

Research Notes

Genetic divergence in land races of rice

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Abstract

Genetic diversity was assessed in 29 land races of rice using Mahalanobis's D² statistics. Eight quantitative characters including grain yield were considered for the study. Based on genetic distances, the 29 genotypes were grouped into five clusters. The mode of distribution of genotypes from different geographic regions into various clusters was at random indicating that geographical diversity and genetic diversity were not related .The characters days to first flowering and single plant yield contributed maximum towards genetic divergence. The maximum inter cluster distance was recorded between cluster IV and cluster V. The genotypes in these clusters *Vattan* and *Vellai Chitraikar* (cluster IV) and *Thulasi Manjari* (cluster V) may serve as potential donors for future hybridization programmes.

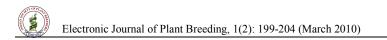
Key words:

Land races, Genetic divergence, D² analysis

Rice (Oryza sativa.L) the prime, most essential and important food crop of the world is also popularly called as 'Global grain' . Land races plays an important role in the local food security and sustainable development in agriculture (Tang et al.,2002). The major objective in rice breeding programme is to maintain the desirable traits with an increase in the yield potential of these land races. Genetic improvement mainly depends on the amount of genetic variability present in the population. The estimation of genetic diversity between different genotypes in the crop of interest is the first and foremost process in any plant breeding programme. However assessment of genetic diversity of rice land races has not given much thrust. We need to identify the genetically diverse accession with desired genes for better utilization in crop breeding programme. Hence the present study was undertaken to evaluate 29 rice land races for genetic divergence.

Department of Plant Breeding and Genetics. Pandit Jawaharlal Nehru College Of Agriculture and Research Institute. Karaikal 609603 Email: atr.agri@gmail.com The experimental materials consist of 29 rice land races received from different sources (Table 1). The genotypes were sown in raised nursery bed during Kharif 2008 at Pandit Jawaharlal Nehru College of Agriculture and Research Institute, Karaikal. After 25 days old seedlings were transplanted to the main field in a randomized block design replicated thrice. Each genotype was transplanted in three rows of 3 m length adopting a spacing of 30x20 cm. Normal package of practices and need based plant protection measures were followed. In each replication, five plants were selected at random and the following biometrical observations viz., days to first flowering, plant height (cm), numbers of productive tillers per plant, panicle length (cm), panicle weight (g), number of filled grains per panicle, 1000-grain weight (g) and single plant yield (g) were recorded .The genetic divergence was estimated using Mahalanobis's D² statistics (Mahalanobis, 1928). All the genotypes were grouped into clusters on the basis of D² values, as suggested by Tocher (Rao, 1952)

The analysis of variance revealed highly significant difference among the genotypes for all the traits (Table 2) indicating genetic diversity among the stocks used for the present study. Based on the D^2



analysis, all genotypes were grouped into five different clusters (Table 3). Cluster I has largest with 15 genotypes followed by cluster III and cluster II having 7 and 4 genotypes respectively .Cluster IV and V have lesser number of genotypes with 2 and one respectively. The clustering pattern showed that genotypes collected from the same geotropic region got distributed in several clusters. It might be due to selection differential and or genetic drift under diverse environmental condition within same geographical regions. This pattern of clustering further indicated that there was no association between geographical distribution of genotypes and genetic divergence .Similar findings was also reported by Murty and Arunachalam (1996), Selvakumar et al. (1989) and Vivekanandan and Subramanian(1993).

Maximum intra cluster distance was observed between the genotypes viz., Pant Kalanamak 3131, Patnai 23, Cherthallai Pokkali, Ponnarayan, Red Thriveni, Sivappu Chitraikar and Vellaikurikar in cluster III indicating the existence of wide genetic divergence among the constituent genotypes in it. High degree of divergence among the genotypes within a cluster produces more segregating breeding materials. Selection within such clusters might be executed based on maximum mean value for the desirable characters. On the other hand .cluster I had minimum intra cluster distance with more than one genotype, indicating the unidirectional selection which might have been practical in the past that could lead to uniformity with less deviation between the genotypes.

The intra cluster distance ranged from 22.75 (Cluster I) to 28.35(Cluster III). The highest inter cluster distance was observed between the clusters IV and V (49.04) followed by between cluster II and V (41.69). The least distance was recorded between the cluster III and IV (30.01) (Table 4). Thus hybridization between genotypes under the highly divergent clusters should result in maximum hybrid vigour and

highest numbers of useful segregants for the trait studied.

The contribution of different character to that of total divergence was estimated based on ranking system (Table 5). Among the traits, days to first flowering has contributed maximum (25.61 per cent) to the total divergence followed by single plant yield (25.12 per cent). The comparison of cluster means (Table 6) revealed that cluster IV recorded high mean values for four traits followed by cluster V .The cluster II had the minimum value for all the traits except for 1000-grain weight which indicates less genetic diversity among the genotypes. The present study suggested that hybridization among genotypes in the diverse Vattan and Vellai Chitraikar (cluster IV) and Thulasi Manjari (cluster V) could give high heterotic combinations and thus produced large variability and better segregates in the segregating generations.

References

- Mahalanobis, P. C. 1928. A statistical study at Chinese head measurement. J. Asiatic Soc. Bengal., 25: 301-317.
- Murty, B. R. and V. Arunachalam. 1996. The nature of genetic divergence in relation to breeding system in some crop plants. *Indian J. Genet.*, 26: 188-198.
- Rao, C. R. 1952. Advanced statistical methods in biometrical research. John Wiley and Sons. Inc., New York, 390 pp.
- Selvakumar, K. S., G. Saundrapandian and A. Amirthadevarathinam. 1989. Genetic divergence for yield and yield components in cold tolerant rice. *Madras Agric. J.*, 76: 688-694.
- Tang, S. X., Y. Z. Jiang, X. H. Wei, Z. C. Li and H. Y. Yu. 2002. Genetic diversity of isozymes of cultivated rice in china. *Acta Agron. Sin.*, 28: 203-207.
- Vivekanandan, P. and S. Subramanian. 1993. Genetic divergence in rainfed rice. *Oryza*, 30: 60-62.



Table 1. Origin and mean perforamance of land races of rice for various characters

Genotypes	Origin	Days to first flowering	Plant height (cm)	No.of productive tillers/ plant	Panicle length (cm)	Panicle weight (g)	No. of filled grains / panicle	1000- grain weight (g)	Single plant yield (g)
Orumanayoor Anakkodan	Kerala	91	183	9	33.66*	4.41	129	20.95	19.29
Vytilla Anakkodan	Kerala	91	181	11	31.33	4.91*	150	30.28*	28.52*
Chettivirippu	Kerala	93	179	7	32.00*	4.73*	140	30.06*	16.85
Chettivirippu Kannamalai	Kerala	93	171	8	31.66*	4.78*	141	30.04*	17.93
Chithyankottai	Tamil Nadu	86*	171	11	33.66*	5.81*	239*	20.33	39.90*
Chitteani	Kerala	96	173	11	34.33*	5.61*	172*	20.97	26.35
Gopalbhag	Bangladesh	104	148*	11	27.33	4.12	236*	10.68	20.14
Pokkali	Kerala	94	195	10	31.33	5.83*	145	30.08*	23.11
Jodumani	Kerala	89*	166	14	27	4.61*	125	20.85	23.97
Kadamakudy Pokkali	Kerala	88*	167	7	35.33*	5.33*	159	20.79	24.28
Kethanur	Kerala	105	170	17*	24.66	3.67	115	20.91	26.32
Koorgood	Kerala	86*	162	14	37*	3.71	108	20.42	26.95
Kuzhavazhai	Tamil Nadu	105	100*	17*	24.66	2.58	116	10.87	25.36
Vettaikaraniruppu Kulivedichan	Tamil Nadu	94	109*	25*	25	2.18	98	20.1	24.57
Vedaranyam Kulivedichan	Tamil Nadu	68*	126*	24*	25.33	2.07	85	20.82	28.56*
Njavara	Kerala	74*	98*	22*	26	2.39	140	10.5	18.57
Pallipuram Pokkali	Kerala	94	176	7	32*	4.70*	157	30.08*	16.57
Pant kalanamak3131	Uttar Pradesh	103	168	13	33.33*	3.64	244*	10.39	21.1
Patnai 23	Kerala	114	175	14	27	3.99	151	20.84	23.19
Cherthallai Pokkali	Kerala	87*	176	7	34.33*	4.38	140	30.03*	19.52
Edavanakad Pokkali	Kerala	95	175	10	31.66*	4.93*	141	30.12*	20.97
Ponnararyan	Kerala	88*	159	7	35.33*	4.76*	173*	30.02*	19.69
Red Thriveni	Kerala	76*	168	8	32.66*	4.64*	180*	20.89	19.6
Sivappu Chitraikar	Tamil nadu	107	173	16*	27	3.2	109	30.00*	23.34
Sivappu Koompalai	Tamil Nadu	70*	117*	17*	26	2.3	85	20.93	20.78
Thulasi Manjari	Bihar	103	173	17*	30	2.92	310*	9.8	30.08*
Vattan	Kerala	85*	175	10	34*	5.08*	194*	20.4	36.11*
Vellai Chitraikar	Tamil Nadu	78*	178	19*	28	3.86	105	20.44	24.59
Vellaikurikar	Tamil Nadu	105	163	17*	25.66	3.36	110	20.81	36.24*
Grand mean		91.81	161.21	13.1	30.25	4.08	151.54	21.63	24.22
SE		0.76	2.95	1.27	0.66	0.24	4.33	1.61	1.69
CD at 5%		1.52	5.91	2.56	1.32	0.5	8.68	3.24	3.38

* Significant at 5 per cent level.



Source	Replication	Genotypes	Error
Degrees of freedom	2	28	56
	Mean	sum of squares	
Days to first flowering	0.011	388.22**	0.86
Plant height (cm)	51.35	1961.29**	13.07
Number of productive tillers per plant	2.31	82.07**	2.45
Panicle length (cm)	1.25	44.18**	0.65
Panicle weight (g)	0.05	3.64**	0.09
Number of filled grains/ Panicle	61.39	8123.58**	28.188
1000- grain weight (g)	1.00	124.622**	3.93
Single plant yield (g)	7.64	101.30**	4.288

Table 2. Analysis of variance for different characters

** Significant at 1 per cent level

Table 3. Distribution of genotypes to different clusters based on Tocher's method

Cluster number	Total number of genotypes	Genotypes	Origin
		Orumanayoor Anakkodan	Kerala
		Vytilla Anakkodan	Kerala
		Chettivirippu	Kerala
		Chettivirippu Kannamalai	Kerala
		Chithyankottai	Tamil Nadu
		Chitteani	Kerala
		Gopalbhag	Bangladesh
Ι	15	Pokkali	Kerala
		Jodumani	Tamil Nadu
		Kadamakudy Pokkali	Kerala
		Kethanur	Kerala
		Koorgood	Kerala
		Kuzhavazhai	Tamil Nadu
		VettaikaraniruppuKulivedichan	Tamil Nadu
		Edavanakad Pokkali	Kerala
		Vedaranyam Kulivedichan	Tamil Nadu
		Njavara	Kerala
II	4	Pallipuram Pokkali	Kerala
		Sivappu Koompalai	Tamil Nadu
		Pant Kalanamak 3131	Uttar Pradesh
		Patnai 23	West Bengal
		Cherthallai Pokkali	Kerala
III	7	Ponnararyan	Kerala
		Red Thriveni	Kerala
		Sivapu Chitraikar	Tamil Nadu
		Vellaikurikar	Tamil Nadu
		Vattan	Kerala
IV	2	Vellai Chitraikar	Tamil Nadu
V	1	Thulasi Manjari	Bihar

Cluster No	Ι	II	III	IV	V
Ι	517.782 (22.75)	1070.701 (32.72)	615.004 (24.79)	652.144 (25.53)	1738.195 (41.69)
II		794.239 (28.18)	1399.443 (37.40)	713.264 (26.70)	3278.139 (57.25)
III			803.849 (28.35)	900.833 (30.01)	1527.549 (39.08)
IV				564.994 (23.77)	2405.027 (49.04)
V					0.000 (0.00)

Table 4. Average intra (diagonal) and inter cluster D ²	Values
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D Values are in parenthesis

Table 5. Contribution of characters towards genetic divergence

Characters	Times ranked first	Contribution (Per cent)
Days to first flowering	104	25.61
Plant height (cm)	47	11.57
Number of productive tillers per plant	12	2.95
Panicle length (cm)	23	5.66
Panicle weight (g)	3	0.73
Number of filled grains per panicle	67	16.50
1000- grain weight (g)	48	11.82
Single plant yield (g)	102	25.12



			Clusters		
Characters —	Ι	П	III	IV	V
Days to first flowering	93.95	<u>76.66</u>	97.19	81.83	102.66
Plant height (cm)	163.26	<u>129.33</u>	168.9	176.66	173.33
Number of productive tillers per plant	12.133	17.5	<u>11.66</u>	14.66	17
Panicle length(cm)	30.71	<u>27.33</u>	30.76	31	30
Panicle weight(g)	30.71	<u>27.33</u>	30.76	31	30
Number of filled grains per panicle	147.51	<u>116.5</u>	158.04	149.83	310
1000-grain weight(g)	22.5	20.58	22.42	20.42	<u>9.8</u>
Single plant yield (g)	24.3	<u>21.12</u>	23.24	30.35	30.08

Table 6. Cluster means for different traits

Underlined and **boldfaced** indicates minimum and maximum cluster mean values respectively.