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Research Article

Comparative patterns of principal component and cluster analysis under sodicity and normal soil conditions in rice (*Oryza sativa* L.)

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Abstract
Rice is an important food crop that feeds majority of world population. The crop is sensitive to sodicity stress and the area under sodicity is gradually increasing, resulting in decline in productivity. The present investigation aimed to study the genetic diversity patterns of rice germplasm under sodicity and normal soil conditions using principal component and hierarchical cluster analysis. The germplasm was raised at two different environments and the observations were subjected to principal component and hierarchical cluster analysis. The principal component analysis identified four principal components having eigen value greater than one under sodic as well as normal soil environments. The genotypes that exhibited higher values for a particular trait were identified using the biplot as they were located closer to the trait vector. The comparison of biplots revealed that trait vectors for DFF, FLB, HGW and SPY were located at different quadrants under sodic and normal soil environments. Hierarchical cluster analysis grouped the rice genotypes into five clusters under both environments. The tolerant (TG63, TG121 and TG17) and susceptible (TG54, TG55, TG86 and TG185) genotypes were identified by comparing the clustering pattern of these genotypes under sodic and normal soil conditions. Identification of clusters with higher genetic distance (cluster I and cluster V) could be employed in plant breeding programmes to produce higher frequency of transgressive segregants and develop sodicity tolerant rice varieties.

Keywords: Rice, Diversity, PCA, Hierarchical cluster analysis

INTRODUCTION

Rice (*Oryza sativa* L.) is one of the most important staple crops globally, serves as a primary source of food and sustenance for a significant portion of the world's population. However, the cultivation of rice is often constrained by various environmental stresses, including soil salinity and sodicity. Among these stresses, sodicity, characterized by excessive accumulation of sodium ions (Na^+) in the soil, poses a significant threat to rice production and productivity, particularly in regions with high soil sodicity (Yu *et al.,* 2014).

Preliminary understanding of the genetic basis of sodicity tolerance in rice is crucial for developing improved varieties that can thrive under such conditions that are unfavourable for crop growth and development (Shanthi *et al.,* 2011). The development of improved

varieties that are tolerant to the sodicity minimizes the yield loss and sustains food security. Assessment of genetic diversity present in a population and identifying distinct heterotic groups are the basic and prime steps before crop improvement (Yadav *et al.,* 2011).

Multivariate analysis such as Principal Component Analysis (PCA) and cluster analysis emerged as a valuable approach to unravel the underlying genetic structure and diversity patterns within rice population (Singh *et al.,* 2022). Among a large volume of datasets generally handled by plant breeders, PCA can identify the key traits that contribute to total variation and allows focus on specific traits. PCA was then used to reveal patterns and reduce redundancy in the datasets as genetic variations often occur in crop species (Maji and Shaibu 2012).

Cluster analysis serves as a fundamental tool in plant breeding programmes, enabling the identification of desirable traits and the selection of appropriate parental lines for hybridization. Cluster analysis aids breeding materials to be classified into different heterotic groups and identification of best parental lines (Aarthi *et al.,* 2021). With this background, the present study has been framed to explore the genetic diversity of rice germplasm collections and compare it among sodicity and normal soil environment using PCA and cluster analysis. By leveraging the power of this statistical methods, we aim to identify key genetic factors and gain insights into the relationships among various rice genotypes under sodic and normal soil environments, facilitating the development of superior sodicity tolerant rice varieties.

MATERIALS AND METHODS

The present study was carried out using a set of 150 germplasm accessions consisting of landraces, improved varieties and Harvestplus lines (**Table 1**). The field experiment was operated at Dept. of Genetics and Plant Breeding farm, Anbil Dharmalingam Agricultural College and Research Institute, Trichy (10º 45' 16'' N, 78º 36' 12'' E) as a sodicity stress environment (pH- 9.1, EC- 0.19, ESP- 36.7) and in Karur, Tamil Nadu, India (10º 57' 34'' N, 78º 00' 42'' E) in normal soil (pH- 7.15, EC- 0.21, ESP- 8.3) as an irrigated crop. The seeds were sown in raised nursery bed and were transplanted to main field 27 days after sowing following a spacing of 20 × 20 cm. The experiment was carried out in Augmented complete block design with 144 test entries and 6 checks. All recommended package of practices were followed to maintain a healthy crop.

Different morphological and biometrical observations *viz*., Days to 50% flowering (DFF), Plant height (PH), Number of tillers (NT), Number of productive tillers (NPT), Flag leaf length (FLL), Flag leaf breadth (FLB), Panicle length (PL), Number of filled grains per panicle (FPP), Spikelet sterility (SS), Panicle weight (PW), Hundred grain weight (HGW) and Single plant yield (SPY) were recorded at crop maturity. All observations were recorded as per Standard Evaluation System (IRRI, 2002).

Statistical analysis: The adjusted mean values for the genotypes were calculated using "augmentedRCBD" package in R software v4.1.2 for both the environments. The mean values were further used for principal component and cluster analysis. The principal

Table 1. List of genotypes used in the present study

Code	Name	Code	Name	Code	Name
TG1	*Mapillai Samba*	TG22	IR 36	TG48	*Kalarkar*
TG2	CK 275	TG25	*Sorna kuruvai*	TG50	*Sornavari*
TG3	*Senkar*	TG26	*Rasacadam*	TG51	RPHP 134
TG4	*Murugankar*	TG31	*Chinthamani*	TG53	IR 68144-2B-2-2-3-1-127)
TG5	CHIR 6	TG32	*Togai Samba*	TG54	PTB 19
TG6	CHIR5	TG33	*Malayalathan Samba*	TG55	IG 67 (EC 729050-120988)
TG7	*Kudai Vazhai*	TG34	RPHP 125	TG56	RPHP 59
TG8	CHIR 8	TG35	CK 143	TG57	RPHP 103
TG9	*Kuruvai Kalanjiyam*	TG36	*Kattikar*	TG58	*Kodaikulathan*
TG11	CSR36	TG37	*Shenmolagi*	TG59	RPHP 68
TG12	*Vellaichithiraikar*	TG39	*Kattu ponni*	TG60	*Rama kuruvaikar*
TG13	*Pokkali samba*	TG40	Pusa 44	TG61	FL478
TG14	Jothi	TG41	*Godavari Samba*	TG63	IG 71 (EC 728651-117588)
TG15	*Palkachaka*	TG42	*Earapalli Samba*	TG66	*Seevanasamba*
TG17	*Sivapuchithiraikar*	TG43	RPHP 129	TG67	RPHP 106
TG18	CHIR 11	TG44	*Mangam samba*	TG68	IG 63 (EC 728711-117674)
TG20	*Kalvalai*	TG46	IG 4 (EC 729639-121695)	TG69	RPHP 48

Table 1.Cont.,

Code	Name	Code	Name	Code	Name
TG70	*Karthi samba*	TG95	*Jeeraga samba*	TG115	IG 43(EC 728788-117759)
TG72	*Aarkadu kichili*	TG96	RP BIO 226	TG116	RPHP 27
TG74	ARB 65	TG98	IG 5(EC 729642-121698)	TG117	IG 65(EC 729024-120958)
TG76	*Matta kuruvai*	TG100	IG 7(EC 729598-121648)	TG118	*Ponmani samba*
TG77	*Karuthakar*	TG102	*Varakkal*	TG120	*Thattan samba*
TG80	IG 66(EC 729047-120985)	TG103	*Mattaikar*	TG121	IG 74(EC 728622-117517)
TG81	CB 07701-252	TG104	IG 53(EC 728752-117719)	TG122	*Kaliyan samba*
TG82	*Thooyamalli*	TG105	IG 6(EC 729592-121642)	TG123	IG 2(EC 729808-121874)
TG83	RPHP 93	TG106	*Katta samba*	TG124	IG 29(EC 728925-117920)
TG85	RPHP 104	TG107	RH2-SM-1-2-1	TG126	*Kallimadayan*
TG86	RPHP 102	TG108	*Red sirumani*	TG127	IG 10
TG88	ASD19	TG109	*Vadivel*	TG128	IG 75(EC 728587-117420)
TG89	IR 83294-66-2-2-3-2	TG110	*Norungan*	TG129	IG 38(EC 728742-117707)
TG90	CSR27	TG111	TRY3	TG130	IG 39(EC 728779-117750)
TG91	IG 23(EC 729391-121419)	TG112	IG 35(EC 728858-117843)	TG131	RPHP 90
TG92	IG 49(EC 729102-121052)	TG113	IG 45(EC 7287698-117736)	TG132	IG 33(EC 728938-117935)
TG94	CSR23	TG114	RPHP 159	TG133	IG 42(EC 728798-117774)

Code	Name	Code	Name	Code	Name
TG134	IG 9(EC 729682-121739)	TG159	*Sembala*	TG182	ARB 59
TG135	RPHP 161	TG160	IG 72(EC 728650-117587)	TG183	RPHP 163
TG136	IG 8(EC 729601-121651)	TG161	*Panamara samba*	TG184	IG 18(EC 728892-117880)
TG139	CO43	TG162	IR 64	TG185	RPHP 36
TG141	IG 44(EC 728762-117729)	TG163	*Mikuruvai*	TG186	IG 28(EC 728920-117914)
TG142	Sasyasree	TG164	*Thillainayagam*	TG187	*Vadakathi samba*
TG143	IG 46	TG165	ARB 64	TG188	RPHP 80
TG144	Apo	TG166	RPHP 140	TG189	IG 41(EC 728800-117776)
TG145	IG 60(EC 728730-117695)	TG168	*Haladichudi*	TG190	IG 26(IC 0590943-121899)
TG147	IG 58(EC 728725-117689)	TG169	IG 24(EC 728751-117718)	TG191	IG 15(IC 728910-117901)
TG149	RH2-SM-2-23	TG170	RPHP 42	TG192	*Nootri pathu*
TG151	IG 32(EC 728838-117823)	TG172	IG 25(EC 729728-121785)	TG231	*Kalanamak*
TG152	RPHP 47	TG173	IG 73(EC 728627-117527)	TG249	TRY4
TG153	BPT5204	TG174	IG 51(EC 728772-117742)	TG250	TRY5
TG154	IG 48	TG175	*Vellai kudaivazhai*		
TG156	IG 12(EC 729626-12168)	TG176	*Kodai*		
TG157	*Karungan*	TG181	IG 52(EC 728756-117723)		

component analysis was carried out using "FactoMineR" (Le *et al.,* 2008) and "factoextra" (Kassambara and Mundt 2020) packages of R software v4.3.0. Similarly, hierarchical cluster analysis was carried out using Ward's method based on Euclidean distances using "stats" package in R software.

RESULTS AND DISCUSSION

Principal component analysis: The genotypes raised in both sodic and normal soil environment were subjected to principal component analysis. The results indicated significant difference in pattern of variation in sodic and normal soil environments. A scree plot was made by plotting principal components against eigen vector values (**Fig. 1**). It revealed first four principal components (PC1, PC2, PC3 and PC4) having eigen value greater than one contributed up to 65.15 and 66.37 per cent of variation under sodicity and normal irrigated environment, respectively (**Table 2**). Shoba *et al*. (2019) also reported four principal components having eigen value greater than one for evaluating their rice germplasm.

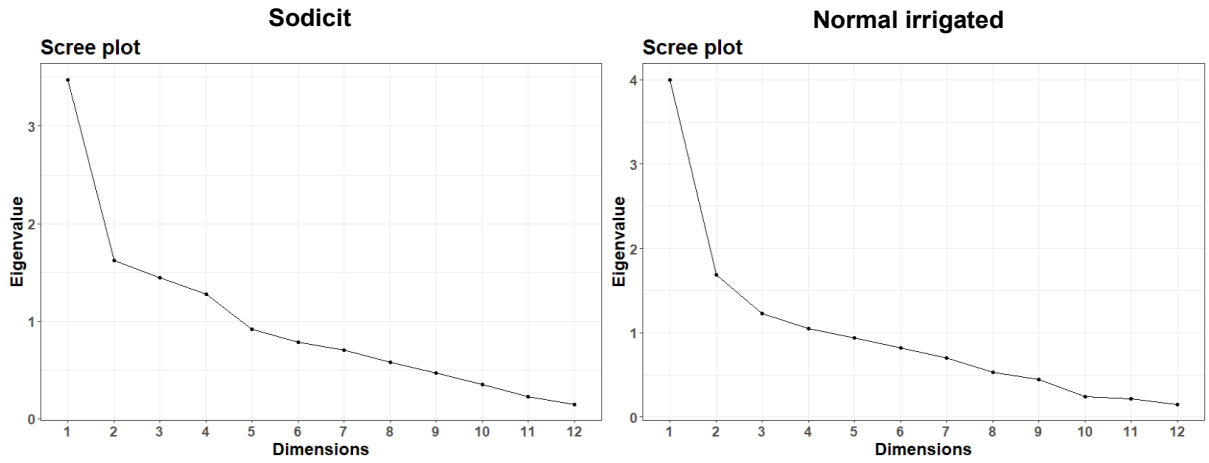

Fig. 1. Scree plot for different principal components in rice genotypes

Table 2. Contribution, Eigen values and proportion of variance of yield and its contributing traits to different principal components

Environment	Sodicity				Normal irrigated			
Traits	Dim.1	Dim.2	Dim.3	Dim.4	Dim.1	Dim.2	Dim.3	Dim.4
DFF	0.047	0.319	**0.709**	-0.052	0.208	**-0.457**	0.169	**0.418**
PH	0.521	0.027	0.090	**0.548**	0.462	0.261	**0.627**	0.246
NT	0.612	**0.502**	**-0.465**	0.082	0.573	**0.459**	**-0.449**	0.268
NPT	**0.654**	**0.465**	**-0.484**	0.058	0.640	0.422	**-0.434**	0.298
FLL	0.459	0.024	0.285	**0.616**	**0.656**	0.155	**0.442**	-0.034
FLB	0.268	0.424	**0.520**	-0.117	0.286	**-0.586**	-0.067	**0.382**
PL	**0.658**	-0.196	0.188	0.016	0.540	-0.211	-0.064	**-0.350**
FPP	**0.678**	-0.025	0.168	**-0.494**	**0.761**	-0.425	-0.027	-0.130
SS	-0.300	**0.484**	0.217	0.229	-0.402	0.200	0.145	**0.558**
PW	0.714	-0.336	0.144	-0.320	**0.792**	-0.312	0.114	0.060
HGW	0.129	**-0.668**	0.031	**0.407**	0.355	**0.532**	0.370	-0.194
SPY	**0.779**	-0.190	-0.038	-0.069	**0.842**	0.100	-0.201	-0.116
Eigen Value	**3.48**	**1.62**	**1.45**	**1.28**	**4.00**	**1.69**	**1.23**	**1.05**
% of variance	**28.96**	**13.49**	**12.05**	**10.64**	**33.33**	**14.08**	**10.23**	**8.74**
Cumulative % of variance	**28.96**	**42.46**	**54.51**	**65.15**	**33.33**	**47.41**	**57.63**	**66.37**

DFF- Days to 50% flowering, PH- Plant Height, NT- No. of tillers, NPT- No. of productive tillers, FLL- Flag leaf length, FLB- Flag leaf breadth, PL- Panicle length, FPP- No. of filled grains per panicle, SS- Spikelet sterility %, PW- Panicle weight, HGW- Hundred grain weight, SPY- Single plant yield

PC1 component under sodicity contributed for 28.96 per cent variation, which is very much similar to PC1 component under normal irrigated environment (33.33 per cent). The comparison of factor loadings for PC1 component under these environments showed almost similar contribution from investigated traits. The highest positive loading for PC1 component was exhibited by SPY under sodicity (0.779), as well as under normal irrigated environment (0.842). Upadhyay *et al.* (2022) also reported higher positive loadings for SPY under sodicity. Negative loadings for PC1 was exhibited by SS under both sodic (-0.300) and normal irrigated environments (-0.402).

Similarly, the contribution for total variation by subsequent principal components (PC2, PC3 and PC4) were found to be 13.49, 12.05 and 10.64 respectively, under sodicity and 14.08, 10.23 and 8.74 respectively, under normal irrigated environment. Further, difference in

contribution was observed for these subsequent principal components. The traits HGW (-0.668), DFF (0.709) and FLL (0.616) contributed highest factor loadings under sodicity, for PC2, PC3 and PC4 respectively, whereas in normal irrigated environment, these traits recorded comparatively lower loadings. Besides, the traits, FLB (-0.586), PH (0.627) and SS (0.558) contributed highest factor loadings under normal irrigated environment for PC2, PC3 and PC4 respectively. These results were in accordance with Upadhyay *et al.* (2022) for DFF under sodicity and Aishwarya *et al.* (2023) for FLB under normal soil conditions. Among them, HGW under sodicity and FLB under normal irrigated environment contributed negative loadings to the principal components.

The PC1 Vs PC2 biplot (**Fig. 2**) indicate the PC values for the evaluated genotypes under sodicity and normal irrigated environment. The trait vectors located in Ist quadrant have higher positive PC1 and PC2 components indicating that these genotypes have higher values for DFF, PH, NT, NPT, FLL and FLB under sodicity. Similarly, under normal irrigated environment, the genotypes located in Ist quadrant had higher PH, NT, NPT, FLL, HGW and SPY. The trait vectors in quadrant II also had positive PC1 values and negative PC2 values in both the environments. The genotypes in quadrant II had higher values for PL, FPP, PW, HGW and SPY under sodicity as against DFF, FLB, PL, FPP and PW under normal irrigated environment. The observations were derived

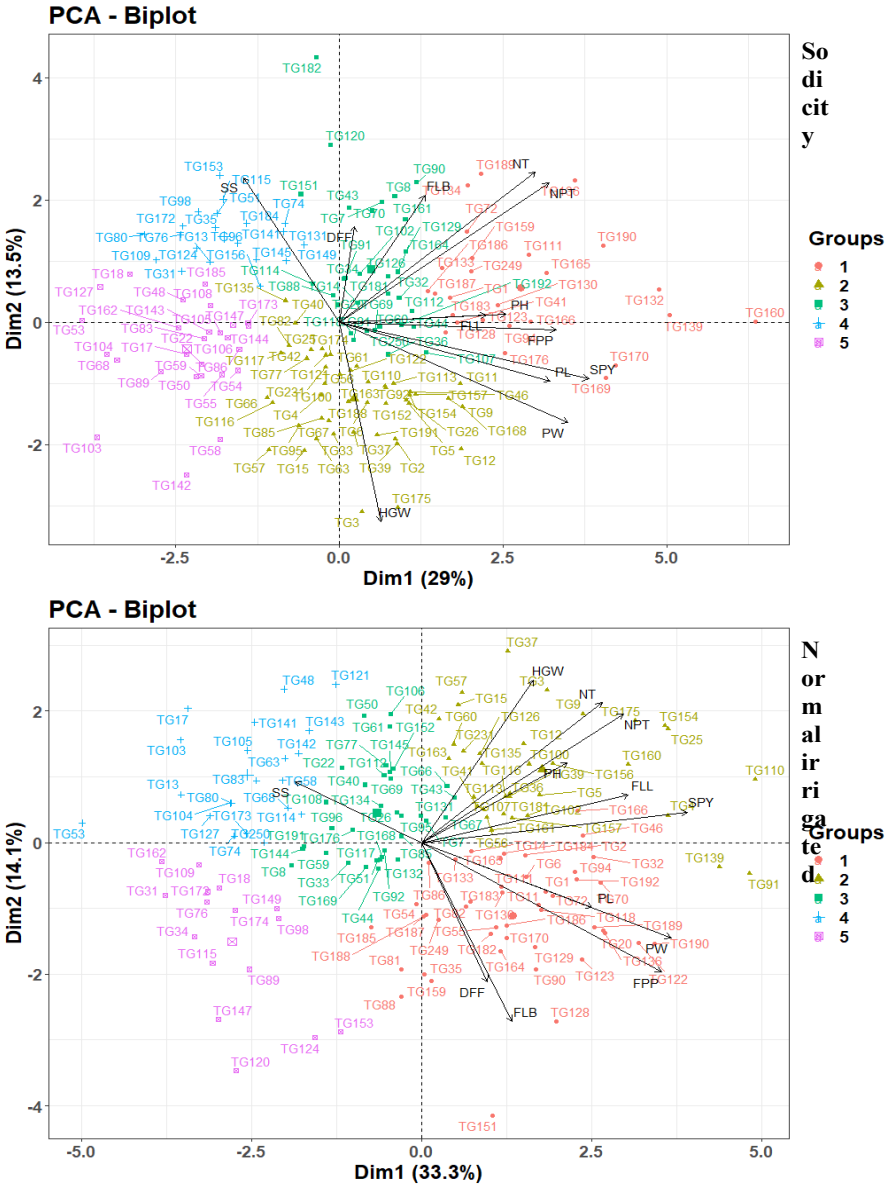

Fig. 2. PC1 Vs PC2 biplot for rice genotypes, yield and its contributing traits

based on the results presents by Ariharasutharsan *et al.* (2023). The trait vector for SS was located in quadrant IV indicating that it had negative PC1 values and positive PC2 values.

Hierarchical Cluster analysis: The genotypes were grouped by using Ward's method based on Euclidean distance values for the principal components (**Fig. 3**). The genotypes were grouped into five groups for both sodicity and normal irrigated environment (**Table 3**). Shoba *et al.* (2019) also classified their germplasm into five clusters for their study based on hierarchical cluster analysis. Also, non-hierarchical clustering was used by Singh *et al.* (2020) to classify their germplasm into ten clusters. The largest cluster in the present study was found to be cluster II under sodicity containing 46 genotypes and cluster I under normal irrigated environment containing 45 genotypes. Other clusters also had significant number of genotypes in both the environments, but it had a clear difference in grouping based on cluster mean values.

The cluster mean values, intra and inter cluster distances between each cluster was calculated to analyse the genotype present in each cluster and its utilization in breeding programmes. The cluster mean values for SPY was found to be highest for cluster I (20.38 g) with 26 genotypes under sodicity followed by cluster II with 16.37 g (**Table 4**). Singh *et al.* (2020) also estimated the cluster mean values for SPY and identified best yielding genotypes under sodic conditions. Cluster I of the present study contains tolerant check varieties *viz*., TG94, TG111, TG139 and TG249 along with best performing genotypes TG160, TG169 and TG190. The susceptible check varieties TG40 and TG88 were grouped in clusters II and III respectively. The other known susceptible varieties were grouped along with susceptible genotypes in clusters IV and V. Similarly, under normal irrigated environment cluster II containing 34 genotypes possess highest mean value for SPY (33.04 g) followed by cluster I (29.45 g). The tolerant and susceptible varieties were distributed across different clusters since each genotype express their potential yield and there were no clear difference between their tolerance and susceptibility nature.

The comparison among the high yielding and low yielding clusters under sodic and normal irrigated environment reveals highly tolerant and susceptible genotypes. The genotypes TG63, TG121 and TG174 which were found to be in low yielding clusters in normal irrigated environment were classified with high yielding cluster in

Table 3. Clustering of rice genotypes using yield and its contributing traits computed by Ward's method based on hierarchical cluster analysis

Cluster (Sodicity)	Cluster size	Genotypes
I	26	TG1, TG41, TG72, TG94, TG111, TG123, TG128, TG130, TG132, TG133, TG134, TG136, TG139, TG159, TG160, TG165, TG166, TG169, TG170, TG176, TG183, TG186, TG187, TG189, TG190, TG249
II	46	TG2, TG3, TG4, TG5, TG6, TG9, TG11, TG12, TG15, TG25, TG26, TG33, TG37, TG39, TG40, TG42, TG46, TG56, TG57, TG61, TG63, TG66, TG67, TG77, TG82, TG85, TG92, TG95, TG100, TG110, TG113, TG116, TG117, TG121, TG122, TG135, TG152, TG154, TG157, TG163, TG168, TG174, TG175, TG188, TG191, TG231
III	31	TG7, TG8, TG14, TG20, TG32, TG34, TG36, TG43, TG44, TG60, TG69, TG70, TG81, TG88, TG90, TG91, TG102, TG107, TG112, TG114, TG118, TG120, TG126, TG129, TG151, TG161, TG164, TG181, TG182, TG192, TG250
IV	20	TG13, TG31, TG35, TG51, TG74, TG76, TG80, TG96, TG98, TG109, TG115, TG124, TG131, TG141, TG145, TG149, TG153, TG156, TG172, TG184
V	27	TG17, TG18, TG22, TG48, TG50, TG53, TG54, TG55, TG58, TG59, TG68, TG83, TG86, TG89, TG103, TG104, TG105, TG106, TG108, TG127, TG142, TG143, TG144, TG147, TG162, TG173, TG185
Cluster (Normal irrigated)	**Cluster size**	**Genotypes**
I	45	TG1, TG2, TG6, TG11, TG14, TG20, TG32, TG35, TG46, TG54, TG55, TG70, TG72, TG81, TG82, TG86, TG88, TG90, TG94, TG111, TG118, TG122, TG123, TG128, TG129, TG130, TG133, TG136, TG151, TG159, TG164, TG165, TG166, TG170, TG182, TG183, TG184, TG185, TG186, TG187, TG188, TG189, TG190, TG192, TG249
II	34	TG3, TG4, TG5, TG9, TG12, TG15, TG25, TG36, TG37, TG39, TG41, TG42, TG56, TG57, TG60, TG91, TG100, TG102, TG107, TG110, TG113, TG116, TG126, TG135, TG139, TG154, TG156, TG157, TG160, TG161, TG163, TG175, TG181, TG231
III	34	TG7, TG8, TG22, TG26, TG33, TG40, TG43, TG44, TG50, TG51, TG59, TG61, TG66, TG67, TG69, TG77, TG85, TG92, TG95, TG96, TG106, TG108, TG112, TG117, TG131, TG132, TG134, TG144, TG145, TG152, TG168, TG169, TG176, TG191
IV	21	TG13, TG17, TG48, TG53, TG58, TG63, TG68, TG74, TG80, TG83, TG103, TG104, TG105, TG114, TG121, TG127, TG141, TG142, TG143, TG173, TG250
V	16	TG18, TG31, TG34, TG76, TG89, TG98, TG109, TG115, TG120, TG124, TG147, TG149, TG153, TG162, TG172, TG174

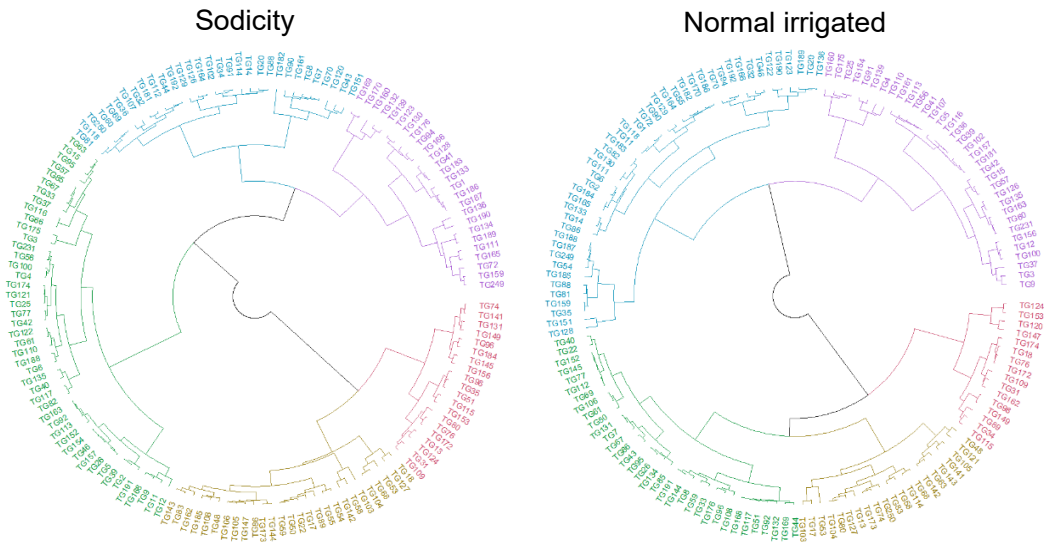

Fig. 3. Dendogram showing different clusters using Ward's method based on hierarchical cluster analysis

Table 4. Cluster means for yield and its contributing traits in rice genotypes

Cluster means- Sodicity												
Clusters	**DFF**	**PH**	**NT**	**NPT**	**FLL**	**FLB**	**PL**	**FPP**	**SS**	**PW**	**HGW**	**SPY**
I	92.60	122.31	16.22	13.48	33.98	1.47	19.55	145.11	25.14	3.11	2.08	20.38
II	90.35	108.28	10.50	7.97	33.35	1.23	17.05	112.16	23.88	2.65	2.36	16.37
III	96.62	109.25	12.83	10.04	34.41	1.45	16.87	120.70	32.42	2.36	1.92	15.11
IV	96.13	103.62	11.90	8.91	29.30	1.28	12.34	87.04	37.47	1.53	1.77	9.79
V	87.50	89.85	9.37	7.09	24.57	1.16	13.74	80.07	30.22	1.70	2.12	9.34
Cluster means- Normal irrigated												
Clusters	**DFF**	**PH**	**NT**	**NPT**	**FLL**	**FLB**	**PL**	**FPP**	**SS**	**PW**	**HGW**	**SPY**
I	98.68	144.53	19.40	14.80	44.50	1.79	20.18	206.97	6.44	3.52	2.00	29.45
II	93.63	156.90	22.12	17.41	48.16	1.53	18.58	180.00	7.00	3.24	2.41	33.04
III	92.08	144.19	18.38	13.90	41.87	1.53	17.75	136.38	10.04	2.63	2.12	24.90
IV	85.01	129.30	18.17	12.91	32.98	1.41	13.87	101.83	10.36	2.05	2.09	18.94
V	100.68	130.36	14.36	9.92	30.19	1.67	15.32	129.78	9.48	2.23	1.69	17.02

sodic environment. This indicated the stability of these genotypes under sodic stress conditions. Similarly, the genotypes which were grouped as high yielding genotypes under normal irrigated environment (TG54, TG55, TG86 and TG185) were grouped as low yielders under sodic stress environment indicating their susceptibility reaction.

The intra and inter cluster distance values were calculated for each cluster (**Table 5**). The maximum and minimum intra cluster distance values were exhibited by cluster III (7.81) and cluster V (5.50) respectively under sodicity. Similarly, cluster I (8.28) and cluster V (6.61) recorded maximum and minimum intra cluster distance respectively under normal irrigated environment.

In case of inter cluster distances, the maximum distance (11.01) was recorded between cluster I and cluster V under sodicity. Similarly, under normal irrigated environment, the maximum inter cluster distance (10.31) was recorded between cluster II and cluster IV. This indicated maximum divergence between these genotypes and crossing between them results in development of several transgressive segregants for sodicity tolerance. These results were in accordance with the results presented by Dhakal *et al.* (2020) and Deepika *et al.* (2021).

The present study aimed to explore the genetic diversity of rice genotypes and compare the pattern of variations under sodicity and normal soil environment. The principal

Table 5. Average intra and inter cluster Euclidean distance values

	Cluster distance - Sodicity					Cluster distance - Normal irrigated				
Clusters	**I**	**II**	**III**	**IV**	**V**	**I**	**II**	**III**	**IV**	**V**
I	**7.13**					**8.28**				
II	9.01	**6.64**				8.80	**7.39**			
III	9.52	8.56	**7.81**			8.75	8.69	**6.30**		
IV	9.76	8.21	8.36	**7.60**		9.11	10.31	7.20	**6.39**	
V	11.01	8.73	8.97	7.56	**5.50**	8.27	9.89	7.65	7.42	**6.61**

component analysis revealed four principal components that accounts for maximum amount of variation in the rice genotypes. The PCA biplot indicated genotypes that are located closer to different trait vectors and exhibiting higher values for that trait. The differences in quadrants were observed for the traits DFF, FLB, HGW and SPY under sodic and normal soil environments. This may be due to the impact of sodic stress on diversity of rice genotypes.

Hierarchical cluster analysis grouped the rice genotypes into five clusters. The genotypes (TG63, TG121 and TG17) present in low yielding cluster in normal irrigated environment were classified with high yielding genotypes in sodic environment. This indicated these genotypes were comparatively stable despite lower yield in other genotypes under sodicity stress. The genotypes in clusters with higher genetic distance (cluster I and cluster V) may be utilized in plant breeding programme to develop sodicity tolerant rice varieties.

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REFERENCES

Aarthi, M., Subramanian, A., Jeyaprakash, P. and Rajanbabu, V. 2021. Multivariate analysis of wild rice MAGIC population under sodic soil condition. *Electronic Journal of Plant Breeding*, **12** (3):748-756. [Cross Ref]

Aishwarya, D., Jebakani, S., Pramitha, J.L., Ramchander, S., Devasena, N., Wilson, D., Kumar, P.D. and Kumar, P.R. 2023. Evaluating the variability parameters among rice (*Oryza sativa* L.) landraces and varieties from Tamil Nadu. *Electronic Journal of Plant Breeding*, **14** (2):487-495. [Cross Ref]

Ariharasutharsan, G., Geetha, S., Saraswathi, R., Raveendran, M. and Krishna Surendar, K. 2023. Identification of newer stable genetic sources for high grain number per panicle and understanding the gene action for important panicle traits in rice. *Plants*, **12** (2):250. [Cross Ref]

Deepika, K., Lavuri, K., Rathod, S., Yeshala, C.M., Jukanti, A.K., Reddy, S.N., LV, S.R. and Badri, J. 2021. Multivariate analysis of geographically diverse rice germplasm for genetic improvement of yield, dormancy and shattering-related traits. *Plant Genetic Resources*, **19** (2):144-152. [Cross Ref]

Dhakal, A., Pokhrel, A., Sharma, S. and Poudel, A. 2020. Multivariate analysis of phenotypic diversity of rice (*Oryza sativa* L.) landraces from Lamjung and Tanahun Districts, Nepal. *International journal of agronomy*, **2020**:1-8. [Cross Ref]

IRRI. 2002. Standard Evaluation System for Rice (SES). International Rice Research Institute, Los Baños, Philippines.

Kassambara, A. and Mundt, F. 2020. Factoextra: Extract and Visualize the Results of Multivariate Data Analyses. *R package version 1.0.7. https://CRAN.R-project.org/package=factoextra*.

Le, S., Josse, J. and Husson, F. 2008. FactoMineR: An R Package for Multivariate Analysis. *Journal of Statistical Software*, **25** (1):1-18. [Cross Ref]

Maji, A. and Shaibu, A. 2012. Application of principal component analysis for rice germplasm characterization and evaluation. *Journal of Plant Breeding and Crop Science*, **4** (6):87-93. [Cross Ref]

Shanthi, P., Jebaraj, S. and Geetha, S. 2011. Study on gene action for sodic tolerance traits in rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*, **2** (1):24-30.

Shoba, D., Vijayan, R., Robin, S., Manivannan, N., Iyanar, K., Arunachalam, P., Nadarajan, N., Pillai, M.A. and Geetha, S. 2019. Assessment of genetic diversity in aromatic rice (*Oryza sativa* L.) germplasm using PCA and cluster analysis. *Electronic Journal of Plant Breeding*, **10** (3):1095-1104.[Cross Ref]

Singh, H.P., Raigar, O.P. and Chahota, R.K. 2022. Estimation

of genetic diversity and its exploitation in plant breeding. *The Botanical Review*:1-23. [Cross Ref

Singh, P., Verma, O.P., Singh, V., Singh, P.K. and Debnath, A. 2020. Genetic divergence analysis in rice (*Oryza sativa* L.) under sodic soil condition. *The Pharma Innovation Journal*, **9** (10):343-346. [Cross Ref]

Upadhyay, S., Rathi, S., Choudhary, M., Snehi, S., Singh, V., Singh, P. and Singh, R. 2022. Principal component analysis of yield and its attributing traits in advanced inbred lines of rice under sodicity condition (*Oryza sativa* L.). *Biological Forum – An International Journal*, **14** (2):1273-1276.

Yadav, R., Kushwaha, G., Chaudhary, R. and Pankaj, K. 2011. Genetic diversity of yield, its components and seed traits in rice under sodic soil. *Plant Archives*, **11** (1):137-139.

Yu, H., Yang, P., Lin, H., Ren, S. and He, X. 2014. Effects of sodic soil reclamation using flue gas desulphurization gypsum on soil pore characteristics, bulk density, and saturated hydraulic conductivity. *Soil Science Society of America Journal*, **78** (4):1201-1213. [Cross Ref]