Plant Archives Vol. 20 No. 1, 2020 pp. 1557-1567 **e-ISSN:2581-6063 (online), ISSN:0972-5210**

GENETIC DIVERGENCE IN RICE (*ORYZA SATIVA* L.) GENOTYPES BASED ON SEED YIELD AND QUALITY PARAMETERS UNDER COASTAL SALINE ECOSYSTEM

S. Sabarinathan[1] , S.T. Ponsiva[2]*, S. Periyar Selvam[3], A. Anandan[4], N. Senthil Kumar[5] and S. Thirugnanakumar[6]

[1,2*,5and6] Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalai Nagar – 608 002 (Tamilnadu), India.
[3]School of Bio Engineering, SRM Institute of Science and Technolgy, Kattankulathur, Chennai- 603 203 (Tamilnadu), India.
[4]Divison of crop improvement, National Rice Research Institute, Cuttack (Odisha), India.

Abstract

Twenty six genotypes were evaluated over two seasons. The ANOVA for individual seasons and Pooled analysis indicated significant differences among all the traits of our interest, over the seasons. D^2 analysis (Tocher method) of the twenty six genotypes based on thirty traits confirmed the presence of high genetic diversity among the genotypes by their resolution into as many as five clusters in S1; eleven clusters in S2, and eleven clusters in the Pooled analysis. Genotypes of different eco-geographic origins were grouped in a single cluster as well as in different clusters and they were also being jumped in different clusters. This is to identify the potential parents for further hybridization and selection based on genetic diversity. The genotypes which were consistently grouped in different clusters in two seasons of interest may be declared as the choice of parents and be utilized to evolve high yielding heterotic lines as well as high yielding transgressive segregants. The traits *viz.*, DPPH antioxidant activity and seed yield per plant contributed consistently maximum towards total genetic divergence. Hence, they may be declared as the choice of traits.

Key words: Rice, Seed quality, Cooking quality, Genetic divergence.

Introduction

Rice is life for the majority of Asian's. Rice is cultivated in all the continents except Antartica. Rice is cultivated in almost all the states. In Tamil Nadu rice is cultivated in all the districts, in an area of 43.99 million hectares with a production of 109.70 million MT (2016-2017, WAP). East coast area of Tamil Nadu comprises the 13 districts. Urbanization has led the farmers to extend the area of rice cultivation to the east coast regions. The present study was conducted to ascertain the genetic divergence among medium duration rice genotypes for 30 traits of economic importance. India has entered the WTO and exports rice to fetch considerable valuable foreign exchange. Hence, seed yield, seed quality, cooking quality, physicochemical traits assume special importance in evolving high quality and saline tolerant rice genotypes.

***Author for correspondence :** E-mail : thirugnanakumar1962@gmail.com

Materials and methods

The seeds of 26 medium duration rice genotypes were obtained from Tamil Nadu Rice Research Institute (TNAU), Aduthurai, Tamil Nadu, India. The studies were conducted at the plant breeding farm, Faculty of Agriculture, Annamalai University, Tamil Nadu, India (MSL 5 m; EC of soil 4.2 dS m^{-1}; EC of water 1.7 dS m^{1}). The seeds were sown in raised beds. The seedlings were transferred to the main field, 28 days after sowing. The seedlings were transplanted in three rows bed of 4.5 m length, with a spacing of 20×15cm, in Randomized Block Design, with three Replications. The experiment was conducted in two season's *viz.*, S_1-Navarai (December- 2016 to April- 2017) and S_2-Samba (June to October - 2017). Recommended agronomic practices and need based plant protection measures were judiciously taken. Observations were recorded on 10 randomly

selected plants, leaving border plants, for 30 seed yield, seed quality, cooking quality, physicochemical traits and seed technological parameters, as listed in Table 1. The mean values were computed and multivariate analyses, as suggested by Mahalanobis' (1936) and Panse and Sukhatme (1978). Group constellation was done by adopting Tocher's method (Rao, 1952). Statistical analysis was performed with windostat version 9.1 from Indostat services, Hyderabad Licensed to National Rice Research Institute Cuttack, India.

Results

Analysis of variance indicated that the 26 genotypes differed among themselves for all the 30 traits in S_1. Whereas, 29 traits were formed similar for S_2 and pooled analysis except density of kernels before cooking in. It amply indicated that further analysis is appropriate (Table 1).

The range was maximum for germination percentage trait in S_1, S_2 and pooled analysis. Desirable genotypes were identified by computing population mean + CD @ 5%. The genotype, which recorded higher than the population mean + CD @ 5% were identified as elite genotypes. Accordingly, 10 genotypes for X1, X3, X9, and X26 were identified as desirable genotypes. Apart from this 11 genotypes for X15, 12 genotypes for X17, 13 genotypes for X22 and 11 genotypes for X24 were culled out as elite genotypes, in S_1. In S_2, 12 genotypes for X1, 10 genotypes for X5, X8 and 11 genotypes for X14, 10 genotypes for X17, X20 and 11 genotypes for X24 were identified as novel genotypes.

Coefficient of variation was higher for X4, X7, X9, X10, X11, X12, X19, X21, X25, X28 and X29 in S_1. In S_2, the CV was higher for X25, X28 and X29. In the pooled analysis, the CV was higher for X4, X12, X19, X21, X22, X25, X28 and X29. Among the 30 traits investigated X28 followed by X29, X12 and X21 were recorded higher CV % in S_1. In S_2, the traits *viz.*, X29, X28, X25 registered higher CV%. In the pooled analysis, the traits *viz.,* X22, X28, X29, X21, X12, X19, X4, and X25.

In S_1, X22 followed by X24, X27 and X30 contributed the maximum towards genetic divergence. In S_2, X24 followed by X30 and X17 contributed the maximum towards genetic divergence. In the pooled analysis, X24 followed by X26, X30 and X27 contributed the maximum towards genetic divergence.

D^2 analysis confirmed the presence of high genetic diversity among the genotypes of interest by their resolution into as many as five clusters in S_1 (Fig. 1) and eleven clusters in S_2 (Fig. 2) and pooled analyses (Fig. 3). The inter-cluster distance was maximum between the clusters IV and V in S_1 (Fig. 4). In S_2 (Fig. 5), the inter-cluster distance was maximum between the clusters III and IX. In a pooled analysis (Fig. 6), the inter-cluster distance was maximum between the clusters VI and IX. The intra -cluster distance was maximum in the cluster IV in S_1. In S_2 and pooled analysis, the intra -cluster distance was maximum in the cluster I.

Discussion

The crosses between genetically diverse parents are likely to produce highly heterotic effects and more variability in segregating generations. Genotypes are often manifested with differential phenotypic response to different seasons. The Mahalanobis' D^2 statistic is used to estimate the genetic divergence among the genotypes.

Considering these points in mind, the results were discussed based on the extent of genetic divergence and variability envisaged in 26 genotypes of rice over two seasons. Thirty important traits relating to seed yield, seed quality, cooking quality, risk efficiency, seed technological parameters and their components were studied. A Mahalanobis' D^2 statistic is a potential tool for estimating genetic diversity as has been emphasized by many workers (Thirugnanakumar, 1991; Sangeeta Banu, 2016; Anbarasu, 2017).

Analysis of Variance

The mean value of 30 traits of the 26 genotypes was transformed into standardized uncorrelated values and D^2 values were computed. The analysis of variance for individual as well as pooled analysis revealed significant differences among the 26 genotypes for all the 30 traits indicating the existence of high genetic variability among the genotypes. Hence, further analysis is appropriate. The results obtained here are in conformity with Sabesan (2005), Rajasekaran (2006), Sangeeta Banu (2016) and Anbarasu (2017). The variation could be used in distinguishing different genotypes.

Mean Performance

In S1, eight genotypes exceeded the population mean seed yield. The genotypes *viz.*, G_1, G_3, G_5, G_9, G_{10}, G_{11}, $G_{16,}$ and G_{20}. Out of which G_3, $G_{5,}$ and G_1 recorded the maximum seed yield per plant (28.70, 26.04 and 23.90 g respectively). In S2, seven genotypes exceeded the grand mean yield per plant. Among the genotypes *viz.*, G_3, G_5, G_8, G_9, G_{10}, G_{16} and G_{20}. Out of which G_3, $G_{5,}$ and G_9 recorded the maximum seed yield per plant (29.57, 27.51 and 25.01 g, respectively). In a pooled analysis nine genotypes were formed higher than the population mean. Among the genotypes *viz.*, G_1, G_3, G_5, G_8, G_9, G_{10}, G_{11},

G_{16} and G_{20}. Out of which G_3, G_5 and G_9 registered higher seed yield per plant (29.14, 26.78 and 24.24g, respectively). Hence, the genotype *viz.*, AD 07312, ADT-49, CO- 43, CO- 49, KJT 15- 1- 36- 5- 28- 1 and OR 2163- 14 stand for merit consideration as they recorded higher seed yield in all the two seasons and in the pooled analysis.

In S1, the consistently high yielding genotype *viz.*, G_3 had the highest mean for three component traits (X4, X10, and X22). The genotype G_5 which consistently registered high mean seed yield per plant also recorded high mean for eleven traits (X1, X2, X3, X6, X8, X9, X14, X16, X18, X20 and X25) of interest. The genotype G_9 which registered high mean for seed yield also possessed high mean for ten component traits (X4, X6, X10, X17, X19, X23, X25, X26, X27 and X29). The Genotype G_{10} which evinced consistent high mean for seed yield also possessed high mean for ten component traits (X1, X4, X10, X13, X15, X17, X19, X20 X22 and X24). The genotype *viz.*, G_{16} which showed a high mean seed yield also had the highest mean for nine component traits (X5, X7, X8, X14, X16, X18, X20, X24 and X25). The genotype G_{20}, which recorded high mean for seed yield also witnessed high mean for four component traits (X1, X8, X15, and X26).

In S2, consistently high yielding genotype *viz.*, G_3 had the highest mean, for one component traits (X10). The genotype G_5 which consistently showed a high mean seed yield per plant also recorded high mean for fourteen traits (X1, X2, X5, X7, X8, X11, X14, X15, X20, X23, X24, X27, X28 and X29) of interest. The genotype G_9 which registered high mean for seed yield also possessed high mean, for eight component traits (X1, X11, X13, X17, X26, X27, X28 and X29). The Genotype G_{10} which evinced consistent high mean for seed yield also possessed high mean for seven component traits (X1, X5, X7, X8, X13, X17 and X24). The genotype *viz.*, G_{16} which showed a high mean seed yield also had higher mean, for eight component traits (X1, X5, X13, X17, X21, X24, X28 and X29). The genotype G_{20}, which recorded high mean for seed yield also witnessed high mean for nine component traits (X1, X5, X7, X8, X12, X13, X17, X21 and X23).

In the pooled analysis, the genotype G_3 which evinced high seed yield was endowed with high mean for the density of the seed, length/ breadth ratio of the kernel before cooking. The genotype G_5 which consistently showed a high mean seed yield per plant recorded high mean for eighteen traits (X1, X2, X3, X6, X7, X8, X9, X11, X14, X16, X18, X20, X23, X24, X25, X27, X28 and X29) of interest. The genotype G_9 which registered high mean for seed yield also possessed high mean for eleven component traits (X1, X4, X6, X10, X13, X17, X19, X23, X26, X27 and X29). The Genotype G_{10} which evinced high mean for seed yield also possessed high mean for seven component traits (X1, X5, X7, X8, X13, X17 and X24). The genotype G_{16} which showed a high mean seed yield also had the highest mean for eleven component traits (X1, X5, X7, X13, X14, X16, X17, X20, X24, X25 and X29). The genotype G_{20}, which recorded high mean, for seed yield also witnessed high mean, for eight component traits (X1, X5, X7, X8, X15, X17, X23 and X26).

A critical perusal of the *per se* performance of the high seed yielding genotypes in S1 revealed the importance of X1, X4, X8, X10, X18, X20 and X25 in the improvement of seed yield, seed quality, cooking quality, risk efficiency and seed technological parameters. In S2, X1 followed by X5, X7, X8, X13, X17, X28 and X29 were found to be important. In Pooled analysis, X1, X5, X6, X7, X10, X13, X17, X23, X24 and X29 were found to be important. All the analyses have clearly indicated the importance of 100 seed weight in determining seed yield, seed quality, cooking quality, risk efficiency and their seed technological parameters. The identified genotypes *viz.*, G_3, G_5, G_9, G_{10}, $G_{16,}$ and G_{20} were analyzed for their seed yield, seed quality, cooking quality and risk efficiency. Accordingly, in S1, the high yielding genotypes had the highest mean for X4, X8, X10, X18, X20 and X25 apart from X1 where as in S2, the high yielding genotypes showed high *per se* performance for X5, X7, X8, X13, X17, X28 and X29 apart from X1. In Pooled analysis, the high yielding genotypes also showed higher mean for X5, X6, X7, X10, X13, X17, X23 and X24 apart from X1.

In S1, Length/ breadth ratio of the seed was high with the G_9, G_{10} and G_2 (long slender seeds); Govindasami (1985). In S2, it was higher with G_{24}, G_{23} and G_2 (long slender seeds). In Pooled analysis, it was high with G_{10}, G_9 and G_2 (long slender seeds). The Length/ Breadth ratio of the kernel before cooking was high with G_3, $G_{10,}$ and G_9 in S1. It was high with G_2, G_{23} and G_{21} in S2 and it was high with G_3, $G_{10,}$ and G_9 in Pooled analysis. The Length/ Breadth ratio of the kernel after cooking was high with G_1, G_{24} and G_{25} in S1. In S2, it was high with G_1, G_2 and G_{25}. In Pooled analysis, it was high with G_1, G_2 and G_{15}. The genotype G_1 evinced high Length/ Breadth ratio of the kernel after cooking in all the analyses. In S1, Length/ Breadth ratio of the kernel after cooking of G_1 was 4.44 mm. It was 4.05 mm before cooking. The difference between the two parameters was 0.39 mm. So, the genotype G_1 may be utilized in crossbreeding programs to evolve long slender seeds.

The water uptake ratio was high with the G_{10}, $G_{14,}$ and G_1 in S1. In S2, it was high with the G_{15}, G_{13} and G_8. In Pooled analysis, it was high with G_{10}, G_{14} and G_{26}. The kernel elongation ratio was higher with the G_{10}, $G_{4,}$ and G_5 in S1; G_8, G_6 and G_4 with S2 and G_8, G_4 and G_5 with Pooled analysis. The volume expansion ratio was higher with G_7, G_{18} and G_{15} in S1; G_{15}, G_{11} and G_{16} in S2 and G_{15}, G_7 and G_{13} in Pooled analysis.

The total phenolic content was higher with the G_{15}, G_{14} and G_{19} in S1. It was higher with G_{14}, G_{24} and G_3 in S2. In Pooled analysis, it was higher with G_{14}, G_{15} and G_3. The genotype G_{14} consistently showed higher total phenolic content in all the analysis. The flavonoid content was higher with G_{19}, G_2 and G_{24} in S1. In S2, it was higher with G_{20}, G_{11} and G_{23}. In Pooled analysis, it was higher with G_{11}, G_{20}, G_{19} and G_{24}. The DPPH Antioxidant activity was higher with G_{18}, G_{10} and G_{22} in S1. It was high with G_{20}, G_{11} and G_{13} in S2. In Pooled analysis, it was high with G_{18}, G_{10} and G_1. The genotype G_{18} consistently showed higher mean for DPPH Antioxidant activity. It may be a risk efficient genotype.

The vigor index was high with G_{18}, G_9, G_{26} and G_5 in S1. It was high with G_{26}, G_5 and G_{18}, in S2. In Pooled analysis, it was high with G_{26}, G_{18} and G_5. The genotypes namely ADT- 49, NDR 359 and WGL 633 were adjudged as efficient genotypes with regard to seed technological parameters (Sabarinathan, 2018).

Genetic Divergence

D^2 analysis of 26 genotypes confirmed the presence of high genetic diversity among the genotypes by their resolution into five clusters in S1; eleven clusters in S2 and eleven clusters in Pooled analysis. Genotypes of different eco-geographic region were grouped in different clusters. Similarly, genotypes of same geographic origin were grouped in different clusters.

The genotypes originating from Coimbatore and Aduthurai origin were found mostly scattered in different clusters in the different seasons and pooled analyses. This indicated that the presence of a wide range of genetic diversity among the genotype of

Table 1: Analysis of variance for seed yield, seed quality, cooking quality, physicochemical traits and seed technological parameters in 26 genotypes of rice

Trait	Traits	Mean squares								
No.		Replicationsdf=2			Genotypesdf=25			Errordf=50		
		S1	S2	Pooled analysis	S1	S2	Pooled analysis	S1	S2	Pooled analysis
X1	100 Seed weight (g)	0.000188	0.006621	0.001465	0.238710**	0.375505**	0.281481**	0.002847	0.006318	0.002260
X2	Length of the seed (mm)	0.009696	0.026017	0.000994	2.982621**	3.361543**	2.324793**	0.007197	0.117241	0.031008
X3	Breadth of the seed (mm)	0.034713	0.024640	0.025073	1.695557**	0.047772*	0.434531**	0.020822	0.014194	0.009252
X4	Length / Breadth ratio of the seed	1.386604	0.110573	0.572117	50.475359**	0.676680**	12.693059**	1.659209	0.102421	0.452911
X5	100 Seed volume (cc)	0.027436	0.010769	0.005417	0.125087**	0.430651**	0.143104**	0.009503	0.009036	0.004350
X6	Density of the seed (g/cc)	0.0165075	0.000047	0.006867	0.196192**	0.020009*	0.043195**	0.007638	0.005930	0.002653
X7	100 kernel weight before cooking (g)	0.050221	0.002155	0.016271	0.146434**	0.191995**	0.117375**	0.017850	0.012742	0.007596
X8	Length of the kernel before cooking (mm)	0.018932	0.013209	0.014097	1.543993**	1.666059**	1.264670**	0.046940	0.013989	0.012821
X9	Breadth of the kernel before cooking (mm)	0.042409	0.001258	0.009932	0.585129**	0.039870**	0.168871**	0.014660	0.004939	0.005767
X10	Length / Breadth ratio of the kernel before cooking	1.722292	0.011009	0.426817	73.513647**	0.476998**	19.077441**	0.620934	0.035952	0.174103
X11	100 Kernel volume before cooking (cc)	0.0466665	0.003462	0.013878	0.086195**	0.135179**	0.071615**	0.024533	0.007195	0.010512
X12.	Density of the kernel before cooking (g/cc)	0.069327	0.011450	0.005842	0.268403*	0.026784	0.078128	0.090094	0.011849	0.030253
X13.	100 Kernel weight after cooking (g)	0.042655	0.002294	0.012909	1.122709**	1.720913**	0.893033**	0.026775	0.022042	0.013724
X14.	Length of the kernel after cooking (mm)	0.007447	0.004024	0.000363	2.343753**	3.085014**	1.868517**	0.031607	0.014454	0.011109
X15.	Breadth of the kernel after cooking (mm)	0.012277	0.005104	0.001717	0.252055**	0.263903**	0.115324**	0.004610	0.024172	0.006795
X16.	Length / Breadth ratio of the kernel after cooking	0.025973	0.009924	0.000755	0.776565**	0.509233**	0.413535**	0.012300	0.019647	0.007620
X17.	100 Kernel volume after cooking (cc)	0.000513	0.0077306	0.019840	1.929379**	1.980785**	1.303862**	0.015179	0.007308	0.006373
X18.	Density of the kernel after cooking (g/cc)	0.002532	0.0050425	0.004117	0.213327**	0.094468**	0.085909**	0.005875	0.002610	0.002122

the present study. These genotypes could well be exploited in heterosis breeding as well as in recombination breeding.

Crosses among the divergent parents are likely to yield desirable combinants. Therefore, a crossing program should be initiated between the genotypes belonging to different clusters. In this context, two important points to be considered are (i) choice of the particular cluster from which genotypes are to be used as parent in crossing programs and (ii) selection of a particular genotype from selected groups.

The greater the distance between two clusters, the wider the genetic diversity among the parents to be included in hybridization program. Parents combining high yield potential with wider genetic diversity are likely to yield superior segregants within a short period.

The tendency of genotypes from diverse geographical regions to group together in one cluster or scattered distribution of genotypes of the same origin in different clusters has been observed in the present study. The studies of several workers confirmed this tendency, that the geographical diversity could not be directly related in any of the crops [Allam *et al.,* (2015); Bhati *et al.,* (2015); Kumari Priyanka *et al.,* (2015); Mohan *et al.,* (2015); Sarwar *et al.,* (2015); Shobana *et al.,* (2015); Srinivas *et al.,* (2015); Vijay Kumar (2015); Chamundeswari (2016); Chandramohan *et al.,* (2016); Lakshmi and Surendar (2016); Mamta Kumari *et al.,* (2016); Nirosha *et al.,* (2016); Thippeswamy *et al.,* (2016); Sangeeta Banu (2016) and Anbarasu, (2017)].

Genetic drift and selection in different environment could cause greater diversity than the geographical distance (Murthy, 1965). However, geographical isolation could be important in the alteration of the breeding structure as pointed out by Wallace (1963).

The intra-cluster distance was maximum in cluster IV in S1. It included three genotypes (G_5, G_6 and G_1). Intra-cluster distance was maximum in cluster I in S2. It included sixteen genotypes (G_{17}, G_{22}, G_6, G_{16}, G_{26}, G_{18}, G_{10}, G_{25}, G_{21}, G_{15}, G_9, G_{24}, G_{12}, G_7, G_{14} and G_{13}). Intra-cluster distance was maximum in cluster I in Pooled analysis. It included fifteen genotypes (G_{16}, G_{17}, G_{22}, G_6, G_{26}, G_{24}, G_{25}, G_{21}, G_8, G_7, G_{13}, G_{12}, G_{14}, G_{15} and G_{20}). This may indicate that these genotypes were dissimilar. The limited gene exchange, the type of selection for diverse traits could be responsible for such intra-cluster divergence. By effecting crosses among these genotypes one may likely to get iso-responsive genotypes.

Cluster III and V (monotypic) in S1, Cluster II, III, IV, V, VI, VII, VIII, IX, X and XI (monotypic) in S2 and Cluster II, III, IV, VI, VII, VIII, IX, X and XI (monotypic)

Table 2: Mean, range and CV for 30 traits of interest.

Trait	Population mean			Range			SE			CD 5%			Number of desirable genotypes		CV (%)			Contribution towards divergence		
No.	S_1	S_2	P	S_1	S_2	P	S_1	S_2	P	S_1	S_2	P	S_1	S_2	S_1	S_2	P	S_1	S_2	P
X1	1.56	2.07	1.82	0.96–2.18	1.40–2.72	1.19–2.41	0.03	0.04	0.02	0.08	0.13	0.07	10	12	3.39	3.82	2.60	0	0	0
X2	7.78	8.32	8.05	5.39-9.78	6.59-10.13	6.63-9.66	0.04	0.19	0.10	0.13	0.56	0.28	8	8	1.08	4.11	2.18	308	0	0
X3	1.74	1.85	1.80	0.37-2.90	1.57-2.00	1.09-2.43	0.08	0.06	0.05	0.23	0.19	0.15	10	0	8.26	6.42	5.33	0	0	0
X4	6.01	4.50	5.25	2.56-18.39	3.55-5.47	3.50-11.21	0.74	0.18	0.38	2.11	0.52	1.10	5	4	21.41	7.11	12.79	0	0	0
X5	1.41	1.91	1.66	1.07-1.83	1.20-2.57	1.20-2.18	0.05	0.05	0.03	0.15	0.15	0.10	6	10	6.89	4.97	3.96	0	0	0
X6	1.13	1.09	1.11	0.80-1.85	0.96-1.27	0..95-1.51	0.05	0.04	0.02	0.14	0.12	0.08	7	1	7.70	7.00	4.61	0	0	0
X7	0.84	1.54	1.20	0.50-1.14	1.06-2.04	0.79-1.52	0.07	0.06	0.05	0.21	0.18	0.14	3	6	15.78	7.28	7.26	0	0	0
X8	5.80	6.12	5.96	4.61-7.62	4.93-7.83	5.14-7.73	0.12	0.06	0.06	0.35	0.19	0.18	9	10	3.73	1.93	1.89	0	246	215
X9	0.99	1.59	1.30	0.25-1.68	1.38-1.84	0.83-1.72	0.06	0.04	0.04	0.19	0.11	0.12	10	3	12.13	4.39	5.83	0	0	0
X10	7.71	3.84	5.77	3.30-20.55	3.12-4.76	3.21-12.08	0.45	0.10	0.24	1.29	0.31	0.68	6	4	10.21	4.93	7.22	0	0	154
X11	0.94	1.26	1.10	0.70-1.30	0.93-1.73	0.82-1.50	0.09	0.04	0.05	0.25	0.13	0.16	2	4	16.50	6.68	9.24	0	0	0
X12	0.94	1.22	1.08	0.43-1.64	1.08-1.42	0.80-1.42	0.17	0.06	0.10	0.49	0.17	0.28	1	1	31.87	8.86	16.03	0	0	0
X13	4.28	4.00	4.14	3.16-5.99	2.63-5.65	2.99-5.36	0.09	0.08	0.06	0.26	0.24	0.19	7	9	3.81	3.70	2.82	0	215	338

in Pooled analysis recorded the minimum intra-cluster distance value.

In S1, inter-cluster distance was maximum between the clusters IV and V. Cluster IV had three genotypes and cluster V had only one genotype. Cluster IV showed higher mean for 100 seed weight, Length of the seed, Density of the kernel after cooking and DPPH antioxidant activity. Cluster V had a desirable mean for 100 Seed volume, 100 kernel weight before cooking, Length of the kernel before cooking, Breadth of the kernel before cooking, Density of the kernel before cooking, 100 Kernel weight after cooking, Length of the kernel after cooking, Length / Breadth ratio of the kernel after cooking, 100 Kernel volume after cooking, Volume expansion ratio and Total phenolic content. The genotypes originating from these clusters may be recombined to evolve high yielding lines.

In S2, inter-cluster distance was maximum between the clusters III and IX. Cluster III comprised of only one genotype and cluster IX comprised of only one genotype. Cluster III had the highest mean for Density of the seed and Volume expansion ratio. Cluster IX had the highest mean for Breadth of the kernel before cooking, Length / Breadth ratio of the kernel after cooking and DPPH antioxidant activity. The genotypes originating from these clusters may be recombined to evolve high yielding genotypes.

In Pooled analysis, inter-cluster distance was maximum between the clusters VI and IX. Cluster VI recorded high mean for Density of the seed, Length of the kernel after cooking and Density of the kernel after cooking. Cluster IX recorded highest mean for 100 Seed weight, 100 Kernel volume before cooking, 100 Kernel weight after cooking, Breadth of the kernel after cooking and Water uptake ratio. The genotypes of these clusters may be crossed to develop desirable genotypes.

As pointed out by Sokal (1965), the choice of trait is important in multivariate analysis and the choice made in the present study appears to be appropriate. Cyclic breeding and crossing may be helpful in bringing new genes into a population of rice and thus expanding the

Table 3: Trends in clustering of genotypes in two seasons.

Geno -type	Name of the Genotype	Origin	Cluster number	
code			S1	S2
G1	AD 08-142	Tamilnadu Rice Research Institute, Aduthurai	IV	IX
G2	AD 06207	Tamilnadu Rice Research Institute, Aduthurai	I	VIII
G3	AD 07312	Tamilnadu Rice Research Institute, Aduthurai	II	X
G4	ADT- 46	Tamilnadu Rice Research Institute, Aduthurai	I	VII
G5	ADT- 49	Tamilnadu Rice Research Institute, Aduthurai	IV	XI
G6	CB 05- 031	Paddy breeding station, Coimbatore	IV	I
G7	CN 1744- 313- 19- 19- 8-8	Tamilnadu Rice Research Institute, Aduthurai	I	I
G8	CN 1755-9-7-5-MLD-20	Tamilnadu Rice Research Institute, Aduthurai	I	IV
G9	CO- 43	Paddy breeding station, Coimbatore	III	I
G10	CO- 49	Paddy breeding station, Coimbatore	II	I
G11	CO- 50	Paddy breeding station, Coimbatore	I	III
G12	CR 2643- 1- 4- 3- 1	Central Rice Research Institute, Orissa	I	I
G13	CR 3299- 11- 1- 1-1	Central Rice Research Institute, Orissa	I	I
G14	HKR 08- 1	Rice Research Station, Kaul	II	I
G15	HUR 1204	Banaras Hindu University , Varanasi	V	I
G16	KJT 15- 1- 36- 5- 28- 1	Regional Agriculture Research Station, Karjat	I	I
G17	MTU 1158	Agricultural University, Marteur	I	I
G18	NDR 359	Narendra Deva University of Agriculture and	I	I
		Technology, Faizabad		
G19	OR 1895- 2	Central Rice Research Institute, Orissa	II	II
G20	OR 2163- 14	Central Rice Research Institute, Orissa	I	VI
G21	PAU 3835- 62- 5- 1	Punjab Agriculture University, Ludhiana	I	I
G22	RNR 2448	Acharya N.G. Ranga Agricultural university, Rajendra Nagar	I	I
G23	RNR 2836	Acharya N.G. Ranga Agricultural university, Rajendra Nagar	I	V
G24	UPR 3330- 9- 12	GB Pant university of agriculture and technology, Panthanagar	I	I
G25	WGL 536	Regional agricultural research station, Warangal	I	I
G26	WGL 633	Regional agricultural research station, Warangal	I	I

range of adaptation. As brought out by Mather (1943), polygenic variability, which is necessary for prospective, adaptive and evolutionary change need doesn't exist as a true phenotypic variation which effective fitness. Therefore, phenotypic uniformity to genetic diversity within population appears to be very useful in rice. In fact, this is possible with a proper use of the suggested parents in the formation of gene complexes to replace the existing varieties.

It can be concluded that there is no relationship between genetic and geographical diversity in the material under investigation. Inter and intra-cluster distances were also not related. The grouping pattern was not consistent across seasons, indicating genotype × season interaction affect genetic diversity.

It is highly desirable that the extent of genetic diversity between the populations reflected in any analysis comparatively stable over the seasons and the environment to be of utility of plant breeders. The differential grouping of different genotypes of varying

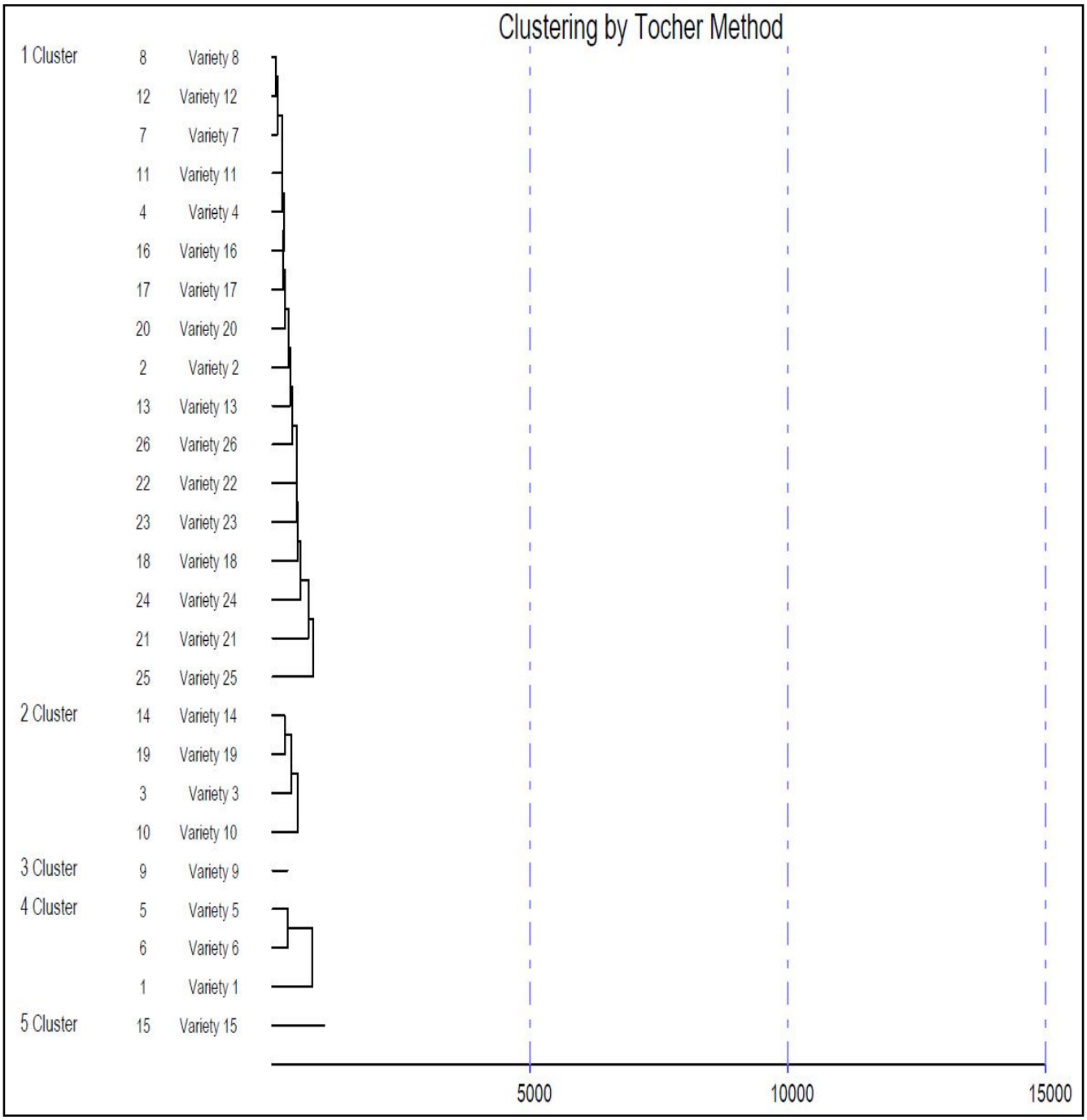

Fig. 1: Composition of D^2 clusters for 26 rice genotypes in S1.

origin in different season necessitate that a breeder should study the genetic divergence over varying seasons as well as environments.

The approach suggested by Thirugnanakumar (1991) is followed in the present study to suggest the parents based on the divergence pattern in varying seasons.

a. One may select the parents on the basis of divergence exhibited in the richest and most productive environment because it provides opportunity for the fullest expression of genetic potential of a genotype. Seed yield was higher in S2. Using this criterion divergent genotype in S2 may be selected from different clusters having high inter-cluster distances. Accordingly, clusters *viz.*, III and IX exhibited high inter-cluster distance. Cluster III composed of only one genotype and cluster IX composed of only one genotype. Cluster III recorded high mean for Density of the seed and volume expansion ratio. Cluster IX registered maximum mean for Breadth of the kernel before cooking, Length / Breadth ratio of the kernel after cooking and DPPH antioxidant activity. Hence, by effecting crosses among the genotypes gathered in these clusters, one may expect desirable genotypes.

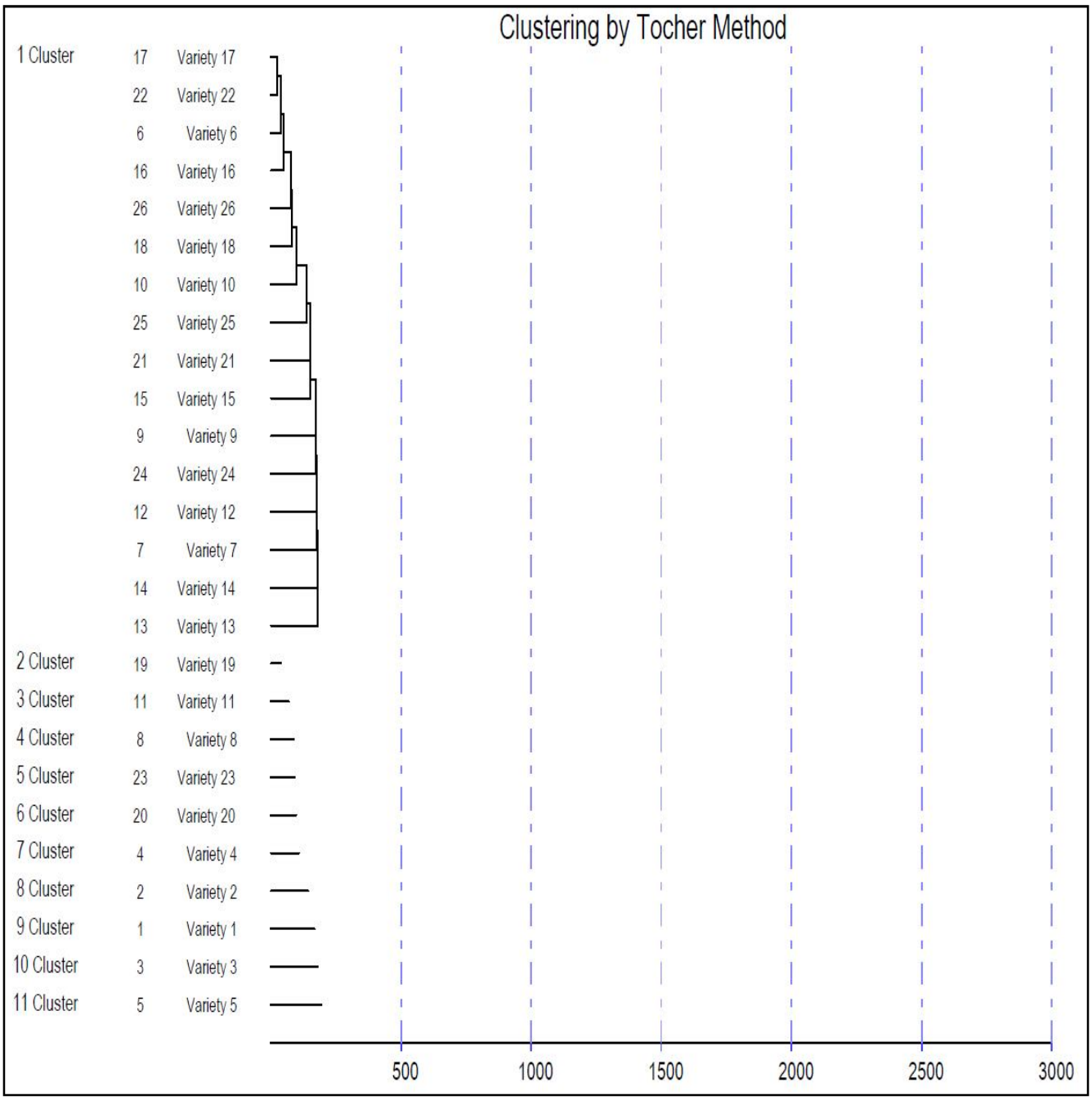

Fig. 2: Composition of D^2 clusters for 26 rice genotypes in S2.

b. Selection of parents can also be made on the basis of divergence which is consistent over two seasons. This can be taken as reliable indicators of genetic divergence. Utilizing this criterion among the genotypes studied, the genotypes namely, CN 1744- 313- 19- 19- 8-8, CR 2643- 1- 4- 3- 1, CR 3299- 11- 1- 1-1, KJT 15- 1- 36- 5- 28- 1, MTU 1158, NDR 359, OR 1895- 2, PAU 3835- 62- 5- 1, RNR 2448, UPR 3330- 9- 12, WGL 536 and WGL 633 were gathered in the same cluster in all the two seasons (Table 3). Hence, it may be suggested that one may effect crosses between these 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 eleven clusters of Pooled analysis may be crossed to evolve

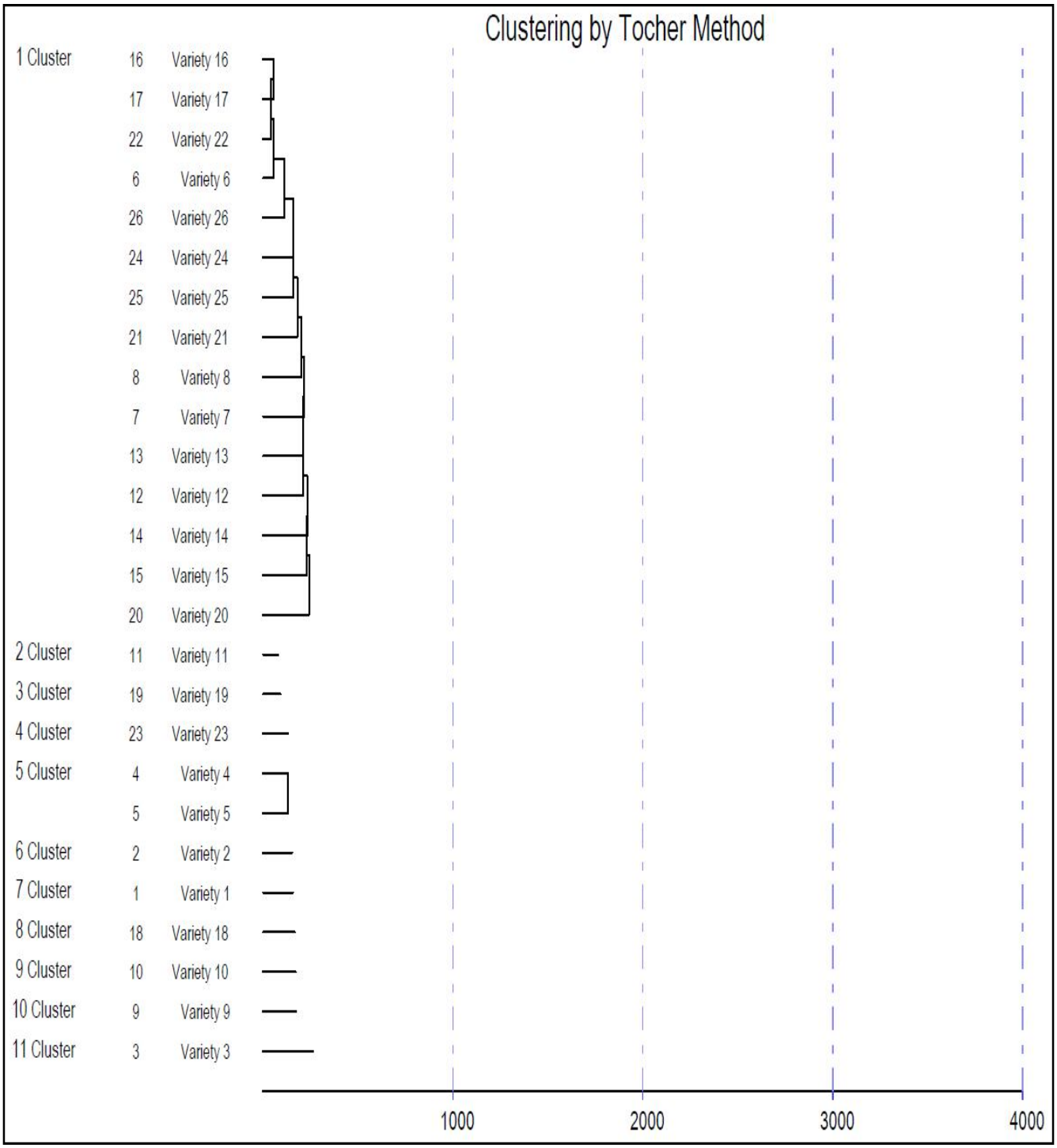

Fig. 3: Composition of D^2 clusters for 26 rice genotypes in Pooled Analysis.

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 underestimation of genetic divergence, because of measures of divergence estimated in different seasons may cancel each other in Pooled analysis.

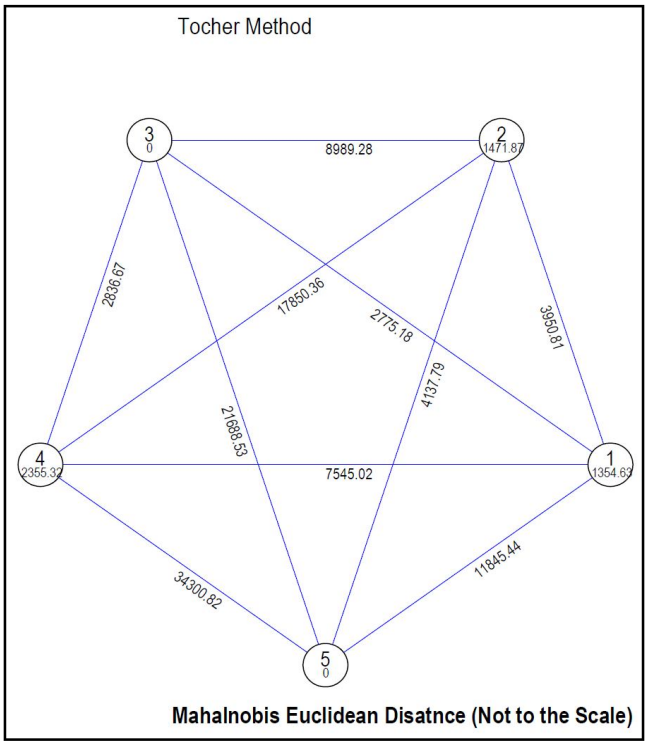

Fig. 4: Intra - and Inter - cluster average of D^2 and the extent of diversity among the clusters- S1.

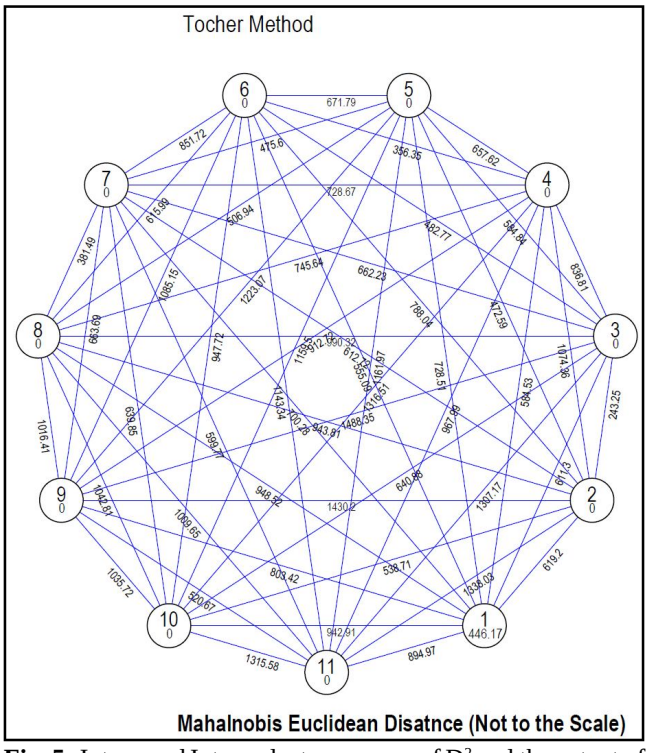

Fig. 5: Intra - and Inter - cluster average of D^2 and the extent of diversity among the clusters- S2.

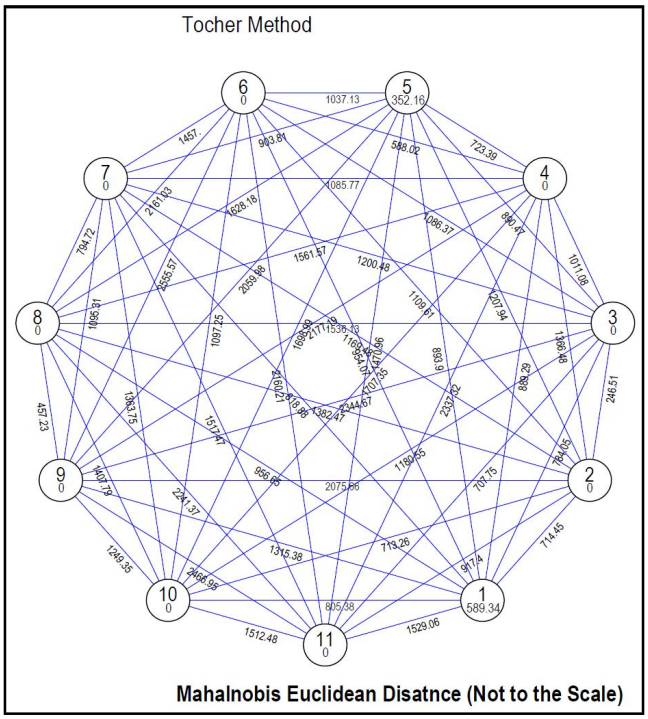

Fig. 5: Intra - and Inter - cluster average of D^2 and the extent of diversity among the clusters- Pooled Analysis.

Trait contribution towards genetic diversity

The relative ranking of the contribution of thirty traits towards genetic diversity based on D^2 statistic revealed that in S1, total phenolic content followed by DPPH antioxidant activity, root length and seed yield per plant contributed the maximum towards genetic diversity. In S2, DPPH antioxidant activity followed by seed yield per plant and Length of the kernel after cooking contributed the maximum towards genetic diversity. In Pooled analysis, DPPH antioxidant activity followed by shoot length and seed yield per plant contributed the maximum towards genetic diversity. The traits *viz.*, DPPH antioxidant activity and seed yield per plant contributed consistently maximum towards total genetic divergence. Hence, they may be declared as choice of traits (Table 3).

Acknowledgement

The authors submit their sincere thanks to the Director, Tamil Nadu, Rice Research Institute (TNAU), Aduthurai, Tamil Nadu for supplying breeder seeds and to P. Anand Babu and Reshma B Nambiar of School of Bio Engineering, SRM Institute of science and technology, kattankulathur, Chennai, Tamilnadu, India for helping the observation of physicochemical traits.

References

Allam, C.R., H.K. Jaiswal and A. Qamar (2015). Analysis of divergence for yield and quality traits in some elite basmati rice genotypes (*Oryza sativa* L.) *Journal of Progressive Agriculture,* **(2):** 1-6.

Anbarasu, M. (2017). Studies on genetic divergence in medium duration genotypes of rice (*Oryza sativa* L.) over seasons. M.Sc (Ag). Thesis submitted to Annamalai University, Annamalai Nagar, India.

Bhati. K.P., S.K. Singh, S.Y. Dhurai and Amita Sharma (2015). Genetic divergence for quantitative traits in rice germplasm. *Electronic J. Plant Breeding,* **6(2)**: 528-534.

Chamundeswari, N. (2016). Studies on nature of genetic divergence in rice (*Oryza sativa* L.) *International J. Science,* 4018-4023.

Chandarmohan, Y., S. Srinivas, S. Thippeswamy and D. Padmaja (2016). Diversity and variability analysis for yield parameters in rice (*Oryza sativa* L.) genotypes. *Indian J. Agric. Res.,* **50(6):** 609-613.

Du Toit, R., Y. Volsteedt and Z. Apostolides (2001). Comparison of the antioxidant content of fruits, vegetables and teas measured of vitamin c equivalents. *Toxicology,* **166:** pp. 63 - 69.

Kumari Priyanka, H.K. Jaiwal, Showkat A. Waza and T. Sravan (2015). Genetic divergence in indigenous aromatic rice (*Oryza sativa* L.) *Electronic J. of Plant Breeding,* **6(4):** 1096-1102.

Lakshmi, L. and C.H. Surendar Raju (2016). Genetic diversity in advanced generations of aromatic rice. *Bioinolet.,* **13(2B):** 357-363.

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

Mamta Kumari, G. Suresh Babu and Nithin B. Patil (2016). Genetic diversity analysis of rice (*Oryza sativa* L.) germplasm under aerobic condition. *Bangladesh J. Bot.,* **45(3):** 727-732.

Mohan, Y.C., S. Thippeswamy, K. Bhoomeshwar, B. Madhailatha and Jameema Samreen (2015). Diversity analysis for yield and gall midge resistance in rice (*Oryza stiva* L.) in northern telangana zone, India. *Sabrao J. of Breeding and Genetics,* **47(2):** 160-171.

Murthy, B.R. (1965). Heterosis and combining ability in relation to genetic divergence in flue cured tobacco. *Indian J. Genet.,* **25:** 46-56.

Nirosha, R.S. Thippeswamy, V. Ravindrababu, V. Ram Reddy and B. Spandana (2016). Genetic diversity analysis of zinc, iron, grain protein content and yield componenets in rice. *Electronic J. of Plant Breeding,* 371-377.

Panse, V.G. and P.V. Sukhatme (1978). Statisiacal methods for agricultural workers. 3rd Edn., Indian Council of Agricultural Research, New Delhi, India.

Rajasekaran, A. (2006). Studies on genetic divergence of Indica and Japonica (*Oryza sativa* L.) Genotypes. *M.Sc., (Ag) Thesis,* Annamalai Univ., Annamalainagar.

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

Sabarinathan, S. (2018). Studies on genetic divergence in medium duration of rice (*Oryza sativa* L.) genotypes grown over seasons based on seed yield, seed quality, cooking quality, risk efficiency traits and seed technological parameters under saline condition. M.Sc (Ag). Thesis submitted to Annamalai University, Annamalai Nagar, India.

Sabesan, T. (2005). Studied on the genetics of quality traits in rice (*Oryza sativa* L.). *Ph.D Thesis,* Annamalai Univ., Annamalainagar, India.

Sangeeta Banu, V.P.T. (2016). Studies on genetic divergence in rice (*Oryza sativa* L.) Over seasons. *M.Sc (Ag). Thesis Submitted to* Annamalai University, Annamalai nagar, India.

Sarwar. G., M.H. Rashid, S. Parveen and M.S. Hossain (2015). Evalution of genetic diversity in agromorphological traits of forty two aman rice genotypes (*Oryza sativa* L.) *AJEA,* **8(5):** 280-288.

Shobana, N., P. Sheela Rani, M. Sathish kumar and S.K. Ganesh (2015). Studies on genetic diversity among land races for sodicity tolerance in rice (*Oryza sativa* L.) *Trends in Biosciences,* **8(15):** 3988-3991.

Singleton, V.L. and Rossi (1965). Colorimetry of total Phenolics with Phosphomolybdic – Phosphotungestic acid reagent, *American Journal of Enology and Viticulture*, **16:** pp. 144 – 158.

Sokal, R.R. (1965). Statistical analysis in rice systematics. *Biol. Rev.,* **40:** 337-391.

Srinivas, D., C.H. Anuradha, M. Sujatha and A. Sivasankar (2015). Assessment of genetic diversity in rice. *Ijta @ Serial Publications,* 199-202.

Thippeswamy, S.Y. Chadramoha, B. Srinivas and D. Padmaja (2016). Selection of divergence parental lines for heterotic hybrid development in rice (*Oryza sativa* L.) *Sabrao J. of Breeding and Genetics,* **48(3):** 285-294.

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

Vijay Kumar (2015). Genetic diversity and character association studies for some economic traits in rice (*Oryza sativa* L.) *The Bioscan,* **10(2):** 899-904.

Wallace, B. (1963). Models of reproduction and their genetic consequences in statistical genetics and plant breeding. *Symb. Raleigh.* pp. 3-20.

World Agricultural production (2018). United States Department of Agriculture. *Foreign Agricultural Service,* 6-8.

Zhinshen, J., T. Mengcheng and W. Jianming (1999). The determination of flavonoid contents in mulberry and their scavenging effects on superoxide radicals. *Food Chemistry,* **64:** 555-559.