^2g}{\sigma^2p} \times K \times \sigma^2p$$

Where,

K = Selection differential at 5 % selection intensity (2.06).

Genetic advance as per cent of mean was calculated as follow:

$$GA (\%) = \frac{\text{Genetic advance}}{\bar{x}} \times 100$$

Where, $\bar{x}$ = Grand mean of character under consideration

The simple correlation between different characters at genotype (g) and phenotype (p) level were estimated as follow (9):

Correlation coefficient (r) between character x and y ,

$$r = \frac{Cov_{xy}}{\sqrt{\text{Var. } x \times \text{Var. } y}}$$

Where

r_{xy} = Correlation coefficient between character x and y

Cov xy = Covariance between character x and y

Var. x = Variance for x character

Var. y = Variance for y character

The significance of correlation coefficient was tested by comparing at an appropriate level of significance. The significance value (r) at ($n - 2$) d.f., where 'n' is number of varieties.

The significance of phenotypic correlation coefficient was tested against ($n - 2$) d.f. at 5 and 1 % probability level, where 'n' is the number of genotypes on which observation was recorded. The significance of environmental correlation coefficient was tested against error d.f. -1 at 5 and 1 % probability level.

Path-coefficient was carried out and the grain yield was assumed to be dependent variable (effect) which was influenced by all the 13 characters, the independent variables (causes), directly as

well as indirectly through other characters (10). The variation in grain yield unexplained by the 13 causes was presumed to be contributed by a residual factor (χ) which is uncorrelated with other factors. Path-coefficients were estimated by solving the following simultaneous equations indicating the basic relationship between correlation and path-coefficient. The equations used are as follows:

$$r_{iy} = P_{iy} + \sum_{j=1}^{12} r_{ij}P_{ij}$$

For $i=1, 2, \dots, 12$.

The above equation can be written in the form of matrix.

$$[A_{1 \times 12}] = [B_{1 \times 12}] [C_{1 \times 12}]$$

Where,

A is column vector of correlation r_{iy}

B is the correlation matrix of r_{ij}

C is the column vector of direct effects, P_{ij}

Residual factor was calculated as follows:

$$P_{xy} = \sqrt{1 - R^2}$$

Where,

$$R^2 = \sum_j p_{ij} r_{iy}$$

The r_{iy} 's i.e., $r_{1.2}$ to $r_{1.12}$ denote correlation between all possible characters and P_{1y} to P_{12y} denotes direct effect of various characters on character y .

r_{ij} = Correlation coefficient between i^{th} and y characters.

p_{ij} = Direct effect of i^{th} character on y .

Results and Discussion

Analysis of variance

The analysis of variance for RBD revealed highly significant differences among the 24 genotypes for all the characters studied, indicating the presence of considerable genetic variability among the genotypes (Table 1). The mean square due to replication were non-significant for most of the trait except days to 50 % flowering, plant height, panicle length, grains per panicle, flag leaf area and number of fertile spikelets per panicle.

The estimates of mean, range, PCV, GCV, heritability and genetic advance as percent of mean for yield and yield contributing traits were presented in Table 2. A wide range of variability was observed among the genotypes for several traits. The highest of variability was recorded for number of fertile spikelets per panicle (74.566–162.230), whereas the lowest range was observed for a number of productive tillers per plant (Fig. 1)

Coefficient of variation

For all characteristics, the magnitude of PCV was greater than GCV. There was a wide range of phenotypic and genotypic coefficients of variability found. The high magnitude ($> 20\%$) of PCV along with GCV was observed for flag leaf area (30.07) and PCV ($> 20\%$) was observed for grains per panicle (22.82), number of fertile spikelets/panicle (22.13) (15–21). Moderate estimates of PCV along with GCV (20–10 %) were recorded for number of productive tillers per plant (16.92) (22), harvest index (15.22), biological yield per plant (12.81) and days to 50 % flowering (11.47) and PCV (20–10 %) were recorded for grain yield per plant (12.38) and GCV (20–10 %) were recorded for grains per panicle (18.45), number of fertile spikelets per panicle (17.75). Low estimates ($< 10\%$) of PCV and GCV were

recorded for days to maturity (9.66) (22) spikelet fertility (9.17), 1000-grain weight (8.70), panicle length (8.48) and GCV ($< 10\%$) were recorded for plant height (9.94) and grain yield per plant.

Heritability and genetic advance

The estimates of heritability in broad sense (h^2_{bs}) varied between 97.8 % in case of days to 50 % flowering to 28 % in case 1000-grain weight (g) (Table 2). The high estimate of heritability in broad sense was recorded in days to 50 % flowering (97.8 %) (15, 23, 24). The moderate estimate of heritability in broad sense was observed for plant height (76.7 %). The low estimate of heritability in broad sense were recorded for grains per panicle (65.3 %) followed by number of fertile spikelets per panicle (64.4 %), biological yield per plant (62.7 %). The high value of genetic advance in percentage of mean observed for flag leaf area (30.95 %), followed by grains per panicle (30.70 %) (15, 17, 19, 24–27) while 1000-grain weight (5.023 %) had lowest value for this parameter.

High heritability coupled with high genetic advance were recorded for days to 50 % flowering, days to maturity, grains per panicle, plant height, number of fertile spikelets per panicle and biological yield per plant demonstrating that the reported heritability was the result of additive gene effects, hence selection would be beneficial for these traits. However, high heritability coupled with moderate genetic advance as per cent of mean were observed for traits panicle length, flag leaf area indicating the role of additive and non-additive gene effects for the characters. Further, the information on genetic variation along with heritability and genetic advance estimates has been reported to give a better idea about the efficiency of selection.

Correlation analysis

Both phenotypic and genotypic calculation were estimated. However, the traits observed at the phenotypic level were largely similar to those at the genotypic level (Table 3). Therefore, phenotypic correlation was primarily discussed as they represent the combined influence of genetic and environmental effects (Table 4).

Table 1. Genotype included in the study along with check in salinity

Sl. No.	Germplasm lines	Source (Material received)
1	NVSR 6489	CRS Masodha
2	RNR 28361	CRS Masodha
3	NVSR 6526	CRS Masodha
4	KPS 6343	CRS Masodha
5	CSR 103-10-2	CRS Masodha
6	RP 6684-CGR 13	CRS Masodha
7	CSR 141-11-107	CRS Masodha
8	RP Bio 4919-NSR 85	CRS Masodha
9	CSR 116-10-2	CRS Masodha
10	RP 6682-CSR 11	CRS Masodha
11	CSR 104-10-2	CRS Masodha
12	NVSR 6494	CRS Masodha
13	IIRRH 163	CRS Masodha
14	RNR 29325	CRS Masodha
15	CSAR 9-29-2021	CRS Masodha
16	CSR 141-11-112	CRS Masodha
17	RP 6688-16-397	CRS Masodha
18	FL 478	CRS Masodha
19	RP 6711-MS-SS-20-2-9-5-23-6-1	CRS Masodha
20	Pusa 44	CRS Masodha
Sl. No.	Name of check varieties	Name of check varieties
1.	NDR 2008	CRS Masodha
2.	CSR 36	CRS Masodha
3.	CSR 23	CRS Masodha
4.	CSR 10	CRS Masodha

Table 2. Genetic parameters for yield and yield components in rice

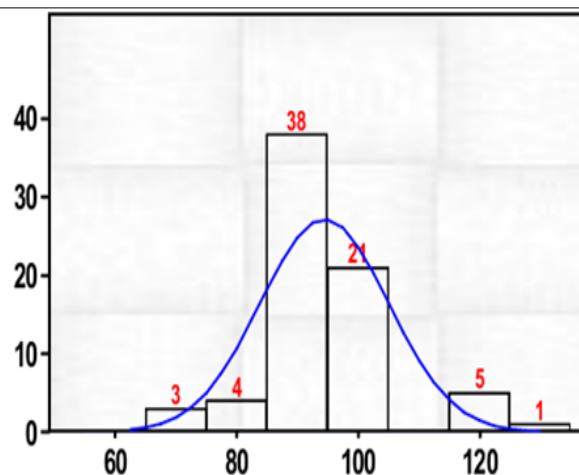
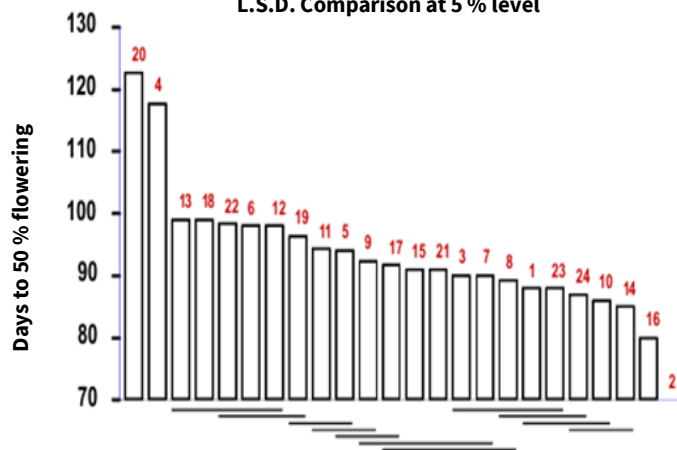
Characters	Grand mean ($\bar{x}$)	Range		Phenotypic coefficient of variation	Heritability broad sense (h^2bs)	Genetic advance (GA)	Genetic advance in percent of mean (GA %)
		Lowest	Highest				
Days to 50 % flowering	93.194	70	122.667	11.472	97.8	21.540	23.113
Days to maturity	116.611	96.666	150	9.662	96.2	22.327	19.147
Plant height (cm)	107.904	87.300	131.233	11.36	76.7	19.367	17.949
Number of productive tillers/plants	10.440	8.066	14.466	16.921	43.8	1.592	15.252
Panicle length (cm)	23.486	20.666	26.600	8.483	54	2.216	9.437
Grains/ panicle	98.470	61.066	135.566	22.822	65.3	30.238	30.708
Flag leaf area (cm ²)	25.275	16.973	43.6433	30.070	50	7.823	30.950
Number of fertile spikelets/panicle	122.741	74.566	162.230	22.122	64.4	36.012	29.340
Spikelet fertility (%)	79.738	63.710	86.08	9.179	34.5	5.201	6.523
Biological yield/plant (g)	38.127	32.586	49.273	12.815	62.7	6.307	16.541
Harvest index (%)	39.919	28.436	49.236	15.277	48.7	6.119	15.329
1000-grain weight(g)	25.332	22.266	27.733	8.707	28	1.273	5.023

Table 3. Estimates of genotypic correlation coefficient between different characters in rice under saline conditions

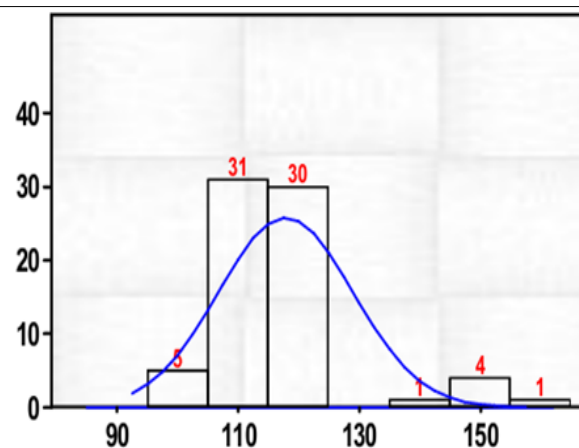
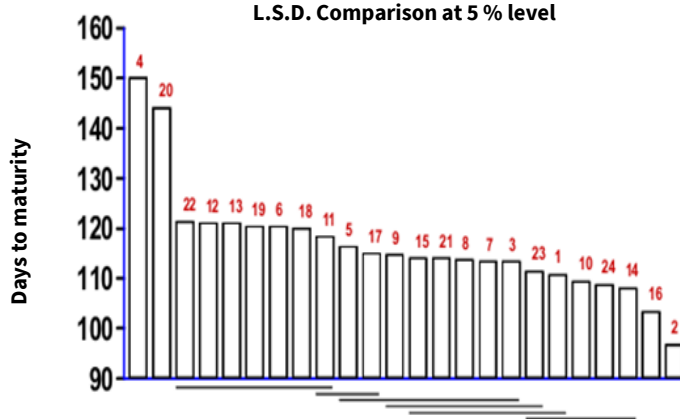
Traits	Days to 50 % flowering	Days to maturity	Plant height (cm)	No. of productive tillers/plant	Panicle length (cm)	Grain/ panicle	Flag leaf area (cm ²)	No. of fertile spikelets / panicle	spikelet fertility (%)	Biological yield/plant	Harvest index (%)	1000-grain weight	Grain yield/ plant
Days to 50 % flowering	1.000	0.989**	0.154	0.90	0.0279*	0.264*	0.227	0.207	0.400**	-0.319**	0.221	-0.116	-0.065
Days to maturity		1.000	0.096	0.093	0.307**	0.320**	0.374**	0.267*	0.391**	-0.268*	0.183	-0.026	-0.054
Plant height (cm)			1.000	0.004	0.633**	0.283*	0.075	0.250	0.429**	-0.044	0.074	0.124	0.060
No. of productive tillers / plant				1.000	0.183	-0.280*	0.216	-0.308**	-0.214	0.254*	0.053	0.299*	0.345**
Panicle length (cm)					1.000	0.381**	0.239*	0.324*	0.396**	-0.267*	0.585**	0.240*	0.453**
Grain/ panicle						1.000	0.602**	0.985**	0.364**	0.327**	0.011	0.437**	0.264*
Flag leaf area (cm ²)							1.000	0.639**	-0.106	0.246*	-0.216	0.511**	0.098
No. of fertile spikelets / panicle								1.000	0.227	-0.052	-0.052	0.500**	0.209
spikelet fertility (%)									1.000	-0.33**	0.288*	-0.142	-0.013
Biological yield/plant										1.000	-0.565**	0.942**	0.314**
Harvest index (%)											1.000	-0.796**	0.596**
1000-grain weight												1.000	0.093

*Significant at 5 % level; **Significant at 1 % level.

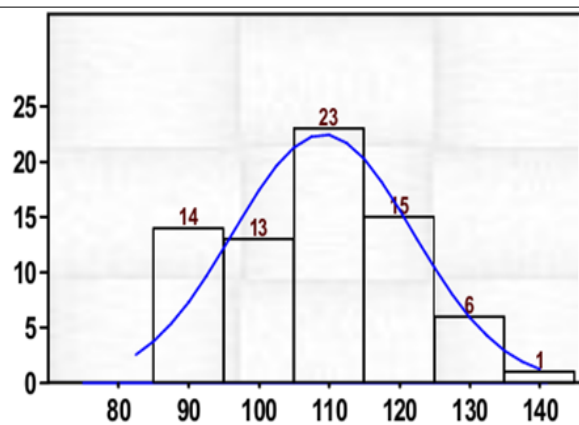
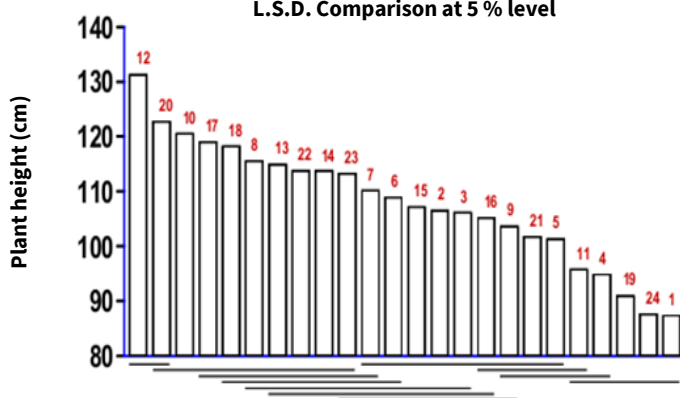
L.S.D. Comparison at 5 % level



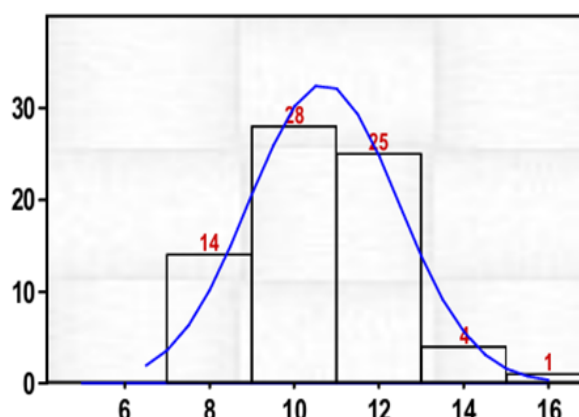
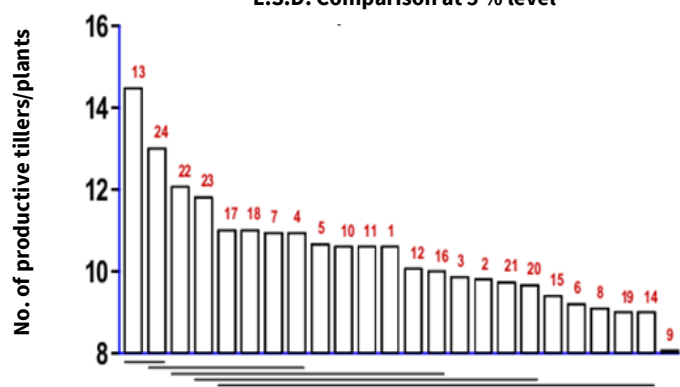
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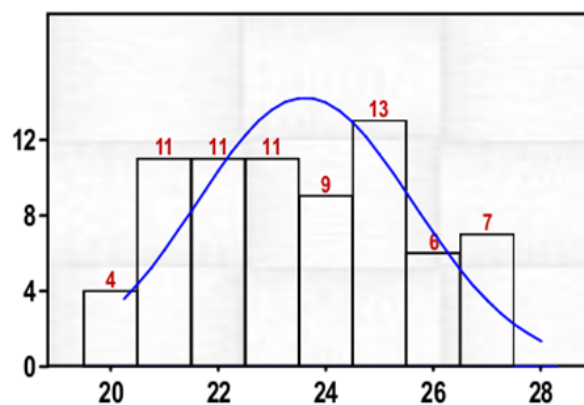
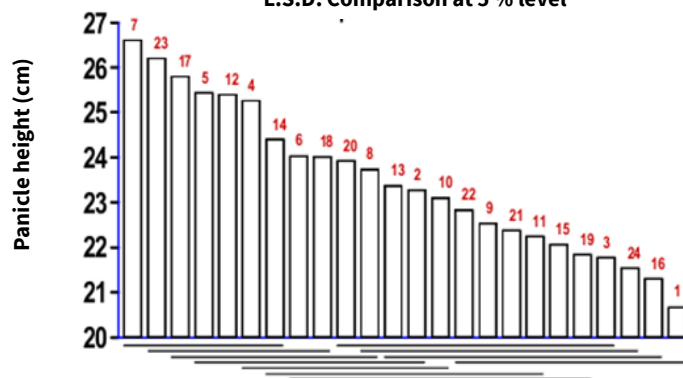
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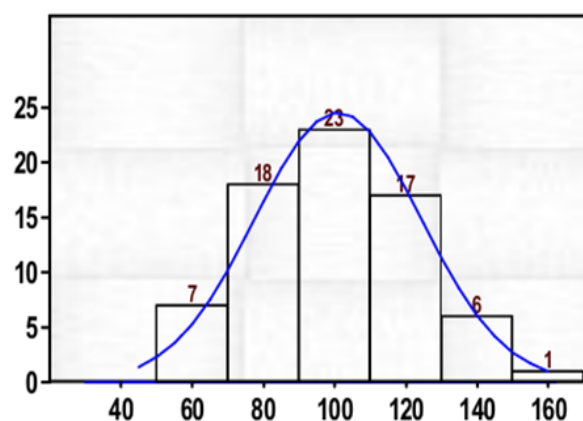
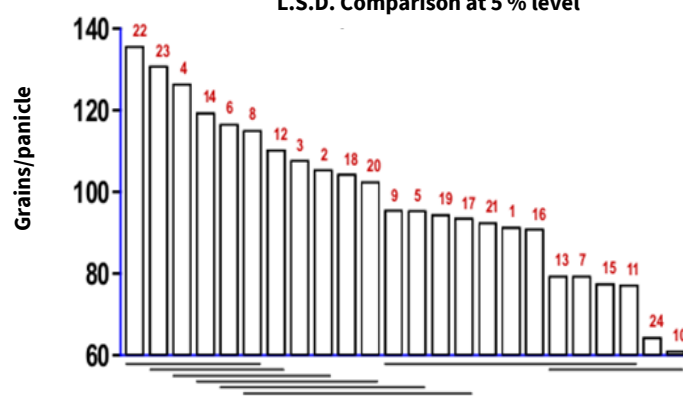
L.S.D. Comparison at 5 % level



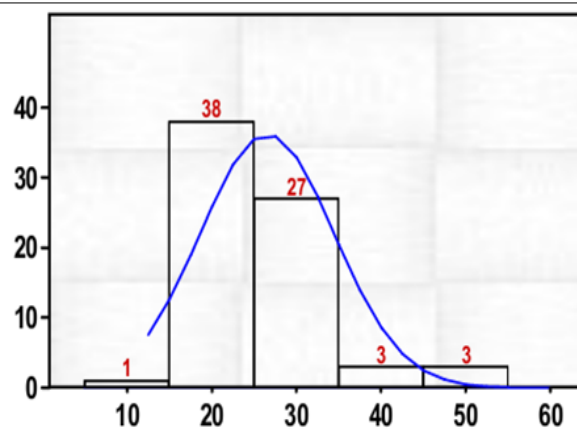
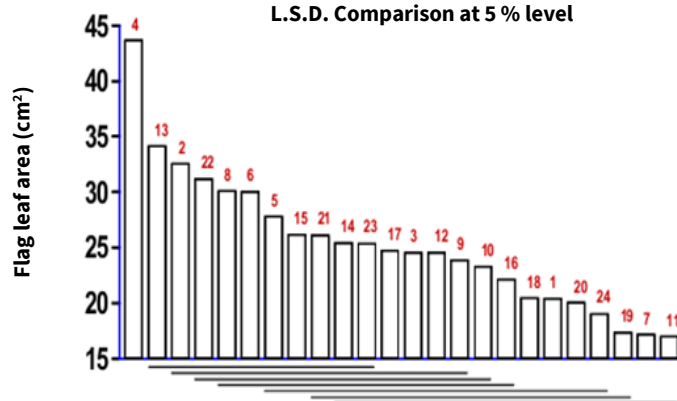
L.S.D. Comparison at 5 % level



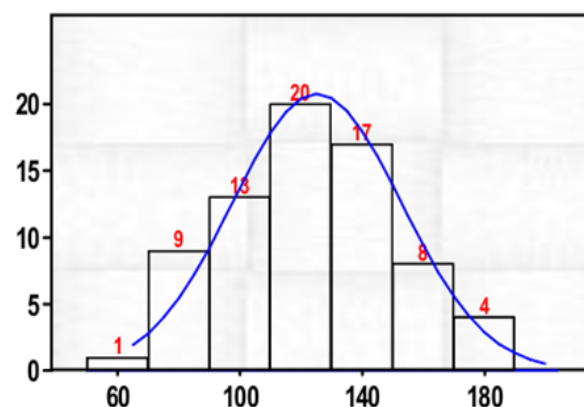
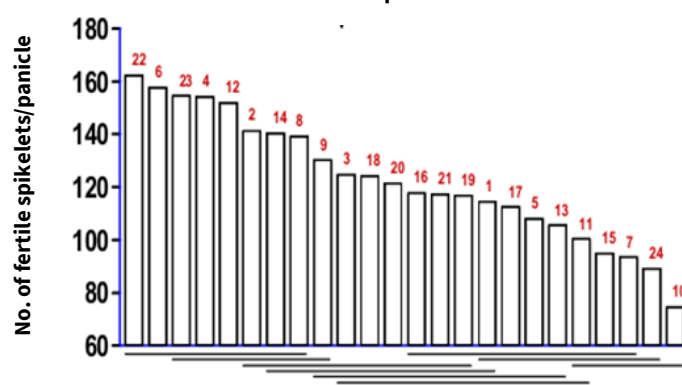
L.S.D. Comparison at 5 % level



L.S.D. Comparison at 5 % level



L.S.D. Comparison at 5 % level



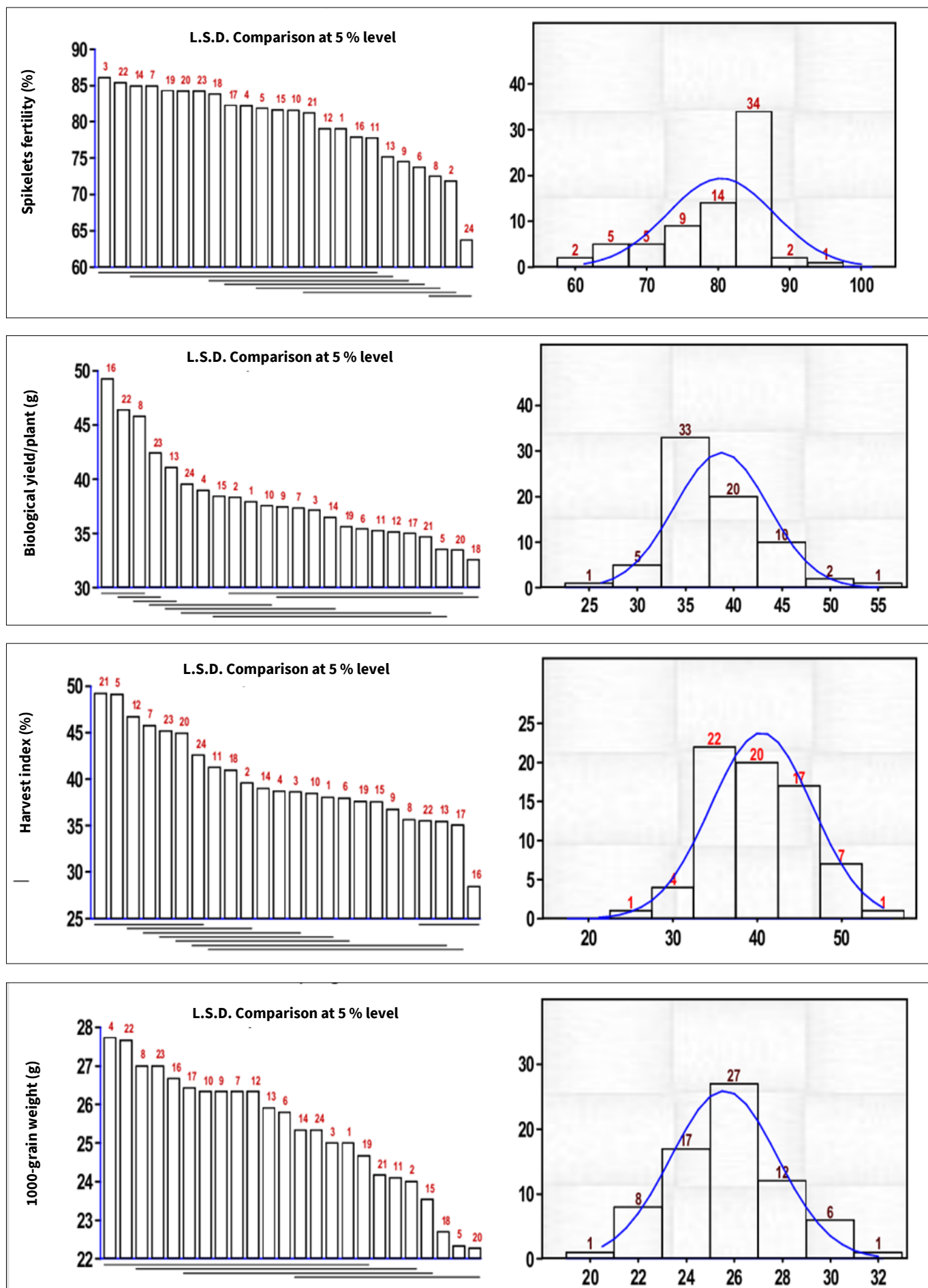


Fig. 1. Scott-knot test grouping in alternate colour for observations under research.

Table 4. Estimates of phenotypic correlation coefficient between different characters in rice under saline conditions

Traits	Days to maturity	Plant height (cm)	No. of productive tillers /plant	Panicle length (cm)	Grain/ panicle	Flag leaf area (cm ²)	No. of fertile spikelets /panicle	spikelet fertility (%)	Biological yield/plant	Harvest index (%)	1000-grain weight	Grain yield/ plant
Days to 50 % flowering	0.965**	0.13	0.09	0.22	0.22	0.15	0.18	0.23	-0.268*	0.18	-0.08	-0.04
Days to maturity		0.07	0.04	0.235*	0.260*	0.232*	0.22	0.23	-0.23	0.15	0	-0.04
Plant height (cm)			-0.02	0.404**	0.18	0.12	0.18	0.15	-0.01	0.03	0.09	0.05
No. of productive tillers /plant				0.06	-0.08	0.1	-0.09	-0.08	0.21	0.03	0.1	0.253*
Panicle length (cm)					0.337**	0.268*	0.236*	0.240*	-0.17	0.252*	0.14	0.19
Grain/ panicle						0.388**	0.909**	0.285*	0.17	-0.06	0.19	0.11
Flag leaf area (cm ²)							0.402**	-0.08	0.22	-0.15	0.261*	0.06
No. of fertile spikelets / panicle								-0.02	0.17	-0.07	0.238*	0.09
spikelet fertility (%)									-0.11	0.05	-0.05	-0.05
Biological yield/plant										-0.626**	0.415**	0.21
Harvest index (%)											-0.18	0.617**
1000-grain weight												0.22

*Significant at 5 % level; **Significant at 1 % level.

The estimates of phenotypic correlation coefficient between different characters are shown in Table 3. A perusal of these results revealed that the grain yield per plant exhibited highly significant and positive correlation for harvest index (0.617) followed by number of productive tillers per plant (0.253) (28–32) and however, grain yield per plant was shown to be, non-significant and negatively associated with spikelet fertility (-0.052) followed by days to 50 % flowering (-0.038) and days to maturity (-0.036) (33–36). Studies on inter-character associations for the yield component traits revealed significant and positive association of 1000-grain weight exhibit significant and positive correlation for biological yield per plant (0.415) (35) followed by flag leaf area (0.261) and number of fertile spikelets per panicle (0.238). Harvest index exhibits significant and positive correlation for panicle length (0.252) (36, 37). Biological yield per plant showed non-significant and positive correlation for flag leaf area (0.222) (38) followed by number of productive tillers per plant (0.208), number of fertile spikelets per panicle (0.166). Spikelet fertility exhibits significant and positive correlation for grains/panicle (0.285) (39, 40) and panicle length (0.240). Number of fertile spikelets per panicle showed significant and positive correlation for grains/panicle (0.909) (23) followed by flag leaf area (0.402), panicle length (0.236). Flag leaf area exhibits significant and positive correlation for grains/panicle (0.388) (41) followed by panicle length (0.268), days to maturity (0.232). Grains/panicle exhibits significant and positive correlation for panicle length (0.337) (42) followed by days to maturity (0.260). Panicle length showed significant and positive correlation for plant height (0.404) (43) and days to maturity (0.235). Number of productive tillers per plant exhibits non-significant and positive correlation for days to 50 % flowering (0.092) and days to maturity (0.043). Plant height exhibits non-significant and positive correlation for days to 50 % flowering (0.130) and days to maturity (0.043). Days to maturity exhibits significant and positive correlation for days to 50 % flowering (0.965) and the heatmap of character association is shown in Fig. 2. However, their significant and positive correlation with grain yield per plant suggested the necessity for careful selection of these features when enhancing grain yield.

Path coefficient analysis

In order to determine the direct and indirect impacts of various characters on seed yield per plant, the path coefficient analysis was conducted utilising the genotypic and phenotypic correlation coefficients between 13 characters. The estimations of the phenotypic and genotypic levels of the direct and indirect effects of various characteristics on seed yield per plant are shown in Table 5. It showed that the highest positive direct effects on grain yield per plant were exerted by harvest index (1.20), followed by biological yield per plant (0.96), panicle length (0.0485) (28, 33, 44–46). However, negative direct effects on grain yield per plant were exerted by days to maturity -0.091, number of fertile spikelets per panicle (-0.056), spikelet fertility -0.40 and number of productive tillers / plant (-0.003) (47). The positive indirect effects on grain yield / plant via harvest index (0.617), further supported by the indirect effect through 1000-grain weight via biological yield per plant (0.399), panicle length via harvest index (0.302), days to 50 % flowering via harvest index (0.215), flag leaf area via biological yield per plant (0.213), number of productive tillers per plant via biological yield per plant (0.199), days to maturity via harvest index (0.176) and number of fertile spikelets per panicle (0.159) (48). However, negative direct effects on grain yield per plant were

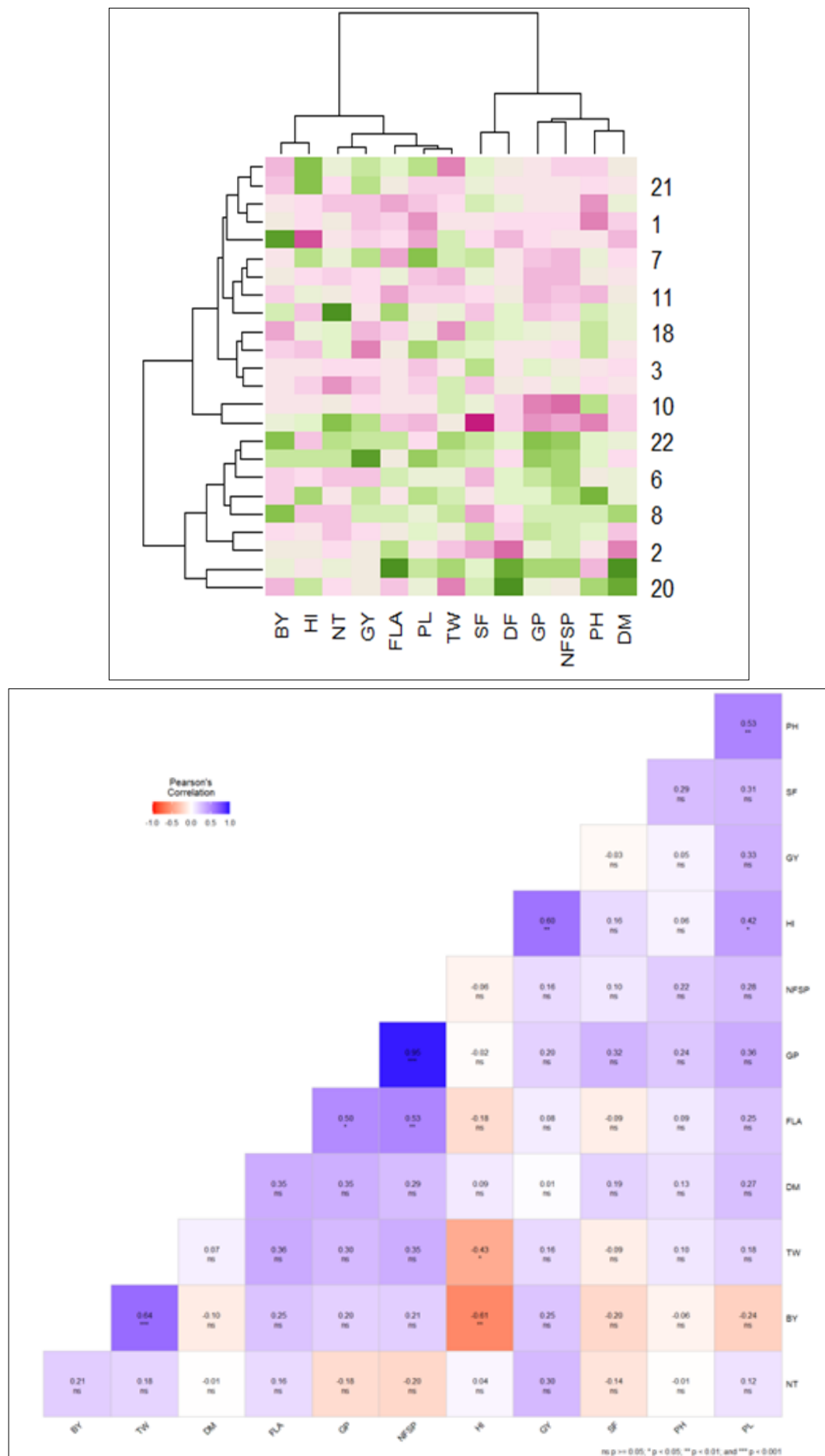


Fig. 2. Representation of heatmap for correlation coefficient between different characters in rice under saline conditions.

DF: days to 50 % flowering; DM: days to maturity; PH: plant height; NT: No. of productive tillers per plant; GP: grains per panicle; FLA: flag leaf area; NFSP: No. of fertile spikelet per panicle; SF: spikelets fertility; BY: biological yield per plant; HI: harvest index; TW: test weight; GY: grain yield per plant.

Table 5. Direct and indirect effects (phenotypic path coefficients) of yield and yield components on grain yield in rice

Trait	Days to 50 % flowering	Days to maturity	Plant height (cm)	No. of productive tillers /plant	Panicle length (cm)	Grain/ panicle	Flag leaf area (cm ²)	No. of fertile spikelets /panicle	spikelet fertility (%)	Biological yield/plant	Harvest index (%)	1000-grain weight	Grain yield/ plant
Days to 50 % flowering	0.0198	-0.0088	0.0003	-0.0004	0.0104	0.0072	0.0022	-0.0099	-0.0094	-0.2572	0.2156	-0.002	-0.038
Days to maturity	0.0191	-0.0091	0.0002	-0.0002	0.0114	0.0086	0.0034	-0.0124	-0.0092	-0.217	0.1763	0	-0.036
Plant height (cm)	0.0026	-0.0006	0.0023	0.0001	0.0196	0.006	0.0017	-0.0099	-0.0061	-0.0111	0.0393	0.0023	0.048
No. of productive tillers /plant	0.0018	-0.0004	0	-0.0039	0.0031	-0.0026	0.0015	0.0053	0.0033	0.1999	0.0367	0.0027	0.253*
Panicle length (cm)	0.0043	-0.0021	0.0009	-0.0002	0.0485	0.0112	0.0039	-0.0134	-0.0098	-0.1621	0.3024	0.0036	0.191
Grain/ panicle	0.0043	-0.0024	0.0004	0.0003	0.0164	0.0332	0.0056	-0.0514	-0.0116	0.1588	-0.066	0.005	0.109
Flag leaf area (cm ²)	0.0031	-0.0021	0.0003	-0.0004	0.013	0.0129	0.0145	-0.0227	0.0031	0.2136	-0.1765	0.0068	0.062
No. of fertile spikelets /panicle	0.0035	-0.002	0.0004	0.0004	0.0115	0.0302	0.0058	-0.0565	0.0006	0.1599	-0.087	0.0062	0.089
spikelet fertility (%)	0.0046	-0.002	0.0003	0.0003	0.0116	0.0095	-0.0011	0.0009	-0.0407	-0.1081	0.0632	-0.0014	-0.052
Biological yield/plant	-0.0053	0.002	0	-0.0008	-0.0082	0.0055	0.0032	-0.0094	0.0046	0.9609	-0.7524	0.0109	0.214
Harvest index (%)	0.0036	-0.0013	0.0001	-0.0001	0.0122	-0.0018	-0.0021	0.0041	-0.0021	-0.6013	1.2024	-0.0046	0.617**
1000-grain weight	-0.0015	0	0.0002	-0.0004	0.0068	0.0064	0.0038	-0.0134	0.0021	0.3992	-0.2108	0.0262	0.224

Diagonal values indicate direct effect; Residual effect = 0.151; *Significant at 5 % level; ** Significant at 1 % level.

exerted by spikelet fertility (-0.052), days to 50 % flowering (-0.038), days to maturity (-0.036) further supported by the indirect effect through biological yield per plant via harvest index (-0.752), harvest index via biological yield per plant (-0.601), days to 50 % flowering via biological yield per plant (-0.257) and days to maturity via biological yield per plant (-0.217). The remaining estimates of the indirect effects in the analysis were too low to be considered. The estimates of residual effect were very low (0.151) indicating that the traits include in the analysis explained a major proportion of the variability in grain yield. The relatively low residual value suggests that the selected characters were adequate in explaining the variation in grain yield under saline condition.

Genetic divergence

On the basis of 13 qualitative and quantitative characteristics, the Mahalanobis D² cluster analysis was used to investigate the genetic divergence present among 24 rice germplasm collections as shown in (Table 6). The pseudo-*F*-test showed that grouping the 24 genotypes into 5 groups was appropriate. As a result, 24 genotypes were included in the group and split into 5 distinct clusters. Cluster I, which contains 10 genotypes, followed by cluster II and cluster III have 5 genotypes in each cluster (Fig. 3). The lowest number of genotypes observed in cluster IV and cluster V having 2 genotypes in each cluster. The highest intra cluster distance observed in cluster IV (215.37) and lowest intra cluster distance recorded in cluster III (55.11) (Fig. 4). The maximum inter cluster distance were recorded between cluster IV and cluster V (1519.35) and minimum inter cluster distance observed between cluster I and cluster II (86.755). Genotypes with significantly varied mean performance for various characters were divided into different clusters based on the intra-cluster group means of 5 clusters (Fig. 5).

For hybridisation, when selecting different parents. Furthermore, the mean genotype performance for various characteristics as well as the inter-cluster distances should be considered. It is possible to choose lines as parents from different clusters with good mean performance in the desired directions for different attribute.

Breeder implication

The strong positive direct effect of harvest index and biological yield on grain yield suggests that these traits should be given greater emphasis in selection program aimed at improving rice productivity under saline environment. Genotypes belonging to widely separate clusters with superior mean performance may serve as potential parent for hybridisation to exploit maximum genetic variability.

Table 6. Estimation of intra cluster and inter clusters distance in rice genotypes

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
I	59.609	86.755	92.659	272.121	689.584
II		55.291	130.924	239.387	880.264
III			55.115	435.329	449.376
IV				215.373	1519.357
V					116.974

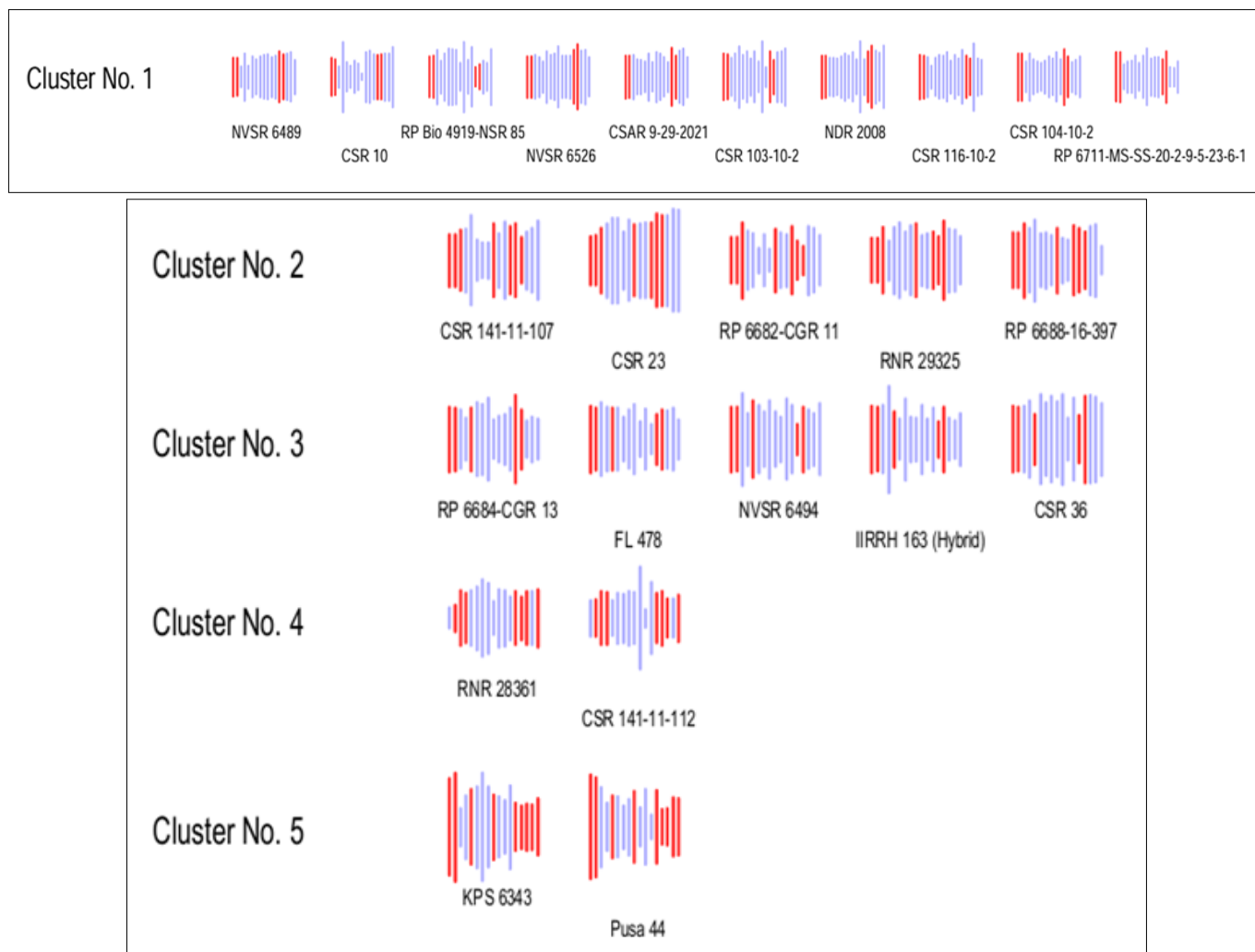


Fig. 3. Diagrammatic representation of number of genotypes involved in each cluster.

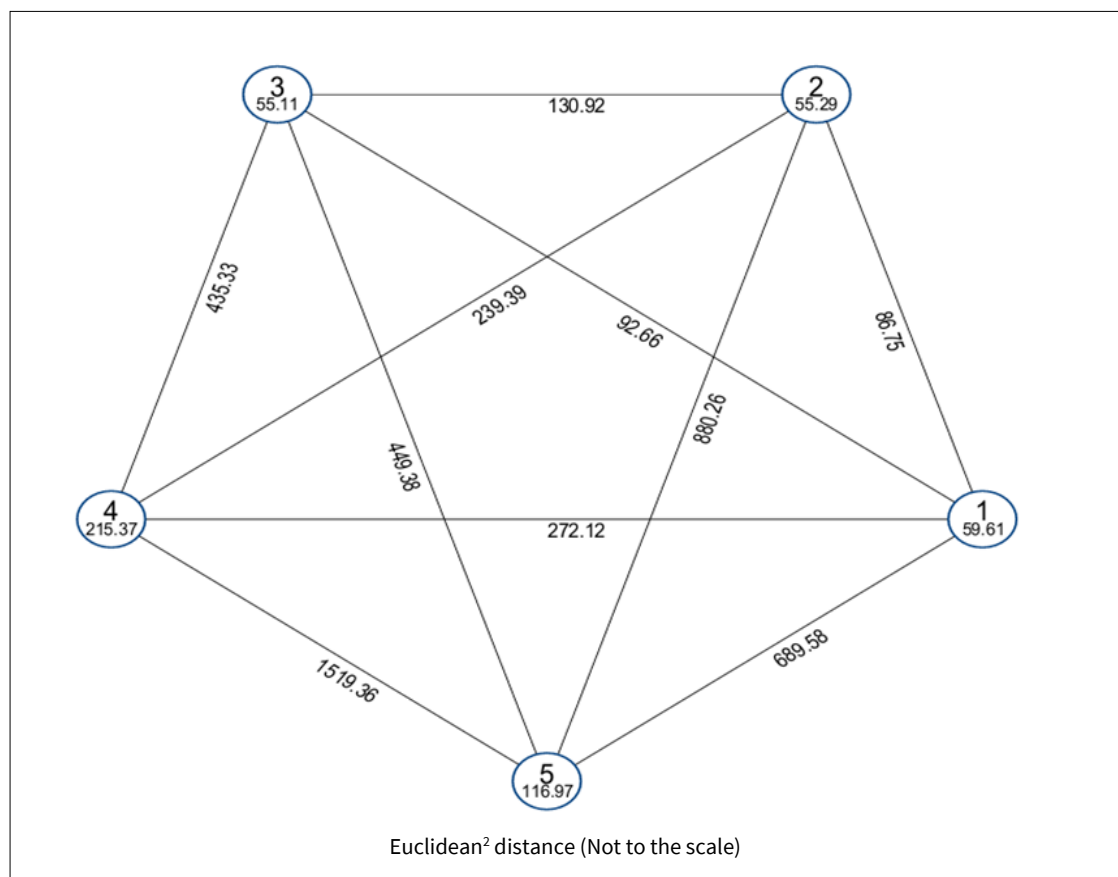


Fig. 4. Diagrammatic representation of intercluster and intra cluster distance in rice genotypes.

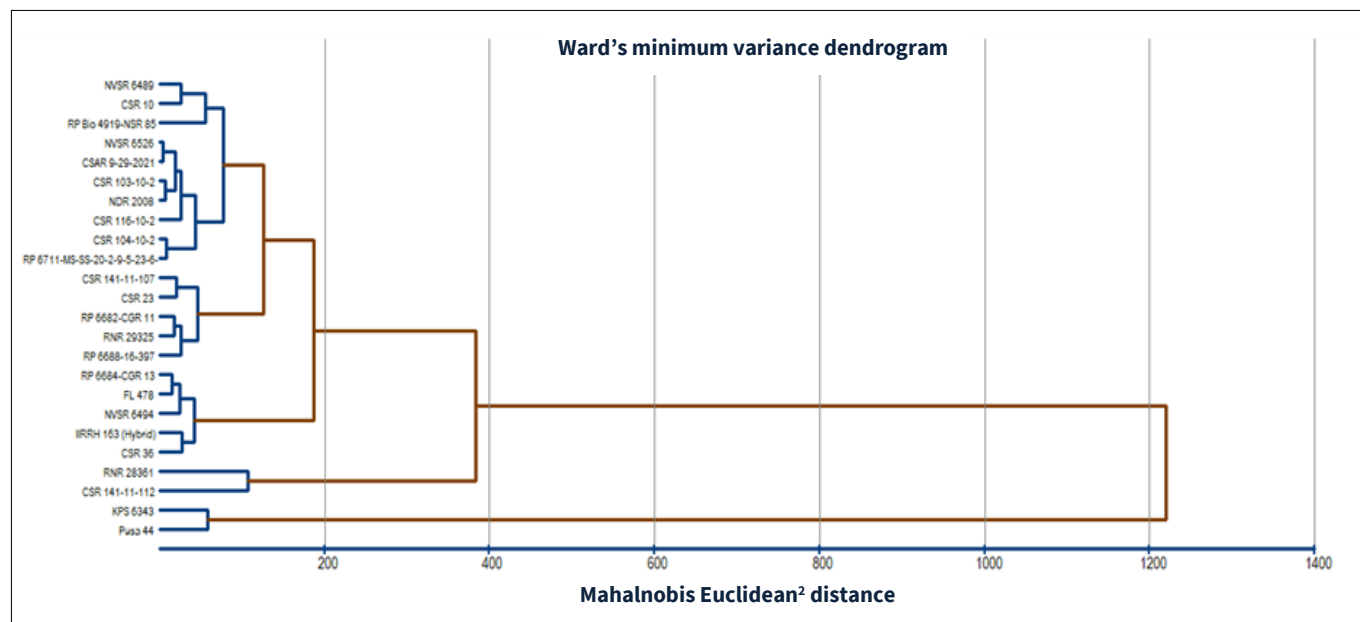


Fig. 5. Ward's minimum variance dendrogram of 24 rice genotypes based on Mahalanobis Euclidean² distance.

Conclusion

The investigation presents several key findings and inferences regarding the genetic diversity and yield potential of 24 rice germplasm collections. The main findings of the study are summarised as follows:

Genetic diversity

The study found a high degree of genetic variability among the rice germplasm for various traits, as indicated by broad variance ranges and significant differences in mean performance among genotypes.

Promising genotypes

The genotype CSAR 23 exhibited the highest grain yield per plant 19.16 g. Other notable genotypes included:

- RNR 28361 for days to 50 % flowering (70 days) and days to maturity (96.66 days).
- NVSR 6489 for plant height (87.30 cm).
- IIRRH 163 (hybrid) for number of productive tillers per plant (14.4).
- CSR 141-11-107 for panicle length (26.60 cm).
- CSR 36 for grains per panicle (135.56) and number of fertile spikelets per panicle (162.23).
- KPS 6343 for flag leaf area (43.64 cm²).
- NVSR 6526 for spikelet fertility (86.08 %).
- CSAR 141-11-112 for biological yield per plant (49.29 g).
- NDR 2008 for harvest index (49.23 %).

High genotypic coefficient of variation and phenotypic coefficient of variation

High genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for flag leaf area indicate substantial genetic variability and suggest that this trait is less influenced by environmental factors. This variability produce greater scope for selection and improvement of photosynthetic efficiency, which may ultimately enhance grain yield under saline conditions.

Heritability and genetic advance

High heritability coupled with high genetic advance (GA) for days to 50 % flowering suggests the predominance of additive gene action. Such trait can be effectively improved through direct selection in early generation. Early flowering genotype may also escape prolonged exposure of saline stress, making this trait important in breeding program targeting salt affected environments.

Character associations

The study identified significant positive correlations between grain yield per plant and several traits, particularly harvest index (0.617), biological yield per plant (0.96) and panicle length (0.0485). However, grain yield was negatively associated with spikelet fertility (-0.052), days to 50 % flowering (-0.038) and days to maturity (-0.036).

Path analysis

The path analysis revealed that the highest direct effect on grain yield per plant was from harvest index (1.20), followed by biological yield per plant (0.96). Negative direct effects were noted from days to maturity (-0.091) and spikelet fertility (-0.052).

Cluster analysis

Using Mahalanobis D² cluster analysis, the 24 genotypes were grouped into 5 clusters. Cluster I had the most genotypes (10), while clusters IV and V had the fewest (2 each). The highest intra-cluster distance was in cluster IV (215.37), indicating greater diversity within that cluster, while the lowest was in cluster III (55.11). The maximum inter-cluster distance was between clusters IV and V (1519.35), suggesting significant genetic divergence.

Hybridisation potential

The findings suggest that genotypes with good mean performance and significant genetic divergence should be selected as parents for hybridisation programs aimed at developing high-yielding rice varieties suitable for saline conditions.

In conclusion, the study emphasises the importance of selecting diverse genotypes with favorable traits for breeding programs to enhance rice yield under challenging environmental conditions. The identified traits and their associations with yield can guide future breeding strategies.

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Authors' contributions

AS and NY carried out conceptualisation, data curation, formal analysis, writing original draft and review and editing. GS and SS helped in formulation of collected data and SCV guided the entire research. All authors have read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: The authors declared that they have no any conflict of interest.

Ethical issues: None

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