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Short Communication

Multivariate analysis for yield and its component traits in rice (*Oryza sativa* L.) under alkaline soil condition

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Abstract

A study was undertaken to assess the response of rice genotypes grown under alkaline soil condition using various multivariate analytical tools. ANOVA and MANOVA revealed significant differences among 33 genotypes for different traits. Principal component analysis (PCA) grouped the traits into three components, which jointly explained 67 % of the total variation. Largest variation was explained by total biomass, spikelet per panicle and grain yield per panicle. When different alkalinity groups were compared in pairwise fashion using SIMPER analysis, it was found that there is no common trait to differentiate between the groups. Considering all traits together, Vikas and KMR 3 were identified as the most suitable genotypes which can be utilized as donors for tolerance to alkalinity.

Key words: Rice, soil alkalinity, principal component axes, SIMPER analysis, grain yield

Rice (*Oryza sativa* L.) is one of the most important staple food crops for more than half of the world's population. Rice is grown under varied agro-climatic conditions. Several abiotic factors affect the genetic potential of yield. Salinity and alkalinity are most important abiotic factors causing wide-spread problems. Salt-affected soils in arid and semi-arid regions of Asia, Africa, and South America cause considerable yield losses. In Asia alone, 21.5 million ha of land area is thought to be salt affected (of which 12 million ha is due to saline conditions and the remaining 9.5 million ha is due to alkaline/sodic conditions). In India 8.6 million ha is salt-affected area including 3.4 million ha of sodic soils [1].

Rice has been reported to be salt-sensitive at the seedling and reproductive stages [2, 3] leading to a reduction in crop productivity [4]. To increase rice production in problematic soils requires the development of alkalinity tolerant cultivars with higher yields. Rice varieties are known to exhibit wide variation in their tolerance to salinity and alkalinity [5, 6]. Development of salt-tolerant rice varieties through traditional breeding approach can only be realized if the genes for salt tolerance are available in germplasm. To identify suitable germplasm for salt tolerance, multivariate analytical tools *viz*., Principal Component Analysis (PCA), Cluster Analysis, Multivariate Analysis of Variance (MANOVA) and Similarity Percentage (SIMPER) analysis were employed to classify the available genotypes into distinct groups on the basis of their genetic diversity.

The material for the present study consisted of 33 genotypes of rice collected from All India Coordinated Research Project on Rice, University of Agricultural Sciences, Bangalore, India and International Rice Research Institute, Philippines. Field experiment was conducted at Zonal Agricultural Research Station, Vishveshwaraiah Canal Farm (Cauvery command area), Mandya, Karnataka State of India. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications.

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Each genotype was planted in three rows of 3.8 meter length with a spacing of 20 x 15 cm. All cultural practices were followed as per package of practices adapted for irrigated rice. Soil samples from the experimental site were collected and analyzed for parameters such as pH, electrical conductivity, organic carbon, available nitrogen, phosphorus and potassium using standard procedures [7-10]. Out of seventy-five plants, five competitive plants were randomly selected from each genotype to record observation on plant height, days to 50 per cent flowering, productive tillers per plant, panicle length, spikelets per panicle, spikelet fertility, total biomass, thousand grain weight, harvest index and grain yield per plant. Visual determinations based on descriptors, provided in standard evaluation system of rice, IRRI, Philippines for identifying rice genotypes tolerant to alkaline soils, was used for scoring all the 33 rice genotypes. Genotypes were scored for tolerance to alkalinity using 0-9 scale [14]. Plant growth habit was determined by phenotypic appearance based on scores 0 (tolerant) to 9 (susceptible), genotypes with the scores 3 and 7 were moderately tolerant and susceptible genotype, respectively.

Data collected on the traits were subjected to analysis of variance (ANOVA). Variability among the cultivars was further analyzed using pattern analysis which involves the use of both principal component analysis and cluster analysis. Hierarchical clustering of genotypes was performed using the Ward's method of clustering. SIMPER analysis, Cluster analysis and PCA were performed using PAST statistical software [12]. Data from the soil analysis revealed that experimental soils were characterized by a relatively less EC < 4 dS/m (1.2), high pH > 8.2 (9.6) and exchangeable sodium percentage is more than 15 (alkali soils). Analysis of variance revealed significant differences among the genotypes for all the characters studied indicating wide genetic variability among the genotypes. PCA carried out for ten quantitative characters revealed that three principal components (PC) together explained 69% of variation. Breakdown of this cumulative variance revealed contribution of 31.6%, 21.3% and 16.6% for PC 1, PC 2 and PC3, respectively. PCA loadings for component 1 (PC 1) indicated that the total biomass, spikelets per panicle, yield per plant, panicle length and days to 50% flowering had high correlation with PC1 (Table 1); component 2 (PC 2) comprised spikelet fertility and harvest Index and PC 3 consisted plant height, 1000 grain weight and days to 50% flowering. Grouping of yield components into PC 1 was in agreement with previous reports [13, 14]. Discriminating power of traits present in PC 1 (3.17) was high, whereas traits present in PC 3 (1.66) were low as also reported by Hosan *et al.* [15]. PCA scatter diagram depicting genotype by trait (GT) biplot of component 1 and component 2 is given in Fig. 1. Vertex genotypes were KMR 3, Mandya Vijaya, KMP-102, Budda and Dodda batta. These genotypes are either superior or inferior for the traits studied. Total biomass, spikelets per panicle and grains per panicle had more influence on yield as indicated by the length of their vectors on GT-biplot (Fig. 2).

Table 1. Principal component analysis for the first three principal coordinates of rice germplasm

Principal Components	PC 1	PC 2	PC 3
Eigen value	3.17	2.13	1.66
% variance	31.69	21.33	16.60
Cumulative variance	31.69	53.02	69.62
Traits		Loadings	
Plant height (cm)	-0.28	0.11	-0.76
Days to 50% flowering	-0.52	0.06	0.66
Productive tillers per plant	-0.42	0.33	-0.32
Panicle length (cm)	-0.53	-0.42	-0.26
Spikelets per panicle	-0.81	-0.39	0.09
Spikelet fertility (%)	0.00	-0.84	-0.12
Total biomass (g)	-0.93	-0.02	-0.09
Thousand grain weight (g)	0.45	-0.10	-0.64
Harvest index (%)	0.07	0.86	-0.01
Yield per plant (g)	-0.80	0.47	-0.18

Genotype by trait (GT) bi-plot can also indicate inter-relationship between traits. Number of productive tillers, panicle length, total biomass and spikelets per panicle had positive association with yield per plant as indicated by acute angle between them whereas with thousand grain weight had negative association (obtuse angle). Mohamed *et al*. [16] have reported that panicle length and 1000-grain weight had significant positive correlation with grain yield. Bhatti *et al.* [17] have reported positive correlation between 1000-grain weight and grain yield; this indicates that genotypes with bold seed size have short panicle length, reduced number of spikelets and reduced total biomass finally resulting in reduced yield. Genotype by trait (GT) bi-plot can be used to identify superior cultivars for different traits. Yan and Rajcan [18] analysed various

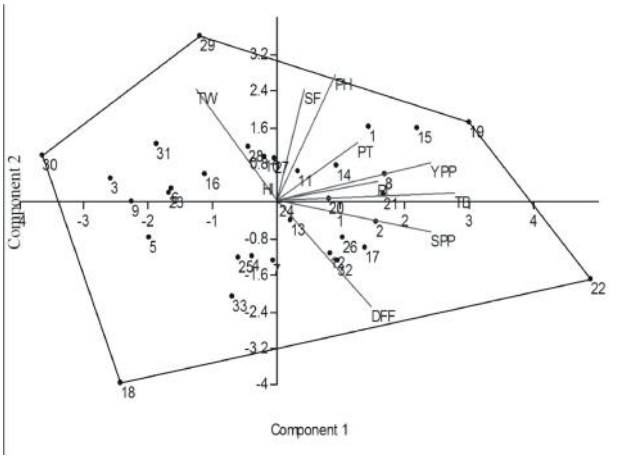

Fig. 1. Patterns of relationships among 33 rice genotypes due to the first two principal co-ordinates. Genotypes 1-33; 1=IR-30864; 2=IR-20; 3=IR-1329; 4=IR-67684B; 5=IR-68902B; 6=IR-70366B; 7=CRMS-32B; 8=KCMS-22B; 9=Sarasa-B; 10=IRYLINE-1; 11=IET-8116; 12=IET-7575; 13=Jaya; 14=KRH-2; 15=Vikas; 16=Tellahamsa; 17=KMP-101; 18=KMP-102; 19=KMR-3; 20=KMR-4; 21=Pragathi; 22=Mandya Vijaya; 23=Mysore mallige; 24= Moroberekan; 25=Prakash; 26= Pusa-205; 27=Rasi; 28=CTH-3; 29=Dodda batta; 30=Budda; 31=Azucena; 32=BR-2655; 33=ES-18; PH=Plant height (cm); DFF=Days to 50% flowering; PT=productive tillers/plant; PL=panicle length; SPP=Spikelets/panicle; SF=Spike fertility; TB=Total biomass; TW=test weight' HI=harvest index; YPP=yield/plant

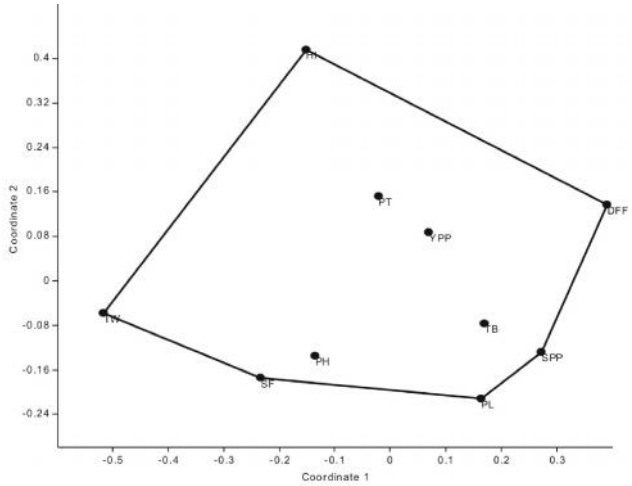

Fig. 2. Discrimination power of different traits studied under alkaline condition

yield components in soybean for six years and reported 52-63% of the total variation of the data among 28 soybean cultivars. Genotype KMR-3 had narrow angle with yield vector (YPP) followed by genotype Pragati indicating the potentiality of these genotypes to give high yield under alkaline conditions.

Genotypes were screened for tolerance to soil alkalinity, which ranged from 0 (normal growth) to 9 (almost all plants dyeing). Six genotypes were tolerant, 12 medium tolerant and seven were classified as susceptible and most susceptible (Table 2). MANOVA was used to test variation in genotypes among four alkalinity groups. Wilk's lambda and Pilai trace test indicated significant overall differences between the groups (Table 3). Traits responsible for distinguishing between groups were determined using similarity percentage (SIMPER) analysis [19]. Spikelet fertility and panicle length contributed more towards differentiating tolerant (T) and moderate tolerant (MT) groups, whereas panicle length and yield per plant were the major contributors in differentiating tolerant genotypes from susceptible (S) and most susceptible (MS) groups, respectively. Plant height contributed more towards differentiating moderate tolerant (MT) from susceptible (S) and most susceptible (MS) group

Table 2. Classification of rice genotypes based on response to soil alkalinity using SES score

Category	Genotypes
Tolerant (T)	Vikas, IR-30864, IR-20, Pragathi, KMR-3, Rasi
Medium tolerant (MT)	IR-1329, Sarasa-B, IR-67684B, IR-70366B, CRMS-32B, Jaya, Tellahamsa, KMP-101, Pusa-205, Doddabatta, Budda, ES-18
Susceptible (S)	KCMS-22B, IRYLINE-1, IET-8116, KMR-4, Mandya vijaya, Mysore mallige, CTH-3
Most susceptible (MS)	KRH-2, IET-7575, KMP-102, Moroberekan, Prakash, Azucena, BR-2655

Table 3. Multivariate ANOVA (MANOVA) for yield and yield components in rice genotypes under alkaline soil condition

MANOVA	Wilk's Lambda	Pilai trace
	0.1241	1.435
df1	30	30
df2	53.51	60
F	1.847	1.835
P	0.025	0.023

Table 4. Similarity Percentage (SIMPER) to identify the traits responsible for differentiating between different alkalinity groups

Traits	T vs MT	T vs S	T vs MS	MT vs S	MT vs MS	S vs MS	Overall
PT	38.97	10.43	-131.00	27.94	37.19	**37.25**	12.59
TB	60.50	18.94	-27.59	-29.96	21.24	17.06	12.14
SF	**102.50**	12.77	-335.40	7.40	6.68	15.95	-12.87
DFF	12.06	12.74	-238.20	-0.97	24.97	15.41	-17.25
TW	32.95	7.33	-40.90	-14.45	40.19	13.94	11.03
SPP	39.14	17.03	-53.83	-5.49	48.58	2.65	14.27
PH	82.03	12.83	-333.00	**36.56**	**62.20**	-5.72	0.00
YPP	39.33	18.22	**7.87**	-40.36	32.93	-12.55	9.06
PL	82.15	**19.97**	-82.95	-3.77	17.10	-13.46	10.77
HI	79.58	15.98	-49.57	19.27	14.15	-24.24	**16.61**

PT=Productive tillers per plant; TB=Total biomass (g); SF=Spikelet fertility (%); DFF=Days to 50% flowering; TW=Test weight (g); SPP= Spikelets per panicle; PH=Plant height (cm); YPP=Yield per plant (g); PL=Panicle length (cm); HI=Harvest index (%); T=Tolerant; MT=Moderate Tolerant; MS=Most Susceptible; S=Susceptible

(Table 4). Cultivars were grouped into clusters using Ward's method of clustering which grouped them into three clusters. Cluster 1 included 11 genotypes which belonged to 'IR' series and wild genotypes most of which were moderately tolerant to salt stress. Genotypes in cluster 2 were mostly cultivars released for commercial cultivation and did not belong to any specific tolerance group (Fig. 3). Comparison of cluster means for all the characters indicated that cluster 2, a group consisting of released cultivars, had high yield, high harvest index and more number of productive tillers. Genotypes in cluster 3 had more number of spikelets per panicle and were mostly susceptible to salinity stress. Cluster 1 flowered earlier than other two, recorded high thousand grain weight and five out of six salinity tolerant genotypes were found in this group (except KMR 3) (Table 2 and Fig. 3). Based on the clustering, it can be suggested that intermating of genotypes belonging to different groups will enhance yield and alkalinity tolerance.

In the present study, various multivariate analytical tools like Principal component analysis (PCA), Cluster analysis, MANOVA and SIMPER analysis were used to analyze different rice genotypes grown under alkaline soil condition. Principal component analysis grouped traits into three components which together explained 67 per cent variation. ANOVA and MANOVA revealed significant differences among genotypes for different traits. Largest variation was explained by traits like total biomass, spikelet per panicle and yield per panicle

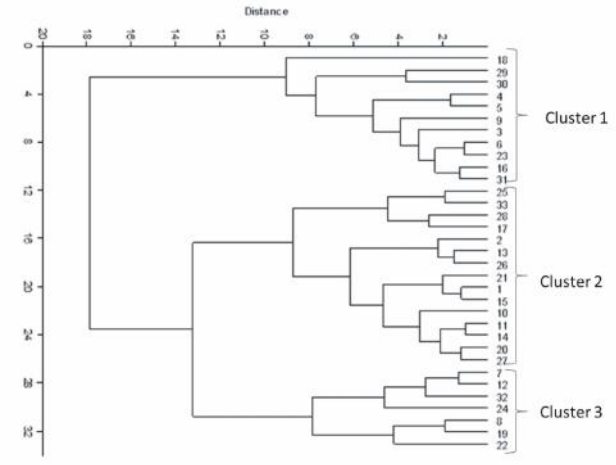

Fig. 3. Dendrogram depicting genetic diversity in 33 rice cultivars grown in alkaline soils. Genotypes 1-33; 1=IR-30864; 2=IR-20; 3=IR-1329; 4=IR-67684B; 5=IR-68902B; 6=IR-70366B; 7=CRMS-32B; 8=KCMS-22B; 9=Sarasa-B; 10=IRYLINE-1; 11=IET-8116; 12=IET-7575; 13=Jaya; 14= KRH-2;15=Vikas;16=Tellahamsa;17=KMP-101; 18=KMP-102; 19=KMR-3; 20=KMR-4; 21=Pragathi; 22=Mandya Vijaya; 23=Mysore mallige; 24= Moroberekan; 25=Prakash; 26= Pusa-205; 27=Rasi; 28=CTH-3; 29=Dodda batta; 30=Budda; 31=Azucena; 32=BR-2655; 33=ES-18

but when different alkalinity groups were compared in pairwise fashion, contribution of traits in identifying groups was different among various pair-wise comparisons. Multivariate analytical tools identified

superior genotypes Vikas and KMR 3 to be tolerant to alkalinity. Such genotypes can be utilized as donors for tolerance to alkalinity in future breeding programme.

References

1. **Sahi C., Singh A., Kumar K., Blumwald E. and Grover A.** 2006. Salt stress response in rice: genetics, molecular biology, and comparative genomics. Funct. Integr. Genomics, **6**: 263-284.
2. **Zeng L., Shannon M. C. and Lesch S. M.** 2001. Timing of salinity stress affects rice growth and yield components. Agric. Water Manage., **48**: 191-206.
3. **Moradi F. and Ismail A. M.** 2007. Responses of photosynthesis, chlorophyll florescence and ROS-scavenging systems to salt stress during seedling and reproductive stages in rice. Ann. Bot., **99**: 1161-1173.
4. **Zeng L. and Shannon M. C.** 2000. Salinity effects on seedling growth and yield components of rice. Crop Sci., **40**: 996-1003.
5. **IRRI.** 2006. *Standard Evaluation System for Rice*. Los Banos, Laguna, Philippines: International Rice Research Institute.
6. **Pathak M. D., Singh U. S., Kumar T., Pandey S., Singh D., Singh A. N. and Mishra R. P.** 2005. Tolerance to soil alkalinity and other constraints in aromatic rices. *In*: Scented Rices of Uttar Pradesh and Uttaranchal (eds). R.K. Singh and U.S. Singh. New Delhi, Kalyani Publishers. pp. 42-56.
7. **Piper C. S.** 1966. Soil and plant analysis. Inter. Sci.Pub., Inc., New York.
8. **Jackson M. L.** 1973. Soil Chemical Analysis, Prentice Hall India Pvt. Ltd., New Delhi.
9. **Subbaiah B.V. and Asija** 1956. A rapid procedure for estimation of available nitrogen in soils. Curr. Sci., **25**: 259-260.
10. **Richards L. A.** 1954. Diagnosis and improvement of saline an alkali soils. (ed.), Hand book No.60, *U.S. Dept. Agric.,* Washington, D.C.
11. **Nanda J.S.** 1997. Standard Evaluation System. *In*: Manual for rice breeding. pp. 80-100.
12. **Hammer Oyvind, Harper D. A. T. and Ryan P. D.** 2009. PAST - PAlaeontological Statistics, ver. 1.89.
13. **Kaya Y., Palta C. and Taner S.** 2002. Additive main effects and multiplicative interactions analysis of yield performances in bread wheat genotypes across environments. Turk. J. Agric. For., **26**: 275-279.
14. **Hosseini S. J., Tahmasebi Z. and Pirdashti H.** 2012. Analysis of tolerance indices in some rice (*Oryza sativa* L.) genotypes at salt stress condition. Int. Res. J. Appl Basic Sci., **3**: 1-10.
15. **Hosan S. M., Sultana N., Iftekharuddaula K. M., Ahmed M. N. U. and Mia S.** 2010. Genetic divergence in landraces of Bangladesh rice (*Oryza sativa* L.). The Agriculturists, **8**: 28-34.
16. **Mohamed K. A., Idris A.E., Mohammed H.I. and Adam K. A.O**. 2012. Ranking rice (*Oryza sativa* L.) genotypes using multi-criteria decision making, correlation and path coefficient analysis. British Biot J., **2**: 211-228.
17. **Bhatti M. K., Ijaz M., Akhter M., Rafig M. and Mushtag Ch**. 2005. Correlation coefficient analysis of yield and yield components in fine rice lines/ varieties. Proc. International seminar on rice crop at Rice Research Institute. Kala Shah Kaku, Pakistan. p. 2-3.
18. **Yan W. and Rajcan J.** 2002. Biplot analysis of test sites and trait relations of soybean in Ontario. Crop Sci., **42**: 11-20.
19. **Clarke K. R.** 1993. Non-parametric multivariate analyses of changes in community structure. Aust. J. Ecol., **18**: 117-143.