# Morphological characterization of major paddy cultivars in seed chain of Tamil Nadu

R. VIGNESHWARI\*, A. VIJAYAKUMAR AND M. BHASKARAN<sup>1</sup>

Department of Seed Science and Technology, Tamil Nadu Agricultural University, COIMBATORE (T.N.) INDIA (Email:vigneshwari\_17@yahoo.co.in)

**Abstract :** Morphological characterization of 13 paddy varieties in seed chain of Tamil Nadu were done using 31 morphological traits in a field trial carried out in Paddy Breeding Station (PBS) of Tamil Nadu Agricultural University, Coimbatore during 2011 - 2012. The results of morphological characterization clearly indicated that the plant characters showed no variation among the varieties, while the grain characters showed clear variation among the varieties. Cluster analysis based on morphological characters grouped the varieties of medium and long slender grain type in one cluster and short bold grain type into another cluster at about 65% similarity level. The similarity indices range of 0.52 to 0.90 indicated remarkable homogeneity among the rice cultivars in the present study. So advanced technologies like molecular methods can be employed for unambiguous and quick identification of similar or closely related varieties.

Key Words: Rice, Morphological, Cluster analysis, Similarity

View Point Article: Vigneshwari, R., Vijayakumar, A. and Bhaskaran, M. (2014). Morphological characterization of major paddy cultivars in seed chain of Tamil Nadu. Internat. J. agric. Sci., 10 (1): 280-285.

Article History : Received : 27.07.2013; Revised : 21.10.2013; Accepted : 19.11.2013

# INTRODUCTION

Rice (Oryza sativa L.) is the staple food for more than 65 per cent of the people of India which plays an important role in the food security of the nation. It accounts for about 43 % of total food grain production and 46 % of total cereal production in the country. Among the rice growing countries, India has the largest area (42.56 million hectares) followed by China. Though the area is larger the productivity is very less compared to China. The average productivity of rice in India is 2.2 tons/ha, with annual production of 95.98 million tonnes from 42.56 million ha. Among the major rice producing states of India, Tamil Nadu ranks sixth with the contribution of 7.06% with the annual production of 62.53 lakh tonnes from 20.16 lakh ha (Anonymous, 2011). In order to meet the domestic demand of the increasing population the production of milled rice has to be increased to 125 million tons by the year 2030 (Shanker, 2010). Therefore, to sustain the self sufficiency in rice, additional production

\* Author for correspondence <sup>1</sup>Seed Centre, Tamil Nadu Agricultural University, COIMBATORE (T.N.) INDIA

of 1.5 million tons is needed every year. Since there is not much scope to increase the area of rice cultivation (due to urbanization and severe water constraints), the additional production will have to come from less land, less water and less human labour (Gujja and Thiyagarajan, 2009). The expected production can be achieved only by the use of high yielding improved varieties. The performance of any commercially cultivated rice variety mainly depends on the true to type of the variety which is mainly decided by the quality seed. It has been estimated that 1% impurity in seed lot may decrease the potential yield of varieties and hybrids by about 100 kg/ha (Mao *et al.*, 1996).

High seed quality can be obtained only by a thorough control of the entire seed production process, step by step from planning to final delivery. In a country like India, where certified seed production is done by registered farmers and private sector (Mishra *et al.*, 2003), monitoring genetic purity at each stage of seed production becomes necessary. That requires science, technology, expertise, experience, good management and certainly, the most important, an absolute and unconditional commitment with quality. Seed testing for quality assurance is one important step in the process of production of high quality seed. Conventionally, differences in morphology, cultural characteristics, and pedigree serve as the initial basis to differentiate the proposed variety from existing ones (Anderson and Wu, 2007). In general seed genetic purity is assessed based on grow out test (GOT). So, morphological descriptors of varieties of crop species are required for verifying varietal identity and determining varietal purity. With this view, the study was carried out to assess the morphological variability of rice cultivars which are in the present seed chain and commercial cultivation of Tamil Nadu.

# **MATERIAL AND METHODS**

#### Morphological characterization :

#### Plant material:

The experimental material consists of thirteen paddy varieties which are in the commercial cultivation of rice belts of Tamil Nadu (Table A). The pure seeds of all these varieties were collected from the Paddy Breeding Station, Tamil Nadu Agricultural University, Coimbatore. The experiment was carried out in Paddy breeding Station (PBS) of Tamil Nadu Agricultural University, Coimbatore during 2011 - 2012.

#### Experimental details:

The trial was conducted as per the DUS guidelines, in a complete randomized block design with three replications. Each entry was sown in plots with rows of 6m length at spacing of 30 cm between rows and 20 cm between plants. The characteristics and their states given as per the National Test Guidelines for distinctness, uniformity and stability (DUS) (Anonymous, 2007) were recorded at different stages of crop growth period. Observations were recorded on ten randomly chosen plants of each variety per replication at appropriate growth stage for thirty one morphological traits (Table B).

## Data analysis :

#### Morphological data:

The multi state data scored on 31 morphological traits were used to analyze the genetic similarities among 13 paddy varieties based on simple matching coefficient (Sokal and Michener, 1958) using NTSYS-pc version 2.02i (Rohlf, 1998). The resulting similarity matrix was first subjected to cluster analysis by the unweighted pair-group method with the arithmetic average (UPGMA) method (Sneath and Sokal, 1973) using sequential agglomerative hierarchical nested cluster analysis (SHAN) programme. A phenetic tree was constructed using the TREEPLOT programme of NTSYS pc.

# **RESULTS AND DISCUSSION**

In the present study 13 paddy varieties which are in the commercial cultivation and also in the seed chain of Tamil Nadu, were characterized using morphological markers to provide useful information to distinguish a variety from other varieties which could be used in seed genetic purity assessment. Among the 31 descriptors studied some of the plant characters like basal leaf sheath colour, leaf anthocyanin colouration, anthocyanin colouration of auricles, shape and colour of ligule, anthocyanin colour of internodes, presence of awns, panicle secondary branching, showed no variation among the varieties.

The traits like intensity of leaf colour, flag leaf attitude of blade and panicle curvature of main axis showed noticeable variation. The light green leaves of White Ponni differentiated it from other varieties. Likewise the horizontal flag leaf

Table A : List of paddy varieties and their parents used in the present study									
Sr. No.	Variety		Parentage						
1.	ADT 37	BG 280 -12	x	PTB 33					
2.	ADT 43	IR 50	х	IW ponni					
3.	ADT 46	ADT 38	х	CO 45					
4.	ASD 16	ADT 31	х	CO 39					
5.	Bhavani	Peta	х	BPI 76					
6.	CO 43	Dasal	х	IR 20					
7.	CO 48	CO 43	х	ASD 19					
8.	CO 49	C 20	х	RNR 52147					
9.	CO 50	CO 43	х	ADT 38					
10.	CR 1009	Pankaj	х	Jagannath					
11.	IR 20	IR 262	х	TKM 6					
12.	IR 50	IR-2153-14-1-6-2	х	IR 28 X IR 36					
13.	IW Ponni	Taichung 65/2	Х	Mayang Ebos-80					

MORPHOLOGICAL CHARACTERIZATION OF MAJOR PADDY CULTIVARS IN SEED CHAIN

Internat. J. agric. Sci. | Jan., 2014| Vol. 10 | Issue 1 | 280-285 Hind Agricultural Research and Training Institute

R. VIGNESHWARI, A. VIJAYAKUMAR AND M. BHASKARAN

Table 1 : Similarity index computed for morphological characters													
	ADT 37	ADT 43	ADT 46	ASD 16	Bhavani	CO 43	CO 48	CO 49	CO 50	CR 1009	IR 20	IR 50	IWP
ADT 37	1.00												
ADT 43	0.71	1.00											
ADT 46	0.68	0.71	1.00										
ASD 16	0.71	0.71	0.52	1.00									
Bhavani	0.58	0.68	0.74	0.58	1.00								
CO 43	0.55	0.77	0.68	0.71	0.77	1.00							
CO 48	0.52	0.71	0.65	0.58	0.71	0.77	1.00						
CO 49	0.52	0.68	0.65	0.61	0.74	0.81	0.84	1.00					
CO 50	0.58	0.71	0.68	0.71	0.81	0.84	0.81	0.84	1.00				
CR 1009	0.61	0.68	0.58	0.71	0.58	0.65	0.58	0.65	0.68	1.00			
IR 20	0.61	0.71	0.65	0.58	0.68	0.77	0.81	0.81	0.81	0.61	1.00		
IR 50	0.58	0.81	0.77	0.65	0.87	0.90	0.71	0.81	0.81	0.61	0.74	1.00	
IWP	0.61	0.68	0.61	0.65	0.68	0.74	0.84	0.71	0.77	0.58	0.77	0.68	1.00

attitude distinguished Bhavani and CO 48 from other varieties (Fig. 1). The varieties ADT 37 and ADT 46 exhibited deflexed panicle curvature among the thirteen varieties, while all other showed drooping type panicles. The grain characters showed clear variation among the varieties (Fig. 2). The length of the grain varied from short to medium while the width of the grain classified the varieties into narrow, medium and broad



Fig. 1: Attitude of flag leaf blade in ADT 37, Bhavani and CO 49



Fig. 2: Morphological variation in grain characters of 13 paddy varieties

types. Based on the decorticated grain shape the varieties were grouped as short bold (ADT 37, ASD 16 and CR 1009), long bold (CO 43), medium slender (CO 48, CO 49, CO 50, IR 20 and Improved White Ponni) and long slender varieties (ADT 43, ADT 46, Bhavani and IR 50) (Table B). This was in accordance with Siddiqui *et al.* (2007) who reported that the Pakistan rice genetic resources showed a great diversity for all the measured grain morphological characters. The level of demarcation was high in this quantitative grain characters compared to qualitative characters. Since in qualitative characters there is a high chance of merging of their states of expression as they are continuous or discrete giving room for human error.

#### **Cluster analysis:**

Cluster analysis based on morphological characters in rice was also reported in several studies, such as, Ghalain (2006), Sarawgi and Bhisne (2007), Mehla and Kumar (2008), Mathure et al. (2010), Li et al. (2010), Zhang et al. (2010) and Nascimento et al. (2011). In this study the dendrogram derived from cluster analysis of 13 paddy varieties based on NTSYS simple matching coefficient showed two major clusters at about 65% similarity level (Fig. 3). Similarity indices estimated based on all the 31 descriptors ranged from 0.52 to 0.90 (Table 1). Among the two major clusters, cluster I consisted of medium and long slender grain type varieties viz., ADT 43, ADT 46, Bhavani, CO 43, CO 48, CO49, CO 50, , IR 20, IR 50 and IW ponni. The cluster II consisted of short bold grain type varieties viz., ADT 37, ASD 16 and CR 1009. Katsuta and Okuno (1992) also showed that the local varieties in northern Pakistan are typically classified into two groups, based on the shape of grain. This clearly indicates that those characters, which clearly delineate the varieties forms the basis of distinguishability.



Fig. 3 : Dendrogram based on morphological characters showing the genetic similarity among 13 paddy varieties using simple matching co-efficient

The dendrogram based on simple matching coefficient showed maximum similarity coefficient of 0.90 between the varieties CO 43 and IR 50. The minimum similarity coefficient of 0.52 between the varieties ASD 16 and ADT 46; and CO 48 and CO 49 with ADT 37 showed that these varieties were phenotypically diverse among all other varieties. The average similarity index of 0.65 indicated remarkable homogeneity among the rice cultivars in the present study. Similar results were reported by Ogunbayo et al. (2005) in assessing phylogenetic diversity and relationship among 40 rice accessions of Nigeria. On the basis of above observation, it is clear that these characters were not enough to distinguish the varieties. So the purpose of distinguishing the closely related varieties can be fine tuned only when it is supported by a parameter which is stable in all environments like molecular markers. Due to the proliferation of many varieties in all major crop species, however, the number of combinations of morphological and physiological descriptors available to establish the uniqueness of a variety has narrowed down (Song et al., 1999). Other than the high similarity level of morphological markers, they also influenced by environmental factors (Li et al. 2002). The necessity of employing the suitable molecular markers for further discrimination of the varieties and to better exploit the diversity is rightly quoted by Zapico et al. (2010).

### **Conclusion:**

The cluster analysis based on morphological characters grouped the thirteen varieties into two major clusters. However the morphological makers were not quite enough to discriminate between the morphological overlap varieties and the morphological identical varieties. So these parameters alone may not be superior enough to discriminate a variety from offtypes during seed production. So, for unambiguous and quick identification of similar or closely related varieties the molecular technology approach can be employed hopefully for genetic purity determinations in seed testing.

# REFERENCES

Anderson, M.P. and Wu, Y.Q. (2007). Fingerprinting of bermuda grass DNA. USGA Turfgrass Environ. Res. Online, 6 (14): 1-8.

Anonymous (2007). Guidelines for the Conduct of Test for Distinctiveness, Uniformity and Stability on Rice (*Oryza sativa* L). *Plant Variety J. India*, **1**(1): 1-25.

**Ghalain, S.S. (2006).** Genetic divergence in rice (*Oryza sativa* L) genotypes grown in Kamaun Himalaya. *Indian J. Genet.*, **66** : 37-38.

**Gujja, Bikshyam and Thiyagarajan, T.M. (2009).** New hope for Indian food security? The system of rice intensification, Gatekeeper Series, No.143, International Institute for Environment and Development (IIED), London, UNITED KINGDOM.

Katsuta, M. and Okuno, K. (1992). Rice cultivars in Northern Pakistan. *Japan J. Breed.*, 42: 707-713.

Li, X., Yan, W., Agrama, H., Hu, B., Jia, L., Jia, M., Jackson, A., Moldenhauer, K., McClung, and Wu, D. (2010). Genotypic and phenotypic characterization on genetic differentiation and diversity in the USDA rice mini-core collection. *Genetica*, **138**: 1221-1230.

Li, Y.C., Korol, A.B., Fahima T., Beiles, A. and Nevo, E. (2002). Microsatellites: genomic distribution, putative functions and mutational mechanisms: a review. *Molecular Ecol.*, **11**: 2453-2465.

**Mao, C.X., Virmani, S.S. and Kumar, I. (1996).** Technological innovations to lower the costs of ybrid rice seed production. In: Virmani SS et al (eds) Advances in hybrid rice technology. Proceedings of Third International Symposium on Hybrid Rice, Directorate of Rice Research, Hyderabad (A.P.) INDIA.

Mathure, S., Shaikh, A., Renuka, N., Wakte, K., Jawali, N., Thengan, R. and Nadaf, A. (2010). Characterization of aromatic rice (*Oryza sativa* L) germplasm and correlation between their agronomic and quality traits. *Euphytica* DOI 10.1007/s10681-010-0294-9.

Mehla, B.S. and Kumar, S. (2008). Use of morphological traits as descriptors for identification of rice genotypes. *Agric. Sci. Digest.*, **28**(2): 101-104.

Mishra, B., Viraktamath, B.C., Ilyas Ahmed, M., Ramesha, M.S. and Vijayakumar, C.H.M. (2003). Hybrid rice research and development in India. In: Virmani SS, Mao CX, Hardy B (eds) Hybrid rice for food security, poverty alleviation, and environmental protection. Proceedings of the 4th International Symposium on Hybrid Rice, 14– 17 May 2002, Hanoi, Vietnam. Los Baños (Philippines), International Rice Research Institute, pp 265–283.

Nascimento, W.F., Silva, E.F. and Veasey, E.A. (2011). Agromorphological characterization of upland rice accessions. *Sci. Agric.*, **68**(6): 652-660. Ogunbayo, S.A., Ojo, D.K., Guei, R.G., Oyelakin, O.O. and Sanni, K.A. (2005). Phylogenetic diversity and relationships among 40 rice accessions using morphological and RAPDs techniques. *Afr. J. Biotechnol.*, **11**: 1234-1244.

**Rohlf, F.J. (1998).** NTSYS-pc Numerical Taxonomy and Multivariate Analysis System, version 20, Exeter Software, Setauket, New York (U.S.A.).

Sarawgi, A.K. and Bhisne, R. (2007). Studies on genetic divergence of aromatic rice germplasm for agro- morphological and quality characters. *Oryza*, 44: 74-76.

**Shanker, L. (2010).** In: Guidelines for seed production of hybrid rice bulletin. Department of Agriculture and Cooperation, Government of India, Ministry of Agriculture. pp. 1-44.

Siddiqui, S.U., Kumamaru, T. and Satoh, H, 2007. Pakistan rice genetic resources–II: Distribution pattern of grain morphological diversity. *Pak. J. Bot.*, **39**(5): 1533-1538.

**Sneath, P.H.A. and Sokal, R.R. (1973).** *Numerical taxonomy* Freeman San Francisco, pp: 573.

**Sokal, R. and Michener, C. (1958).** A statistical method for evaluating systematic relationships. *Univ. Kans Sci. Bull.*, **38**: 1409–1438.

Song, Q.J., Quigley, C.V., Nelson, R.L., Carter, T.E., Boerma, H.R., Strachan, J.L. and Crega, P.B. (1999). A selected set of trinucleotide simple sequence repeat markers for soybean cultivar identification. *Plant Var. Seeds*, **12**: 207-220.

Zapico, F.C.L., Namocatcat, J.A. and Turner, J.L.C. (2010). Genetic diversity analysis of traditional upland rice cultivars in Kihan, Malapatan, Sarangani rovince, Philippines Using Morphometric Markers Philippine. J. Sci., **139** (2): 177-180.

Zhang, C.H., Li, J.Z., Zhu, Z, Zhang, Y.D., Zhao, L. and Wang, C.L. (2010). Cluster analysis on japonica rice (*Oryza sativa* L) with good eating quality based on SSR markers and phenotypic traits. *Rice Sci.*, **17** : 111-121.

10<sup>th</sup> Year \*\*\*\* of Excellence \*\*\*\*\*