Electronic Journal of Plant Breeding, 4(1): 1034-1042 (Mar 2013)
ISSN 0975-928X

Research Article

Genetic diversity analysis of rice (*Oryza sativa*) genotypes for seedling characters under saline - alkaline condition

K Seetharam[1]*, S.Thirumeni[1], K.Paramasivam[1], S.Nadaradjan[2]
[1]Department of Plant Breeding and Genetics, [2]Department of Crop Physiology
Pandit Jawaharalal Nehru College of Agriculture and Research Institute, karaikal, U.T. of Puducherry
* Email: kdseetharam@gmail.com

(Received: 25 Mar 2013; Accepted: 21 Feb 2013)

Abstract

Rice is life for Asians as it provides 43 per cent calorie requirement for more than 70 per cent of the population. The production is often limited by salinity. Understanding of physiological and genetic mechanisms is necessary for a breeding programme to improve crop performance under environmental stresses. Thirty rice genotypes pre-germinated in saline-alkaline water (pH-9.60; EC-10.0; SAR-54.32; RSC- 11.51) were placed in plastic cups filled with sterile soil and the stress was imposed upto 21 days. Genetic diversity was estimated based on the observations recorded on germination per centage, vigor index, shoot length, root length, seedling length, root/shoot ratio, seeding dry weight, Na^+/K^+ ratio. The genotypes were grouped in to five clusters based on the Euclidean coefficient which ranged between 2.09(CSR10 X CSR 13) and 76.29 (IWP X Chettiviruppu). Cluster II was largest (22 genotypes) followed by cluster I (4 genotypes). Genotypes grouped under cluster I showed low Na^+/K^+ ratio which is an important physiological trait for salinity tolerance. Cluster V (MI 48 & IWP) grouped the susceptible genotypes which had high Na^+/K^+ ratio. The hybrids thus developed from the genotypes of cluster I & V may express high magnitude of transgressive segregants.

Key words:
Rice, Salinity, Genetic diversity

Introduction

Rice is an important food crop for the entire world population. While active efforts are being made to increase rice productivity, a considerable amount of rice biomass for which genetic potential exists in the present-day cultivars is not harvested under field conditions, primarily because of the sensitivity of this crop to various stresses (Shimamoto, 1999). Among various stresses, salt stress is certainly one of the most serious environmental factors limiting the productivity and quality of the crop produce (Gepstein *et al.*2006). Globally, 831 million ha soils was salt affected out of which 47.8 per cent (397 million ha) are saline in nature (Salinity news, 2010). In Asia alone, 21.5 million ha of land area is thought to be salt affected (FAO, 2009), with India having 6.73 million ha salt-affected area (Mandal *et al.*, 2009). The use of some management options can ameliorate yield reduction under salinity stress but the implementation is often limited because of cost and availability of good quality water resources. Therefore, the development of salt tolerant varieties would be a practical solution to address this problem. However, efforts to improve crop performance under environmental stress have not been that fruitful because the fundamental mechanisms of stress tolerance in crop plants remain to be completely understood (Yamaguchi and Blumwald, 2005). Understanding of physiological and genetic mechanisms is necessary for a breeding programme, in order to select the desired trait in the different genetic backgrounds (Munns *et al.,* 2006). Thus the present study was carried out with objective to study the genetic divergence of rice genotypes for seedling characters under saline-alkaline condition.

Material and methods

The material used in the study comprise 30 indigenous and exotic genotypes (Table 1) gathered from different rice research stations in India and abroad. All the genotypes were screened for salt tolerance at seedling stage in the Plant breeding laboratory of Pandit Jawaharlal Nehru Collage of Agriculture and Research Institute, Karaikal, U.T.of Puducherry. The germination test was conducted as per ISTA (1999). Randomly selected seeds were surface sterilized with 0.1 per cent $HgCl_2$ and placed in petri plates lined with moist filter paper and kept in seed germinator maintained at 90 per cent relative humidity and 25 $\pm$ 2^0 C temperature for conducting germination test. Salt stress was imposed through moistening of filter paper, by bore well water at varied salt levels and double distilled water was used as control (Table 2).

Ten well germinated seeds of each genotype were sown in perforated plastic cup filled with sterile soil and the cups were placed in plastic tubs filed with bore well water and the stress was imposed for 21 days. To maintain the constant saline-alkaline condition for every two days the bore well water in the tub was replaced. Each entry was replicated thrice in Randomized Complete Block Design. The genotypes were evaluated at 21 days after sowing for the following traits *viz.,* germination per cent (GP), vigor index (VI), shoot length (SL), root length (RL), seedling length

(SDL), root/shoot ratio (R/S), seeding dry weight (SDW), Na^+/K^+ ratio (N/K).

The mean values for different observations recorded under laboratory condition were used to group the genotypes into four categories *viz.*, highly tolerant, moderately tolerant, moderately susceptible and highly susceptible using interval estimation with 95 per cent confidence limit over the genotypic mean. The interval estimation is computed adopting the following formula (Rangaswamy, 1995) to group the genotypes

$$L = GM - SE(GM) \times t_{n-1df,}$$

$$U = GM + SE(GM) \times t_{n-1\,df}$$

Where, GM =Grand mean, SE(GM)=Standard error over genotypic mean, L= Lower confidence limit, U = Upper confidence limit, n= Number of genotypes, t_{n-1df}= table 't' value at n-1 degrees of freedom.

Genotypes with mean values between grand mean and lower confidence limit for a particular trait were considered to be moderately susceptible. Those, with values lower than 'L' were highly susceptible. Genotypic mean values between grand mean and upper confidence limit (U) were grouped as moderately tolerant, while genotypes with mean values higher than 'U' were highly tolerant. The mean over all treatments were used for the diversity analysis. Diversity analysis was conducted using the software NTSYS-pc version 2.1 (Exeter software, Setauket, NY). The seedling characters were standardized prior to cluster analysis. The matrix of average taxonomic distance for individuals and morphological traits was then computed using SIMINIT function and EUCLIDIAN distance coefficient (Rohlf, 1998). This dissimilarity coefficient is based on interval measure data collected for the morpho-physiological traits. Cluster analysis was then conducted on the taxonomic distance matrix with the Unweighted Pair Group Method based on Arithmetic Average (UPGMA) and a dendrogram was generated based on the genetic distance matrix (Sneath and Sokal, 1973).

Result and Discussion

The significant mean square values obtained from the analysis of variance suggest that differences existed between the rice cultivars for all the characters, indicating that they are highly variable (Table 3). The mean performance of thirty genotypes for over two levels of stress and control is presented in the table 4. The characters such as germination per cent, seedling survival, shoot length, root length, seedling length, vigour index and seedling dry weight showed decreasing trend under stress conditions, whereas the sodium potassium ration showed increasing trend over the control. Out of 30 genotypes studied, two genotypes namely Nonobokra and Pokkali grouped as highly salt tolerant whereas Chitteani and Chettivirippu grouped as moderately tolerant. All other genotypes were grouped under susceptible categories. Genotypes grouped under tolerant types also showed low Na^+/K^+ ratio which is an important physiological trait for salinity tolerance.

The mean over all treatments were used for the diversity analysis (Table.5). Taxonomic distance based on seedling character was estimated after standardization. The matrix of average taxonomic distance was estimated using Euclidian distance. The average taxonomic distance ranged from 2.09 and 76.29. The cluster analysis was conducted on average taxonomic distance with UPGMA method. At a Euclidean distance of 21.27 the 30 genotypes were grouped into five clusters (Figure 1). Among them cluster II was found to have large number of genotypes. Genotypes grouped in the cluster I and IV was found to be highly tolerant to saline alkaline condition. When the genotype in these clusters were compared with the seedling data it was found that they have low Na+/K+ ratio with the range of 0.25 (Pokkali) to 0.40 (Chettivrripu) and high seedling length and dry weight. In contrast the genotypes clustered in group V was found to be highly susceptible and they have very high Na+/K+ ratio (Improved White Ponni – 0.67 and MI 48-0.65).

The clustering pattern clearly grouped the genotypes based on their response to salinity. The genotypes with different geographical origin fell in the same cluster in both the methods of clustering, thus indicating that geographical diversity is not necessarily related to genetic diversity. Such a clustering of genotypes from different geographical origin into one cluster was attributed to the free exchange of breeding material from one place to another. This may also be due to the fact that the unidirectional selection for a particular trait practiced in several places produced a similar phenotype and resulted in a segregation of genotypes irrespective of their geographical origin (Singh *et al*, 1990). It suggested that genotypes developed in different geographical regions had genetic similarity, there by indicating that geographical distribution could not be taken as sole criterion of genetic diversity. Crossing between highly divergent genotypes would throw a wide spectrum of variability enabling further selection and improvement. The hybrids, thus developed from the genotypes of these cluster may express high magnitude of heterosis or desirable transgressive segregants.

References

FAO, 2009. FAOSTAT database 2009. Food and Agriculture Organization of The United Nations. http://faostat.fao.org/site/567/ default. aspx#ancor.

Gepstein, S., A. Grover, E. Blumwald. 2006. Producing biopharmaceuticals in the desert: building an abiotic stress tolerance in plants for salt, heat and drought. In: Knablein J, Muller RH (eds) Modern biopharmaceuticals. Wiley-VCH Verlag GmbH, Weinhaum, pp 967–994**.**

ISTA, 1999.International rules for seed testing. *Seed Sci and Technol(Supplement),* **27**:27-31.

Mandal.A.K., R.C. Sharma and Gurbachan Singh. 2009. Assessment of salt affected soils in India using GIS. *Geocarto International.* **24(**6): 437-456.

Munns,R. 2005. Genes and salt tolerance: bringing them together. *New phytologist*, **167**:645-663.

Rangaswamy, R.1995. A text Book of Agriculture statistics. Wiley Eastern limited New Delhi.

Rohlf, F.J. 1998. NTSYS-pc numerical taxonomy and multivariate analysis system. Version 2.02. *Exeter Publications Setauket*, New York

.

Shimamoto, K.1999. Molecular biology of rice, Springer-Verlag, Tokyo.

Singh, R.B., P.C. Ram and B.B. Singh. 1990. Genetic variability in rice genotypes planted in sodic soil. *Int. Rice Res. Newsl.*, **15**(4) : 14.

Sneath, P.H.A and R. R. Sokal. 1973. Numerical taxonomy. W. H. Freeman and Company, San Francisco.

Yamaguchi,T and E.Blumwald.2005.Developing salt tolerance crop palnts:Challenges and opportunities.*TRENDS in Plant Sci.*, **10**: 212-220.

Table 1. Details of the genotypes used in the study

S . No	Genotypes	Pedigree	Origin
1	Chitteani	Land race	Kerala, India
2	Chettivirippu	Land race	Kerala, India
3	Wag wag	Land race	Philippines
4	Nonabokra	Land race	West Bengal, India
5	Ketumbar	Land race	Indonesia
6	Pokkali	Land race	Kerala, India
7	Jhona	Land race	Pakistan
8	IR 72582-10-1-1-3-1	IR 9884 // IR 20 / IR 26	IRRI,Philippines
9	IR 72593-B-3-2-1-2	IR 69195 / IR 20 / IR 24	IRRI,Philippines
10	IR 73678-6-9-B	IR 9884 / *Oryza rufipogan*	IRRI,Philippines
11	IR 72579-B-2R-1-3-2	CSR10 // IR20 / IR26	IRRI,Philippines
12	IR 72593-B-13-3-3-1	IR 69195 / IR20 / IR24	IRRI,Philippines
13	IR 71991-3R-2-6-1	IR5 / IR 52713	IRRI,Philippines
14	BTS 10-10	Somaclone of Pokkali	CARI, Port Blair, A&N Islands
15	BTS 10-12	Somaclone of Pokkali	CARI, Port Blair, A&N Islands
16	BTS 24	Somaclone of Pokkali	CARI, Port Blair, A&N Islands
17	BTS 17-20	Somaclone of Pokkali	CARI, Port Blair, A&N Islands
18	BTS 11-7	Somaclone of Pokkali	CARI, Port Blair, A&N Islands
19	CST 7-1	CSR 1 / IR 24	Canning Town, West Bengal
20	IET 18709	Jaya / CSR 23	CSSRI, Karnal , India
21	KR 0004	IET 14543 / TRY 1	PAJANCOA& RI, Karaikal , India
22	KR 0015	SSRC 92076 / TRY 1	PAJANCOA& RI, Karaikal , India
23	KR 0029	IR 70866-B-P-7-2	PAJANCOA& RI, Karaikal , India
24	KR 0009	SSRC 92076 / TKM 9	PAJANCOA& RI, Karaikal , India
25	CSR 10	M-40-431-24-114 / Jaya	CSSRI, Karnal , India
26	CSR 13	CSR 1/ Basmati 370 / CSR 5	CSSRI, Karnal , India
27	CSR 23	IR 64 // IR 4630-22-2-5-1-3 / IR 9764-45-2-2	CSSRI, Karnal , India
28	TRY 2	IET 6238 / IR 36	Tamil Nadu, India
29	Improved White Ponni	Taching 65 / 2	Tamil Nadu, India
30	MI 48	-	CSSRI, Karnal , India

IRRI - International Rice Research Institute, Philippines
PAJANCOA & RI - Pandit Jawaharlal Nehru College of Agriculture and Researche Institute, Karaikal.
CSSRI - Central Soil Salinity Research Institute, Karnal.
CARI - Central Agriculture Research Institute, Port Blair, Andaman and Nicobar Islands.

Table 2. Characteristics of bore well water used in experiment

Treatment	pH (d S/m)	EC	SAR	RSC (meq/l)
Control (T_0)	6.83	0.13	-	-
Moderate stress (T_1)	8.21	5.00	27.17	10.30
High stress (T_2)	9.60	10.0	54.32	11.51

Table 3. Analysis of variance for seedling traits under saline alkaline condition.

Source of Variation	Degrees of freedom	Mean Square							
		GP	SL	RL	SL	R/S	VI	SDW	Na^+:K^+ ratio
Genotypes	29	247.52**	53.83**	22.74**	140.33**	0.059**	142.86**	0.004**	0.063**
Treatments	2	24943.10**	1580.11**	899.67**	4863.14**	0.007**	6982.10**	0.269**	1.759**
Genotype x Treatment	58	84.61**	2.073**	2.097**	5.62**	0.031**	7.92**	0.004**	0.017**
Error	90	3.96	0.350	0.484	0.974	0.011	0.730	0.003	0.001

GP- Germination percentage, SL- Shoot length (cm), RL- Root length (cm), SDL- Seedling length (cm)
T_0- Control, T1- Moderate stress, T2- High stress, G- Genotype, T- Treatment, GxT- Genotype X Treatment interaction; SEd – Standard error difference, CD – Critical difference
*, ** Significant at 5 and 1 per cent respectively

Table4. Mean performance of genotypes for seedling characters at different salinity levels

	GP			SL			RL			SDL		
Genotypes	To	T1	T2	To	T1	T2	To	T1	T2	To	T1	T2
Chitteani	100	90	76	20.88	15.0	9.00	13.67	11.65	5.76	34.54	26.59	14.76
Chettivirippu	97	98	81	21.89	16.73	11.0	17.28	14.84	8.00	39.17	31.57	19.00
Wag wag	99	76	62	16.92	8.72	4.97	10.00	6.99	4.85	26.00	15.91	9.82
Nona Bokra	96	96	75	24.83	16.91	10.04	17.69	12.94	8.60	29.52	24.52	18.64
Ketumbar	100	80	60	16.79	9.80	7.76	14.30	8.23	5.00	31.10	18.02	12.76
Pokkali	100	96	76	24.07	20.87	14.3	17.68	13.25	7.45	38.75	34.12	21.75
IR72582-10-1-1-3-1	98	73	59	12.98	8.85	4.54	10.21	7.73	4.79	23.18	16.58	9.33
IR72593-B-3-2-1-2	96	79	62	13.47	8.88	3.70	10.00	5.80	3.45	23.46	14.69	7.14
IR73678-6-9-B	100	90	76	12.35	8.46	4.26	8.80	6.03	4.00	21.23	14.49	8.26
IR72579-B-2R-1-3-2	100	77	59	15.01	7.97	4.84	11.97	7.96	3.83	26.99	15.94	8.68
IR72593-B-13-3-3-1	100	83	53	15.76	9.95	5.90	11.58	5.47	3.28	27.35	15.42	9.18
IR71991-3R-2-6-1	100	82	50	13.97	8.53	4.77	10.27	7.02	3.36	24.24	15.55	8.18
BTS 10-10	100	75	47	16.07	7.17	3.16	11.57	5.67	2.91	27.67	12.83	6.07
BTS 10-12	100	80	59	15.02	9.98	5.12	11.97	7.96	3.83	26.99	15.94	8.68
BTS 24	100	74	42	13.81	7.69	3.74	12.14	4.68	2.61	25.94	12.36	6.35
BTS 17-20	100	69	47	13.87	8.53	4.99	11.27	4.95	2.76	25.58	13.47	7.75
BTS 11-7	100	77	51	14.69	7.00	3.04	10.64	6.97	3.02	25.33	13.97	6.07
CST 7-1	100	84	56	13.05	8.13	4.63	12.14	6.92	3.19	25.17	15.05	7.83
KR 0004	100	80	59	15.94	9.08	5.10	9.69	5.95	3.46	25.62	15.03	8.57
KR 0015	100	82	62	14.49	10.75	6.60	11.69	7.07	3.92	26.18	17.82	10.52
KR 0029	100	80	54	15.95	8.97	5.20	11.04	5.81	2.65	26.98	14.78	7.85
IET 18709	100	89	56	13.37	8.89	6.43	9.93	7.72	4.11	23.29	16.61	10.54
TRY 2	100	90	65	13.77	8.3	3.64	10.09	8.39	4.46	24.07	16.69	8.09
IWP	100	65	36	11.96	5.94	3.25	9.79	5.69	2.80	21.75	11.63	6.05
MI 48	100	62	38	13.18	5.00	2.14	10.89	4.50	2.30	24.06	9.50	4.44
CSR 13	100	94	64	15.05	8.39	5.55	11.39	5.94	3.95	26.44	14.33	9.50
CSR 23	100	94	69	17.82	10.76	7.24	13.46	7.79	5.00	31.28	18.54	12.24
CSR 10	100	90	62	16.29	10.89	5.63	13.02	5.69	4.09	29.32	16.58	9.73
Jhona	100	74	51	14.79	7.73	3.96	11.14	7.01	2.73	25.93	14.75	6.70
KR 0009	100	86	60	16.23	7.94	3.96	1.82	7.10	2.50	27.05	15.05	6.45
Mean over treatments		80.34			10.38			7.74			18.13	
Lower Limit		78.61			9.88			7.16			17.30	
Upper Limit		81.99			10.87			80.32			18.95	
	G	T	G xT	G	T	G xT	G	T	GxT	G	T	GxT
SEd	0.81	0.25	1.40	0.24	0.07	0.41	0.28	0.09	0.49	9.40	0.13	0.70
CD (0.05)	2.28	0.72	3.95	0.77	0.13	1.76	0.79	0.25	1.38	1.13	0.35	1.94

Contd..

GP- Germination percentage, SL- Shoot length (cm), RL- Root length (cm), SDL- Seedling length (cm)
T_0- Control, T1- Moderate stress, T2- High stress, G- Genotype, T- Treatment, GxT- Genotype X Treatment interaction
SEd – Standard error difference, CD – Critical difference

Table4. Mean performance of genotypes for seedling characters at different salinity levels (contd..)

Genotypes	R/S			VI			SDW			N/K		
	To	T1	T2	To	T1	T2	To	T1	T2	To	T1	T2
Chitteani	0.66	0.78	0.65	34.54	23.94	11.29	0.29	0.18	0.11	0.28	0.34	0.45
Chettivirippu	0.79	0.88	0.73	38.18	31.09	15.49	0.29	0.22	0.16	0.20	0.26	0.37
Wag wag	0.50	0.80	0.98	26.78	12.02	6.15	0.23	0.16	0.11	0.16	0.24	0.32
Nona Bokra	0.71	0.77	0.85	41.04	28.79	14.07	0.29	0.26	0.17	0.17	0.20	0.28
Ketumbar	0.86	0.85	0.64	31.10	14.41	7.72	0.24	0.17	0.12	0.23	0.36	0.59
Pokkali	0.61	0.64	0.60	38.57	32.93	16.58	0.34	0.26	0.18	0.16	0.19	0.25
IR72582-10-1-1-3-1	0.78	0.87	1.06	22.82	12.17	5.55	0.28	0.15	0.10	0.13	0.22	0.37
IR72593-B-3-2-1-2	0.74	0.66	0.98	22.53	11.67	4.46	0.25	0.17	0.09	0.25	0.38	0.87
IR73678-6-9-B	0.72	0.72	0.94	21.23	13.04	5.78	0.24	0.15	0.11	0.18	0.27	0.43
IR72579-B-2R-1-3-2	0.80	1.00	0.79	26.99	12.28	4.87	0.24	0.14	0.10	0.16	0.34	0.56
IR72593-B-13-3-3-1	0.74	0.56	0.55	24.23	12.81	4.10	0.25	0.16	0.09	0.21	0.31	0.52
IR71991-3R-2-6-1	0.73	0.82	0.70	27.67	9.70	2.88	0.23	0.15	0.08	0.24	0.35	0.77
BTS 10-10	0.72	0.79	0.93	26.73	12.84	4.82	0.23	0.17	0.13	0.28	0.40	0.72
BTS 10-12	0.80	1.00	0.79	25.94	9.12	2.70	0.23	0.14	0.10	0.13	0.20	0.44
BTS 24	0.89	0.60	0.69	25.58	9.29	3.64	0.24	0.15	0.08	0.14	0.27	0.43
BTS 17-20	0.85	0.58	0.55	25.34	10.84	3.12	0.22	0.17	0.04	0.11	0.20	0.65
BTS 11-7	0.73	0.99	0.99	25.19	12.71	4.38	0.22	0.15	0.12	0.16	0.23	0.43
CST 7-1	0.93	0.85	0.69	27.35	12.80	4.86	0.28	0.16	0.12	0.14	0.23	0.35
KR 0004	0.61	0.66	0.68	25.63	12.09	5.05	0.24	0.16	0.12	0.26	0.38	0.87
KR 0015	0.81	0.66	0.62	26.18	14.70	6.54	0.21	0.15	0.11	0.12	0.18	0.37
KR 0029	0.67	0.65	0.53	26.98	11.82	4.28	0.23	0.14	0.10	0.26	0.38	0.73
IET 18709	0.75	0.87	0.64	23.29	14.78	5.96	0.24	0.15	0.12	0.15	0.20	0.32
TRY 2	0.73	1.01	1.25	24.07	15.03	5.27	0.23	0.18	0.14	0.16	0.35	0.87
IWP	0.82	0.96	0.86	21.76	7.54	2.19	0.24	0.11	0.08	0.12	0.29	0.67
MI 48	0.83	0.90	1.08	24.06	5.90	1.70	0.23	0.12	0.07	0.09	0.12	0.28
CSR 13	0.76	0.71	0.71	26.44	13.54	6.09	0.26	0.16	0.13	0.15	0.20	0.32
CSR 23	0.76	0.73	0.69	31.28	17.43	8.50	0.58	0.17	0.15	0.28	0.35	0.58
CSR 10	0.80	0.53	0.73	29.32	14.99	6.03	0.28	0.16	0.12	0.25	0.36	0.84
Jhona	0.76	0.91	0.7	25.93	10.99	3.39	0.24	0.15	0.12	0.14	0.19	0.39
KR 0009	0.66	0.90	0.64	27.05	12.92	3.85	0.25	0.17	0.12	0.24	0.35	0.77
Mean over treatments		0.76			15.99			0.17			0.32	
Lower Limit		0.68			15.28			0.17			0.34	
Upper Limit		0.85			16.71			0.18			0.29	
	G	T	GxT	G	T	GxT	G	T	GxT	G	T	GxT
SEd	0.04	0.01	0.07	0.35	0.11	0.60	0.003	0.001	0.005	0.01	0.004	0.02
CD (0.05)	1.20	0.39	2.10	0.98	0.31	1.68	0.008	0.002	0.014	0.03	0.01	0.06

GP- Germination percentage, SL- Shoot length (cm), RL- Root length (cm), SDL- Seedling length (cm)
T_0- Control, T1- Moderate stress, T2- High stress, G- Genotype, T- Treatment, GxT- Genotype X Treatment interaction, SEd – Standard error difference, CD – Critical difference

Table 5. Mean performance of genotypes for various seedling Character under saline alkaline condition.

Genotypes	GP	SL	RL	SDL	R/S	VI	SDY	N/K
Chitteani	88.83	14.94	10.36	25.3	0.69	23.25	0.19	0.36
Chettivirippu	92.5	16.53	13.37	29.91	0.8	28.26	0.23	0.28
Wag wag	79.5	10.2	7.28	17.48	0.79	14.98	0.16	0.24
Nona Bokra	89.5	17.26	13.07	30.33	0.78	27.96	0.24	0.22
Ketumbar	80.16	11.45	9.17	20.62	0.78	29.42	0.17	0.39
Pokkali	91	19.47	11.79	31.54	0.59	13.51	0.25	0.2
IR 72582-10-1-1-3-1	77	8.79	7.58	16.36	0.91	12.89	0.18	0.24
IR 72593-B-3-2-1-2	79.33	8.68	6.42	15.09	0.79	13.35	0.17	0.29
IR 73678-6-9-B	86.67	8.35	6.31	14.66	0.79	14.8	0.17	0.29
IR 72579-B-2R-1-3-2	78.67	9.27	7.92	17.19	0.86	15.03	0.16	0.35
IR 72593-B-13-3-3-1	78.33	10.53	6.78	17.31	0.62	13.71	0.17	0.34
IR 71991-3R-2-6-1	77.66	9.08	6.88	15.67	0.75	13.41	0.15	0.45
BTS 10-10	74.33	8.79	6.72	15.52	0.82	14.8	0.18	0.46
BTS 10-12	80	10.04	7.92	17.19	0.86	14.8	0.16	0.24
BTS 24	72.16	8.41	6.47	14.88	0.73	12.58	0.16	0.26
BTS 17-20	72	9.13	6.48	15.6	0.66	12.83	0.18	0.28
BTS 11-7	76.33	8.25	6.88	15.1	0.99	13.1	0.16	0.32
CST 7-1	80.16	8.6	7.41	16.02	0.82	14.09	0.19	0.27
KR 0004	79.83	10.04	6.37	16.41	0.65	14.25	0.18	0.26
KR 0015	81.5	1.61	7.56	18.17	0.69	15.8	0.16	0.5
KR 0029	78.16	10.03	6.5	16.54	0.62	14.36	0.16	0.22
IET 18709	81.83	9.56	7.25	16.81	0.75	14.67	0.17	0.46
TRY 2	85	8.63	7.65	16.28	0.99	14.78	0.18	0.22
Improved White Ponni	67.16	7.04	6.09	13.14	0.89	10.49	0.15	0.46
MI 48	66.66	6.77	5.89	12.67	0.93	10.55	0.14	0.36
CSR 13	86.17	9.66	7.09	16.78	0.72	15.35	0.18	0.16
CSR 23	87.83	11.94	8.74	20.68	0.72	19.07	0.2	0.23
CSR 10	84.16	10.94	7.6	18.54	0.69	16.78	0.19	0.4
Jhona	75.17	8.83	6.97	15.79	0.79	13.43	0.17	0.48
KR 0009	82	9.37	6.81	16.18	0.73	14.6	0.18	0.24

GP- Germination percentage, SL- Shoot length (cm), RL- Root length (cm), SDL- Seedling length (cm)
T_0- Control, T1- Moderate stress, T2- High stress, G- Genotype, T- Treatment, GxT- Genotype X Treatment interaction
SEd – Standard error difference, CD – Critical difference

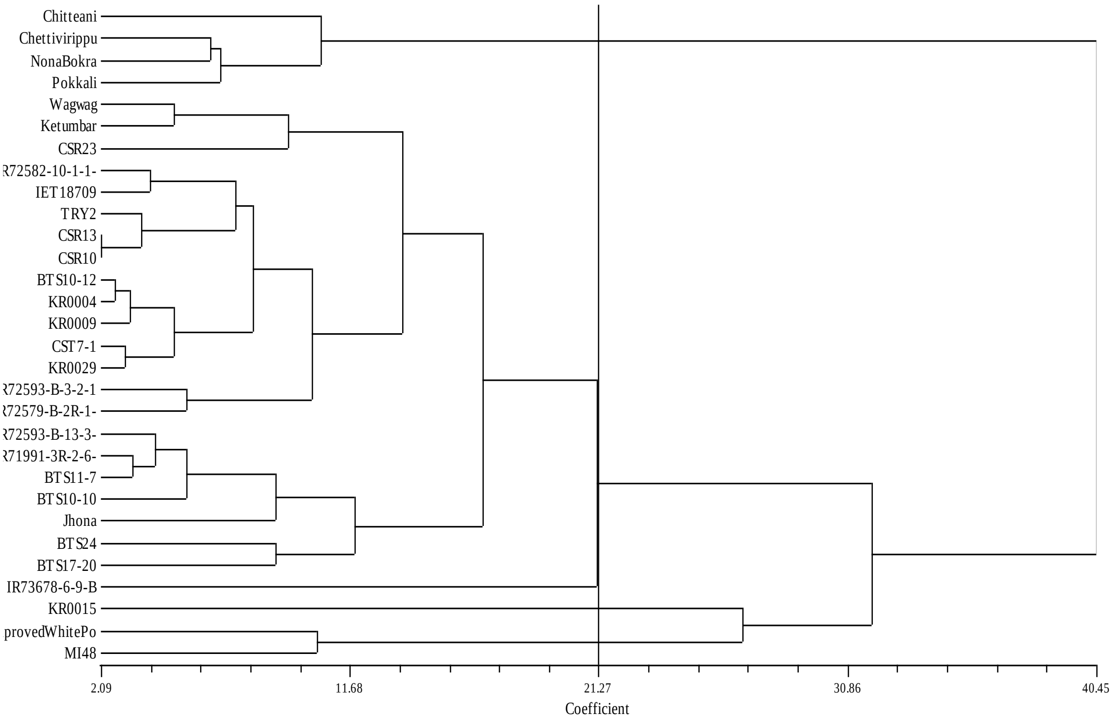

Figure 1. Clustering of 30 rice genotypes based on seedling characters