Journal of Pharmacognosy and Phytochemistry

Available online at www.phytojournal.com

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Morpho-agronomic evaluation for delineation of salinity stress specific response and tolerance status of rice genotypes

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Abstract
Analysis of variance revealed significant differences amongst eighteen rice genotypes evaluated in randomized block design with two replications under normal (pH 8.15 and EC 0.28 dsm^{-1}) and salt affected (pH 9.18 and EC 1.22 dsm^{-1}) field conditions. Considerably higher relative mean values for the eleven morpho-agronomic traits, such as, panicles per plant, panicle length, 100 seed weight, spikelets per panicle, filled grains per panicle, unfilled grains per panicle, root length, root volume, root dry weight, biological yield and grain yield per plant, were recorded in tolerant genotypes compared to moderately tolerant and susceptible genotypes. Root volume, root dry weight and unfilled grains per panicle were observed to be more affected in susceptible genotypes. Keeping into consideration the relative mean performance, the genotypes were categorized as highly tolerant, moderately tolerant and susceptible to saline condition. Eigen vectors from the three principal component axes revealed the importance of panicle length, filled grains per panicle, 100-seed weight, root length and root dry weight as main contributors to genetic divergence among the genotypes. Average taxonomic distance based hierarchical classification and principal component analysis based spatial distribution patterns unambiguously discriminated the tolerant and susceptible genotypes.

Keywords: Rice, morpho-agronomic traits, principal component analysis, reproductive stage, salinity tolerance, phenetic divergence

Introduction
Rice is an important crop which provides food for half of the world's population. Globally, salinity is the foremost hindrance affecting cultivation of crop plants including rice after drought [1] that reduces crop productivity [2]. A substantial proportion of arable lands world-wide is affected by salinity and more areas are being expected to worsen in future due to global climate changes [3, 4]. Apart from salinity stress, several countries are facing severe drought leading to extreme evaporation which results in accumulation of salt in the soil; thereby presenting an increasing threat to plant cultivation [5, 6].

Rice is considered as glycophyte plant and hence it cannot tolerate high concentration of salt. However, there are large numbers of varieties, which show appreciable variation in the level of salt tolerance [7]. The sensitivity to salt stress in the case of rice genotypes has an adverse effect on germination, seedling growth, establishment and grain yield [8]. Salinity leads to inhibition of germination and initial development, leaf area development due to diminished photosynthetic area, reduction in dry matter production, delay in seed set and sterility [8, 9]. Being a salt sensitive crop, it exhibits differential sensitivity to different levels of salinity during different growth and development stages. Rice is considered to be more sensitive to salinity stress during early vegetative and reproductive stages but tolerant during germination and active tillering [10-12]. At reproductive stage, salinity causes an increase in sterile florets by affecting panicle initiation and also reduces panicle length, number of primary branches and spikelets per panicle, fertility and panicle weight, thus reducing grain yield [13, 14]. Keeping all these into consideration, an attempt was made to evaluate a set of rice genotypes for assessment of salinity stress specific response and their tolerance status under saline condition.

Materials and Methods
A set of eighteen rice genotypes was evaluated in randomized block design with two replications in normal (pH 8.15; EC 0.28 dsm^{-1}) and salinized (pH 9.18; EC 1.22 dsm^{-1}) field conditions at the research farm of Dr. Rajendra Prasad Central Agricultural University, Bihar, Pusa. The seeds of all the genotypes (table 1) were grown in nursery and seedling was transplanted after 25 days to the field. Each entry was raised in two rows spaced at 20 cm. The inter-plant distance within a row was maintained at 15 cm.

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Recommended agronomic practices were followed while raising the crop. The observations for panicles per plant, panicle length, 100-seed weight, spikelets per panicle, filled grains per panicle, unfilled grains per panicle, root length, root volume, root dry weight, biological yield and grain yield were recorded on five randomly chosen plants of each genotype in each replication. An average value based on five plants was subjected to statistical analysis. Relative mean value was obtained by dividing the mean value obtained in saline field with the mean value obtained from normal field and expressed in percentage. The relative mean value computed for different morpho-agronomic characters was then averaged to find out the mean index value (MI) and then it was finally compared with the standard deviation. The genotypes were characterized as highly tolerant (>MI+1/2 Sd), moderately tolerant (>MI±1/2 Sd) and susceptible (<MI±1/2 Sd) categories based on their overall relative mean value.

Using morpho-agronomic characters based similarity correlation matrix, principal component analysis was carried out to recognize the relative importance of classification variables [15]. Principal component analysis resulted spatial distribution of genotypes in two dimensional plots along orthogonal coordinate axis. Sequential agglomerative hierarchical nested (SHAN) clustering based on average taxonomic distance was employed for tree building. The dendrogram was constructed by unweighted pair-group

method using arithmetic mean for differentiation and discrimination of genotypes.

Results and Discussion

Analysis of variance for the design of experiment revealed significant genotypic differences for eleven morpho-agronomic characters under both the conditions. Considerably higher extent of variability among the genotypes under evaluation was observed for all characters recorded in the present study. This is also clearly evident from a perusal of range of mean values obtained for different characters. Under normal condition, the number of panicles ranged from 5.8 in CSR-2K- 219 to 10.03 in IR- 64 whereas in salt stressed field, it ranged from 5.3 in CSR-2K-242 to 9.6 in CSR-36 (Table 1). The relative mean value of number of panicles per plant was found to be considerably lower in genotypes swarna (69.74%), IR-36 (69.04%) and IR 64 (72.81%) compared to the genotypes CSR-13 (97.36%) and CSR-30 (97.10%). Therefore, the genotypes IR-36, Swarna and IR-64 showed greater sensitivity to salt affected condition in accordance with the evidence available in the literature [16]. Recognizable reduction in panicle length was observed in salt affected field. Since, salinity adversely affects plant growth and development, panicle length was reduced probably by interfering with the cell metabolism through changes of the water and ionic status in the cells [17, 18]. Among the genotypes under evaluation, CST-7-1 had the maximum relative mean value (98.14%) for panicle length.

Table 1: Mean performance of genotypes for panicles per plant and panicle length under normal and salinized conditions

Genotype	No. of panicles per plant		Relative (%)	Panicle length (cm)		Relative (%)
	Normal	Salinized		Normal	Salinized	
NDRK -11-1	9.30	8.20	88.17	19.70	18.60	94.41
NDRK -11-3	9.95	9.00	90.45	20.20	19.60	97.02
NDRK -11-4	7.00	5.90	84.28	22.30	18.00	80.71
NDRK -11-5	8.70	6.80	78.16	23.40	22.60	96.58
NDRK -11-6	7.90	6.30	79.74	20.00	18.40	92. 00
NDRK -11-7	9.20	7.10	77.17	24.10	22.50	93.36
CST7-1	9.50	8.90	93.68	21.60	21.20	98.14
CSR-2K-219	5.80	5.30	91.39	23.60	23.00	97.45
CSR-2K-242	7.90	5.80	73.41	23.80	23.10	97.05
CSR-2K-262	8.50	7.55	88.82	19.25	18.00	93.50
IR -36	8.75	7.40	69.71	22.90	21.80	95.19
IR -64	10.3	7.50	72.81	21.80	19.20	88.07
Swarna	8.40	6.10	69.04	21.20	19.90	93.86
CSR- 13	7.60	5.80	97.36	23.20	20.10	86.63
CSR -23	7.60	6.90	90.78	20.60	19.20	93.20
CSR -27	7.00	6.75	96.42	19.20	18.10	94.27
CSR -30	6.90	6.70	97.10	19.90	18.95	95.22
CSR -36	9.95	9.60	96.48	22.70	21.60	95.15
CD	2.368	2.324		1.890	1.927	
CV	13.339	15.415		4.107	4.487	

The highest relative mean value for 100 seed weight (Table 2) was observed in CSR 36 (99.56%) followed by CSR-2K-219 (99.17%), whereas the lowest value was recorded in IR-64 (92.99%) followed by NDRK-11-4 (89.49%). Most likely salinity reduced the photosynthetic activity leading to poor sugar production in the ovaries [18]. The highest relative mean value for spikelets per panicle was recorded in genotype CSR-

36 (94.58%) reflecting its tolerance to salinity stress, while the genotype IR-36 had the lowest relative value (73.52%) indicating its susceptibility to salt tolerance.

Spikelet per panicle is an important and sensitive morphological character related to the grain yield. Earlier reports suggested a considerable reduction in spikelets per panicle with increase in salinity levels [16].

Table 2: Mean performance of genotypes for 100 seed weight and spikletes per panicle under normal and salinized conditions

Genotype	100 seed weight		Relative (%)	Spiklets per panicle		Relative (%)
	Normal	Salinized		Normal	Salinized	
NDRK -11-1	2.41	2.37	98.34	124.70	104.10	83.48
NDRK -11-3	2.07	2.02	97.58	124.40	101.10	81.27
NDRK -11-4	2.38	2.13	89.49	137.40	126.40	91.99
NDRK -11-5	2.52	2.44	96.82	134.80	111.40	82.64
NDRK -11-6	2.38	2.26	94.95	132.70	117.00	88.16
NDRK -11-7	2.57	2.52	98.05	110.60	97.10	87.79
CST7-1	2.81	2.73	97.15	113.10	93.40	82.58
CSR-2K-219	2.41	2.39	99.17	99.00	82.80	83.63
CSR-2K-242	2.23	2.20	98.65	93.60	76.10	81.30
CSR-2K-262	3.00	2.89	96.33	1160	105.60	91.03
IR -36	2.89	2.84	98.26	122.55	90.10	73.52
IR -64	2.57	2.39	92.99	106.70	91.10	85.37
Swarna	2.50	2.39	95.60	86.60	73.60	84.90
CSR- 13	2.42	2.30	95.04	86.80	82.10	94.58
CSR -23	2.22	2.17	97.74	101.20	93.70	92.58
CSR -27	2.54	2.43	95.66	123.10	111.60	90.65
CSR -30	2.38	2.28	95.79	111.90	100.60	89.9
CSR -36	2.28	2.27	99.56	108.10	96.10	88.89
CD	0.363	0.271		18.737	20.854	
CV	6.891	5.332		7.798	10.062	

The relative mean value of filled grains per panicle (Table 3) was found to be highest in CSR-23 (98.57%) and lowest in NDRK-11-3 (78.67%), whereas unfilled grains per panicle were highest in CSR-2K-262 (92.52%) and lowest in Swarna (48.31%). Saline field diminishes the number of filled grain and increases the number of unfiled grain per panicle. This might be due to sterility and improper seed set as a result of reduced translocation of soluble carbohydrate to spikelets, accumulation of high sodium and low potassium content in panicle and inhibition of starch synthetase activity in developing grain [19-21].

The highest relative mean value for root length (Table 4) was found in the genotype NDRK-11-5 (91.12%) followed by CST-7-1 (90.52%), whereas the lowest relative value was observed in Swarna (48.31%). An earlier report suggested that root length reduces under saline stress [22-25] as observed in the present study. The relative mean value for root volume was observed maximum in CSR-27(96.42%) and minimum in IR-36 (54.16%).

Table 3: Mean performance of genotypes for filled and unfilled grains per panicle under normal and salinized conditions

Genotype	No. of filled grains/ panicle		Relative (%)	No. of unfilled grains/ panicle		Relative (%)
	Normal	Salinized		Normal	Salinized	
NDRK -11-1	99.50	83.80	84.22	25.20	20.30	80.55
NDRK -11-3	100.80	79.30	78.67	23.60	21.80	92.37
NDRK -11-4	95.70	92.40	96.55	41.70	33.00	79.13
NDRK -11-5	84.60	72.80	86.05	50.20	38.60	76.89
NDRK -11-6	90.80	86.60	95.37	41.90	32.50	77.56
NDRK -11-7	80.80	70.90	87.74	29.60	26.20	88.51
CST7-1	81.50	64.70	79.38	31.60	28.70	90.82
CSR-2K-219	90.20	74.40	82.48	12.90	8.40	65.11
CSR-2K-242	86.90	70.00	80.55	6.70	6.10	91.04
CSR-2K-262	97.95	88.90	90.76	18.05	16.70	92.52
IR -36	91.70	74.60	81.35	30.85	15.50	50.24
IR -64	87.50	76.50	87.42	19.20	13.80	71.87
Swarna	68.80	67.00	97.38	17.80	8.60	48.31
CSR- 13	80.30	66.60	82.93	6.50	5.40	83.07
CSR -23	84.00	82.80	98.57	17.20	12.90	75.00
CSR -27	102.10	97.70	95.69	210	13.90	66.19
CSR -30	98.00	91.90	93.77	13.90	9.70	69.78
CSR -36	95.40	84.70	88.78	33.00	21.40	64.84
CD	16.322	19.606		12.498	13.244	
CV	8.545	11.639		23.989	35.189	

Table 4: Mean performance of genotypes for root length (cm) and root volume (cm³) under normal and salinized conditions

Genotype	Root length (cm)		Relative (%)	Root volume (cm³)		Relative (%)
	Normal	Salinized		Normal	Salinized	
NDRK -11-1	8.50	7.50	88.23	11.50	9.00	78.26
NDRK -11-3	10.70	9.30	86.91	11.00	7.00	63.63
NDRK -11-4	8.40	7.00	83.33	13.50	10.50	77.77
NDRK -11-5	12.40	11.30	91.12	17.00	14.00	82.35
NDRK -11-6	13.10	10.30	78.62	18.50	12.50	67.56
NDRK -11-7	8.90	7.80	87.64	21.50	16.00	74.41
CST7-1	9.50	8.60	90.52	18.50	16.50	89.18
CSR-2K-219	11.30	9.80	86.72	15.00	10.50	70.00
CSR-2K-242	8.50	7.00	82.35	15.50	12.00	77.41
CSR-2K-262	12.50	9.70	77.60	12.50	10.50	84.00
IR -36	10.00	7.10	71.00	12.00	6.50	54.16
IR -64	8.90	5.90	66.29	13.00	9.00	69.23
Swarna	10.00	7.60	76.00	17.50	10.30	58.85
CSR- 13	10.80	9.60	88.88	9.00	8.50	94.44
CSR -23	10.10	9.00	89.10	11.00	8.50	77.27
CSR -27	8.90	8.00	89.88	14.00	13.50	96.42
CSR -30	9.70	7.80	80.41	16.50	15.00	90.90
CSR -36	11.00	10.00	90.90	14.00	12.50	89.28
CD	2.692	2.705		4.901	5.168	
CV	12.437	14.934		15.860	21.408	

Root dry weight showed remarkable difference in the relative mean value, which ranged from 51.93% in IR-64 to 94.87% in CSR-23. The genotype CSR-36 (98.49%) had the maximum relative mean value for biological yield, whereas IR-36 (73.61%) showed the minimum relative mean value (Table 5). The plant height acts an important key of shoot yield and total biomass production [18]. Accordingly, biomass decreases significantly with salinity and might be due to upset in the photosynthesis activity [24]. Therefore, biological yield seems to be a very important trait for evaluation of salinity stress tolerance status.

Table 5: Mean performance of genotypes for root dry weight (gm) and biological yield (gm) under normal and salinized conditions

Genotype	Root dry weight (gm)		Relative (%)	Biological yield (gm)		Relative (%)
	Normal	Salinized		Normal	Salinized	
NDRK -11-1	10.30	7.60	73.78	58.62	54.37	92.74
NDRK -11-3	7.72	4.82	62.43	45.59	36.52	80.10
NDRK -11-4	9.78	7.30	74.64	56.75	45.17	79.59
NDRK -11-5	6.37	4.77	74.88	56.20	44.49	79.16
NDRK -11-6	9.49	6.58	69.33	56.39	48.61	86.20
NDRK -11-7	11.24	7.15	63.61	67.05	61.78	92.14
CST7-1	6.14	5.40	87.94	59.56	57.15	95.95
CSR-2K-219	8.32	5.25	63.10	56.92	51.76	90.93
CSR-2K-242	8.21	5.95	72.47	59.18	52.05	87.95
CSR-2K-262	8.31	6.07	73.04	63.79	60.88	95.43
IR -36	8.83	5.20	58.89	45.26	33.32	73.61
IR -64	6.45	3.35	51.93	50.15	39.25	78.26
Swarna	5.98	3.77	63.04	50.07	38.96	77.81
CSR- 13	5.74	5.34	93.03	59.47	59.05	99.29
CSR -23	3.90	3.70	94.87	59.63	59.52	99.81
CSR -27	5.47	4.23	77.33	55.22	50.84	92.06
CSR -30	7.36	6.39	86.82	60.60	55.91	92.26
CSR -36	5.80	5.03	86.72	60.61	59.70	98.49
CD	2.665	2.487		7.305	10.785	
CV	16.642	21.489		6.045	10.037	

The grain yield recorded the highest relative mean value in genotype CST-7-1 followed by CSR-13, CSR-36, CSR-23, CSR-2K-262, CSR-27 and CSR-30 as compared to the genotypes CSR-2K-242, NDRK-11-1, NDRK-11-7, NDRK-11-6, NDRK-11-3, NDRK-11-5, NDRK-11-1, and CSR-2K-219. The lowest relative mean value for grain yield was recorded in genotype IR-64 followed by IR-36 and Swarna, reflecting their susceptibility to salinity stress (Table 6). Therefore, it was inferred from the results of the present study that the response and tolerance to salinity stress is genotype dependent. Since tolerance is not dependent on a single trait, so there is need to study the mechanism and response of plant under salinity stress. Initially plants face osmotic effects by lowered osmotic potential followed by ionic stress [8, 26]. The tolerant genotypes have an adaptive mechanism to avoid salt tolerance by exclusion, dilusion and compartmentalization [19, 27, 28]. Consequently, differential response of genotypes for different morpho-agronomics traits was noticed. Furthermore, the impact of salinity was different for tolerant and susceptible genotypes in accordance with the reports of earlier researchers [21, 29]. Saline soil contains high concentration of soluble salts [30].

Table 6: Mean performance of genotypes for grain yield per plant under normal and salinized conditions

Genotype	Grain yield per plant (gm)		Relative (%)
	Normal	Salinized	
NDRK -11-1	20.39	18.50	90.73
NDRK -11-3	21.43	19.17	89.45
NDRK -11-4	20.54	18.02	87.73
NDRK -11-5	19.50	17.23	88.35
NDRK -11-6	19.01	17.09	89.90
NDRK -11-7	20.79	18.80	90.42
CST7-1	23.13	22.07	95.41
CSR-2K-219	20.12	17.47	86.82
CSR-2K-242	21.00	19.09	90.90
CSR-2K-262	24.61	22.70	92.23
IR -36	17.67	13.80	78.09
IR -64	18.84	14.77	78.39
Swarna	18.04	14.01	77.66
CSR- 13	23.30	22.12	94.93
CSR -23	22.12	20.43	92.35
CSR -27	22.14	20.39	92.09
CSR -30	24.22	22.24	91.82
CSR -36	22.96	21.61	94.12
CD	2.830	2.466	
CV	6.304	6.145	

While discriminating the genotypes into the categories of highly tolerant (>MI+1/2 Sd), moderately tolerant (MI±1/2Sd) and highly susceptible genotypes (< MI-1/2 Sd) in relation to the mean index (MI) value, the genotypes CSR-13, CSR-23, CSR-27, CSR-30, CSR-36, CST7-1 and CSR-2K-262 were found to be highly tolerant (>MI+1/2 Sd) to salt stress, whereas NDRK-11-1, NDRK-11-3, NDRK-11-4, NDRK-11-5, NDRK-11-6, NDRK-11-7, CSR-2K-219 and CSR-2K-242 were inferred to be moderately tolerant (MI±1/2Sd). The remaining three genotypes, namely, IR-36, IR-64 and Swarna were categorized as highly susceptible to salt stress (< MI-1/2 Sd).

Table 7: Range of variation in relative mean performance for 11 morpho-agronomic characters of 18 rice genotypes

Character	Mean	Standard deviation	Range
PP	85.26	09.91	69.04-97.36
PL	93.43	04.36	80.71-98.14
SW	96.50	02.40	89.49-99.56
SP	86.34	05.23	73.52-94.58
FG	88.20	06.69	78.67-98.57
UG	75.76	13.39	48.31-92.52
RL	83.63	07.28	66.29-91.12
RV	77.50	12.08	54.16-96.42
RDW	73.76	12.24	51.93-94.87
BY	88.43	08.38	73.61-99.81
GY	88.96	05.52	77.66-95.41

PP: Panicles per plant; PL: Panicle length; SW: 100-Seed weight, FG: Filled grain per panicle; UG: Unfilled grain per panicle; RL: Root length; RV: Root volume; RDW: Root dry weight; BY: Biological yield; GY: Grain yield

Being a glycophytic cereal crop, rice is salt sensitive crop and found to be more tolerant at germination stage and tillering stage and sensitive at vegetative and reproductive stage [10, 31]. Basically, tolerance and sensitivity for salt stress is dependent on various factors such as genotypes, their growth stages, salinity levels, treatment stage [9, 32, 33]. Exploitable extent of genetic variability was observed among the genotypes under evaluation as it is evident from a perusal of range of relative mean values obtained for different morpho-agronomic characters (Table 7), providing an opportunity for exploitation in crop improvement programmes.

Positively significant correlation of grain yield per plant was observed with panicles per plant (r = 0.781), spikelets per panicle (r = 0.512), unfilled grains per panicle (r = 0.638), root length (r = 0.770), root volume (r = 0.793), root dry weight (r = 0.781) and biological yield per plant (r = 0.832). Among the component characters, spikelets per panicle exhibited significant positive association with panicles per plant (r = 0.544), filled grains per panicle (r = 0.632), root volume (r = 0.621), root dry weight (r = 0.575) and biological yield per plant (r = 0.598). Similarly, the association of panicles per plant with root length (r = 0.640), root volume (r = 0.748), root dry weight (r = 0.713) and biological yield per plant (r = 0.748) was found significantly positive. Among the rest of the morpho-agronomic characters, root length, root volume and root dry weight exhibited significant positive association among themselves and also with biological yield per plat. Negatively significant association was recorded between spikelets per panicle and panicle length (r = -0.552) and between filled grains per panicle and 100-seed weight (r = -0.475).

Principal component analysis based on similarity correlation matrix was used for evaluation of relative importance of classification variables. The eigen values from the first, second and third principal components axes accounted for 47.86%, 25.22% and 10.71% with cumulative contribution of 83.80% to total variation. A comparison of the relative magnitude of eigenvectors from the first principal component axis indicated that grain yield per plant, biological yield, root volume, root dry weight, panicles per plant, root length and spikelets per panicle were the important characters that contributed positively in descending order of magnitude (Table 8). This shows that these morpho-agronomic characters were the important classification variables with positive contribution. From the second principal component axis, 100-seed weight, panicle length and root length appeared to be the important classification variables with positive contribution, whereas filled grains per panicle and spikelets per panicle were negative contributors. Similarly, the variance explained by the third principal component axis was mainly contributed by filled grains per panicle, 100-seed weight, panicle length and root dry weight with positive contributors, whereas unfilled grain per panicles with negative contribution. The importance of some of these characters as main contributors to phenetic divergence among genotypes of rice has been emphasized by earlier researchers [34, 35].

Table 8: Eigen vectors from three principal component axes for 11 morpho-agronomic characters of 18 rice genotypes

Character	Principal component axis		
	1	2	3
PP	0.864	0.019	0.099
PL	0.023	0.880	0.303
SW	0.135	0.888	0.323
SP	0.665	-0.681	0.063
FG	0.083	0.755	0.494
UG	0.477	0.155	0.795
RL	0.769	0.304	0.032
RV	0.877	-0.126	-0.174
RDW	0.869	-0.088	0.203
BY	0.894	0.103	0.145
GY	0.951	0.153	-0.164

PP: Panicles per plant; PL: Panicle length; SW: 100-Seed weight, FG: Filled grain per panicle; UG: Unfilled grain per panicle; RL: Root length; RV: Root volume; RDW: Root dry weight; BY: Biological yield; GY: Grain yield

Spatial distribution pattern of rice genotypes in two dimensional ordinations along orthogonal coordinate axes, as reflected by principal component analysis using relative mean performance based taxonomic distance, unambiguously discriminated the tolerant and susceptible genotypes and classified them into two well separated broad groups (Fig. 1). The first group consisted of highly tolerant and moderately tolerant genotypes, whereas the second group consisted of three salt susceptible genotypes. Hierarchical classification pattern of genotypes generated by employing sequential agglomerative hierarchical nested analysis using arithmetic mean dependent unweighted pair-group method based on similarity coefficient matrix also separated the genotypes into two broad clusters (Fig. 2). At higher phenon level, the first multi-genotypic cluster was further divided into two sub-clusters. The first sub-cluster (A) consisted of fourteen

genotypes, whereas the second sub-cluster (B) comprised of NDRK-11-4. The second multi-genotypic cluster consisted of three salt susceptible genotypes by accommodating IR-36, IR-64 and Swarna. Using multiple agronomic characters and physiological indices, cluster analysis has also been performed by earlier researchers for evaluation of salt tolerance among rice genotypes [31, 36] which clearly differentiated rice cultivars into different clusters. It was clearly evident from the results of the present study that salinity had differential impact on different morpho-agronomic characters in tolerant and susceptible genotypes, corroborating the finding of earlier researchers [21, 29]. Therefore, the tolerant genotypes seemed to possess an adaptive mechanism to avoid the adverse effects of salt tolerance, clearly reflecting that the tolerance to salinity stress is genotype dependent.
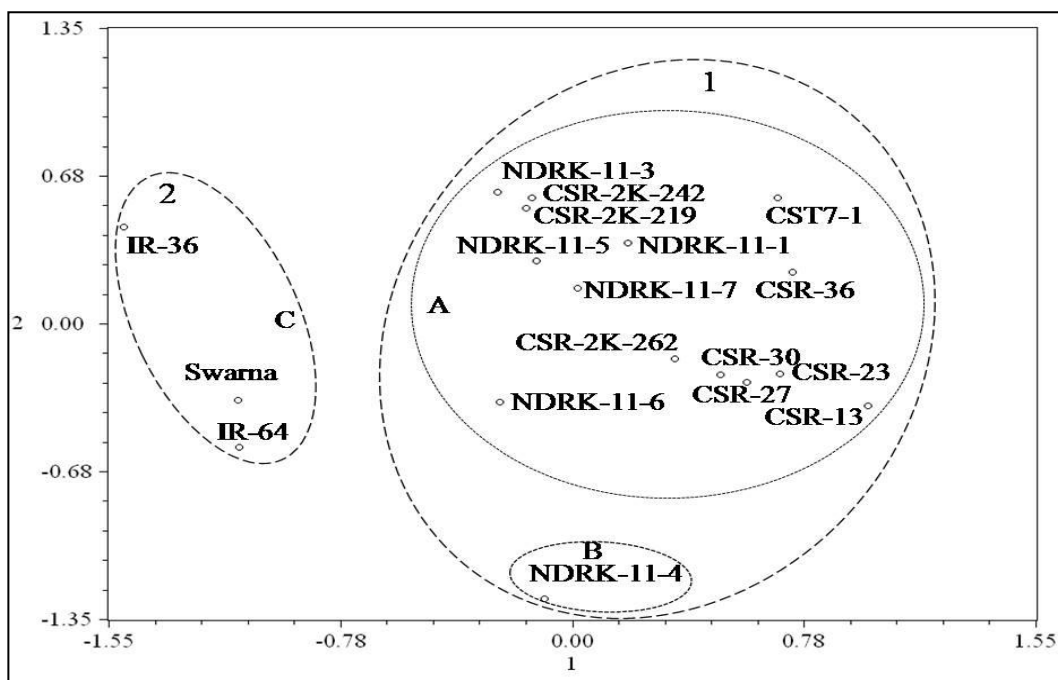

Fig 1: Spatial distributions of 18 rice genotypes along orthogonal coordinate axes
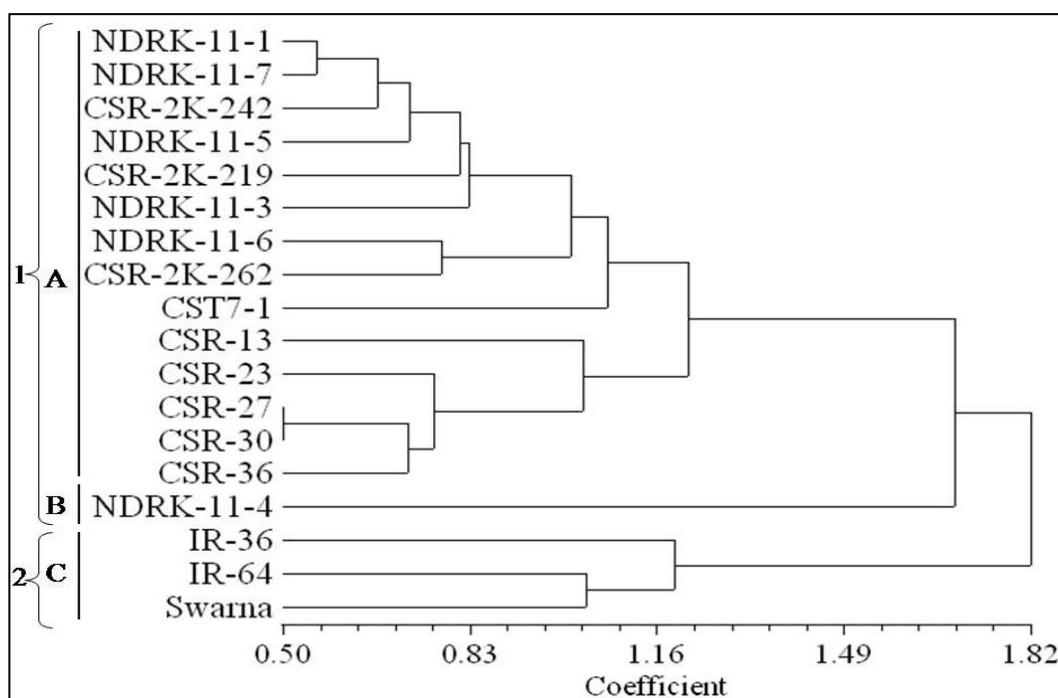

Fig 2: Dendogram based on taxonomic distance among 18 rice genotypes

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