

Genetic correlation, path and multivariate analysis in rice under coastal saline ecosystem of Tamil Nadu

A. Nandini¹, M. Venkatesan^{2*} , D. Sathyaraj¹ and M.S. Aneesa Rani³

¹Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalai Nagar, Chidambaram-608 002, India

²Department of Plant Breeding and Genetics, Horticultural College and Research Institute, Paiyur, Krishnagiri - 635 115, India

³Horticultural College and Research Institute, Paiyur, Krishnagiri - 635 115, India

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*Corresponding Author Email: venkatjack@rediffmail.com

*ORCID: <https://orcid.org/0000-0002-0949-0259>

Abstract

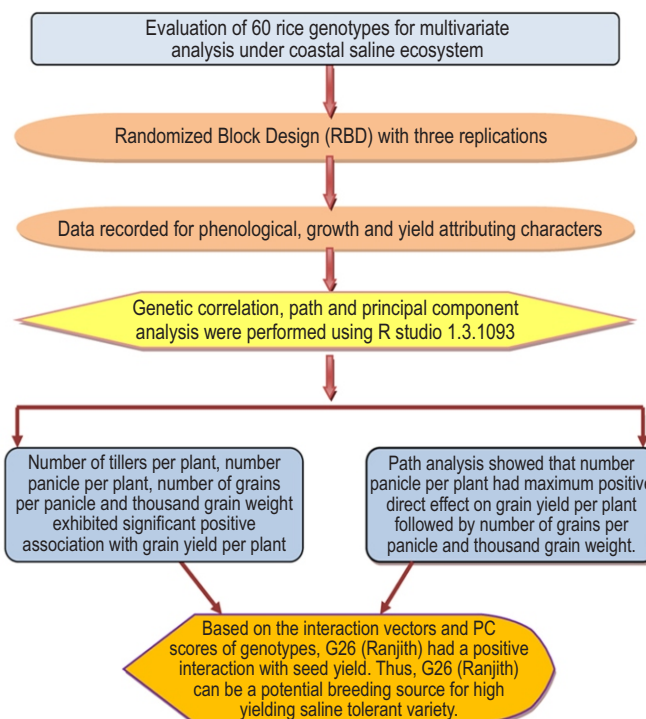
Aim: The present experiment was investigated to elucidate the correlation and their interrelationship among different characteristics and evaluate the direct and indirect impact traits of rice genotypes under east coastal region of Chidambaram, Tamil Nadu (India).

Methodology: The study was conducted under the coastal saline ecosystem at the Plant Breeding Farm, Department of Genetics and Plant Breeding, Annamalai University, during the major planting season of 2022-23. The experiment was laid out in a Randomized Block Design with three replicates.

Results: Character association analysis indicated that among the nine agro-morphological traits, four traits number of tillers per plant, number panicles per plant, number of grains per panicle and thousand grain weight had significant and positive association with grain yield per plant. Path coefficient studies showed that the number of panicles per plant, number of grains per panicle and thousand grain weight had maximum direct effect on the grain yield per plant. Principal component analysis disclosed that the first four components with Eigen values greater than 1.00 contributed about 70.49% of the total variability in the studied accessions involving all the nine characters.

Interpretation: Correlation studies indicated that yield can be enhanced by prioritizing the number of tillers per plant, number panicles per plant, number of grains per panicle and thousand grain weight during selection. The study also revealed that direct selection of the number panicles per plant, number of grains per panicle and thousand grain weight could be exploited for improving grain yield in saline breeding programme. Based on the interaction vectors and PC scores of genotypes, G26 (Ranjith), G44 (STBN 4), G60 (Pokkali) and G34 (IR64) were identified as high yielding which can be widely utilized for the development of new diverse varieties for enhanced grain yield under saline conditions.

Key words: Coastal saline ecosystem, *Oryza sativa*, Path analysis, Yield traits



Introduction

Rice (*Oryza sativa* L.) is grown widely in the most diverse agroecosystems of tropical and subtropical regions of the world. It is a semi aquatic, annual crop that belongs to family Poaceae (2n=24). Rice is the main staple and nutritional source for more than three billion people of the world and forms the backbone to the Indian agriculture. Worldwide, rice is the third largest cereal cultivated in 162 million ha area, with annual production of 755 million tons (FAO, 2023). In India, the total area under rice cultivation was 46.38 million hectares with a production of about 130.29 million tonnes and productivity of 2809 kg ha⁻¹. In Tamil Nadu, the area and production of rice was about 2.21 million hectares and 8.07 million tones and productivity of 3658 kg ha⁻¹ respectively (Sathyaraj and Sabesan, 2024). It is estimated that over 20% of the world's cultivable land is impacted by high salinity, leading to a reduction in the agricultural productivity. Worldwide, approximately 45 million ha of irrigated land and 32 million ha of rain-fed agricultural land are impacted by soil salinity. In India, of the total 8.0 M ha of land is affected by soil salinity, and more than 2.10 M ha area is affected due to coastal salinity.

Additionally, practices such as brackish water irrigation, along with natural events like tidal surges and tsunamis, continue to exacerbate soil salinization (Schroeder et al., 2013). Projections suggest that by 2050, up to 50% of currently arable land could be affected by salinity (Wang et al., 2003). Globally, the major rice production constraints included several stress factors namely biotic and abiotic, which led to notable yield loss in rice production. Soil salinity is the severe abiotic stressors, followed by drought (Islam et al., 2019). Rice is canonically a salinity stress-sensitive crop and its sensitivity significantly diminishes during germination, early seedling and booting stages (Palao et al., 2013). Furthermore, saline stress negatively affects well plant establishment, tillers, panicles, time to heading and leaf area index (Singh et al., 2021). Consequently, there is an urgent need to investigate and harness natural genetic resources to identify novel genes and alleles that confer resistance to high salinity, thereby ensuring sustained crop productivity in saline-affected areas.

Mitigating salinity stress to enhance rice production necessitates the application of a comprehensive understanding of the underlying mechanisms that govern salinity tolerance in plants. Salinity is a major problem in the rice producing coastal low lands of Tamil Nadu, especially in Cuddalore district. For this reason, currently salinity tolerant improved rice cultivar is required for saline affecting coastal low lying areas. Developing rice cultivars with tolerance of salinity and agronomic traits acceptable to farmer is a feasible approach to address this current problem. Developing stress tolerant rice varieties has been an effective approach to cope with the adverse effects of soil salinity. The present investigation is oriented towards breeding for coastal saline tolerance, much emphasize was given to understand the association between grain yield and its components. Correlation studies permit only a degree of relationship between two variables. Furthermore, grain yield and

associated traits may also partition into direct and indirect effects. Principal component analysis is an implausibly propitious tool for clarifying the relationship among the traits in a complex multi-trait system such as quantitative traits and yield contributing traits. Despite increasing challenges posed by soil salinity in coastal agro-ecosystems, particularly in regions such as Cuddalore in Tamil Nadu, research over the past years has remained fragmented in addressing the multifactorial nature of salinity tolerance in rice. Existing studies have predominantly focused on molecular or physiological aspects, or narrowly targeted individual traits, thereby overlooking holistic approaches that integrate phenotypic variability, trait interrelationships, and multivariate statistical frameworks (Bhandari et al., 2020). The present study was investigated by keeping the above aspects in consideration to elucidate the character association and direct and indirect effects of yield component characters towards grain yield and saline tolerance using correlation and path analysis, and to quantify the genetic diversity of 60 distinct rice genotypes using PCA analysis.

Materials and Methods

Rice materials: The experimental materials for the present study comprised of diverse 60 elite rice genotypes collected from various research institutes are presented in (Table 1).

The study was conducted under the coastal saline ecosystem at the Plant Breeding Farm of Department of Genetics and Plant Breeding, Annamalai University, Annamalai Nagar, the study cite is situated 11° 24' N latitude, 79° 44' E longitude 5.79 m above mean sea level during the rice growing season (Samba season 2022 and 2023 July-December). The field is situated 15 km away from the sea shore (Bay of Bengal). The soil was clay loamy with pH 7 and electrical conductivity greater than one (slightly saline), also the soil had poor nitrogen content, whereas phosphorous and potassium were present in optimum levels. The pooled data was taken for multivariate analysis. The experiment was laid out in a Randomized Block Design with three replicates. The 60 rice genotypes were sown in two lines per entry under raised bed nursery (1 m with 20 m length) and soil was excavated from the interspace between two genotypes. The sown nursery area was covered with rice straw and coconut leaves to prevent soil moisture from evaporating. The twenty-one day old healthy and sturdy seedlings were transplanted in the well puddle main field in two rows 3 m long with a spacing of 20 x 15 cm. The recommended agronomic practices were judiciously followed along with necessary prophylactic plant protection measures to raise a good crop.

In the present study, the morphological data was recorded on ten randomly selected plants of each genotype at different stages for nine quantitative traits viz. days to first flower, plant height, number of tillers per plant, number of panicles per plant, panicle length, number of grains per panicle, thousand grain weight, grain L/B ratio and grain yield per plant. Phenotypic and genotypic correlations were worked out by using the formulae suggested by

Table 1: List of genotypes of interest and their geographic origin

Geno. Code	Name of the genotypes	Origin	Geno. Code	Name of the genotypes	Origin
G1	CARI 1	CIARI, Andaman, India	G31	PY 1	Regional Research Station, Paiyur, TN, India
G2	CARI 2	CIARI, Andaman, India	G32	BPT 5204	A.N.G.R.A.U. Research station, AP, India
G3	CARI 3	CIARI, Andaman, India	G33	MTU 1010	A.N.G.R.A.U. Research station, AP, India
G4	CARI 4	CIARI, Andaman, India	G34	IR 64	IRRI, Philippines
G5	CARI 5	CIARI, Andaman, India	G35	CR 1009	NRRI, Cuttack, India
G6	ANR 16	CIARI, Andaman, India	G36	NDR 59	NDUAT, Kumarganj, India
G7	ANR 21	CIARI, Andaman, India	G37	Basmati SPS	CSSRI, Karnal, India
G8	ANR 37	CIARI, Andaman, India	G38	Pusa Basmati 1	CSSRI, Karnal, India
G9	ADT 36	TRRI, TN, India	G39	Pusa Basmati 1121	CSSRI, Karnal, India
G10	ADT 37	TRRI, TN, India	G40	Supermoti	CSSRI, Karnal, India
G11	ADT 38	TRRI, TN, India	G41	STBN 1	IIRR, Hyderabad, India
G12	ADT 43	TRRI, TN, India	G42	STBN 2	IIRR, Hyderabad, India
G13	ADT 45	TRRI, TN, India	G43	STBN 3	IIRR, Hyderabad, India
G14	Bora	Landrace, Assam, India	G44	STBN 4	IIRR, Hyderabad, India
G15	Shali	Landrace, Assam, India	G45	STBN 5	IIRR, Hyderabad, India
G16	Porimol	Landrace, Assam, India	G46	STBN 6	IIRR, Hyderabad, India
G17	Sampada	Landrace, Assam, India	G47	STBN 7	IIRR, Hyderabad, India
G18	Chhatoki	Landrace, Assam, India	G48	STBN 8	IIRR, Hyderabad, India
G19	Shabagidhan	Landrace, Assam, India	G49	STBN 9	IIRR, Hyderabad, India
G20	Burmadhan Black	CIARI, Andaman, India	G50	STBN 10	IIRR, Hyderabad, India
G21	CSR 10	CSSRI, Karnal, India	G51	STBN 11	IIRR, Hyderabad, India
G22	CSR 36	CSSRI, Karnal, India	G52	STBN 12	IIRR, Hyderabad, India
G23	CSR 43	CSSRI, Karnal, India	G53	STBN 13	IIRR, Hyderabad, India
G24	CO 43	AC & RI, Coimbatore, India	G54	STBN 14	IIRR, Hyderabad, India
G25	CO 47	AC & RI, Coimbatore, India	G55	STBN 15	IIRR, Hyderabad, India
G26	Ranjith	NRRI, Cuttack, India	G56	STBN 16	IIRR, Hyderabad, India
G27	Gayathri	NRRI, Cuttack, India	G57	STBN 17	IIRR, Hyderabad, India
G28	Swarna	NRRI, Cuttack, India	G58	STBN 18	IIRR, Hyderabad, India
G29	Jaya	IIRR, Hyderabad, India	G59	STBN 19	IIRR, Hyderabad, India
G30	C 14-8	CIARI, Andaman, India	G60	Pokkali	Kerala Agricultural University, India

Falconer and Mackay (1996). Path coefficient analysis was carried out following the method suggested by Dewey and Lu (1959) for partitioning the correlation coefficients into direct and indirect effects. The PCA analysis reduces the dimensions of a multivariate data to a few principal axes, generates an Eigen vector for each axis and produce component scores for the characters (Sneath *et al.*, 1973). The mean data of the trait were used to perform Principal Component Analysis using R v.4.2.1.

Results and Discussion

Salinity tolerance is a complex quantitative trait controlled by multiple genes (Chinnasamy *et al.*, 2005). Rice has been grouped as a salt susceptible cereal. Salt stress confines rice production in vast areas world and the problem is increasing because of climate change, global warming and secondary salinization, with consequent rise in sea level, particularly in the coastal areas. Salt stress affects the development of the rice genotypes during seedling and reproductive stage (Rajamadhan *et al.*, 2011). Therefore, studying genotypes and their traits at this stage will be appropriate for further progress in developing saline tolerant rice genotypes. The grain yield per plant or economic

yield is the primary trait for selection in breeding programmes for the breeders. The identification of vital yield components and information about their relationships is beneficial for developing an efficient breeding strategies for evolving high yield varieties under salinity. One of the ways to break productivity ceiling is through manipulation of these quantitative traits by exploiting underlining the association between genotypic variations and biometrical characters in a large population of rice genotypes which helps to identify the genetic markers associated with salt tolerance. Furthermore, principal component analysis is a statistical tool that allows for the identification of the most influential traits contributing to salt tolerance. By applying three approaches in combination reliable and accurate evaluation of rice genotypes for salt tolerance can be achieved, leading to the development of improved salt-tolerant varieties and ultimately ensuring food security in areas affected by salinity stress.

Association between characters: Correlation studies gives an estimate of degree of conglomeration of seed yield with its components. In this study, the rank, correlation coefficients indicated the degree and direction (positive and negative) of the associations between the characters. Positive correlation

Table 2: Phenotypic and genotypic correlation coefficients among yield attributing characters in rice genotypes under coastal saline condition (Pooled analysis)

Characters		Days to first flower	Plant height	Number of tillers per plant	Number of panicles per plant	Panicle length	Number of grains per panicle	Thousand grain weight	L/B ratio	Grain yield per plant
Days to first flower	P	1.00	-0.026	0.048	0.073	0.156*	0.138	-0.049	-0.047	0.037
	G	1.00	-0.003	0.077	0.138	0.276*	0.139	-0.075	-0.066	0.047
Plant height	P		1.00	-0.149*	-0.151*	0.079	-0.11	0.301**	-0.033	-0.119
	G		1.00	-0.193	-0.23	0.092	-0.113	0.399**	-0.04	-0.116
Number of tillers per plant	P			1.00	-0.086	0.072	0.352**	-0.027	-0.064	0.142
	G			1.00	-0.063	-0.108	0.496**	-0.036	-0.188	0.282*
Number of panicles per plant	P				1.00	0.09	0.322**	-0.055	-0.088	0.511**
	G				1.00	0.037	0.430**	-0.173	-0.183	0.731**
Panicle length	P					1.00	0.101	0.076	-0.018	0.044
	G					1.00	0.148	-0.013	-0.111	0.108
Number of grains per panicle	P						1.00	-0.026	-0.303**	0.784**
	G						1.00	-0.022	-0.369**	0.841**
Thousand grain weight	P							1.00	-0.105	0.198**
	G							1.00	-0.125	0.260**
L/B ratio	P								1.00	-0.213
	G								1.00	-0.216**
Grain yield per plant	P									1.00
	G									1.00

Significant* $p < 0.005$ and Significant** $p < 0.001$

between desirable traits is favorable to the plant breeder because it helps in simultaneous enhancement of both characters, while the negative association hinders the same. A positive significant association due to gene effects can be the result of the presence of strong coupling phase linkage between their genes or the characters may be result of pleiotropic genes that control these characters in the same direction. The correlation co-efficient among the various yield and yield associating traits in rice genotypes under coastal saline environment (pooled analysis) are shown in Table 2. The results demonstrated that the values of genotypic correlations coefficients were higher than the phenotypic correlations. Genotypic correlation is more stable and of much significance to the plant breeder to bring about genetic improvement in one character by selecting the other character of the pair that is genetically correlated (Anbuselvam *et al.*, 2023).

The findings of this study showed that, at both the genotypic and phenotypic levels, the grain yield per plant was significantly and positively correlated with the number of grains per panicle (0.841**, 0.784**), number of panicles per plant (0.731**, 0.511**), and thousand grain weight (0.260**, 0.198**) whereas days to first flower and plant height were not significantly correlated with grain yield per plant. This can be improved by selecting early maturing lines. The grain yield per plant had no significant correlation with days to first flower (Islam *et al.* (2016) and plant height (Faysal *et al.*, 2022). Genotypic correlation was found significant grain yield with number of tillers per plant (0.282*). This was in conformity with the findings of Kiruthikadevi *et al.* (2020) for number of grains per panicle and number of panicles per plant; Rajamadhan *et al.* (2011) for thousand grain

weight. Grain yield was also significant and negatively associated with grain L/B ratio (-0.216*) at both phenotypic and genotypic level. The characters viz., days to first flowering (0.047, 0.037) and panicle length (0.044, 0.108) recorded positive non significant association with grain yield per plant whereas plant height (-0.119,-0.116) exhibited negative non-significant association with grain yield both at genotypic and phenotypic level. These findings corroborate with the results of Manohara and Singh (2015) who reported negative non-significant association between grain yield and plant height in rice. Since, the characters number of grains per panicle, number of panicles per plant, thousand grain weight, panicle length and days to first flower were less affected by salt stress, selection based on these traits would be effective.

Days to first flower had a strong significant and positive inter correlation with panicle length (0.276*, 0.156*). However, with other traits it showed a non-significant positive correlation (Table 1). The inter correlation of plant height exhibited a strong significant and positive correlation with thousand grain weight. Similar findings were observed by Krishnamurthy *et al.* (2014). The number of tillers per plant had positive significant inter-correlation with the number of grains per panicle and grain yield per plant at both genotypic and phenotypic level. The number of panicles per plant had positive significant association with the number of grains per panicle and grain yield per plant at both genotypic and phenotypic level. The inter correlation of panicle length showed non-significant correlation with all the traits. From this study, the number of grains per panicle exerted a positive and highly significant correlation with grain yield, which indicated the

Table 3: Path coefficient analysis showing direct and indirect effects of yield attributing characters on grain yield per plant in rice genotypes under coastal saline condition (Pooled analysis)

Character	Days to first flower	Plant height	Number of tillers per plant	Number of panicles per plant	Panicle length	Number of grains per panicle	Thousand grain weight	L/B ratio	Grain yield per plant
Days to first flower	-0.097	0.002	0.003	0.076	0.015	0.092	-0.031	-0.012	0.046
Plant height	0.002	-0.073	-0.007	-0.126	0.004	-0.074	0.166	-0.007	-0.115
Number of tillers per plant	-0.007	0.014	0.037	-0.034	-0.005	0.326	-0.014	-0.035	0.282
Number of panicles per plant	-0.013	0.016	-0.002	0.549	0.002	0.284	-0.072	-0.033	0.731
Panicle length	-0.026	-0.006	-0.004	0.019	0.053	0.097	-0.005	-0.020	0.108
Number of grains per panicle	-0.013	0.008	0.018	0.236	0.008	0.660	-0.009	-0.067	0.841
Thousand grain weight	0.007	-0.029	-0.001	-0.095	0.000	-0.014	0.415	-0.023	0.260
L/B ratio	0.006	0.002	-0.007	-0.100	-0.006	-0.243	-0.052	0.184	-0.216

Residual effect – 0.2339 Direct effect – Diagonal bold values Indirect effect – Unbold values

Table 4: Extracted Eigen values, percentage of variances and cumulative percentage of variances for each principal components under coastal saline condition (Pooled analysis)

Principal components	Eigen values	Variance per cent	Cumulative variance per cent
PC 1	2.55	28.36	28.36
PC 2	1.46	16.27	44.63
PC 3	1.19	13.25	57.88
PC 4	1.14	12.61	70.49
PC 5	0.84	9.35	79.84
PC 6	0.77	8.54	88.38
PC 7	0.62	6.89	95.27
PC 8	0.38	4.20	99.47

importance of this trait for progeny selection under salt stress, whereas negative significant association with L/B ratio. Thousand grain weight showed a negative significant correlation with grain L/B ratio. Inter-correlation of grain L/B ratio was found to be strong negative and significant with grain yield per plant. The close relation of phenotypic and genotypic correlation coefficients is studied from the correlation study which indicates the masking effect of environment on character association. The findings of this study confirmed that the essential yield related traits were number of tillers per plant, number of panicles per plant, number of grains per panicle and thousand grain weight, which could be used as selection standards for rice grain yield enhancement under saline breeding programme.

Knowledge of the association among phenotypic traits and their impact on grain yield would be vital for selecting desired accessions to be integrated with a breeding program and for releasing new varieties (Dhavaleshvar *et al.*, 2019). The correlation between two variables can be divided into direct and indirect effect through other factors based on path coefficient analysis. Path coefficient study provides an effective way of determine the direct and indirect sources of correlations. In order to find out the cause and effect relationship between yield and its related component traits were studied in the present study.

Direct positive effect on grain yield per plant of some traits indicates that selection of these traits will provide ample scope for improving the grain yield whereas negative indirect effects exhibited that opportunity for yield improvement through other associated traits. The genotypic correlation coefficient recorded for nine yield component traits on grain yield were partitioned into direct and indirect effects of yield components as grain yield was undertaken in the present investigation and the results obtained are presented in Table 3.

The estimated residual effect under salinity stress condition was 0.2339. The path analysis revealed that the highest positive direct effects on grain yield per plant was found with the number of grain per panicle (0.660), number of panicles per plant (0.549), and thousand grain weight (0.415), indicating a true relationship among these traits. Thus, direct selection for these attributes will be beneficial for improvement under saline conditions. Similar observations of high direct effect of grains per panicle on grain yield was earlier reported by Shanthi Priya *et al.* (2017) and number of panicles per plant and thousand grain weight on grain yield by Saravanan and Sabesan (2010) and Venkatesan *et al.* (2019). The number of tillers per plant (0.037) and panicle length (0.053) had negligible direct effects on grain yield per plant. The negative negligible effect was obtained by days to first flower (-

Table 5: Rotated component matrix (Eigen vectors) for the different characters for the principal components under coastal saline condition (Pooled analysis)

Parameters	PC 1	PC 2	PC 3	PC 4
Days to first flower	0.13	-0.04	0.66	-0.22
Plant height	-0.15	0.63	0.07	0.02
Number of tillers per plant	0.26	-0.11	-0.24	-0.71
Number of panicles per plant	0.41	-0.14	0.11	0.56
Panicle length(cm)	0.11	0.19	0.66	-0.11
Number of grains per panicle	0.56	0.03	-0.08	-0.14
Thousand grain weight	0.02	0.67	-0.18	0.03
L/B ratio	-0.27	-0.24	0.04	0.21
Grain yield per plant	0.57	0.13	-0.13	0.23

0.097) and plant height (-0.073). These two characters do not have any effect on improving grain yield. However, the residual effect was lesser (0.2339) indicating that the three characters under this study contributed 76.61 percent of the total variability in grain yield per plant studied.

The number of tillers per plant had positive indirect effects on grain yield per plant through number of grains per panicle (0.326). Vennila and Palaniraja (2018) found that a higher number of tillers per plant indirectly increased grain yield by enhancing the number of grains per panicle. This suggests that tiller count plays a key role in improving the overall yield potential. Number of panicles per plant exhibited positive indirect effects on grain yield via number of grain per panicle (0.284). Manivelan *et al.* (2022) observed that an increase in the number of panicles per plant positively influenced the grain yield by boosting the number of grains per panicle. This indirect effect highlights the importance of panicle number in enhancing yield potential. In this research, the indirect and direct effects of yield contributing traits and yield were calculated. The relationship between the effect and a causal factor was similar to its direct effect, thus true relationship was explained and plant breeder could directly select for these traits. As a result, indirect selection based on these traits should be examined simultaneously for yield enhancement. Principal component analysis is a well known multivariate technique in clarifying the relationship among traits in complex multi trait system such as the growth characters, yield and yield attributing traits (Prafull Kumar *et al.*, 2015).

In the present study, PCA was performed in 60 rice genotypes using nine quantitative traits under salt stress (pooled analysis) condition. The percent of variance, cumulative proportion of variances and Eigen values are shown in Table 4. Under saline stress, PCA analysis showed that out of nine quantitative traits, four most informative PCs with Eigen values of 2.55, 1.46, 1.19 and 1.14 accounted 70.49% of the cumulative variance. PC1 showed 28.36% whereas PC2, PC3 and PC4 accounted 16.27%, 13.25% and 12.61% variance, respectively. Venkata Ratnam *et al.* (2023) reported that out of fourteen traits studied in 37 rice genotypes, 3 PCs exhibited more than 1.0 eigen values and showed about 78.33% total variability among the

characters studied. The study explained by the first four axes with an Eigen value of greater than unity indicates that, the identified traits within the axes exhibited great influence on the phenotype of genotypes studied. Remaining components with Eigen values <1 contributed 29.51 percent variability. Principal components with values <1 were considered non-significant.

Scree plot elucidated the variation percent associated with each principal component by drawing a graph between Eigen values (X-axis) and percentage of variation explained (Y-axis) (Fig. 1). Scree plots display the eigen values order of greatest to smallest as well as percentage of variability in terms of primary component and eigen value. PC1 showed 28.36% variability with eigen value 2.55, thereafter graph gradually declined for another PC. Steep curve followed by bend and then straight found for different PCs. Scree plot maximal variation expressed in saline stress, PC1 expressed the most variance compared to nine PCs, although PC1, PC2, PC3 and PC4 account for the highest variation since their Eigen value were more than one. The remaining factors contribute minimally to the overall variability and are considered less critical. Shivangi *et al.* (2021) similarly observed that the first few principal components (PC1–PC4) explained the majority of variation, while the remaining components had minimal impact. This indicates that these factors are less influential in determining the overall grain yield.

The principal component scores of all the nine characters under study were estimated presented in Table 5. Interpretation of the principal components are based on the findings where variables are strongly correlated with each component. Eigen values close to -1 or 1 indicate that the variable strongly influences the component. Values close to 0 indicate that the variable has a weak influence on the component. In this study, the important characters contributed in positive factor loading value for PC 1 were grain yield per plant (0.57), number of grains per panicle (0.56), number of panicles per plant (0.41), number of tillers per plant (0.26), days to first flower (0.13) and panicle length (0.11). Traits like grain L/B ratio (-0.27) and plant height (-0.15) showed negative contribution to PC 1 indicating that genotypes with negative values of PC1 had reduced height and grain breadth. PC 2 contributed positively with the grain yield per plant

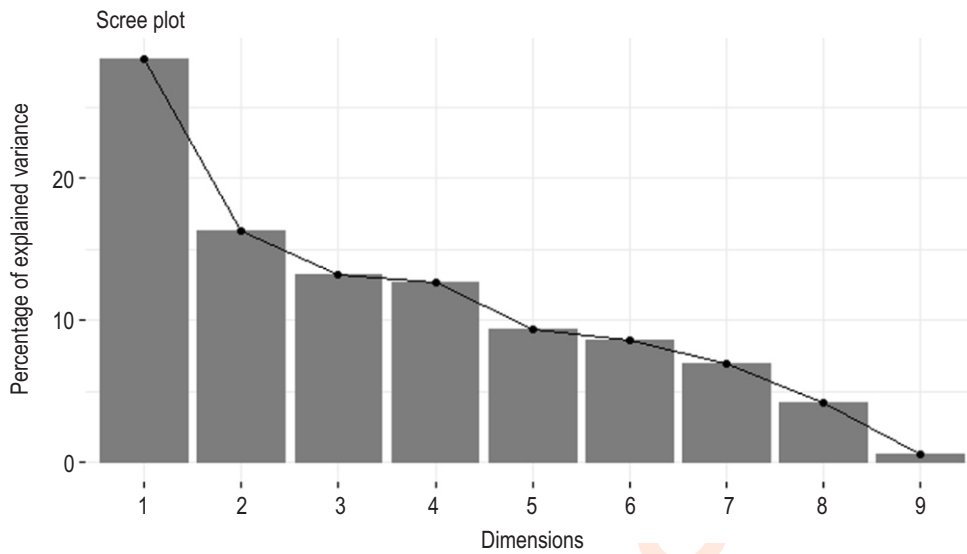


Fig. 1: Scree Plot of principal component analysis for rice genotypes between their Eigen value, percentage of variance, cumulative percentage variance and the number of principal components under coastal saline condition (Pooled analysis).

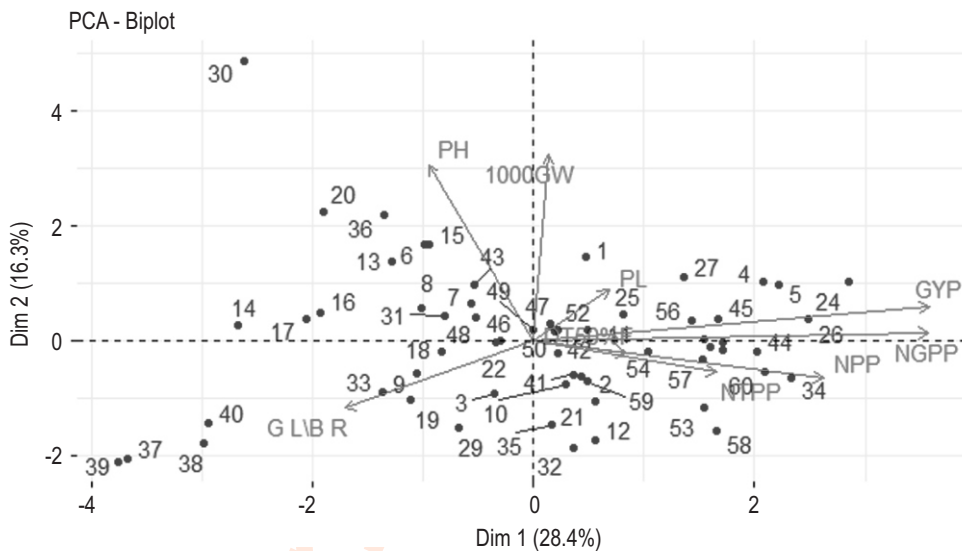


Fig. 2: PCA biplots of the various rice genotypes and characters represented in two major principal components under coastal saline condition (Pooled analysis).

(0.13), number of grains per panicle (0.67), panicle length (0.19) and plant height (0.63), while grain L/B ratio (-0.24) and the number of tillers per plant (-0.11) contributed negatively.

PC 3 related to the characters days to first flower and panicle length (0.66) contributed positively whereas the number of tillers per plant (-0.24) and grain yield per plant (-0.13) contributed negatively. The first three principal component axes explained more than half of the total variability (57.88 %), hence, it

indicated a high degree of correlation among the traits studied. However, PC 4 expressed positive factor loading values for grain yield per plant (0.23), grain L/B ratio (0.21) and number of panicles per plant (0.56), while days to first flower (-0.22), panicle length (-0.11), number of grains per panicle (-0.14) and number of tillers per plant (-0.71) contributed to maximum negative factor loading value. As a whole, PCA was able to identify important characters that were responsible for variability in a population. Christina et al. (2021) and Lakshmi et al. (2022) also found that

the first few principal components captured most of the variability, indicating strong trait interrelationships. They reported both positive and negative trait loadings, helping to identify key contributors to population variability. Biplot diagram analysis between PC1 and PC2 showed that variables and genotypes are super imposed on the plot as vectors. The length of the vector is based on the contribution of the character to the principal component (Table 5, Fig. 2). Moreover, the angle of the character vectors reflects the correlation of variables. The angle between the trait vectors indicates the direction of association between the traits. An acute angle (less than 90°) indicates a highly positive correlation, while obtuse angle (more than 90°) indicates a highly negative correlation. Orthogonal vectors indicate no correlation (Sathyaraj et al., 2024).

The findings of this study showed that the genotypic correlations were found higher than the phenotypic correlation revealing strong inherent association among the various traits. From the results of this study, grain yield per plant showed positive significant association with number of tillers per plant, number of panicle per plant, number of grains per panicle and thousand grain weight at both genotypic and phenotypic levels reflecting that the effective selection on the basis of these traits can lead to achieve higher grain yield. Path analysis revealed that direct selection of the number panicles per plant, number of grains per panicle and thousand grain weight could be exploited for improving grain yield in saline breeding programme. The experiment unraveled the hidden buffering capacity of genotypes for the study. Based on the interaction vectors and PC scores of genotypes, G26 (Ranjith), G44 (STBN 4), G60 (Pokkali) and G34 (IR64) were identified as high yielding, and the most diverse parents which could be used in coastal saline improvement program.

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