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Pedigree analysis of some short duration Indian rice (*Oryza sativa* L.) varieties

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ABSTRACT

Pedigree analysis of 29 rice varieties revealed that their origin was traced to 69 ancestors, of which 25 were from India and remaining 44 from 12 different countries. Three ancestors viz., DEE-GEO-WOO-GEN, CINA AND LATISAIL, were common in 24 out of 29 varieties. IR 8 had the highest foot print value followed by Peta indicating their profound influence in the pedigrees of these 29 rice varieties. Pedigree profiles also revealed that 16 out of 29 rice varieties possess genomes of indica, japonica and javanica sub spp. Clustering based on Coefficient of Co-ancestry (CoC) resulted in grouping of two major clusters with 18 and 11 varieties respectively and culminated in the identification of diverse clusters. Finally, the genetic diversity of the 29 short duration rice varieties was observed to be narrow and, therefore, necessary to broaden the genetic base of the present day rice cultivars, by bringing in genes of agronomic values from large germplasm.

Key words: *Rice-pedigree, coefficient of co-ancestry, genetic base index, foot print value, inbreeding coefficient*

Rice is world's most important food crop that feed over half of the global population. India, where it is planted to 42 mha, has made spectacular progress in rice production and productivity as evidenced from five-fold increase from 21mt in 1950s, to 93mt, in 2006-07 (Shobharani 2010). This was due to the development of high yielding rice varieties (HYV) coupled with adoption of improved cultural practices which heralded the so called "Green revolution". Breakthrough in rice yield was achieved with the development of semi-dwarf varieties characterized by lodging resistance and nitrogen responsiveness (Borlaug 1998). However, on the other side, green revolution led to the depletion of genetic base of rice varieties, as thousands of traditional varieties (landraces) were replaced by a handful of modern rice varieties, resulting in genetic uniformity (Shivkumar *et al.* 1998; Mishra *et al.* 2003). Similar situations have been reported from Japan (Kaneda 1985), United States (Dilday 1990), Taiwan (Lin 1991), Latin America (Cuevas-Perez *et al*. 1992) and Australia (Ko *et al*. 1994), documenting a widespread reduction in genetic diversity of modern rice cultivars due to intensive breeding efforts. Therefore, knowledge of genetic relationships among modern rice cultivars is of prime importance to breeders for understanding of germplasm usage to avoid development of varieties with a narrow genetic base (Shivkumar *et al*.1998; Davierwala *et al*. 2000).

To avoid the pitfalls of narrow genetic base, pedigree information has historically been used to predict performance, compute coefficient of parentage, plan further crosses for cultivar development and trace the inheritance of specific gene variants. Coefficient of parentage (CoP) (Kempthorne *et al*. 1985) or Coefficient of co ancestry (CoC) (Falconer and Mackay 1996) can be calculated from pedigree analysis

and may provide alternative or additional measures that quantify relatedness among genotypes. It indirectly measures the genetic diversity among cultivars by estimating from pedigree records, the probability that alleles, in a locus, are identical by descent. The present study was, therefore, undertaken to quantify the genetic base of short duration rice varieties with the objectives of (1) determining Coefficient of Co-ancestry, (2) calculating the genetic contribution of ancestral lines to the genetic diversity of modern rice varieties, (3) to estimating the inbreeding coefficient, foot print value and genetic base index and (4) to identify set of divergent genotypes for further breeding programmes.

MATERIALS AND METHODS

Plant materials

The materials comprised 29 short duration rice varieties maturing in 105-115 days. Of these, 25 are recommended for cultivation in the states of Tamil Nadu and Puducherry during May/June-August/ September seasons. Two varieties *viz.*, Annada and Tulasi, as popular national varieties and another two varieties: IR 72 and IR 74 as popular IRRI varieties (IRRI bred varieties cultivated in many countries) were included for comparison. These rice varieties were bred in different rice research stations of Tamil Nadu Agricultural University, Coimbatore and Peruthalaivar Kamaraj Krishi Vigyan Kendra (PKKVK) of Puducherry (Table 1).

Pedigree data

Details of ancestors *i.e.*, pareents, grandparents, great grandparents and so on of all the 29 short duration rice varieties were gathered from several sources in the literature (Ghouse *et al.* 1960; Subramanian and Manuel 1998; Sharma and Rao 2004; Shobharani *et al.* 2008) web site (www.iris.irri.org) and from personal communication (Dr. Alcantara Researcher of Data Administration Team, INGER, IRRI Philippines). PEDITREE software package, developed by Vanberloo and Hutten (2005) was used to analyze the pedigree data thus collected. Data were provided in the form of a Microsoft access database containing a single table with the pedigree data. Using peditree software measures of Inbreeding Coefficient (IBC), Coefficient of Co ancestry (CoC) and foot print value were calculated and images of pedigree tree and Pedi graph were also produced. Inbreeding coefficient (IBC), a measure of genetic relatedness within a variety, was estimated using circular edge walking method as suggested by Falconer and MacKay (1996). Coefficient of Co ancestry (CoC), another similar measure of genetic relatedness, but between a pair of varieties, was calculated for all 406 pair wise combinations following the method of Falconer and Mackay (1996). Foot print value is a measure of a genotype indicating its influence in being used as parent in number of crosses. Such influential genotypes were identified by its higher foot print values using progeny batch tab sheet in the Peditree software. Genotypes with large foot print can be considered to have a relatively large input in the complete set of germplasm involved in development of 29 rice varieties.

Genetic Base Index (GBI)

Genetic base index of the rice varieties can be assessed using inbreeding coefficient and number of ancestors involved in development of a particular variety. It was calculated as follows. Lower the index, broader the genetic base.

$$GBI = \frac{IBC}{\text{Number of ancestors}} \times 100$$

Pedigree tree

The PEDITREE results of an each pedigree (variety) search were displayed as an explorer-like collapsible expandable tree, allowing focus on specific parts of the pedigree giving depth of generation etc.,

Pedi graph

Conventional pedigree diagram of each variety was created by exporting data to a Pedi graph data file to visualize very complex pedigree relationships.

Cluster analysis

The coefficient of co ancestry data generated using PEDITREE software was used in the NTSYS-pc software to cluster the rice varieties. A dendrogram was constructed based on a matrix of the coefficients of ancestry. By using an Unweighted Pair Group Method based on Arithmetic mean (UPGMA) with the

SAHN clustering function of NTSYS-pc package.

RESULTS AND DISCUSSION

Unlike morphological, biochemical and molecular markers, pedigree data do not require the observations to be recorded on the plant material and is not influenced by environment or the technique used (Gopal and Oyama 2005). Geneticists can use pedigree information to estimate the genetic distance among cultivars, or to evaluate the contribution of various genetic pools to current cultivars. Applied plant breeders can use this information to identify parents that are genetically dissimilar and thus have the potential to generate new variability for future crop improvement, or to identify genetic pools that have proven valuable or have been neglected in the past (Calhoun *et al.* 1994). Coefficient of parentage (COP), based on pedigree information provides an indirect measure for the relative genetic similarity of related individuals. If the pedigrees are well documented and reliable, the establishment of groups is possible (Smith *et al.* 1985). Pedigree analysis of 29 rice varieties showed that their origin were traced to 69 ancestors out of which 25 were of Indian origin, contributing 36 per cent of the genes, and the remaining 44 from 12 different countries, contributing 64 per cent of the genes (Table 2,3). In earlier studies, Lin (1991) reported the presence of 65 ancestors in the pedigrees of 99 japonica rice varieties of Taiwan, Shivkumar *et al.* (1998) observed only 37 ancestors in the development of 29 rice varieties in Kerala and (Joshi 2005) noticed 35 ancestors in the

Table 4. Foot print value of some of the genotypes involved

Sl. No.	Genotype	Footprint value	Genotype contribution	Sl. No	Genotype	Footprint value	Genotype contribution
1.	IR 8	14.38	20	34.	IR 3024	2.00	06
2.	PETA	11.25	20	35.	PTB 33	1.88	05
3.	IR 24	6.75	17	36.	IR 50	1.75	04
4.	TN 1	6.38	17	37.	IR 1704	1.75	08
5.	GEB 24	5.75	20	38.	IR 22	1.75	05
6.	IR 262	5.38	20	39.	IR 1614	1.63	04
7.	IR 1561	5.13	18	40.	IR 2061	1.63	04
8.	TAICHUNG 65	3.75	12	41.	CO 18	1.63	06
9.	IR 833	3.75	17	42.	B57-1096	1.50	03
10.	REXORO	3.63	13	43.	IR 42	1.50	03
11.	IR 1721	3.50	15	44.	C 22	1.50	04
12.	IR 127	3.50	14	45.	CH 2	1.50	07
13.	FORTUNA	3.38	16	46.	ADT 3	1.50	07
14.	CENTURYPATNA 231	3.38	10	47.	IR 238	1.50	05
15.	IR 3403	3.00	05	48.	IR 1529	1.38	07
16.	SIGADIS	3.00	08	49.	HSINCHU4	1.38	04
17.	SHINRIKI	3.00	11	50.	IR 28	1.38	05
18.	TKM 6	2.88	10	51.	IR 2153	1.38	05
19.	BLUE BONNET	2.88	11	52.	IR 1416	1.38	04
20.	BPI	2.88	10	53.	B502A2	1.25	04
21.	B 5580	2.75	14	54.	IR 746 A	1.25	07
22.	IR 20	2.63	06	55.	CR 94	1.25	04
23.	IR 36	2.50	05	56.	IR 2042	1.25	04
24.	IR 579	2.38	11	57.	IR 1402	1.25	05
25.	IR 747	2.38	11	58.	IR 2040	1.25	05
26.	ADT 31	2.25	05	59.	SLO 17	1.25	05
27.	IR 1539	2.25	10	60.	BLUE ROSE SUPRME	1.25	07
28.	CUL 340	2.13	07	61.	TJEREMAS	1.25	05
29.	IR 733	2.13	05	62.	IR 2147	1.13	05
30.	IR 1737	2.13	09	63.	IR 400	1.13	04
31.	RSBR	2.00	08	64.	TAINUNG 16	1.13	05
32.	TEXASPATNA	2.00	08	65.	IR 1541	1.13	05
33.	IR 3185	2.00	06	66.	PTB 21	1.00	04

Table 2. Details of depth of generations, ancestry, sub spp composition, IBC and GBI of rice varieties

S.No.	Variety	Depth of generations	Ancestors	Sub spp/ related spp composition					IBC	GBI
				indica	japonica	javanica	Other spp	Unknown*		
1.	ADT 36	6	8	8	-	-	-	0	0.035	0.438
2.	ADT 37	6	8	8	-	-	-	0	0.002	0.025
3.	ADT 41	0	1	1	-	-	-	0	0.000	-
4.	ADT 42	7	11	7	4	-	-	0	0.016	0.146
5.	ADT 43	14	23	14	5	2	1	1	0.017	0.074
6.	ADT 45	14	24	17	3	2	1	1	0.017	0.071
7.	ADT 47	15	24	15	5	2	1	1	0.004	0.016
8.	ADT 48	15	22	14	3	2	1	2	0.035	0.159
9.	IR 36	10	16	10	3	1	1	1	0.023	0.144
10.	IR 42	11	14	9	2	2	-	1	0.038	0.271
11.	IR 50	13	20	13	3	2	1	1	0.068	0.340
12.	IR 64	14	21	13	3	2	1	2	0.139	0.661
13.	IR 72	5	12	4	4	-	-	4	0.031	0.258
14.	IR 74	15	24	17	3	2	1	1	0.158	0.658
15.	TKM 9	3	4	4	-	-	-	0	0.000	-
16.	TKM 11	4	7	5	1	1	-	0	0.000	-
17.	TKM 12	5	9	7	1	1	-	0	0.016	0.178
18.	PY 2	4	6	5	1	-	-	0	0.049	0.817
19.	PY 3	12	22	15	3	2	1	1	0.048	0.218
20.	PY 5	5	8	7	1	-	-	0	0.008	0.100
21.	PMK 1	6	9	6	3	-	-	0	0.001	0.011
22.	PMK 2	14	17	12	2	2	-	1	0.063	0.371
23.	PMK 3	9	17	10	3	2	-	2	0.037	0.200
24.	ASD 16	6	9	6	3	-	-	0	0.188	2.08
25.	ASD 18	14	24	14	6	2	1	1	0.018	0.075
26.	CO 47	14	21	14	3	2	1	1	0.076	0.362
27.	MDU 5	1	2	1	-	-	1	0	0.000	-
28.	ANNADA	2	3	3	-	-	-	0	0.000	-
29.	TULASHI	5	9	5	2	1	-	1	0.002	0.022

* Sub spp status is not known

evolution of 28 Nepalese rice varieties. Pedigree images of all the 29 varieties were obtained and the image of ADT 37 is shown as an example in Figure 1. Depths of generations indicate number of crossings involved in evolution of a particular variety. Screen shot of the depth of generations for ADT 36 is shown in Figure 2.

In the present study, 31 out of 69 ancestors occurred only once in the pedigree of 29 rice varieties which is similar to that reported earlier (Shivkumar *et al.* 1998) where in 11 out of 37 ancestors appeared only once (Table 2). Further, it was observed that only 18 landraces contributed for the development of more than 10 varieties. DEE-GEO-WOO-GEN was the most frequently used ancestor due to its source of dwarfing gene (sd-1) and it appeared in as many as 25 (86.20 %) varieties. This was followed by CINA and LATISAIL each in 24 (82.70%), for photo period-insensitivity (used as maternal parent) and for non-

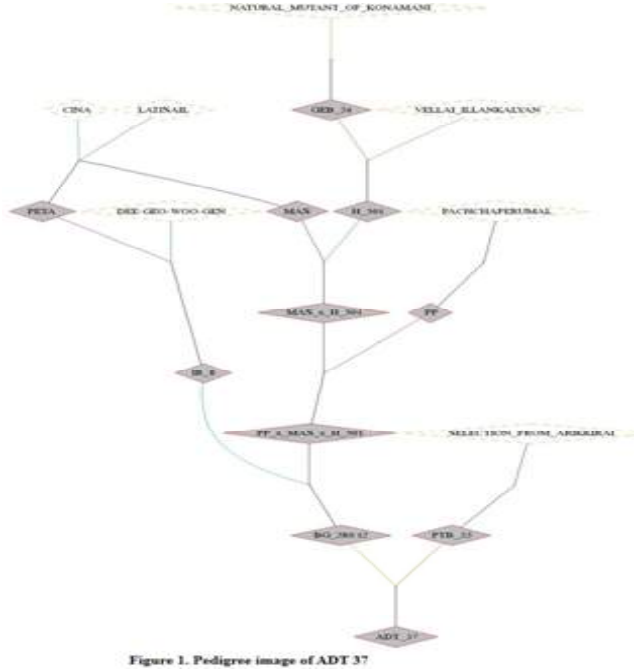

Figure 1. Pedigree image of ADT 37

Table 3. Details of sub spp., origin, frequency, varietal contribution and special features of ancestors of rice varieties

Sl No	Landrace	Sub spp.	Origin	Frequency (%)	Varietal contribution	Special features
1	Anaikomban	indica	India	3.4	1	
2	Arikkirai	indica	India	13.7	4	Res. to all biotypes of BPH
3	Azucena	japonica	Philippines	10.3	3	Aromatic rice
4	Basmathi 370	indica	India	3.4	1	Res. to stem rot, blast
5	Benong	javanica	Indonesia	44.8	13	Rainfed, low land
6	Bhogjira	indica	India	6.8	2	Res. to BLB, stripped borer
7	Bulk h9	-	-	3.4	1	
8	Chow-sung	japonica	S.Korea	6.8	2	Aromatic rice
9	Cina	indica	China	82.7	24	Photo-insensitive
10	Dasal	indica	India	6.8	2	Salt tolerance
11	Dee-Geo-Woo-Gen	indica	Taiwan	86.2	25	Dwarf, drought, upland
12	Eravapandi	indica	India	34.4	10	Res.to RTV, GLH, BPH
13	Gampai	indica	Thailand	34.4	10	Res. to RTV, blast
14	Garikasannavari	indica	India	3.4	1	-
15	Gowdalu	indica	India	3.4	1	-
16	Italy tau	-	Taiwan	3.4	1	-
17	Iwataasahi	japonica	Japan	3.4	1	-
18	Iyosengokku	japonica	Japan	3.4	1	-
19	Jeeragasamba	indica	India	3.4	1	-
20	Jojutla	indica	Mexico	31	9	-
21	Kameji	japonica	Japan	24.1	7	-
22	Kavunginpoothala	indica	India	3.4	1	-
23	Kiryouyoshi	japonica	Japan	20.6	6	Tolerance to flooding
24	Konamani	indica	India	68.9	20	-
25	Korangu samba	indica	India	3.4	1	Eating quality, Res. to stem borer
26	Kullakar	indica	India	6.8	2	-
27	Kuruvai	indica	India	10.3	3	-
28	Kuruvai kalayan	indica	India	3.4	1	-
29	Kyonishiki	-	Taiwan	3.4	1	-
30	Lambayeque-1	indica	Peru	3.4	1	-
31	Latisail	indica	India	82.7	24	Non lodging, non shattering, Res. to RTV, drought tolerance
32	Machakanta	indica	India	3.4	1	-
33	Marong paroc	-	Philippines	51.7	15	-
34	2 Mayangebos 80	indica	Malaysia	6.8	2	-
35	Meijiho	-	-	3.4	1	-
36	Mifb322-1	javanica	Philippines	3.4	1	-
37	Milek kunning	indica	Malaysia	3.4	1	-
38	Mudgo	indica	India	13.7	4	Res. to BPH, WBPH
39	Nallarlu	indica	India	3.4	1	-
40	Nanhng mon	-	Thailand	6.8	2	-
41	Nippon tau	-	Taiwan	3.4	1	-
42	Norin 8	japonica	Japan	3.4	1	-
43	O.glaberrima	other spp	Africa	3.4	1	-
44	O16	-	-	3.4	1	-
45	Oluanchu	japonica	Taiwan	13.7	4	-
46	O.nivara	other spp	-	41.3	12	Res. to grassy stunt virus
47	Os 4	-	Nigeria	3.4	1	-
48	Osakaashi	indica	Japan	3.4	1	-
49	Pachchaperumal	indica	Srilanka	6.8	2	-
50	Pachiam	javanica	-	55.1	16	-
51	Palwan	indica	Philippines	10.3	3	-
52	Pokkali	indica	India	3.4	1	Tolerance to salt & Fe toxicity

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Sl No	Landrace	Sub spp.	Origin	Frequency (%)	Varietal contribution	Special features
53	Seraup Besar 15	indica	Malaysia	7.2	5	-
54	Siam 29	indica	Thailand	3.4	1	Res. to gall midge
55	Sinawpagh	japonica	Philippines	51.7	15	Res. to blast, BLB, stem borer
56	Tadukan	indica	Philippines	44.8	13	
57	Tainaniku 487	japonica	Taiwan	31	9	-
58	Tsai-yuan-chung	indica	Taiwan	65.5	19	Good agronomic base
59	Tetep	indica	Vietnam	17.2	5	Res. to blast
60	Thavalakannan	indica	India	3.4	1	Res. to RTV, BPH
61	Thekkan	Indica	India	34.4	10	Res. to RTV, BPH, gall midge
62	Unknown India	indica	India	44.8	13	-
63	Un. Japanese	japonica	-	51.7	15	-
64	Urang urangan	indica	Indonesia	3.4	1	-
65	Vellai illankalayan	indica	Srilanka	6.8	2	-
66	Vellaikar	indica	India	58.6	17	-
67	W1543	indica	India	41.3	12	-
68	Waikoku	indica	China	3.4	1	-
69	Yokichisen	indica	Japan	3.4	1	-

shattering, respectively. Further GEB 24, for good grain quality, in 20 (69 %) varieties and TSAI- YUAN-CHUNG, for good agronomic base, in 19 (66 %) varieties. It was revealed that three ancestors *viz.*, DEE-GEO-WOO-GEN, CINA and LATISAIL, the parents of IR 8, are common in 24 out of 29 varieties. This is in accordance with the earlier reports of Hargrove *et al.* (1985), Shivkumar *et al.* (1998) and Joshi (2005). In India out of 298 rice varieties released between 1966 and 1986 by Central Variety Release committee (CVRC), 90 % of the varieties are semi-dwarf bearing the blood of DEE-GEE-WOO-GEN (Krishnamurthy 1986) while in Cuba, 98 % of rice varieties carry the same semi-dwarfing genes from DEE-GEO-WOO-GEN (Foster and Rutger 1978). In addition, most of these parental varieties used in hybridization programs trace to the same maternal parent: CINA, resulting in a very uniform cytoplasm (Fuentes *et al.* 1999). It is interesting to note from the pedigree profiles that 16 out of 29 rice varieties possess genomes of *indica*, *japonica* and *javanica* while seven possess indica and japonica only. This in contrast to the finding of Joshi (2005) in pedigree analysis of 28 Nepalese varieties wherein it was reported 27 out of 28 were purely *indica* genomes only. However, of the 20 wild sp. of rice only O. nivara, source of grassy stunt virus gene (Gsy), was traced as ancestor in 11 out of 29 varieties. Even though 20,000 accessions of wild sp. housed in germplasm banks (Zamir 2001) are sources of resistance to various biotic/ abiotic stresses (Khush 1999) only *O. nivara* was found utilized in the pedigrees of 29 rice varieties.

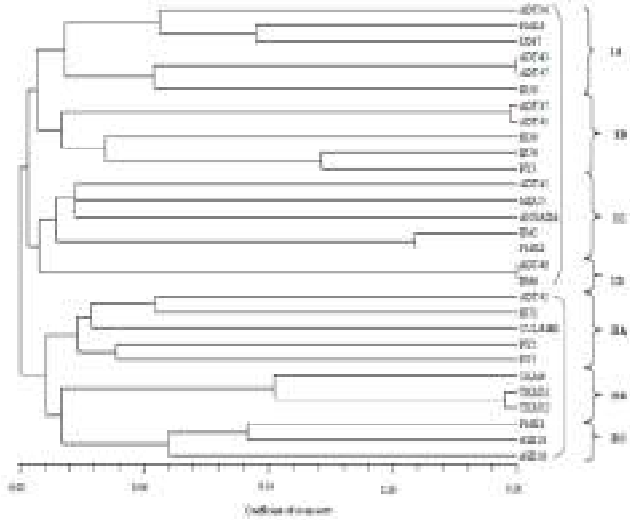
Clustering based on Coefficient of Co-ancestry (CoC) resulted in grouping of two major clusters I and II with 18 and 11 varieties respectively (Figure 3). All rice varieties bred at Aduthurai (except ADT 42) and IRRI (except IR 72) were found grouped in Cluster I

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

Sl. 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 O.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 & RI,Madurai
28)	ANNADA	MTU 15 x Waikoku	1987	NRRI,Cuttack
29)	TULASHI	CR 151 x CR 1014	1988	NRRI,Cuttack

*Released in Indonesia

TRRI, Tamil Nadu Rice Research Institute, IRRI, International Rice Research Institute, RRS, Rice Research Station, PKKVK, Perunthalaivar Kamaraj Krishi Vigyan Kendra, ARS, Agricultural Research Station, PBS, Paddy Breeding Station, AC & RI, Agrl. College & Research Instt. NRRI, National Rice Research Institute



while varieties bred at Tirurkuppam and Ambasamudram were observed in Cluster II. Grouping of IRRI lines with ADT lines may be due to more frequent use of IRRI lines as parents in the breeding programmes at Aduthurai rice research station. Further the usage of their own breeding lines/varieties in their breeding programmes may be another reason for clustering together of varieties of particular breeding station. Similar results were earlier reported for clustering Cuban varieties (Fuentes *et al.* 2005) and Indian rice varieties (Davierwala *et al*. 2000). Clustering analysis culminated in the identification of diverse clusters I A (ADT 36, PMK 3, C0 47, ADT 43 ADT 47 and IR 50) and cluster II C (PMK 1, ASD 18 and ASD 16) and hybridization programmes involving

these varieties may throw superior segregants besides broadening the genetic base.

Upon skimming of the pedigree data, it was observed that IR 8 had the highest foot print value of 14.38 (Table 4) followed by Peta with 11.25. In a similar study, Davierwala *et al*. (2000) reported the usage of IR 8, TN 1 and TKM 6 most frequently in the breeding programmes. The influence of IRRI bred varieties/lines was very evident from the fact that IR 8, the miracle rice variety developed during 1966, six years after IRRI was established (Khush 1999), was used directly or indirectly as parent in 19 out of 23 non IRRI bred varieties taken in the present investigation. Further, it indicated that out of 66, 35 were from IRRI which is indicative of the strong influence of IRRI coded lines in the breeding programmes of many rice research stations under National Agricultural Research Systems (NARS).

Inbreeding coefficient (IBC), a measure of genetic relatedness, indicates the presence of genotypes several times in the pedigree of a variety. On the other hand, more the number of ancestors involved in the development of a variety, more its genetic base. IBC alone may not be a reliable measure of genetic base because in certain varieties with few unrepeated ancestors the IBC will be 0.00 indicating broad genetic base. Therefore, by considering both IBC and number of ancestors, a genetic base index (GBI) was worked out. Among 29 varieties studied, PMK 1 (0.011) was found to be genetically broadest followed by ADT 47 (0.016) and TULASHI (0.022) (Table 2). Varieties bred at Aduthurai, compared to other centers, had broad genetic base. Even though genetic base of ADT varieties is broader they are genetically similar owing to sharing of common ancestry. In this study, ADT 43 and ADT 47 are genetically broader because of involvement of more number of ancestors in their pedigrees with lower IBC but they are genetically similar as indicated in the dendrogram (Figure 3) and inferred from the pedigree details of these two varieties (ADT 43 is one of the parents of ADT 47: Table 1).

In conclusion, 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 of agronomic value, resistance to biotic and abiotic stresses from large germplasm comprising landraces and wild spp. Widening the genetic base of rice cultivars can be accelerated by two approaches: (1) Thousands of landraces with wide allelic versions of desirable genes, left hitherto unutilized/underutilized, can be put into use by forming core collections using DNA markers (Xu *et al*. 2004). This provides breeders access to choose diverse genetic stocks for further hybridization. (2) Gene reserves from wild spp. can also be roped in by offsetting crossability barriers that come in the way of wide hybridization, through tissue culture techniques and constructing introgression Lines (ILs) using molecular markers by backcrossing (Zamir 2001). This ILs, comprising of marker-defined exotic segments of wild spp. introgressed onto the background of elite varieties, enables the breeders to discover and characterize genes that underlie traits of agricultural value.

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