Path analysis and Principal component analysis for seedling and reproductive stage salinity tolerance in rice (*Oryza sativa* L.)

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ABSTRACT

The present investigation was carried out to determine the relationship and genetic diversity among 76 rice germplasm using principal component analysis and path analysis at both seedling and reproductive stage salinity tolerance. Principal Component Analysis (PCA) was utilized to estimate the relative contribution of various traits for total variability. During seedling stage, the first two principal components together accounted for 78.92% of the variability. The PC1 and PC2 showed eigen value more than 1 and contributed 46.83 and 18.59 percent of variability respectively. During reproductive stage, the first three components were found to have eigen value more than 1.00 and contributed 40.58, 17.80 and 13.65 per cent of variability. All the three PC's accounted for 81.31% of the total variability. Path analysis revealed that high direct effects was exhibited by shoot Na^+ concentration at seedling stage; and similarly, high direct effects was exhibited by number of productive tillers, number of grains per panicle at reproductive stage. Hence, selection based on these characters would be more effective to meet higher grain yield. The residual effect under path analysis was very low and negligible.

Introduction

Rice is the most important staple crop in the world. It belongs to Gramineae family (Poaceae) with a basic chromosome number (n) of 12 (2n=24). Various abiotic stresses namely, drought, flood and salinity needs more attention because they are the reason for direct barrier in rice production. Among these abiotic stresses, salinity affects approximately10 m ha of inland and coastal areas. Unfortunately, cultivation of rice is only available to the farmers in the saline-prone coastal regions where anything else can be grown, and is critical to the food security of these resource-poor farmers.

Prior to recognizing the new method to break the yield barrier, it is essential to study the correlation for yield and it's at tributes under salinity and clustering them into diverse groups based on the diversity among the genotypes. Correlation studies can be used to determine the relative importance of indi-

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vidual traits. Path coefficient analysis gives an understanding of a trait's direct and indirect contribution to yield, allowing the breeder to evaluate the genetic traits according to their contribution. Knowing the nature and degree of genetic divergence can help in choice of the traits useful for breeding programme.

Materials and Method

The experimental material consists of 76 rice genotypes comprising of released rice varieties and advanced breeding lines from Regional Agricultural Research Station, Maruteru; Agricultural Research Station, Machilipatnam; and Agricultural Research Station, Bapatla along with few private research hybrids. Data was collected on different traits *viz.*, 10th day salt injury score, 16th day salt injury score, shoot Na$^+$ concentration, shoot K$^+$ concentration, shoot length, root length and Na$^+$/K$^+$ under seedling stage salinity. During reproductive stage, data on salinity score, days to 50% flowering, plant height (cm), panicle length (cm), number of productive tillers plant^{-1}, number of filled grains panicle^{-1}, total number of grains panicle^{-1}, spikelet fertility (%) and grain yield per plant (g) was collected. The data was collected on the above characters was analyzed using path coefficient analysis and principal component analysis.

Results and Discussion

Principal component analysis

PCA during seedling stage identifies the traits that contribute towards the variation within a group of genotypes. In the present study, first two components were recorded with eigen value greater than

1.00 (Table 1 and Figure 1) and together contributed for 78.92% of the total variation. Principal component 2(PC2) with the eigen value of 1.30 and accounted for 65.43% of total variation, while PC1 with eigen value of 3.27, contributed 46.83% of the total variation. In the first principal component, the traits 10th day and 16th day salt injury score, shoot Na$^+$ concentration and Na$^+$/K$^+$ ratio contributed better for total variation due to their high loadings. The traits 10th day and 16th day salt injury score are the important attributes in the second principal component. In third principal component, 10th day and 16th day salt injury score, shoot length, shoot Na$^+$ and shoot K$^+$ concentration are the important traits. According to the results it was evicted that the first three PCs comprising of characters 10th and 16th day salt injury score which recorded high factor loadings are responsible for maximum variability. Rotated component matrix revealed that first three PCs were representing maximum variability (78.92%) and hence, the traits falling in these three PCs must be given due importance for salt tolerance rice breeding program. The positive and negative loading reveals the presence of constructive and destructive
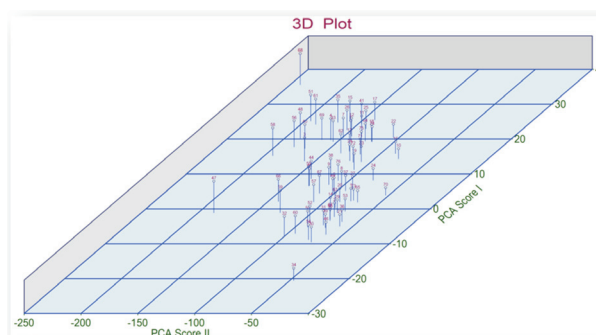

Fig. 1. 3D plot representing the diversity among 76 rice genotypes under seedling stage salinity

Table 1. Factor loadings for different characters under seedling stage salinity of first three principal components

S.No.	Character	PC 1	PC 2	PC 3
1.	10th day salt injury score	0.40	0.15	0.17
2.	16th day salt injury score	0.44	0.15	0.27
3.	Shoot length	-0.39	0.02	0.41
4.	Root length	-0.26	-0.33	-0.63
5.	Shoot Na$^+$ concentration	0.17	-0.79	0.26
6.	Shoot K$^+$ concentration	-0.41	-0.24	0.48
7.	Na$^+$/ K$^+$ ratio	0.46	-0.38	-0.09
	Variability (%)	46.83	18.59	13.49
	Cumulative Variability (%)	46.83	65.43	78.92
	Eigen Values	3.27	1.30	0.94

correlation trends among the components and the variables. Therefore, the above mentioned traits with high positive loadings were found to be contributed more towards diversity.

Under reproductive stage salinity, the first three components recorded with eigen value greater than 1.00 (Table 2) and together contributed for 81.31% of the total variation. Principal component 1(PC1) with eigen value of 3.65 accounted for 40.58% of the variation, while PC2 with the eigen value of 1.60, contributed 58.38% of the total variation and PC3 with an eigen value of 1.23 accounted for 72.03% of the total variation. In the first principal component, the traits salinity score, days to 50% flowering, plant height, number of productive tillers, panicle length, number of filled grains/panicle, number of total grains/panicle and grain yield/plant contributed more for total variation due to their high loadings. Days to 50 % flowering, total number of productive tillers and spikelet fertility were the important traits in the second principal component. The salinity score and days to 50% flowering are the important traits in third principal component, whereas spikelet fertility was recorded as the important trait in fourth principal component. Based on PCA, important yield and its component traits for salt tolerance were present in PC1 (Table 2), (Figure 2). Rotated component matrix revealed that first four PCs were representing maximum variability (81.31%) and hence, the traits falling in these four PCs must be given importance in salinity tolerance breeding programme in rice. The positive and negative loadings represent the presence of both constructive and destructive correlation trend amid the components and variables.
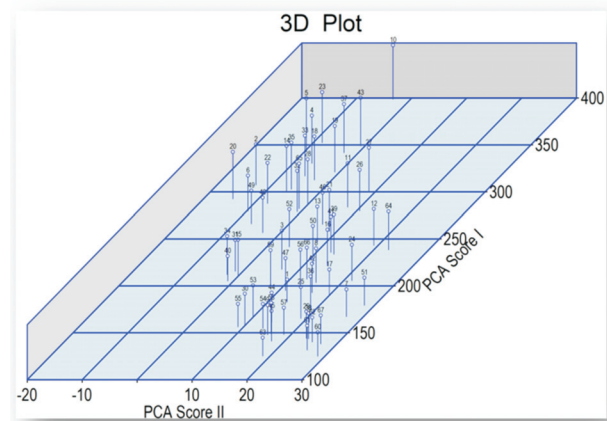

Fig. 2. 3D plot representing the diversity among 76 rice genotypes under reproductive stage salinity

Path Analysis

A correlation study allows to measure the association between two traits. The definite contribution of atraits and its effect through the other characters could be arrived, only by partitioning the genotypic correlation coefficient into both direct and indirect effects by path coefficient analysis. This will be very much helpful in giving due weight age importance to yield traits under selection process. In the current study, path coefficient analysis was conducted for different root, shoot growth parameters, Na^+ concentrations, K^+ concentrations and the results were furnished in Table 3 and Figure 3.

A perusal of the results on path coefficient analysis reveals, a residual effect of 0.351, indicating that variables studied in the current study explained about 64.90 per cent of variability for Na^+/K^+ ratio and the other attributes, contributing for salt toler-

Table 2. Factor loadings for different characters under reproductive stage salinity of first four principal components

S.No.	Character	PC 1	PC 2	PC 3	PC 4
1.	Salinity Score	0.12	0.03	0.71	0.57
2.	DFF	0.31	0.38	0.29	-0.01
3.	Plant height	0.24	-0.44	-0.23	0.26
4.	No. of productive tillers	0.33	0.46	-0.04	0.00
5.	Panicle length	0.25	-0.55	0.03	0.29
6.	No. of filled grains/panicle	0.47	-0.05	-0.16	-0.11
7.	No. of total grains/panicle	0.49	-0.08	-0.05	-0.25
8.	Spikelet fertility	-0.11	0.33	-0.55	0.66
9.	Grain yield/plant	0.43	0.16	-0.16	0.11
	Variability (%)	40.58	17.80	13.65	9.28
	Cumulative Variability (%)	40.58	58.38	72.03	81.31
	Eigen Values	3.65	1.60	1.23	0.84

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ance. High and positive direct effects of shoot Na⁺ concentration were noticed in the current investigation, indicating the effectiveness of direct selection for this trait in improvement of salt tolerance. However, negative direct effects were noticed for shoot K⁺ concentration, along with negative significant correlation with Na⁺/K⁺ ratio, resulting indirect effects as the cause of correlation.
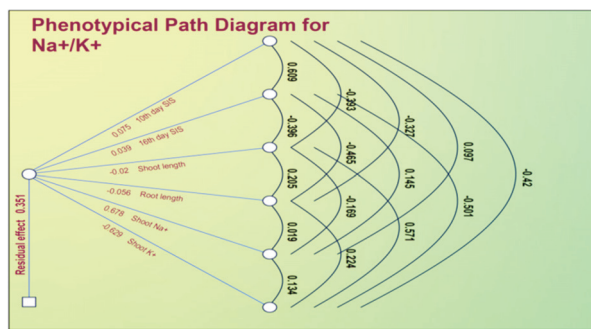

Fig. 3. Path Analysis For Different Traits Seedling Stage Salinity

The path coefficient analysis on yield and yield attributing traits under reproductive stage salinity revealed, the residual effect of 0.261 and 0.295 at both phenotypic and genotypic levels respectively, representing that characters studied in the current investigation explained about 73.90, 70.5 per cent of variability for grain yield per plant. Results on path analysis of yield components and quality characters on grain yield per plant are presented in Table 4 and Figs. 4 and 5. High and positive direct effects of productive tillers per plant and number of filled grains per panicle on grain yield per plant were noticed in the present study. These traits also recorded high positive and significant association with grain yield per plant, indicating the effectiveness of direct selection for these traits in improvement of grain yield

per plant under reproductive stage salinity. However, negative direct effects were noticed for plant height, along with non-significant association with
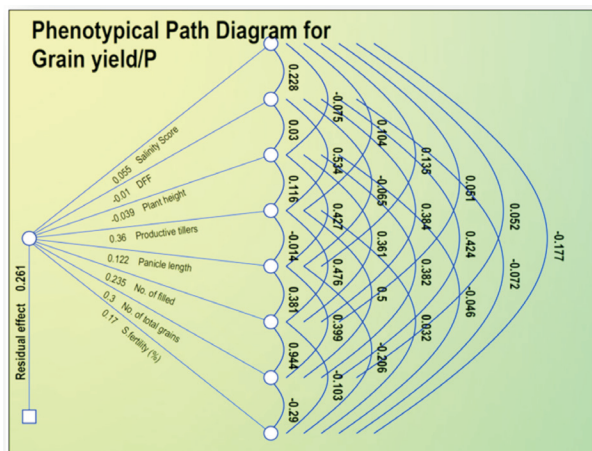

Fig. 4. Phenotypical Path Analysis For Yield And Yield Attributing Traits Under Reproductive Stage Salinity Tolerance
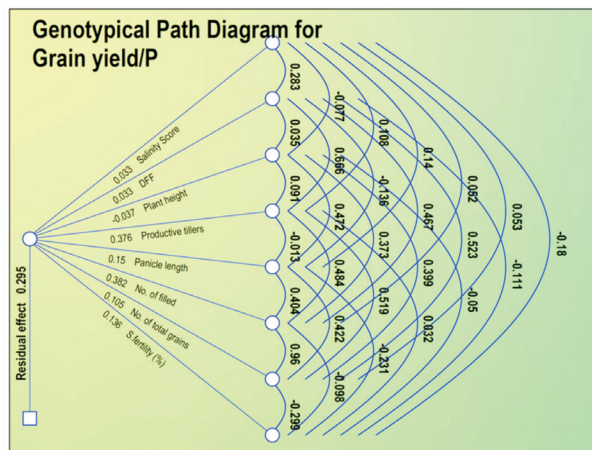

Fig. 5. Genotypical Path Analysis For Yield And Yield Attributing Traits Under Reproductive Stage Salinity Tolerance

Table 3. Path analysis on different traits under seedling stage salinity tolerance

	10th day SIS	16th day SIS	Shoot length (cm)	Root length (cm)	Shoot Na⁺	Shoot K⁺	Na⁺/K⁺
10th day SIS	**0.0748**	0.0456	-0.0294	-0.0245	0.0073	-0.0315	0.4550**
16th day SIS	0.0235	**0.0386**	-0.0153	-0.0179	0.0056	-0.0193	0.5320**
Shoot length	0.0080	0.0080	**-0.0202**	-0.0041	0.0034	-0.0116	-0.5500**
Root length	0.0184	0.0262	-0.0115	**-0.0564**	-0.0011	-0.0126	-0.2310*
Shoot Na⁺	0.0659	0.0986	-0.1147	0.0129	**0.6780**	0.0905	0.6090**
Shoot K⁺	0.2642	0.3150	-0.3588	-0.1409	-0.0839	**-0.6285**	-0.6130**
Na⁺/K⁺	0.4548	0.5320	-0.5500	-0.2309	0.6093	-0.6130	**1.0000**

Residual Effect = 0.351; * and ** Significant at 5 % and 1 % levels respectively; Diagonal bold values indicate direct effects

Table 4. Path analysis on yield and other yield attributing traits under reproductive stage salinity tolerance

		Salinity Score	Days to 50% flowering	Plant height (cm)	Productive tillers	Panicle length (cm)	No. of filled grains/panicle	No. of total grains/panicle	Spikelet fertility (%)	Grain yield/Plant
Salinity Score	P	**0.0546**	0.0125	-0.0041	0.0057	0.0074	0.0028	0.0029	-0.0097	0.1070
	G	**0.0327**	0.0093	-0.0025	0.0035	0.0046	0.0017	0.0017	-0.0059	0.1070
Days to 50% flowering	P	-0.0023	**-0.010**	-0.0003	-0.0053	0.0006	-0.0038	-0.0042	0.0007	0.3910**
	G	0.0094	**0.0330**	0.0012	0.0220	-0.0045	0.0154	0.0173	-0.0037	0.4890**
Plant height (cm)	P	0.0029	-0.0012	**-0.0389**	-0.0045	-0.0166	-0.0140	-0.0149	0.0018	0.2420*
	G	0.0029	-0.0013	**-0.0372**	-0.0034	-0.0176	-0.0139	-0.0149	0.0018	0.2440*
Productive tillers	P	0.0374	0.1922	0.0417	**0.3595**	-0.0051	0.1710	0.1798	0.0114	0.6210**
	G	0.0404	0.2502	0.0343	**0.3757**	-0.0048	0.1819	0.1948	0.0120	0.6400**
Panicle length (cm)	P	0.0165	-0.0079	0.0521	-0.0017	**0.1221**	0.0465	0.0487	-0.0251	0.2830*
	G	0.0210	-0.0204	0.0707	-0.0019	**0.1499**	0.0606	0.0632	-0.0346	0.2950*
No. of filled grains/panicle	P	0.0121	0.0901	0.0846	0.1117	0.0894	**0.2347**	0.2215	-0.0242	0.7030**
	G	0.0199	0.1786	0.1424	0.1850	0.1544	**0.3821**	0.3669	-0.0374	0.7150**
No. of total grains/panicle	P	0.0157	0.1274	0.1148	0.1503	0.1198	0.2836	**0.3005**	-0.0873	0.6850**
	G	0.0055	0.0549	0.0419	0.0544	0.0442	0.1007	**0.1049**	-0.0314	0.6930**
Spikelet fertility (%)	P	-0.0300	-0.0121	-0.0078	0.0054	-0.0349	-0.0175	-0.0493	**0.1696**	0.0370
	G	-0.0245	-0.0151	-0.0067	0.0043	-0.0314	-0.0133	-0.0406	**0.1358**	0.0370
Grain yield/Plant	P	0.1070	0.3910**	0.2420*	0.6210**	0.2830*	0.7030**	0.6850**	0.0370	**1.0000**
	G	0.1070	0.4890**	0.2440*	0.6400**	0.2950*	0.7150**	0.6930**	0.0370	**1.0000**

Residual Effect = 0.261 (P), 0.295 (G); * and ** Significant at 5 % and 1 % levels respectively; Diagonal bold values indicate direct effects

grain yield per plant, indicating indirect effects as the cause of correlation. Similarly, the direct effects of component traits on grain yield were reported earlier for number of grains per panicle by Mohana Krishna *et al.* (2009), for plant height by Reddy *et al.* (1997) and for panicle length by Deepa Sankar *et al.* (2006). Similar results were found for number of grains per panicle by Choudhury and Das (1998), Yogameenakshi *et al.* (2004) and Panwar *et al*. (2007). Thus, direct selection for these attributes will be gratifying for yield enhancement under saline soils.

Individual plants with more number of tillers per plant and number of filled grains per panicle with more panicle weight can be selected from the segregating generations for improvement of yield under saline condition. Commencing the experimental findings it could be accomplished that grain yield per plant exhibited a very strong positive association with panicle length, number of filled grains per panicle, panicle weight at phenotypic and genotypic level which indicates that, these traits were the strongest associates of grain yield per plant, under reproductive stage salinity.

Conclusion

Path analysis revealed that the traits with high direct effects and significant positive association, *i.e.* shoot Na$^+$ concentration during seedling stage and number of productive tillers/plant, number of grains per panicle during reproductive stage must be considered as useful selection criteria for improvement of salt tolerance. Further, PCA revealed characters *viz.*,10th day and 16th day salt injury score, shoot Na$^+$ concentration contributed for most towards the variation among genotypes studied during seedling stage, whereas the traits *viz.*, reproductive stage salt score, days to 50% flowering, panicle length, plant height, number of productive tillers, number of filled grains, number of total grains, grain yield and spikelet fertility during reproductive stage con-

tributed most towards the variation among genotypes studied. Hence, these results will be of greater benefit to the breeder to identify parents and the selection of characters for future hybridization program for salinity tolerance.

Acknowledgement

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