MAHALANOBIS, D.² AND GAUCH'S AMMI ANALYSES IN MEDIUM DURATION RICE (*ORYZA SATIVA* L.) GENOTYPES GROWN OVER SIX SEASONS UNDER COASTAL ECO-SYSTEM

[1]Ponsiva, S.T., [1]S. Sabarinathan, [1]S.R. Kirubhakaran, [1]N. Senthilkumar, A. [2]Anandan and [1*]S. Thirugnanakumar

Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University,
Annamalai Nagar – 608 002, Tamilnadu, India.
[2]Divison of crop improvement, National Rice Research Institute, Cuttack, Odisha, India
[*]Corresponding author, Email: thirugnanakumar1962@gmail.com
Mobile: 9788598493

Abstract

D² analyses of 26 genotypes over six seasons and pooled analysis based on 13 agronomical traits confirmed the presence of high genetic diversity among the genotypes studied. The 26 genotypes were grouped into as many as thirteen clusters in S_1; six clusters in S_2 and S_4; five clusters in S_3 and pooled analysis; eight clusters in S_5 and four clusters in S_6. The genotypes hailing from different geographical origin were grouped in a single cluster and *vice versa*. The pattern of clustering demonstrated that genetic diversity was not fully related to geographical diversity. Seed yield per plant contributed maximum towards genetic diversity in all the six seasons. Selection of parents has been suggested based on consistency in genetic divergence. Accordingly, the following genotypes were culled out as divergent from the rest of the genotypes of interest. They are: AD 08-142 and AD 06207. AMMI analysis revealed that the genotypes *viz.,* G1, G5, G9, G11, G20, G22 and G26 among them G1, G9, G20 and G22 had high mean seed yield and hence, recommended for all the seasons.

***Key words*:** Genetic diversity, Stability, Rice and Over seasons.

Introduction

Rice is considered moderately sensitive to salinity. Urbanization has led to the farmers look in for coastal area for rice cultivation. The identified saline tolerant cultivars are not suitable for modern agriculture. Evolving high yielding but saline tolerance rice genotypes are in pipeline. Genetic diversity plays an important role in crop evolution. Quantification of genetic diversity against paramount importance in evolving high yielding superior genotypes. Genotypes with high combining ability are naturally genetically diverse enough. Highly combining parents result in higher heterosis in F1 generation and yield novel segregants in F2 and also in later segregating generations. Genetic diversity has been classically measured with mahalanobis' D² method. Estimates of genetic diversity is influenced by environments, seasons, years and locations. Hence, the breeder ought to measure the genetic divergence over seasons and year. Identification of genotypes with stable grain yield under salinity condition and to evaluate genotype × season interaction requires more sophisticated statistical tool. Additive main effects and multiplicative interaction (AMMI) gains momentum in selection for stable genotypes. It was observed that AMMI uniquely separates G, E and GE.

The objective of this research are: i.) to assess the genetic divergence among 26 medium duration rice genotypes under coastal eco-system, over six seasons, ii.) To cull out the trait(s) consistently contributing to genetic diversity over seasons, iii.) To determine the basis of adaptive response for seed yield in different seasons using the AMMI statistical model, iv.) To find the association between genotype and trait as well as trait and season using biplot technique and v.) To identify genetically divergence but phenotypically stable genotype(s). Therefore the present investigation provide insight into the selection strategies required for identifying elite genotypes for coastal ecosystem.

Materials and Methods

Twenty six medium duration rice genotypes were grown in six seasons *viz.,* S1- Samba (2013), S2- Navarai (2014), S3- Samba (2015), S4- Navarai (2016), S5- Navarai (2017) and S6- Samba (2018) and investigated for genetic worthiness of the genotype for breeding for seed yield, seed quality and their component traits. The crop was planted in Randomized Block Design with three replication's, with a spacing of 20 × 15 cm, in a five rows plot of 4.5 meter length. Recommended agronomic practices and need based plant protection measures were judiciously taken. Observations were recorded on ten randomly selected

plants per replication on the following traits; X1) Days to 50% flowering, X2) Plant height at maturity (cm), X3) Number of tillers per plant, X4) Number of productive tillers per plant, X5) Length of the panicles (cm), X6) Number of seeds per panicle, X7) Length of the seed (mm), X8) Breadth of the seed (mm), X9) Length/Breadth ratio of the seed, X10) 100 Seed weight (g), X11) Total dry matter production (g), X12) Harvest index (%) and X13) Seed yield per plant (g). Both individual and pooled analyses were performed. All the thirteen traits were utilized to measure the genetic divergence. But, phenotypic stability was tested for the traits which contributed maximum towards genetic divergence consistently over analyses.

Genetic diversity was measured with use of Mahalanobis' generalized distance D^2 statistic (Mahalanobis', 1936) and clustering of genotypes was done by Tocher's method (Rao, 1952). To analyze the Genotype × Environment interaction, the AMMI model was used (Gauch, 1988). The AMMI statistical model is a combination of customary analysis of variance (ANOVA) and principal component analysis (PCA). The equation of this model is:

$$Y_{ge} = \mu + \alpha_g + \beta_e + \pounds_n \, \alpha_n \perp_{gn} \_{en} + P_{ge} + K_{ger}$$

with Y_{ge} is the trait of genotype g in environment e; μ is the grand mean, α_g is the genotypes deviation from grand mean and the environment deviation β_e, α_n is the eigen value of PCA axis n; $\perp_{gn}$ and $\_{en}$ are the genotype and environment PCA scores for PCA axis n; P_{ge} is the residual of AMMI model and K_{ger} is the random error. AMMI utilizes standard ANOVA to analyze the main effects and PCA TO quantify the non-additive residual (interaction) left over by the ANOVA model. PCA decomposes the interaction into PCA axes 1 to N and a residual remains if all axes are not used. The interaction between any genotype and environment can be estimated by multiplying the score of the interaction principal component axis (ICPA) of the genotypes by an environment IPCA score. The AMMI analysis was performed for 100 seed weight, total dry matter production, harvest index and seed yield per plant, as the aforementioned traits consistently contributed maximum towards total genetic divergence. All the analyses were done with use of Windostat Version 9.1 from Indostat Services, Hyderabad licensed to National Rice Research Institute, Cuttack. The study was conducted at plant breeding farm, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalai Nagar (Latitude/Longitude- 11° 23' 30" N / 79° 42' 47" E; 3.9 dsm^2; altitude 5 m MSL; EC of soil 4.2 dS m^{-1}; EC of water 1.7 dS m^1)

Results and Discussion

Highly significant variations were found amongst the rice genotypes with regard to all the thirteen traits studied. On the basis of D^2 values for the 676 possible pairs of genotypes, the 26 genotypes were grouped into thirteen clusters in S1; six clusters in S2; five clusters in S3; six clusters in S4; eight clusters in S5; four clusters in S6 and five clusters in pooled analysis (Table 1). The dispersion pattern of genotypes over a large number of clusters with a maximum of four genotypes in cluster I in S1; six genotypes in cluster I and IV in S2; fifteen genotypes in cluster II in S3; fourteen genotypes in cluster III in S4; six genotypes in cluster I in S5; fourteen genotypes in cluster IV in S6 and pooled analysis indicated the presence of high degree of genetic divergence and genetic heterogeneity among the genotypes.

Rice genotypes exhibited a distinct and wide spread clustering pattern and high inter-cluster distances thereby indicating a huge amount of genetic divergence and heterogeneity. The determinants such as gene frequencies, mutations, male sterility, random genetic drift, preferential selection pressures and distantly exchange of germplasm by the people, microclimates and erratic changes in the environmental conditions are likely to be the predominant factors responsible for infusing such a high degree of divergence and heterogeneity. The greater the distance between two clusters, the wider the genetic diversity amongst the genotypes of the two clusters.

Intra-cluster divergence was maximum in cluster XI in S1 (675.11); in cluster II in S2 (487.02); in cluster I in S3 (155.50); in cluster V in S4 (92.68); in cluster VIII in S5 (1057.31); in cluster IV in S6 (716.57); and in cluster V in pooled analysis (578.04) Table 2 to 8. All inter-cluster distance was found more than the intra-cluster distances. The high inter-cluster distance was recorded between clusters III and XII (3670.73) in S1; clusters III and V (1113.36) in S2; clusters I and V (557.42) in S3; clusters II and VI (349.05) in S4; clusters V and VI (1625.97) in S5; clusters I and III (1836.91) in S6 and clusters IV and V (569.29) in pooled analysis. Inter-cluster distances amongst the remaining clusters were recorded low.

High mean values (Table 9 to 15) for seed yield per plant was recorded in cluster XII (60.00 g) in S1; cluster III (28.47 g) in S2; cluster I (19.64 g) in S3; cluster I (22.24 g) in S4; cluster VII (33.90 g) in S5; cluster IV (17.94 g) in S6 and cluster IV (22.43 g) in pooled analysis. Cluster XII in S1 included only one genotype; Cluster III in S2 included four genotypes; Cluster I in S3 included five genotypes; Cluster I in S4 included four genotypes; Cluster VII in S5 included

three genotypes; Cluster IV in S6 and pooled analysis included fourteen genotypes. Lowest mean value for days to 50 percent flowering was recorded in cluster IV in S1 (91.66 days); cluster II in S2 (94.08 days); cluster IV in S4 (101.53 days); cluster VII in S5 (97.16 days); cluster IV in S6 (101.28 days) and cluster II in pooled analysis (101.17 days). Cluster IV in S1 comprised two genotypes; Cluster III in S4 and cluster IV in S6 comprised fourteen genotypes.

The approach suggested by Singh *et al.* (1988) and Thirugnanakumar (1991) was followed in the present study to suggest the parents based on the divergence pattern in varying seasons.

(a) One may select the parent on the basis of divergence exhibited in the richest and most productive season, because it provides opportunity for the fullest expression of genetic potential of a genotype, seed yield was higher in S_1. Using this criterion, divergent genotypes in S_1, may be selected, from different clusters having high inter-cluster distances. Cluster III and XII showed maximum inter-cluster distances in S_1. Cluster III composed of two genotypes and cluster XII composed of only one genotype. Cluster III recorded low mean for days to 50% flowering and high mean for number of seeds per panicle. Cluster XII recorded low mean for plant height and high mean for number of productive tillers per plant as well as seed yield. Hence, by effecting crosses among the genotypes gathered in these clusters, one may expect earliness coupled with higher seed yield.

(b) Selection of parents can also be made on the basis of divergence which is consistent over six seasons. This can be taken as reliable indication of genetic divergence. Utilizing this criterion among the genotypes studied, the genotypes namely, AD 08-142 and AD 06207 were consistently differed from the remaining genotypes. Hence, it may be suggested that one may effect crosses between the genotypes to evolve desirable lines.

(c) One may argue that the divergence expressed in Pooled analysis may be reliable estimate and therefore should be used for selecting the parents. If this criterion is followed, the genotypes that were grouped in the fourth and fifth clusters of Pooled analysis may be crossed to evolve heterotic lines and segregants.

Out of three approaches one may prefer approach 'b', as it suggested the genotypes based on consistency in the divergence. The approach 'a' suffers from seasonal influence and approach 'c' suffers from the under estimation of genetic divergence, because of measures of divergence estimated in different seasons may cancel each other in Pooled analysis.

The highest contribution towards total genetic divergence was rendered by seed yield per plant in S1 (41.84); S2 (42.46); S3 (39.07); S4 (32.92); S5 (34.76); S6 (41.23) and pooled analysis (29.53). It was followed by total dry matter production in S1 (21.84) and S6 (22.46); grain length in S2 (14.46) and S5 (14.76); harvest index in S3 (25.23); S4 (32.61) and pooled analysis (20.92) (Table 16).

Stability Analysis (AMMI)

The interactions of the seasons are highly varied. All the seasons are highly interactive. Navarai 2015, samba 2016 and samba 2018 were unfavorable seasons. Navarai 2013 was favorable season. The genotypes namely G6, G4, G14, G24, G22, G20, G1 and G9 have difference only in main (additive) effects. The two groups of genotypes namely G24, G14, G17, G15 and G25, G3, G22, G20 and G16, G12, G26, G5, G1, G9, and G11 have differences in the interaction effects. While, the genotypes G26, G13, G21 and G7 have difference both in main and interaction effects. The genotypes G12 and G16 were rather similar respect to both main and interaction effects. The genotypes *viz.*, G22, G20, G26, G1, G5, G9 and G11 had low interaction and hence they were stable. Among them, G22, G20, G1 and G9 had high mean values and hence, recommended for all the seasons. The other genotypes had high interaction with seasons and hence, they are suited for specific seasons. The genotypes *viz.*, G26, G5 and G11 had higher mean and positive interaction. Hence, they are suitable for favorable seasons. Conversely the genotypes G16, G12 with high mean and negative interaction are suited for unfavorable seasons (Table 17 and 18; Fig. 1).
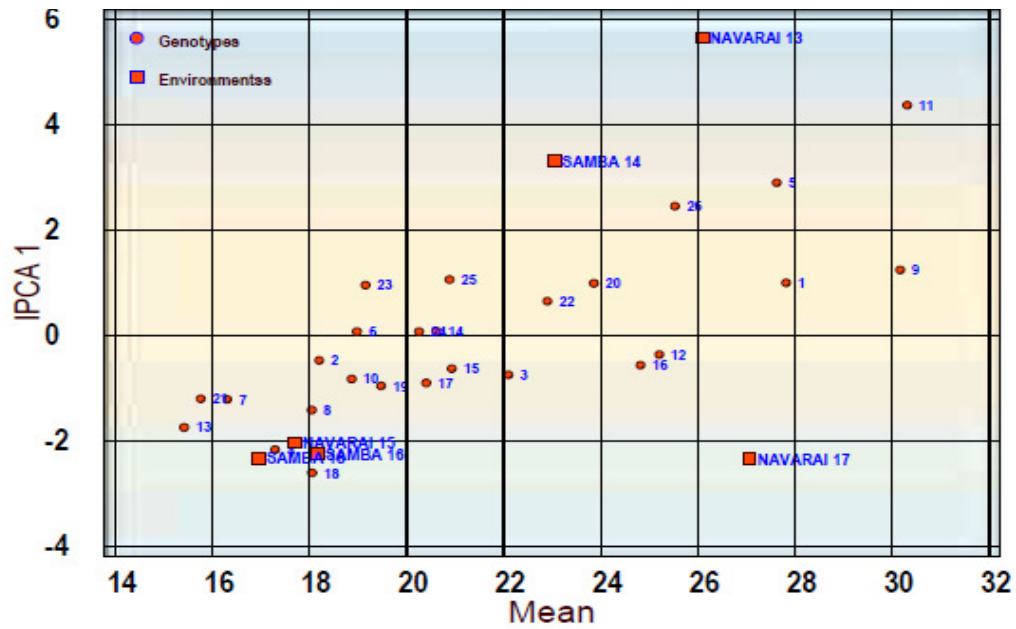
Fig. 1 : Biplot (AMMI) for seed yield

Table 1 : Trends in clustering of genotypes in two seasons.

S. No	Genotype code	Name of the Genotype	Cluster number						
			S1	S2	S3	S4	S5	S6	Pooled
1.	G_1	AD 08-142	I	I	I	I	I	I	I
2.	G_2	AD 06207	I	I	I	I	I	I	I
3.	G_3	AD 07312	I	I	I	II	I	I	IV
4.	G_4	ADT- 46	I	I	II	I	I	I	II
5.	G_5	ADT- 49	XII	I	II	III	I	I	IV
6.	G_6	CB 05- 031	VI	I	II	III	IV	III	IV
7.	G_7	CN 1744- 313- 19- 19- 8-8	IV	II	II	III	IV	I	IV
8.	G_8	CN 1755-9-7-5-MLD-20	III	II	II	III	II	IV	IV
9.	G_9	CO- 43	II	II	V	III	IV	IV	IV
10	G_{10}	CO- 49	VII	III	II	III	V	IV	IV
11.	G_{11}	CO- 50	XIII	III	I	II	I	IV	IV
12.	G_{12}	CR 2643- 1- 4- 3- 1	IV	II	II	III	VII	I	IV
13.	G_{13}	CR 3299- 11- 1- 1-1	X	V	II	II	V	III	IV
14.	G_{14}	HKR 08- 1	XI	V	I	III	II	IV	I
15.	G_{15}	HUR 1204	VII	VI	II	III	IV	II	I
16.	G_{16}	KJT 15- 1- 36- 5- 28- 1	XI	VI	II	III	VII	IV	IV
17.	G_{17}	MTU 1158	V	VI	II	III	III	IV	III
18.	G_{18}	NDR 359	V	VI	II	III	III	IV	III
19.	G_{19}	OR 1895- 2	VIII	III	II	III	IV	III	IV
20.	G_{20}	OR 2163- 14	II	III	II	I	V	II	IV
21.	G_{21}	PAU 3835- 62- 5- 1	X	V	V	VI	VIII	IV	V
22.	G_{22}	RNR 2448	VI	IV	IV	IV	VI	IV	IV
23.	G_{23}	RNR 2836	VIII	IV	III	V	VIII	IV	V
24.	G_{24}	UPR 3330- 9- 12	III	V	III	III	VI	IV	II
25.	G_{25}	WGL 536	IX	VI	V	V	VIII	IV	V
26.	G_{26}	WGL 633	IX	VI	IV	IV	VII	IV	V

Mahalanobis, D.^{2} and Gauch's ammi analyses in medium duration rice (*Oryza sativa* L.) genotypes grown over six seasons under coastal eco-system

Table 2 : Inter and Intra (diagonal) cluster average of D^2 and D (values in parantheses) and the extent of diversity among the clusters- S1

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
I	467.65 (21.62)	607.04 (24.63)	463.88 (21.53)	421.27 (20.52)	447.46 (21.15)	363.07 (19.05)	585.03 (24.18)	58.13 (18.92)	587.10 (24.23)	885.43 (29.75)	423.52 (20.58)	2775.34 (52.68)	1561.28 (39.51)
II		85.30 (9.23)	1094.38 (33.08)	416.71 (20.41)	520.81 (22.82)	337.31 (18.36)	170.48 (13.05)	352.12 (18.76)	178.05 (13.34)	1721.02 (41.48)	752.91 (27.43)	2502.84 (50.02)	427.24 (20.67)
III			120.25 (10.996)	548.51 (23.42)	562.92 (23.72)	437.78 (20.92)	1026.22 (32.03)	516.75 (22.73)	1089.48 (33.00)	351.70 (18.75)	376.44 (19.40)	3670.73 (60.58)	2276.89 (47.71)
IV				143.35 (11.97)	298.38 (17.27)	390.90 (19.77)	398.41 (19.96)	482.50 (21.96)	430.42 (20.74)	1142.79 (33.80)	631.30 (25.12)	2721.12 (52.16)	1432.68 (37.85)
V					143.70 (11.98)	397.81 (19.94)	373.32 (19.32)	471.88 (21.72)	706.46 (26.57)	901.92 (30.03)	592.42 (24.34)	2763.03 (52.56)	1590.86 (39.88)
VI						159.31 (12.62)	344.78 (18.56)	191.94 (13.85)	406.30 (20.15)	776.70 (27.86)	323.87 (17.99)	2715.03 (52.10)	985.34 (31.39)
VII							179.98 (13.41)	373.52 (19.32)	286.94 (16.93)	1585.17 (39.81)	774.76 (27.83)	2803.95 (52.95)	746.49 (27.32)
VIII								230.71 (15.18)	421.50 (20.53)	914.79 (30.24)	364.95 (19.10)	2981.54 (54.60)	948.02 (30.79)
IX									243.65 (15.60)	1854.61 (43.06)	770.71 (27.76)	2524.42 (50.24)	643.40 (25.36)
X										281.95 (16.79)	673.21 (25.94)	3665.78 (60.54)	2945.81 (54.27)
XI											675.11 (25.98)	3044.72 (55.17)	1625.83 (40.32)
XII												0.000 (0.00)	2882.72 (53.69)
XIII													0.00 (0.00)

Table 3 : Inter and Intra (diagonal) cluster average of D^2 and D (values in parantheses) and the extent of diversity among the clusters- S2

Clusters	I	II	III	IV	V	VI
I	331.8 (18.20)	553.90 (23.53)	643.83 (2.37)	351.44 (18.74)	604.36 (24.58)	395.20 (19.88)
II		487.02 (22.06)	895.44 (29.92)	792.93 (28.15)	803.30 (28.34)	563.53 (23.73)
III			448.59 (21.18)	534.48 (23.11)	1113.36 (33.36)	573.00 (23.93)
IV				174.42 (13.20)	548.12 (23.41)	503.60 (22.44)
V					373.85 (19.33)	869.90 (29.49)
VI						478.90 (21.88)

Table 4 : Inter and Intra (diagonal) cluster average of D^2 and D (values in parantheses) and the extent of diversity among the clusters- S3

Clusters	I	II	III	IV	V
I	155.501 (12.470)	177.229 (13.313)	243.835 (15.615)	140.769 (11.865)	557.428 (23.610)
II		116.856 (10.810)	121.257 (11.012)	84.396 (9.187)	290.028 (17.030)
III			48.492 (6.964)	101.982 (10.099)	215.570 (14.682)
IV				113.871 (10.671)	289.173 (17.005)
V					146.736 (12.113)

Table 5 : Inter and Intra (diagonal) cluster average of D^2 and D (values in parantheses) and the extent of diversity among the clusters- S4

Clusters	I	II	III	IV	V	VI
I	87.129 (9.334)	119.609 (10.937)	89.459 (9.458)	55.175 (7.428)	124.558 (11.161)	150.174 (12.255)
II		51.673 (7.188)	93.568 (9.673)	80.730 (8.985)	164.255 (12.816)	349.056 (18.683)
III			86.673 (9.310)	60.989 (7.810)	110.570 (10.515)	211.664 (14.549)
IV				29.586 (5.439)	76.501 (8.747)	158.041 (12.571)
V					92.686 (9.627)	205.806 (14.346)
VI						0.000 (0.000)

Table 6 : Inter and Intra (diagonal) cluster average of D^2 and D (values in parantheses) and the extent of diversity among the clusters- S5

Clusters	I	II	III	IV	V	VI	VII	VIII
I	847.205 (29.107)	531.040 (23.044)	670.175 (25.888)	1376.323 (37.099)	1027.681 (32.057)	889.603 (29.826)	1448.594 (38.060)	854.221 (29.227)
II		171.188 (13.084)	391.019 (19.774)	953.785 (30.883)	480.938 (21.930)	967.866 (31.111)	956.704 (30.931)	699.649 (26.451)
III			181.438 (13.470)	1370.799 (37.024)	887.808 (29.796)	936.592 (30.604)	1267.103 (35.596)	912.449 (30.207)
IV				823.647 (28.699)	1092.854 (33.058)	1197.754 (34.609)	622.420 (24.948)	1086.373 (32.960)
V					884.274 (29.737)	1625.979 (40.323)	1046.261 (32.346)	1110.499 (33.324)
VI						298.162 (17.267)	1304.293 (36.115)	696.035 (26.382)
VII							663.591 (25.760)	1166.912 (34.160)
VIII								1057.315 (32.516)

Table 7 : Inter and Intra (diagonal) cluster average of D^2 and D (values in parantheses) and the extent of diversity among the clusters- S6

Clusters	I	II	III	IV
I	278.821 **(16.698)**	305.947 **(17.491)**	1836.913 **(42.859)**	571.305 **(23.902)**
II		72.812 **(8.533)**	1687.264 **(41.076)**	454.874 **(21.328)**
III			566.160 **(23.794)**	1518.877 **(38.973)**
IV				716.572 **(26.769)**

Mahalanobis, D.² and Gauch's ammi analyses in medium duration rice (*Oryza sativa* L.)
genotypes grown over six seasons under coastal eco-system

Table 8 : Inter and Intra (diagonal) cluster average of D^2 and D (values in parantheses) and the extent of diversity among the clusters- pooled analysis

Clusters	I	II	III	IV	V
I	193.229 **(13.901)**	273.360 **(16.534)**	387.120 **(19.675)**	340.329 **(18.448)**	382.776 **(19.565)**
II		73.887 **(8.596)**	170.311 **(13.050)**	452.090 **(21.262)**	288.141 **(16.975)**
III			84.115 **(9.171)**	504.126 **(22.453)**	488.665 **(22.106)**
IV				446.873 **(21.139)**	569.291 **(23.860)**
V					578.046 **(24.043)**

Table 9 : Cluster means of 26 rice genotypes for various characters in S1

Traits / Clusters	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13
I	102.91	96.99	17.32	11.07	22.99	166.63	7.73	2.36	3.28	1.94	49.09	0.43	22.22
II	105.16	110.09	22.03	13.06	23.10	119.33	7.25	2.55	2.83	1.85	75.68	0.47	36.16
III	94.16	89.55	13.06	6.53	21.42	134.25	8.53	2.26	3.77	2.43	49.33	0.43	19.85
IV	91.66	86.81	17.46	12.06	21.46	108.08	7.00	2.73	2.56	2.01	55.35	0.36	20.80
V	106.33	96.68	15.75	8.40	21.55	70.31	7.36	6.36	2.38	2.53	49.71	0.28	14.81
VI	105.16	95.92	14.90	11.13	24.38	118.64	8.10	2.16	3.74	1.45	63.65	0.41	26.60
VII	110.16	88.44	15.83	11.16	21.79	116.56	6.93	2.45	2.87	1.78	68.90	0.29	20.85
VIII	107.50	104.51	16.33	10.26	23.35	165.89	8.20	2.51	3.28	2.11	65.85	0.35	23.21
IX	102.83	99.11	16.26	11.00	22.91	179.45	6.83	2.20	3.12	1.50	68.28	0.51	35.30
X	101.00	82.60	15.16	11.97	21.89	82.62	9.65	2.52	3.86	1.91	40.75	0.30	12.37
XI	104.16	105.86	16.90	12.13	25.60	153.20	8.45	2.18	3.87	1.81	52.41	0.48	25.63
XII	110.00	99.30	19.53	14.66	21.99	115.50	7.20	2.20	3.27	1.03	27.33	0.45	60.00
XIII	111.00	112.93	20.60	14.40	29.50	134.95	7.83	2.56	3.03	2.13	102.53	0.56	58.17

Table 10 : Cluster means of 26 rice genotypes for various characters in S2

Traits / Clusters	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13
I	105.77	89.96	14.70	10.09	22.17	130.64	7.75	2.35	3.31	1.76	50.00	0.42	21.55
II	94.08	85.00	15.43	10.48	18.95	104.13	7.55	2.60	2.94	2.41	56.03	0.39	22.93
III	110.00	103.71	14.51	10.18	22.81	116.57	7.54	2.63	2.87	2.38	75.79	0.36	28.47
IV	107.00	85.13	13.10	13.33	20.03	149.92	8.23	2.33	3.53	1.45	63.71	0.43	27.25
V	103.08	83.78	13.93	10.32	22.58	97.70	9.35	2.40	3.89	2.25	44.35	0.38	17.32
VI	104.22	93.61	14.23	9.90	21.46	125.08	7.25	2.37	3.06	2.11	59.45	0.38	23.39

Table 11 : Cluster means of 26 rice genotypes for various characters in S3

Traits / Clusters	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13
I	99.62	98.33	18.04	9.02	23.71	173.17	7.90	2.56	3.16	1.49	53.80	39.88	19.64
II	99.30	101.15	18.92	9.12	23.79	163.80	8.49	2.72	3.16	1.75	60.79	31.62	18.00
III	102.10	101.45	19.40	8.13	22.48	150.86	8.48	2.76	3.07	1.77	55.03	23.15	12.59
IV	98.23	100.87	18.50	9.50	23.28	165.83	8.46	2.73	3.12	1.74	62.77	30.36	18.23
V	101.70	98.35	19.16	9.86	23.17	166.53	9.81	2.81	3.47	2.21	45.85	32.77	15.06

Table 12 : Cluster means of 26 rice genotypes for various characters in S4

Traits / Clusters	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13
I	103.03	102.30	19.63	10.06	24.54	181.23	8.70	2.75	3.22	1.79	62.20	38.36	22.24
II	102.75	101.99	16.31	10.15	24.39	163.08	7.67	2.50	3.15	1.46	62.75	35.02	21.67
III	101.53	102.27	18.12	9.50	24.03	166.75	8.44	2.68	3.20	1.75	59.00	33.03	17.73
IV	103.26	101.90	18.66	11.20	23.41	167.06	9.00	2.88	3.12	1.61	60.34	31.63	18.02
V	101.73	106.06	16.96	5.40	23.66	158.63	9.18	2.90	3.07	1.89	48.25	16.47	8.30
VI	104.60	95.33	20.20	11.66	23.76	165.73	10.48	2.60	3.90	2.14	41.28	42.88	17.37

Table 13 : Cluster means of 26 rice genotypes for various characters in S5

Traits / Clusters	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13
I	104.22	92.83	20.25	12.25	23.93	125.77	7.95	1.78	6.25	1.81	52.25	44.56	23.09
II	101.99	103.37	19.71	11.87	23.76	127.84	7.22	1.64	4.39	1.81	57.48	42.35	24.31
III	103.64	89.84	23.73	16.69	21.15	98.99	7.87	2.70	2.90	2.17	74.91	36.64	26.92
IV	102.44	108.02	20.57	11.76	24.19	173.74	7.66	1.14	9.14	1.61	84.14	38.43	32.18
V	104.69	100.52	21.84	13.13	25.10	144.48	6.78	1.40	7.68	1.77	69.53	33.02	22.74
VI	99.89	111.21	21.89	12.43	26.46	133.73	9.22	2.18	4.45	1.66	59.64	52.02	30.99
VII	97.16	105.99	21.47	12.29	25.33	178.82	7.48	1.84	4.09	1.82	91.21	36.92	33.90
VIII	103.27	108.71	20.52	11.75	24.23	153.59	8.35	2.05	4.75	2.05	63.66	38.22	23.24

Table 14 : Cluster means of 26 rice genotypes for various characters in S6

Traits / Clusters	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13
I	101.39	73.58	14.57	10.56	19.40	92.82	8.59	1.82	4.71	1.90	42.35	39.48	16.61
II	104.88	71.62	14.58	10.16	18.11	64.75	8.08	1.88	4.30	2.33	43.06	33.09	14.25
III	102.55	70.86	15.61	11.00	18.67	83.91	7.38	1.78	4.13	1.91	68.24	22.04	14.93
IV	101.28	80.57	14.81	10.55	18.98	87.56	8.41	1.87	4.50	2.15	48.89	37.27	17.94

Table 15 : Cluster means of 26 rice genotypes for various characters in pooled analysis

Traits / Clusters	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13
I	104.87	90.60	17.53	10.66	22.34	140.55	8.16	2.23	4.05	1.86	52.21	27.69	21.89
II	101.17	92.07	17.35	10.04	22.98	128.27	8.63	2.37	3.77	2.09	54.39	21.71	18.77
III	102.70	92.40	19.22	11.79	21.37	105.50	8.06	3.19	3.15	2.23	59.10	23.34	19.23
IV	101.60	97.19	17.32	10.61	22.95	136.69	7.92	2.27	3.99	1.81	61.04	23.58	22.43
V	102.12	93.66	16.25	9.84	21.91	147.84	8.63	2.35	3.82	1.94	56.05	21.58	20.33

Table 16 : Contribution of different traits to genetic divergence in all analysis

S. No	Characters	Mean						
		S1	S2	S3	S4	S5	S6	pooled
1.	Days of 50% flowering	3.3846	7.6923	0.0000	0.3077	0.0000	2.1538	4.0000
2.	Plant height at maturity	0.6154	0.3077	0.6154	0.0000	0.9231	0.6154	0.0000
3.	Number of tillers per plant	0.0000	0.0000	0.0000	0.0000	0.0000	0.3077	0.0000
4.	Number of productive tillers per plant	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
5.	Panicle length	0.0000	0.0000	0.3077	0.3077	0.3077	0.0000	0.0000
6.	Number of grains per panicle	8.0000	1.5385	0.3077	2.7692	8.0000	1.5385	2.7692
7.	Grain length	11.3846	14.4615	6.4615	7.3846	14.7692	0.9231	12.3077
8.	Grain breadth	0.3077	11.0769	0.6154	1.2308	8.6154	0.0000	0.6154
9.	Grain length and breadth ratio	0.3077	0.6154	0.6154	0.6154	3.0769	0.0000	9.2308
10.	Hundred seed weight	5.5385	8.6154	20.0000	17.5385	8.6154	18.7692	15.3846
11.	Total dry matter production	21.8462	8.6154	6.7692	4.3077	12.0000	22.4615	5.2308
12.	Harvest index	6.7692	4.6154	25.2308	32.6154	8.9231	12.0000	20.9231
13.	Grain yield per plant	41.8462	42.4615	39.0769	32.9231	34.7692	41.2308	29.5385

Mahalanobis, D.[2] and Gauch's ammi analyses in medium duration rice (*Oryza sativa* L.)
genotypes grown over six seasons under coastal eco-system

Table 17 : Stability parameters for seed yield in rice

Genotypes	Mean	Index	IPCA I
G1	27.82	6.32	1.00
G2	18.20	-3.30	-0.47
G3	22.10	0.60	-0.75
G4	17.30	-4.20	-2.17
G5	27.62	6.12	2.90
G6	18.98	-2.52	0.07
G7	16.31	-5.19	-1.22
G8	18.05	-3.45	-1.42
G9	30.16	8.66	1.24
G10	18.87	-2.63	-0.83
G11	30.31	8.81	4.37
G12	25.20	3.70	-0.37
G13	15.42	-6.08	-1.75
G14	20.62	-0.89	0.08
G15	20.94	-0.57	-0.63
G16	24.82	3.32	-0.56
G17	20.41	-1.09	-0.90
G18	18.06	-3.44	-2.61
G19	19.48	-2.02	-0.96
G20	23.86	2.36	0.99
G21	15.77	-5.73	-1.20
G22	22.90	1.40	0.65
G23	19.16	-2.34	0.95
G24	20.26	-1.24	0.07
G25	20.89	-0.61	1.06
G26	25.53	4.03	2.45
S_1	26.09	4.59	5.65
S_2	23.04	1.54	3.31
S_3	17.69	-3.81	-2.04
S_4	18.16	-3.34	-2.25
S_5	27.06	5.56	-2.34
S_6	16.96	-4.55	-2.32

Table 18 : AMMI ANOVA for yield

Source of Variations	df	Sum of Squares	Mean Squares	F Ratio
Trials	155	11509.24316	74.25318	1.506
Genotypes	25	2730.00763	109.20031	2.215
Environments	5	2616.86378	523.37276	10.616
G*E Interaction	125	6162.37175	49.29897	38.906
PCA I	29	3961.99747	136.62060	107.820
PCA II	27	1079.49898	39.98144	31.553
PCA III	25	650.53518	26.02141	20.536
PCA IV	23	414.82295	18.03578	14.234
Residual	21	55.51717	2.64367	2.086
Pooled residual	69	2200.37428	22.92057	
Error	312	395.33982	1.26711	
Total	467	11904.58298	25.49161	

References

Gauch, H.G. (1988). Model selection and validation for yield trials with interaction. Biometrics, 44: 705-715.

Mahalanobis, P.C. (1936). On the generalized distance in stastics. Poc. Nat. Sci., India. 2: 49-55.

Rao, C.R. (1952). Advanced stastical method in biometrical research. John Wiley and Sons Inc., New York.

Singh, S.V.; Gupta, P.K. and Sharma, K.P. (1988). Genetic divergence in potato (*Solanum tuberosum* L.) grown in twelve environments. J. Potato Assoc., 15: 45- 52

Thirugnanakumar, S. (1991). Seed genetics in relation to yield in sesame (*Seasmum indicum* L.) *Ph.D. Thesis,* Tamilnadu Agri Univ. Coimbatore.