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RESEARCH ARTICLE :

Genetic divergence for crop improvement in short duration rice varieties as revealed by morphological traits

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SUMMARY : A sustainable breeding programme could be achieved through precise knowledge of genetic divergence for yield components. Hybridization between diverse parents maximizes the chance of higher heterosis as it will give wide range of segregation which will promote chance of selection. It also helps to widen the genetic base of varieties in a breeding programme. With this in view this investigation was carried out with the objective of estimating genetic diversity present in a set of 29 short duration rice varieties recommended for cultivation in Tamil Nadu and Puducherry (U.T.), using morphological traits. Clustering based on average taxonomic distance using morphological traits grouped 29 varieties into two major clusters with 25 and 4 varieties respectively and produced distant genetic pools. The genetic diversity of the 29 short duration rice varieties was observed to be narrow and, therefore, it is necessary to broaden the genetic base of the present day rice cultivars by bringing in genes from large germplasm comprising land races and wild spp.

KEY WORDS :
Genetic diversity,
Short duration rice,
Morphological traits

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BACKGROUND AND OBJECTIVES

Rice occupies, and will continue to occupy a pivotal place in global food and livelihood security systems (Swaminathan, 2006). It is the most important staple food for Indians as it provides 43 per cent calorie requirement for more than 70 per cent of population (Rahman, 2006). India has the large acreage under rice (44 million hectares) with annual production of about 104 million tones and ranks second only to China (Babu *et al*., 2014). To feed the India's burgeoning population the production has to be stepped upto 120 mt by 2025 (Mishra, 2009). Further, several biotic and abiotic stresses adversely affect rice productivity. Changes in insect biotypes and disease races are becoming a continuing threat to rice production. Thus there is urgent need to broaden the rice gene pool through introduction of new genes from new and diverse sources (Brar and Khush, 2002).

Therefore, knowledge of genetic diversity among modern rice cultivars is of

paramount importance to breeders for understanding of germplasm usage to avoid development of varieties with a narrow genetic base (Davierwala *et al*., 2000). With this in background the present study was, therefore, undertaken to estimate the genetic base of short duration rice varieties (less than 115 days), recommended for cultivation in Tamil Nadu and Puducherry (U.T).

RESOURCES AND METHODS

The present investigation was carried out in the Department of Plant Breeding and Genetics, Pandit Jawaharlal Nehru College of Agriculture and Research Institute (PAJANCOA and RI), Karaikal during June-September. The materials chosen in the study comprised 29 short duration rice varieties maturing in less than 115 days. Of these 25 are recommended for cultivation in Tamil Nadu and Puducherry during *Kuruvai* (June–September) and *Navarai* (December-April) seasons. Two varieties *viz.*, Annada and Tulasi, as popular national varieties and another two varieties: IR 72 and IR 74 as popular International varieties (IRRI bred varieties cultivated in many countries) were included for comparison. Details of parentage, year of release and breeding station of rice varieties are given in Table 1. To estimate the genetic diversity, among 29 rice varieties using morphological traits, a field trial was conducted, during *Kuruvai* in the eastern farm of PAJANCOA and RI in Randomized Block Design (RBD) with three replications. Each variety was raised in four rows of one meter length and a spacing of 20 x 15 cm was adopted. Normal agronomical practices and appropriate plant protection measures were followed. In each replication, Observation were recorded on nine different morphological parameters such as days to fifty per cent flowering, plant height, tiller number, panicle length, panicle weight, 1000 seed weight, grain length, grain width and single plant yield.

Computer software, NTSYS-pc (Numerical Taxonomy and Multivariate Analysis System) was used to discover and describe the pattern of biological diversity by using a set of multivariate data (Rohlf, 1998). A similarity distance matrix was calculated based on the means of morphological characters. The data were standardized by subtracting the means from the original values and dividing by the standard deviation using STAND procedure. Similarity matrix was calculated using the SIMINT procedure of NTSYS-pc based on Average Taxonomic Distance (*i.e.*, DIST co-efficient in the procedure). The distance co-efficients (f) were used for cluster analysis and dendrogram was constructed by the unweighted pair group method (UPGMA) (Sneath and Sokal, 1973).

OBSERVATIONS AND ANALYSIS

The genetic improvement of yield and other economically important traits in crop species depends upon the genetic diversity available within crop species. Morphological traits are easily observable and useful for preliminary evaluation because they offer a fast and simple approach for assessing genetic diversity. Morphological traits such as flowering, plant height, grain weight etc., were among the earliest genetic markers used in diversity analysis in crop plants. Differences between genotypes with regard to any of these characteristics are expected to provide information about genetic diversity. If the traits are highly heritable, morphological markers are one of the choices for diversity studies because the inheritance of the marker can be monitored visually without specialised biochemical or molecular technique. However, it poses several limitations, including low polymorphism, low heritability, late expression and vulnerability to environmental influences which in turn may affect the estimation of genetic diversity.

Average taxonomic distances based on morphological characteristics were estimated after standardization. The average taxonomic distance (dissimilarity co-efficient's) among 29 rice varieties ranged from 0.65 (ADT 47 and ADT 43) and 0.66 (ASD 18 and IR 36) to 1.57 in 100 pairs of varieties involving TKM 11, TKM 12, PMK 1 and PMK 2 with remaining 25 varieties. The average taxonomic distance of 406 pairs (0.138) was the cophenetic matrix of average taxonomic distance was used to construct hierarchical clusters and the resulting dendrogram is presented in Fig. 1.

Dendrogram produced two major clusters at genetic distance of 1.50 the first major cluster comprised seven sub cluster grouped various distances. Sub cluster M I A comprised five varieties (ADT 36, IR 36, ASD 18, CO 47 and PY 5), M I B with four varieties (ADT 42, IR 72, IR 74 and PMK 3), M I C with two varieties (IR 42 and TKM 9), M I D with one (IR 64), M I E with four (ADT 43, ADT 47, PY 2 and ADT 45), M I F with six (ADT 37, ANNADA, ADT 48, ASD 16, MDU 5 and

TULASHI), M I G with one variety (IR 50) and M I H with two varieties (ADT 41 and PY 3). Second major cluster comprised only four varieties (TKM 11, PMK 1, PMK 2 and TKM 12).Varieties bred at different Centers clustered mixed in all the sub clusters (Table 2).

Clustering based on average taxonomic distance based on morphological traits grouped 29 varieties into two major clusters M I and M II with 25 and 4 varieties respectively. Four rice varieties *viz.*, TKM 11, TKM 12, PMK 1 and PMK 2, grouped in cluster M II, were distinct from remaining varieties for plant height and days to 50 per cent flowering. ADT 43 and ADT 47 were almost uniform for most of the traits and so clustered together in M I E. Similarly IR 36 and ASD 18, in cluster M I A, were uniform for plant height, tiller number, panicle weight, grain length and grain width. ADT 42 and IR 72, in Cluster M I B, were similar for all the characters except plant height. ADT 37 and ANNADA were similar for grain characters and so grouped in cluster M I F. ADT 41 and PY 3 bore the lengthiest grain compared to other varieties and therefore grouped in M I H. Clustering of rice varieties based on morphological traits employed in this study was earlier reported by many researchers (Shanmugasundaram *et al*., 2000; Chandra *et al*., 2007 and Nadia *et al*., 2014).

Clustering of rice varieties, in the present investigation, gave distant genetic pools comprising cluster M I A with five varieties (ADT 36, IR 36, ASD 18, CO 47 and PY 5) and cluster M II A with four varieties (TKM 11, PMK 1, PMK 2 and TKM 12). Similar

Table 1 : Details of parentage, year of release and breeding station of rice varieties

Sr. No.	Variety	Parentage	Year of release	Breeding station
1.	ADT 36	Triveni x IR 20	1980	TRRI, Aduthurai
2.	ADT 37	BG 280 x PTB 33	1987	TRRI, Aduthurai
3	ADT 41	Natural mutant from Basmathi 370	1992	TRRI, Aduthurai
4.	ADT 42	AD 9246 x ADT 29	1994	TRRI, Aduthurai
5.	ADT 43	IR 50 x Improved whiteponni	1998	TRRI, Aduthurai
6.	ADT 45	IR 50 x ADT 37	2001	TRRI, Aduthurai
7.	ADT 47	ADT 43 x Jeeragasamba	2005	TRRI, Aduthurai
8.	ADT 48	IET 11412 x IR 64	2005	TRRI, Aduthurai
9.	IR 36	IR 1561 x IR 24 x *Oryza nivara* x CR 94	1979	IRRI, Philippines
10.	IR 42	IR 2042 x CR 94	1983	IRRI, Philippines
11.	IR 50	IR 2153 x IR 28 x IR 36	1982	IRRI,Philippines
12.	IR 64	IR 5657 x IR 2061	1989	IRRI,Philippines
13.	IR 72	TN 1 x Chianung 242	1989*	IRRI,Philippines
14.	IR 74	IR 19661 x IR 15795	1991*	IRRI,Philippines
15.	TKM 9	TKM 7 x IR 8	1978	RRS,Tirur,Tamilnadu
16.	TKM 11	C 22 x BJ 11	1998	RRS,Tirur,Tamilnadu
17.	TKM 12	TKM 9 x TKM 11	2002	RRS,Tirur,Tamilnadu
18.	PY 2	Kannagi x Cul 2032	1980	PKKVK,Puducherry
19.	PY 3	IR 3403 x PTB 33 x IR 36	1984	PKKVK,Puducherry
20.	PY 5	Swarnadhan x NLR 9674	1994	PKKVK,Puducherry
21.	PMK 1	CO 25 x ADT 31	1985	ARS,Parmakudi
22.	PMK 2	IR 13564 x ASD 4	1994	ARS,Parmakudi
23.	PMK 3	UPLRI 7 x CO 43	2003	ARS,Parmakudi
24.	ASD 16	ADT 31 x CO 39	1986	RRS,Ambasamudram
25.	ASD 18	ADT 31 x IR 50	1991	RRS,Ambasamudram
26.	CO 47	IR 50 x CO 43	1999	PBS,Coimbatore
27.	MDU 5	*Oryza glaberrimma* x Pokkali	1996	AC and RI,Madurai
28.	ANNADA	MTU 15 x Waikoku	1987	CRRI,Cuttack
29.	TULASHI	CR 151 x CR 1014	1988	CRRI,Cuttack

*Released in Indonesia

Table 2 : Distributions of varieties to different clusters based on UPGMA method in morphological dendrogram

Cluster no.	Total no. of varieties	Varieties	Origin
M I A	5	ADT 36	TRRI, Aduthurai
		IR 36	IRRI, Philippines
		ASD 18	RRS, Ambasamudram
		CO 47	PBS, Coimbatore
		PY 5	PKKVK, Puducherry
M I B	4	ADT 42	TRRI, Aduthurai
		IR 72	IRRI, Philippines
		IR 74	IRRI, Philippines
		PMK 3	ARS,Parmakudi
M I C		IR 42	IRRI, Philippines
	2	TKM 9	RRS, Tirur, Tamilnadu
M I D	1	IR 64	IRRI, Philippines
M I E	4	ADT 43	TRRI, Aduthurai
		ADT 47	TRRI, Aduthurai
		PY 2	PKKVK,Puducherry
		ADT 45	TRRI, Aduthurai
		ADT 37	TRRI, Aduthurai
M I F	6	ANANDA	CRRI, Cuttack
		ADT 48	TRRI, Aduthurai
		ASD 16	RRS, Ambasamudram
		MDU 5	AC and RI, Madurai
		TULASHI	CRRI, Cuttack
M I G	1	IR 50	IRRI, Philippines
M I H	2	ADT 41	TRRI, Aduthurai
		PY 3	PKKVK, Puducherry
M II	4	TKM 11	RRS, Tirur, Tamilnadu
		PMK 1	ARS, Parmakudi
		PMK 2	ARS, Parmakudi
		TKM 12	RRS, Tirur, Tamilnadu

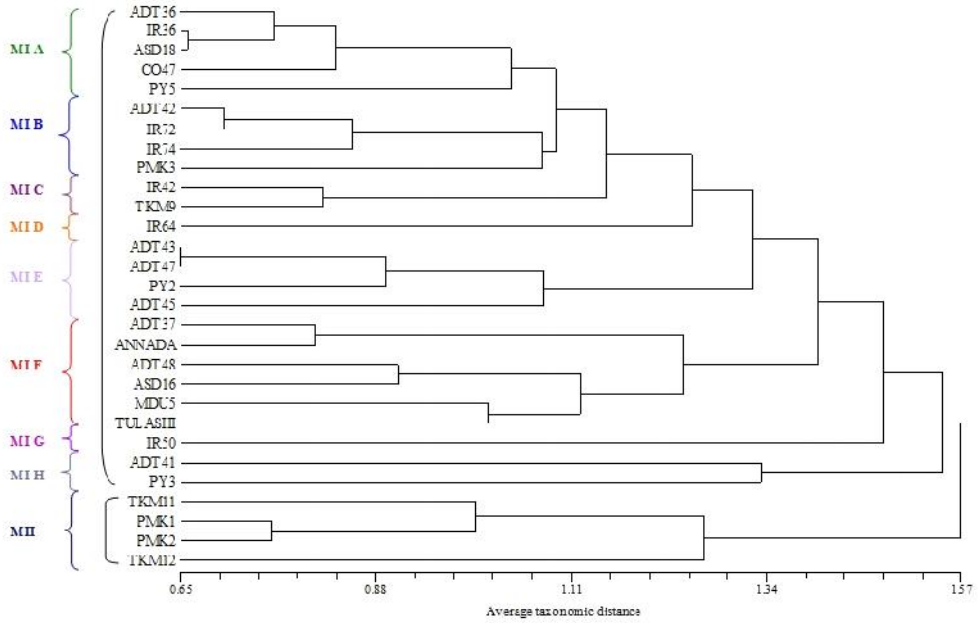

Fig. 1 : Dendrogram showing genetic relationship among 29 rice varieties using morphological characters.

Grouping of rice varieties, in a similar manner, was earlier reported by (Fuentes *et al*., 2005).

In conclusion, the genetic diversity of the 29 short duration rice varieties was observed to be narrow. It is necessary to broaden the genetic base of the present day rice cultivars, by bringing in genes of agronomic value, resistance to biotic and abiotic stresses from large germplasm (Khush, 1999) comprising land races and wild spp.

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