

Genetic Diversity and Evaluation of Rice Genotypes in Response to Salt Stress During Seedling Stage

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INTRODUCTION

Salinity is one of the major constraints for crop production worldwide. In Louisiana, salinity problem is mainly due to hurricane induced salt water intrusion, reduced rainfall, and proximity to the Gulf of Mexico. As a consequence, salinity is emerging as a significant threat to the rice industry of the state. Rice plants in general are sensitive to salinity although some germplasm exhibit considerable degree of tolerance. Under moderate (6dSm⁻¹) salinity level, rice yields can be reduced by about 50%. Therefore, the need for breeding rice with tolerance to salt stress is important.

Our long term goal is to develop rice varieties with salinity tolerance. In this study however, our specific objective is to assess the genetic variability and to characterize the salinity tolerance of the high yielding varieties grown in the Southern US. Hence, the US varieties together with rice landraces procured from IRRI were screened for salinity tolerance at the seedling stage.

MATERIALS & METHODS

Fifty rice lines used for this study consisted of 30 high yielding varieties obtained from the LSU AgCenter Rice Research Station, 6 lines from Germplasm Resource Information Network (GRIN) and 14 rice germplasm from IRRI. The plants were grown in nutrient solution following the IRRI standard evaluation technique for salinity tolerance (Fig. 1). Seven-day old seedlings were subjected to salinity level of 12 dSm⁻¹ and then scored for salt injury when the susceptible check IR29 was almost dying (Table 1). Morphological, physiological, and biochemical traits were measured to assess the degree of salt tolerance and sensitivity.

For genetic characterization, DNA from each genotype was extracted and assayed for PCR using 161 simple sequence repeat (SSR) markers (Fig. 3). Amplicons were then scored as 1 and 0 for the presence and absence of band, respectively.

Phenotypic data were averaged for each line. ANOVA, correlation and Principal Component Analysis (PCA) were done to analyze the data. SSR marker data and quantitative measurements were also analyzed using NTSYS-pc statistical package v. 2.1.

Table 1. Standard visual salinity injury score (SIS) at seedling stage.

Score	Observation	Tolerance
1	Normal growth, no leaf symptoms	Highly tolerant
3	Nearly normal growth, but leaf tips or 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; plants are nearly dying	Susceptible
9	All plants are dead	Highly susceptible

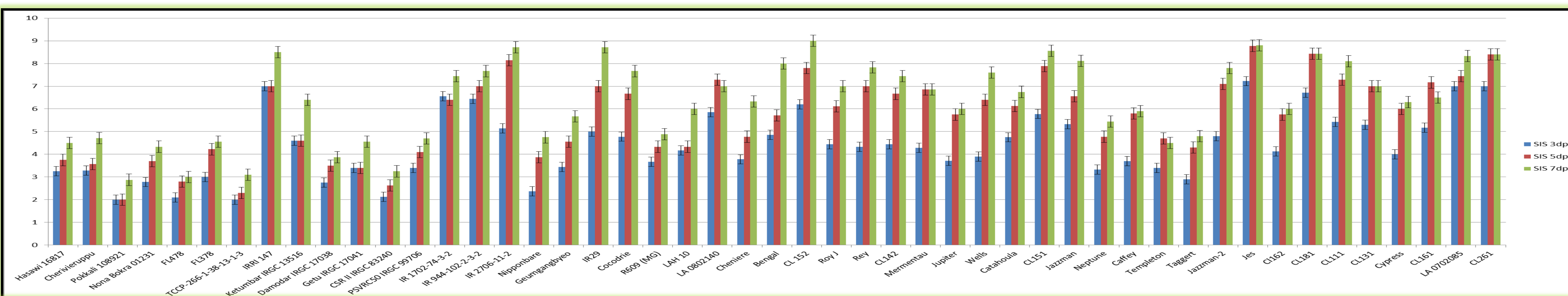


Fig. 1. Time-course progression of visual salinity injury scores on fifty rice genotypes in response to salinity stress (12 dSm⁻¹).

RESULTS

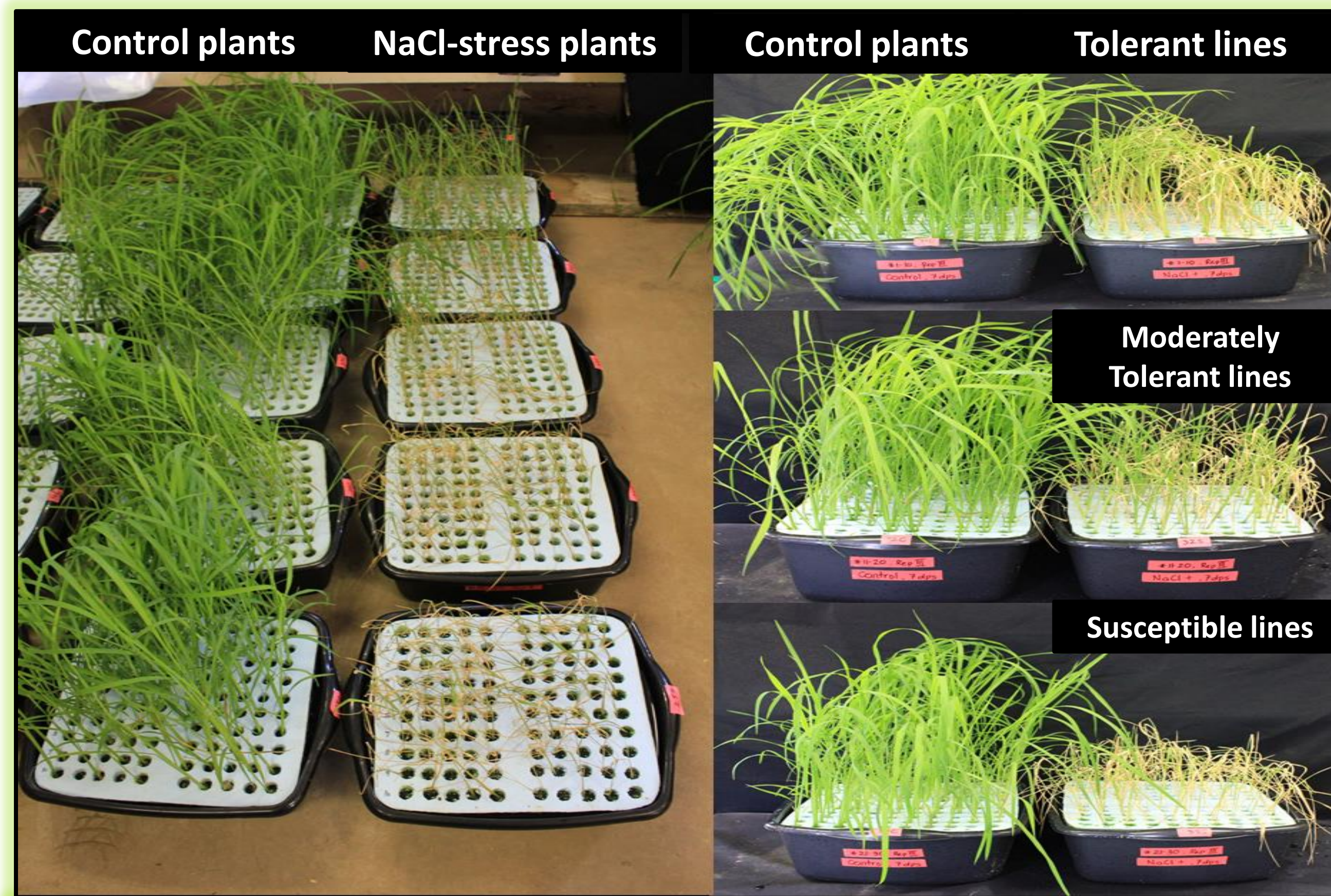


Fig. 2. Seedling screening for salinity tolerance.

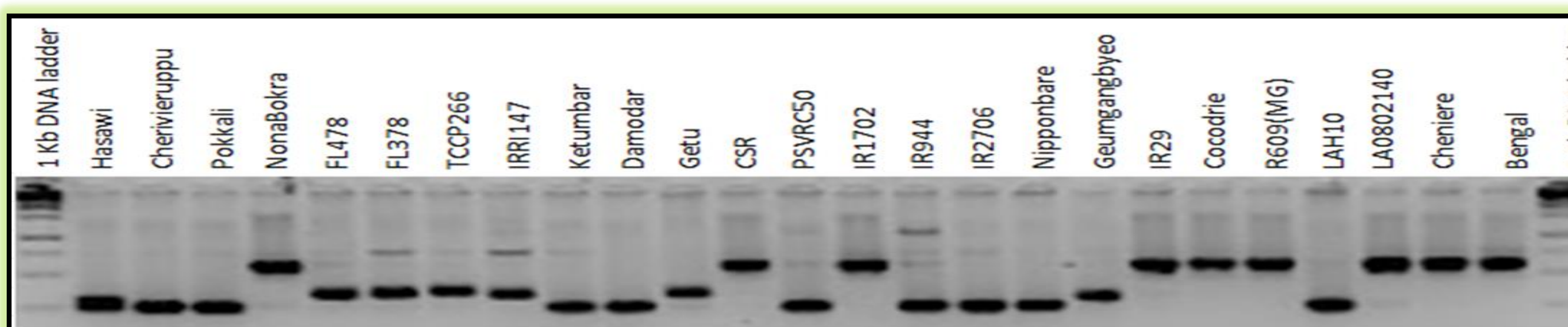


Fig. 3. Genotyping of rice genotypes using SSR marker (RM10864)

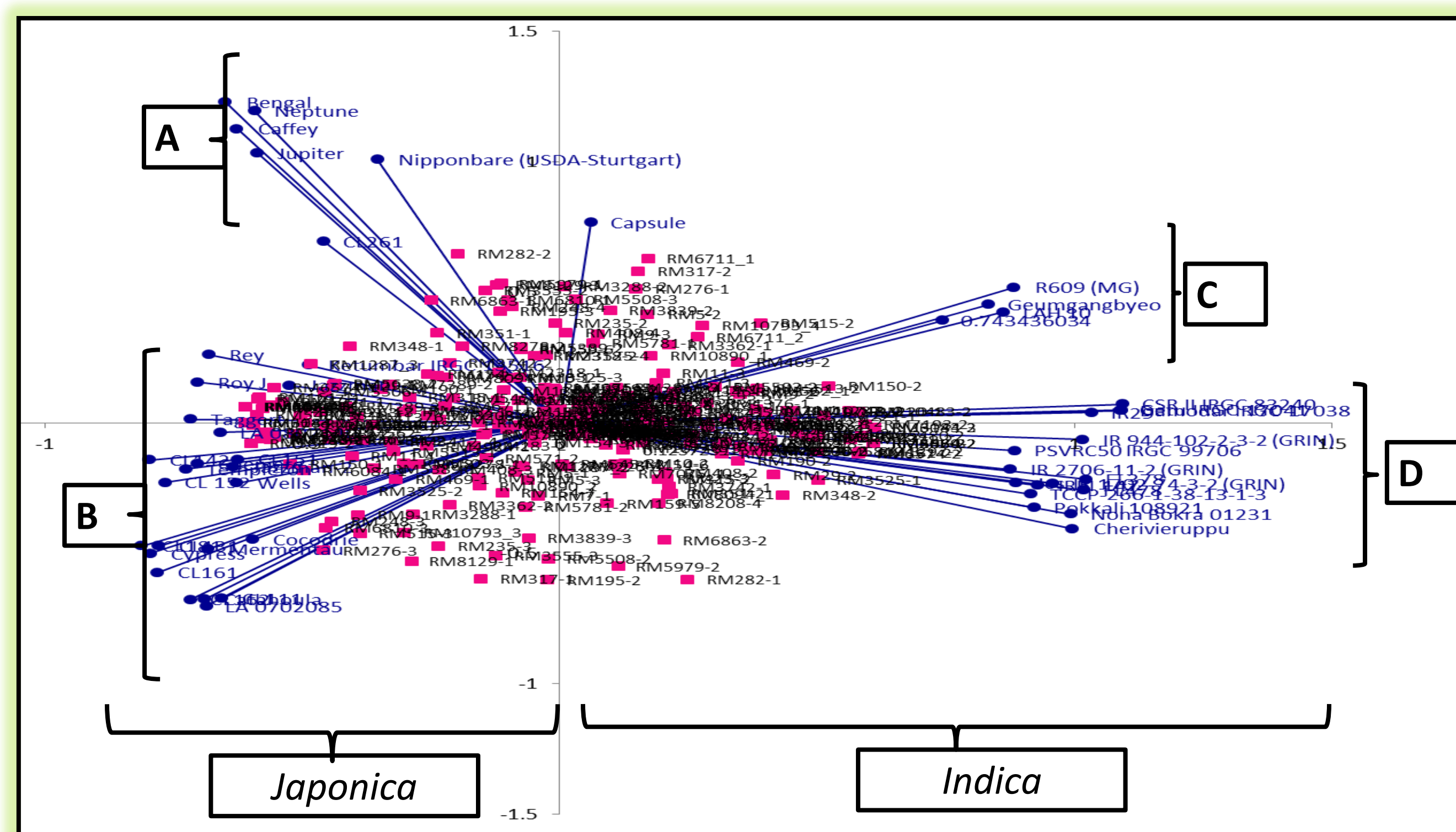


Fig. 4. Biplot of genotype-marker interaction showing the genetic diversity of the fifty rice genotypes.

Table 2. Pearson correlation coefficients between quantitative traits of fifty rice genotypes in response to salinity stress.

Pearson Correlation Coefficients, N = 49 Prob > r under H0: Rho=0											
	SIS	Chl_R	ShL_R	RtL_R	Ion_leak	Rt_Na	Rt_K	Rt_Na/K	Sh_Na	Sh_K	Sh_Na/K
SIS	1.000										
Chl_R	0.669	1.000									
ShL_R	0.509	0.415	1.000								
RtL_R	-0.006	0.018	0.124	1.000							
Ion_leak	0.967	0.900	0.397	0.069	1.000						
Rt_Na	0.469	0.252	0.470	0.069	0.638	1.000					
Rt_K	0.025	0.134	-0.233	-0.136	-0.075	0.258	1.000				
Rt_Na/K	0.864	0.358	0.108	0.350	0.608	0.258	0.258	1.000			
Sh_Na	-0.118	-0.084	-0.106	-0.173	-0.184	0.015	0.015	0.015	1.000		
Sh_K	0.420	0.564	0.468	0.235	0.205	0.073	0.073	0.073	0.073	1.000	
Sh_Na/K	0.143	0.214	-0.024	0.050	0.149	0.493	-0.678	0.493	-0.678	0.493	1.000
Sh_Na	0.326	0.140	0.868	0.733	0.308	0.000	<.0001	0.000	<.0001	0.000	<.0001
Sh_K	0.158	0.223	-0.003	-0.338	-0.138	0.281	0.068	0.122	1.000	0.318	1.000
Sh_Na/K	0.278	0.124	0.983	0.018	0.345	0.051	0.643	0.403	0.026	0.940	0.026
SIS	-0.546	-0.263	-0.435	-0.039	-0.563	0.346	0.222	-0.011	0.318	1.000	0.026
Sh_Na/K	<.0001	0.068	0.002	0.793	<.0001	0.015	0.125	0.940	0.026	0.940	<.0001
Sh_Na	0.469	0.425	0.388	-0.200	0.443	-0.123	-0.200	0.138	0.358	-0.749	1.000
Sh_K	<.0001	0.002	0.006	0.168	0.001	0.399	0.167	0.344	0.012	<.0001	<.0001

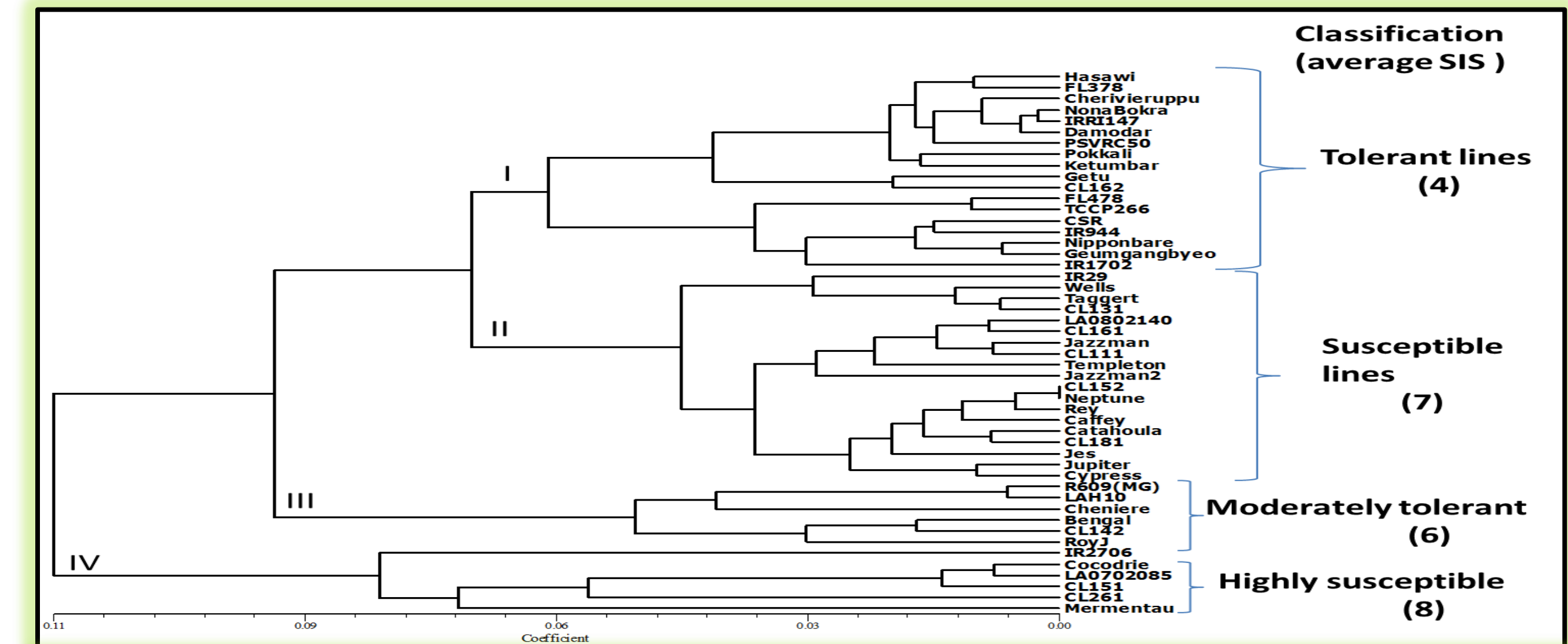


Fig. 5. Clusters of fifty rice genotypes based on Euclidean distance calculated from standardized data matrix of six quantitative traits in response to salinity stress.

- PCA analysis showed a narrow genetic variability among the 30 Southern US rice varieties (groups A, B, C, Fig. 4).
- Geumgangbyeo, LAH10, and R609 are different from Pokkali and Nona Bokra based on genotypic clusters (Fig. 4).
- At seedling stage, tolerant plant has a low Na-K ratio, low reduction in chlorophyll, shoot length, ion leakage and high shoot K concentration (Table 2).
- Geumgangbyeo was grouped together with Pokkali, tolerant check (Group I, Fig. 5).
- Group II included susceptible lines to which most of the US varieties were clustered (with IR29-susceptible check).
- LAH 10, R609 and Cheniere were moderately tolerant to salinity (Group III).

CONCLUSION

- Clustering based on the six highly correlated traits effectively characterized the 30 US Southern rice genotypes for salinity tolerance.
- Geumgangbyeo was identified tolerant (SIS= 4.0) while R609 and LAH10 were moderately tolerant (SIS = 4.4, 4.5).
- Mechanism of salinity adaptation by Geumgangbyeo, LAH10 and R609 may be different from Pokkali and Nona Bokra based on their genetic profile.
- Since Pokkali and Nona Bokra are both photosensitive, the use of Geumgangbyeo as a donor for salinity tolerance will be useful for the rice breeding program of Louisiana.

ACKNOWLEDGMENT

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