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MORPHOLOGICAL AND MOLECULAR BASED GENETIC DIVERSITY STUDIES ON ALKALINITY AND INLAND SALINITY STRESS TOLERANCE IN RICE (*ORYZA SATIVA* L.)

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ABSTRACT

Rice is the predominant staple crop for majority of the people in Asia and South East Asia. Its production is affected by various stresses comprising from biotic to abiotic aspects. In this study, we conducted an extensive evaluation to identify rice genotypes with tolerance to alkalinity and inland salinity stress. A total of 36 rice genotypes were subjected to comprehensive screening, encompassing both morphological and molecular parameters. The screening took place in both hydroponic and field conditions during the *rabi* season at Agricultural Research Station, Kampasagar, in the year 2020-2021 and through in-vitro screening process identified several promising candidates for stress tolerance, including CT 11891, Sahel 177, M 202, KPS 10654, and KPS 10656, all of which exhibited high levels of tolerance (SES 3.0). Additionally, IRRI 154, GSRIR 2, IR 13F 167, Jasmine 85, KPS 10628, KPS 10631, KPS 10633, KPS 10640, KPS 10642, and KPS 10651 were categorized as moderately tolerant (SES 5.0). Field evaluations further confirmed the stress tolerance of CT 11891, Sahel 177, M 202 and KPS 10654, with these genotypes displaying both resilience to stress conditions and promising yield potential. Moreover, a validation study was conducted using SSR markers linked to the *Saltol* QTL. A line KPS 10654 was found to having a similar allele to the resistant check FL 478 for 7 markers. The study revealed varying levels of polymorphic information content (PIC), ranging from 0.27 (RM10843) to 0.64 (RM10793). Overall, the combined analysis of morphological and molecular diversity grouped the evaluated genotypes into four distinct clusters, shedding light on the genetic diversity present in response to alkalinity and inland salinity stress.

Key words : Alkalinity and Inland salinity, Rice, Diversity, Screening.

Introduction

Rice (*Oryza* spp.) is an important cereal crop and a staple food for more than three billion people in the world. Conversion of some highly productive rice lands for industrial and residential purposes has pushed rice cultivation to less productive areas such as saline, drought and flood prone areas. Salinity is a common abiotic stress that severely limits crop growth and development, productivity and causes the continuous loss of arable land, which results in desertification in arid and semi-arid regions of the world (Pons *et al*., 2011). For rice, salinity is next only to drought in limiting its productivity. Salinity is of two types, Coastal and Inland salinity. Coastal salinity is due to influence of sea water whereas, Inland salinity occurs as the name implies, inside the land without the effect of sea water. Indeed, frequent occurrences of the combination of drought, due to declining water resources, and salinity, often due to poor irrigation management have created a situation where rice ecosystem are now highly vulnerable to climate change (Singh *et al*., 2021). Saline soils are characterized by

excess of sodium ions with dominant anions of chloride and sulphate resulting in higher electrical conductivity (>4 dS m^{-1}) and alkalinity refers to the hydrogen ion concentration and it is greater than a pH of 8.5. In general salinity induces an initial osmotic stress and subsequent toxicity as a consequence of ion imbalance. However, damage can also ensure as a result of excessive reactive oxygen species (ROS) such as superoxide radicals (O_2^-), hydrogen peroxide (H_2O_2) and hydroxyl radicals (OH^-) produced at a high rate commonly accumulated in plant tissues due to ion imbalance and hyperosmotic stresses. ROS accumulation leads to lipid oxidation and has a negative effect on cellular metabolism and physiology, thus adversely ruining the membrane integrity (Munns *et al*., 2006).

Due to various reasons, the occurrence of salinity along with alkalinity stress is a common phenomenon in rice growing areas and to counteract it the most effective approach to addressing the challenges of salinity and alkalinity lies in the development of crop varieties, with inherent tolerance to these stressors. The initial step in this endeavour involves the systematic screening of germplasm to identify potential lines exhibiting such tolerance. Field-based screening, while essential, presents certain complexities and limitations. Soil heterogeneity, climatic variations, and other environmental factors can introduce inaccuracies, as they may influence the physiological responses of plants. To mitigate these challenges, screening under controlled environmental conditions offers a viable alternative. The hydroponic system, in particular, presents advantages by eliminating the stress factors associated with soil-related conditions. Traditional methods for selecting salt-tolerant plants are confronted with difficulties, primarily due to the substantial influence of the environment and the inherently low narrow-sense heritability of salt tolerance. Consequently, in-vitro screening emerges as a preferred approach, as it offers distinct advantages over field-based screening by reducing the inherent variabilities associated with the latter.

Salinity tolerance in rice is associated with Na^+ exclusion and increased absorption of K^+ to maintain a good Na^+/K^+ balance in the shoot under saline condition. It is considered that damage of leaves was attributed to accumulation of Na^+ from the root to the shoot in external high concentration (Lin *et al*., 2004). In several species including rice, salt stress might increase or even include the expression of specific genes and repress or completely suppress the expression of others (Hasegawa *et al*., 2000). In addition to ion homeostasis strategies many plants have evolved mechanism to regulate the synthesis and accumulation of compatible solutes such as proline and glycine betaine, which function as osmoprotectants that have a crucial role in plant adaptation to the prevailing stress conditions through stabilization of the tertiary structure of proteins (Munns and Tester, 2008).

With this in background, current study was undertaken to identify genotypes in terms of alkalinity and inland salinity tolerance, diversity analysis for yield and its attributes and validation of markers linked to *Saltol* QTL to identify suitable lines.

Materials and Methods

Experimental material and plan

Thirty-six genotypes were evaluated in the current study comprising of advanced breeding lines and germplasm lines provided by the research station. During the *Rabi* season of 2020-2021 these genotypes were evaluated at Agricultural Research Station, Kampasagar. Each genotype was meticulously examined within the framework of a randomized block design, with each genotype undergoing three replications. The primary field, strategically chosen as a naturally occurring stressed plot, served as the ideal backdrop for screening tolerance to both alkalinity and inland salinity. The soil within this test plot exhibited distinctive characteristics, with a pH level of 9.30, an electrical conductivity (E.C) of 4.68 dSm^{-1}, and an exchangeable sodium percentage (E.S.P) value of 88.0. FL 478 was included as the benchmark for salinity resistance, CSR 23 as the benchmark for alkalinity and inland salinity tolerance, CSR 36 as the alkalinity benchmark, and Pusa44 was the reference for susceptibility to both alkalinity and salinity stress. Data was taken on seedling mortality (%), days to 50% flowering, plant height (cm), panicle length (cm), number productive tillers/hill, number of grains per panicle, number of filled grains per panicle, sterility percentage (%), 1000 grain weight (g) and yield (kg/ha). Data was recorded on five randomly selected plants while the data on days to 50% flowering and seedling mortality were noted on entire plot basis.

Phenotypic study of salinity and alkalinity tolerance at seedling stage in *in-vitro* condition

The rice genotypes were screened for alkalinity and salinity stress tolerance at seedling stage in hydroponic system using the IRRI standard protocol (Gregorio *et al*., 1997). Treatment and control condition setups with 3 replications of each entry was maintained. In the treatment setup a pH of 8.5 and E.C of 4.0 dSm^{-1} were maintained by adding powdered sodium chloride to increase the electrical conductivity and 1N NaOH to

Table 1 : Standard Evaluation System scale (IRRI-SES, 2013).

Score	Observation	Tolerance
1	Normal growth, no leaf symptoms	Highly tolerant
3	Nearly normal growth, but leaf tips of few leaves whitish and rolled	Tolerant
5	Growth severely retarded, most leaves rolled, only a few are elongating	Moderately tolerant
7	Complete cessation of growth, most leaves dry, some plants drying	Susceptible
9	Almost all plants dead or drying	Highly susceptible

increase the pH and regulating it with 1N HCl after 4 days of sowing.

Visual rating of the genotypes for the salinity and alkalinity tolerance was done according to the standard evaluation system (Table 1) (SES, IRRI, 2013). Initial scoring was done 10 days after treatment imposition and final scoring 16 days after treatment imposition.

Molecular screening with SSR markers linked to Saltol QTL

Genomic DNA isolation was carried out using young leaves from 10-15 days old seedlings of 36 lines and the DNA was extracted by following the CTAB method as per Murray and Thompson (1980). Based on published literature (Gregorio *et al*., 1997; Nejad *et al*., 2008; Islam *et al*., 2012; Ganie *et al*., 2014) a total of 15 SSR markers linked with *Saltol* QTL on chromosome 1, were used to study the polymorphism among the genotypes. DNA marker analysis was carried out using SSR marker linked to *Saltol* QTL. The bands obtained from other genotypes were compared to the band obtained from FL 478. FL 478 was used as salt tolerant genotype in this study because it is the standard salt tolerant genotype which is used as a yardstick for *Saltol* QTL.

Statistical analysis

Analysis of variance was carried out using the method of Panse and Sukhatme (1967) for each of the thirty-six genotypes. Genetic divergence was estimated by Mahalanobis' D^2 statistics (1936) on 10 quantitative traits. The genotypes were grouped into a number of clusters by Tocher's method described by Rao (1952). These two analyses were done using WindowStat version 9.1 software.

The allelic data obtained from the molecular analysis, which is in the form of binary data was subjected to cluster analysis, and a dendrogram was constructed using the Unweighted Pair Group Method Arithmetic Mean (UPGMA) through NTSYS-pc version 2.11 software (Rohlf, 1993) at 1000 bootstrap values based on similarity matrices calculated using the simple matching (SM) coefficient (Nei and Li, 1979). Polymorphic information content (PIC) values were calculated for each SSR primer according to the formula given by Smith *et al*. (1997).

Results and Discussion

***In-vitro* screening of genotypes for salt tolerance at seedling stage**

In the absence of salinity stress, all genotypes exhibited robust growth, displaying uniform green coloration and height. However, upon the imposition of salinity treatment, a diverse range of phenotypic responses became evident, with scores varying from 3 (indicative of tolerance) to 9 (reflecting high susceptibility) (Table 2). Specifically, ten genotypes achieved a score of 3, while ten others attained a score of 5. Furthermore, eleven genotypes were assigned a score of 7 and five entries received the highest score of 9. Remarkably, the prevailing stress conditions exerted a more pronounced detrimental impact on the growth of the shoot system compared to the root system. This disparity may be attributed to the leaves' heightened sensitivity to alterations in pH and electrical conductivity, in contrast to the roots. This observation aligns with findings from a study conducted by Mazher *et al* (2007), which also highlighted the shoot system's heightened susceptibility to salinity stress.

The manifestation of stress symptoms was particularly evident in the first and second leaves, characterized by leaf rolling, browning, whitening of leaf tips, stunted growth, leaf desiccation, and a reduction in root growth, ultimately culminating in the complete cessation of seedling growth and, in some cases, seedling mortality. Among the genotypes, CT 11891, Sahel 177, M 202, KPS 10654, and KPS 10656 demonstrated significant tolerance to the stress conditions. Conversely, KPS 10661, KPS 10672, KPS 10316 and KPS 10321 exhibited high susceptibility, as indicated by their respective scoring.

Rice exhibits a notable ability to thrive in salt-affected soils, primarily owing to its capacity to flourish in flooded conditions, which effectively leaches soluble salts from the topsoil. However, it's important to recognize that salt tolerance in rice is not uniform and varies significantly among different genotypes. This variation is attributed to the diverse strategies for ion homeostasis that rice genotypes have evolved over time to contend with excessive ion concentrations during salinity and alkalinity

Table 2 : SES scores of genotypes under invitro stress conditions.

S. no.	Genotype name	Remarks	SES score
1.	IR 69726	Germplasm Collection	7
2.	IR 77186	Germplasm Collection	7
3.	NSICRC 240	Germplasm Collection	7
4.	IRRI 154	Germplasm Collection	5
5.	GSRIR 2	Germplasm Collection	5
6.	CT 11891	Germplasm Collection	3
7.	IR 13F 167	Germplasm Collection	5
8.	Sahel 177	Germplasm Collection	3
9.	Jasmine 85	Germplasm Collection	5
10.	M 202	Germplasm Collection	3
11.	KPS 10628	Advanced Breeding Line	5
12.	KPS 10631	Advanced Breeding Line	5
13.	KPS 10633	Advanced Breeding Line	5
14.	KPS 10640	Advanced Breeding Line	5
15.	KPS 10642	Advanced Breeding Line	5
16.	KPS 10651	Advanced Breeding Line	5
17.	KPS 10654	Advanced Breeding Line	3
18.	KPS 10656	Advanced Breeding Line	3
19.	KPS 10657	Advanced Breeding Line	7
20.	KPS 10658	Advanced Breeding Line	7
21.	KPS 10661	Advanced Breeding Line	9
22.	KPS 10667	Advanced Breeding Line	7
23.	KPS 10669	Advanced Breeding Line	7
24.	KPS 10672	Advanced Breeding Line	9
25.	KPS 10676	Advanced Breeding Line	7
26.	KPS 10683	Advanced Breeding Line	7
27.	KPS 10316	Advanced Breeding Line	9
28.	KPS 10319	Advanced Breeding Line	7
29.	KPS 10321	Advanced Breeding Line	9
30.	KPS 10329	Advanced Breeding Line	7
31.	FL 478	Salinity tolerant check	3
32.	Pusa 44	Susceptible check	9
33.	CSR 23	Alkalinity and salinity tolerant check	3
34.	CSR 36	Alkalinity tolerant check	3
35.	RNR 11718	Local alkalinity and salinity check	3
36.	KPS 2874	Local check	3

stress. Rice plants endowed with salt-tolerant traits typically excel in maintaining ion homeostasis, particularly by maintaining low Na^+/K^+ ratios or high K^+/Na^+ ratios. This is achieved through the processes of ion exclusion, compartmentalization and partitioning, which effectively regulate the distribution of sodium ions (Na^+) in either shoots or roots, thus minimizing the negative effects of salinity (Blumwald, 2000).

In addition to ion homeostasis, the accumulation of proline serves as another well-established mechanism to combat drought or salinity stress in numerous plant species. Proline assumes a pivotal role in safeguarding subcellular structures and facilitating osmotic adjustment under stressful conditions. Consequently, an experiment aimed at analysing the fluctuations in ion concentrations, particularly sodium and potassium, in cultivated salt-resistant rice varieties throughout the crop's growth cycle holds the potential to provide valuable insights into the underlying survival mechanisms employed by these plants during periods of salinity and alkalinity stress.

Cluster distances and composition

Analysis of variance based on mean values of 10 traits observed across 36 genotypes (Table 3) revealed significant differences across all characters. D^2 statistics grouped these 36 genotypes into four distinct clusters (Table 4). Cluster I accommodated 21 out of 36 genotypes, while Cluster II comprised 13 genotypes. In contrast, Clusters III and IV each included a single genotype, KPS 10661 and Pusa 44, respectively. Clusters III and IV were characterized as monogenic clusters due to their distinct morphological traits, warranting separate categorization. This phenomenon mirrors findings in previous studies, such as Aljumaili *et al.* (2018) analysis of aromatic rice accessions.

Heterosis breeding is integral to breaking yield plateaus and advancing rice production. Emphasizing heterosis breeding is crucial, as it underpins modern plant breeding and yields hybrids with enhanced characteristics, adaptability and morphological traits. The presence of monogenic clusters in this study implies limited intragenotypic variation and, consequently, a lower expectation of heterogeneity in these clusters. Correspondingly, the highest heterogeneity is anticipated in clusters with more diverse genotypes. This aligns with findings by Dey *et al.* (2020) and Islam *et al.* (2018) in their diversity studies on rice genotypes. Overall, the results suggest significant variability among the genotypes studied, making hybridization between genotypes from divergent clusters conducive to gene transfer, with potential for productive crosses between Clusters I and IV.

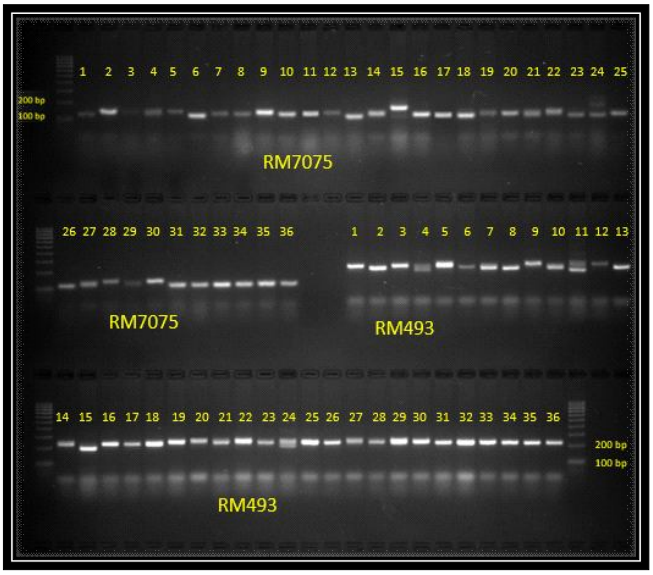

Fig. 1: Genotyping of rice genotypes using the SSR markers, RM 7075 and RM493. 1-FL 478 2-Pusa 44 3-CSR 23 4-CSR 36 5-RNR 11718 6-KPS 2874 7-IR 69726 8-IR 77186 9-NSICRC 240 10-IRRI 154 11-GSRIR 2 13-CT 11891 14-Sahel 177 15-Jasmine 85 16-M 202 17-KPS 10628 18- KPS 10631 19- KPS 10633 20- KPS 10640 21- KPS 10642 22-KPS 10651 23-KPS 10654 24- KPS 10656 25-KPS 10657 26-KPS 10658 27- KPS 10661 28- KPS 10667 29-KPS 10669 30- KPS 10672 31- KPS 10676 32-KPS 10683 33- KPS 10316 34-KPS 10319 35-. KPS 10321 36-KPS 10329.

Genotyping with SSR markers linked to Saltol QTL

Polymorphic information content (PIC) value provides a simple measure of marker-specific allelic diversity and frequency amongst the entries under evaluation, and a relatively higher numerical value indicates a comparatively greater probability of allelic variants detection among the varieties evaluated. Molecular diversity analysis was carried out by using 15 SSR markers linked to "*Saltol* QTL" on chromosome 1 of which the 8 markers which showed differential banding patterns between resistant (FL 478) and susceptible (Pusa 44) checks were further used to study the genotypes. (Table 5, Fig. 1).

The number of alleles indicates the richness of the population and generally, allele numbers of 2 to 7 alleles per locus are considered good (Aljumaili *et al*., 2018). In the present study, a total of 27 alleles were recorded, ranging from 2 (RM 3412) to 5 (RM 10793) with an average of 3.37 per locus. The richness of information a marker otherwise known as polymorphic information content (PIC) of this study differs significantly from 0.27 (RM 10843) to 0.64 (RM 10793). PIC determines the usefulness of the markers for linkage analysis (Elston, 2005). Markers with PIC values of 0.5 or above are considered for the genetic studies since they are the most useful in describing the polymorphism magnitude of a specific locus (Akkaya and Buyukunal Bal, 2004) and in

Table 3 : ANOVA for yield and its traits of the genotypes under study.

Source of variation	d.f	Mean sum of squares									
		SM	DFF	PH	PL	NPT	NGP	NFP	SP	TW	Yield
Replication	2	2	13.481	54.065	42.954	7.148	0.944	95.071	60.731	1.410	1.366
Treatments	35	35	264.073 **	33.978 *	185.597 **	3.806*	1.838**	427.606 **	283.539 **	495.550 **	35.145 **
Error	70	70	9.548	19.246	15.849	2.336	0.364	68.048	51.131	49.715	0.476
Total	107	107	92.877	24.715	71.880	2.907	0.857	186.166	127.332	194.646	11.833

Note: * Indicates significance at 5 percent probability level, ** Indicates significance at 1 percent probability level, d.f – degrees of freedom.

Table 4 : Clustering pattern of rice genotypes studied.

Cluster number	Number of genotypes	Name of genotypes
C- I	21	KPS 10633, KPS 10642, KPS 10651, KPS 10628, KPS 10631, KPS 10683, KPS 10329, KPS 10640, KPS 10658, KPS 10319, KPS 10667, KPS 10657, KPS 10669, KPS 10316, KPS 10321, KPS 2874, RNR 11718, KPS 10656, KPS 10654, KPS 10672, KPS 10676
C- II	13	IR 69726, IR 77186, Jasmine 85, IRRI 154, CSR 36, GSRIR 2, CSR 23, IR 13F167, CT 11891, M 202, Sahel 177, FL 478, NSICRC 240
C- III	1	KPS 10661
C-IV	1	Pusa 44

*C-Cluster.

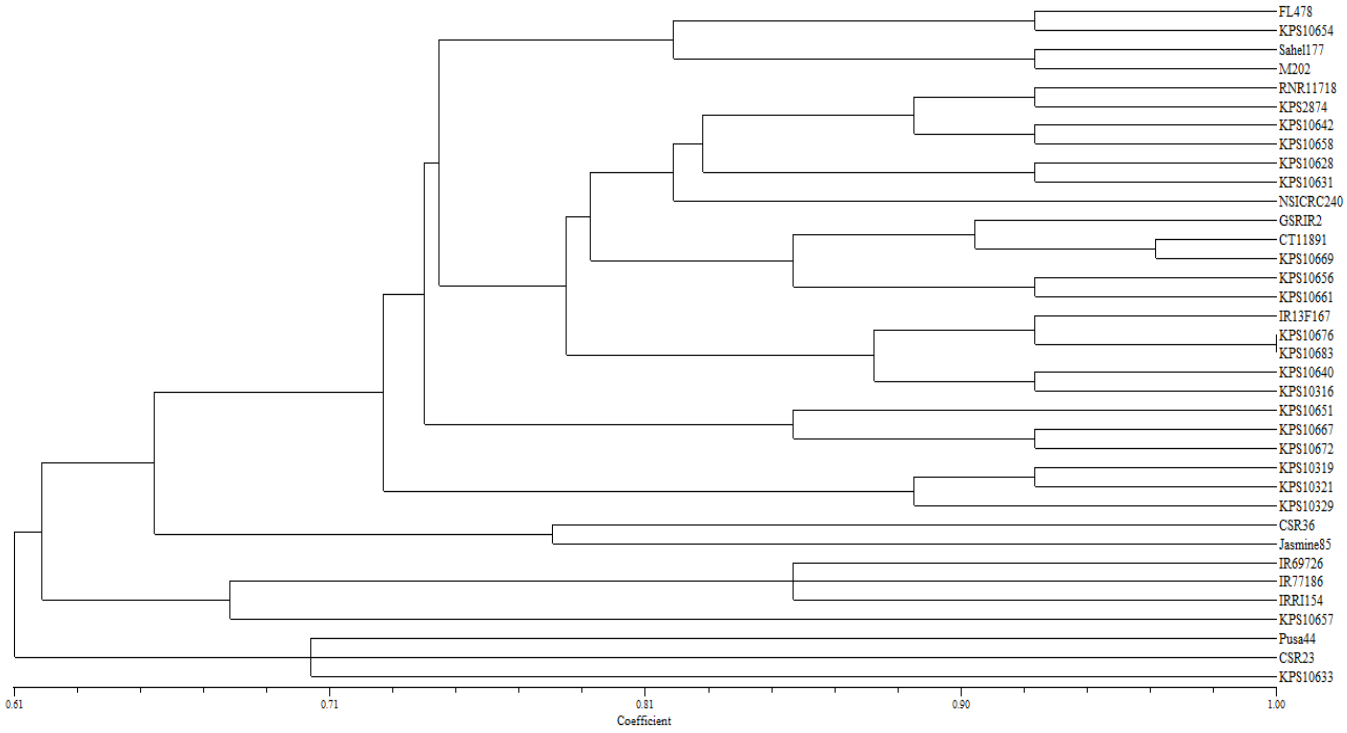

Fig. 2: Dendrogram of rice genotypes studied using *Saltol* linked SSR markers by UPGMA method.

the present study, the most informative primer based on the PIC value was RM 10793 (0.64) followed by RM 7075 (0.57). Nei's genetic diversity and Shannon's information index ranged from 0.29 (RM 10843) to 0.64 (RM 7075) with an average of 0.48 and from 0.50 (RM 7075) to 0.83 (RM 10843) respectively. Similar results were reported by Raghavendra *et al.* (2020), while studying landraces from western ghats for new sources of salinity tolerant genotypes.

Cluster analysis is very useful in revealing complex relationships among the populations of diverse analysis in a more simplified manner. UPGMA is one of the simplest and popular clustering algorithms to create a distance-based phylogenetic dendrogram. The distance coefficient ranged from 0.61 to 1.00. Based on the similarity distance coefficient matrix at 0.67 these 36 genotypes were divided into 4 clusters (Table 6, Fig. 2). Matin *et al.* (2012) also reported similar findings of 4 clusters. Lines such as CT11891, M202, Sahel 177 and KPS 10654 were grouped together and causes of similar grouping because they are tolerant to stress conditions and has high yield potential. In the study, we observed that CSR 23 and Pusa 44 were grouped into similar cluster I based on the molecular scoring, which is due to the similar banding pattern for the markers under study.

All the genotypes of cluster II (IR 69726, IR 77186, IRRI 154, and KPS 10657) and III (CSR 36 and Jasmine 85) along with CSR 23 of cluster I from molecular diversity analysis were present in the cluster II of D^2 analysis. Pusa44 which was placed separately in cluster I of D^2 analysis was placed along with CSR 23 and KPS 10633 in cluster I of molecular diversity analysis. Even though both the diversity analysis gave similar number of clusters the molecular diversity analysis gives more variation because marker alleles provide more discrimination. Several reports suggested that molecular diversity provides remarkably higher estimates of genetic diversity than morphological or physiological methods of Beyene *et al.* (2005). A similar pattern was also observed by Weiguo *et al.* (2007). These differences are not an indicator of the failure or limitation or weakness of the methods (Roldán-Ruiz *et al.*, 2001). These results may be due to the diversity at the molecular level, which may not reflect in the diversity at the morphological or physiological level, as described by Karhu *et al.* (1996). In order to obtain a similar diversity pattern among the genotypes studied with both morphological and molecular based diversity we need to use several thousands of markers and the all possible morphological and physiological traits are to be studied.

Genetic divergence study and clustering of rice genotypes for salinity and alkalinity tolerance could help in effective selection of parents in future hybridization programme for utilization of heterotic effect in the F_1 generation and isolation of promising segregants in advance segregating generations.

Table 5 : Allelic diversity generated by polymorphic SSR markers in the study.

Marker	No. of alleles	PIC	Shannon's information index	Nei's index
RM 562	3	0.30	0.81	0.33
RM 7075	4	0.57	0.50	0.64
RM 493	4	0.37	0.72	0.43
RM 10772	3	0.39	0.64	0.48
RM 3412	2	0.33	0.69	0.42
RM 10793	5	0.64	0.50	0.68
RM 10694	3	0.49	0.58	0.56
RM 10843	3	0.27	0.83	0.29
Mean values	**3.38**	**0.42**	**0.66**	**0.48**

Table 6 : Clustering of rice genotypes based on molecular marker diversity analysis.

Cluster	No. of genotypes	Genotype
I	3	KPS 10633, CSR 23, Pusa 44
II	4	KPS 10657, IR 69726, IR 77186, IRRI 154
III	2	CSR 36, Jasmine 85
IVA	6	KPS 10319, KPS 10321, KPS 10329, KPS 10651, KPS 10667, KPS 10672
IVB	21	RNR 11718, KPS 2874, KPS 10642, KPS 10658, KPS 10628, KPS 10631, NSICRC 240, GSRIR 2, CT 11891, KPS 10669, KPS 10656, KPS 10661, IR 13F167, KPS 10676, KPS 10683, KPS 10640, KPS 10316, FL 478, KPS 10654, Sahel 177, M 202

Validation of markers linked to *Saltol* QTL

The genotype KPS 10654 which was found to be the tolerant line in the invitro and field screening had similar allelic scoring to the resistant check FL 478 for 7 SSR markers (RM 7075, RM 493, RM 10772, RM 3412, RM 10793, RM 10694 and RM 10843). The line IR 69726 had similar banding pattern for 6 markers (RM 562, RM 493, RM 10772, RM 10793, RM 10694 and RM 10843).

In our study we found that the alkaline and inland saline resistant check CSR 23 did not have a similar allelic scoring to that of the resistant check FL 478. These results indicated the resistance in this line might be governed by some other QTLs/genes which need to be identified through developing a suitable mapping population to find the new QTLs/genes, which govern the tolerance mechanisms.

Conclusion

The comprehensive examination of rice genotypes for tolerance yielded valuable insights into their responses to stress. When subjected to stress conditions, these genotypes exhibited a wide spectrum of phenotypic scores, ranging from 3 (indicative of tolerance) to 9 (indicating high susceptibility). Notably with the aid of both in-vitro and field screening conditions along with validation of SSR markers linked to seedling stage salinity QTL lines such as CT 11891, M 202, Sahel 177 and KPS 10654, which were found to be tolerant to the stress conditions with good yield capability. Molecular marker analysis further validated the salt-tolerant lines and differentiated them from susceptible ones. The lack of similar allelic scoring for CSR 23, an alkaline and inland saline-resistant check, suggests the involvement of additional genes governing tolerance mechanisms. This study serves as a valuable resource for the selection of lines which can be used as varieties for the stress prone areas or as parents in future hybridization programs to harness heterosis, improving the salt and alkalinity tolerance of rice varieties along with yield capability and facilitating the isolation of promising segregants for further advancements in rice production.

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