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Original Article

Use of Descriptor Codes in Agro-Morphological Characterization: Qualitative assessment of 20 Land Races of Rice (Oryza sativa L.) from West Bengal

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Abstract

Rice is one of the very few crop species endowed with rich genetic diversity which is embodied in the traditional rice landraces or folk varieties. It is one of the most researched crops. Rice genetic resources and human welfare are intricately interlinked. Rice has shaped the history, culture, diet and economy of billions of people of Asia. The diversity data generated in time and space have been valuable to communities, scientists and policy managers to formulate and implement conservation strategies of *in situ*, on-farm as well as *ex situ* conservation and management of genetic resources. West Bengal has rich rice genetic wealth. But this genetic wealth is being silently depleted due to the onslaught of the high-yielding varieties (HYVs) and neglect. Descriptor codes were used for the qualitative evaluation of genetic diversity among the 20 rice genotypes collected from different parts of West Bengal, following the Standard Evaluation System (SES) for rice developed by the International Rice Research Institute (IRRI). There is an urgent need to document, characterize and conserve these varieties.

Keywords: *Rice landraces, descriptor codes, qualitative characterization, SES, genetic diversity*

Introduction

Rice is one of the very few crop species endowed with rich genetic diversity which account over 100,000 folk varieties or landraces. It is one of the most researched crops. Rice (*Oryza sativa* L.) is one of the most important food crops grown worldwide and is the staple food for half of the world population (Sasaki & Burr 2000). Rice genetic diversity has attracted great interest of researchers due to the importance of rice as one of the major world food crops, (Roy *et al.* 2016). This diversity is embodied in the traditional rice landraces or folk varieties.

Rice genetic resources and human welfare are intricately interlinked. Rice being the most important staple food in South and South-East Asia, the conservation of the rice diversity and utilization of the diversity for rice breeding is directly related to the food security of this heavily populated part of the world (Pant, 2010). Morphological evaluation is a preliminary step to estimate the variability and relationship among cultivars.

The use of agro-morphological traits is the most common approach utilized to estimate relationships between genotypes (Bajracharya *et al.,* 2006). Knowledge of the agro-morphological diversity within a crop and its distribution across agro-ecological zones could be of a great help in the management of its germplasm and the development of strategies for its improvement (Odjo *et al.*, 2017). Developing minimal descriptors for characterisation and evaluation of different agri-horticultural crops is a pre-requisite for the National Database on Plant Genetic Resources (Mahajan *et al.,* 2000). The agro-morphological characterization is fundamental in order to provide information for plant breeding programs (Lin, 1991).

Rice Landraces

Landraces offer a valuable gene pool for future breeding program (Patra *et al.,* 2003). For farmers, genetic diversity means varietal diversity, which farmers can clearly distinguish on the basis of agromorphological traits, phenological attributes, postharvest characteristics, and differential adaptive performance under abiotic and biotic stresses (De & Dey, 2013). Landraces are the heterogeneous crop populations that humans deliberately cultivate. The amount of genetic diversity within species is essential for the survival of species and their adaptation to changing environments. (Gao, 2003). Importance of landraces or folk varieties can never be denied in agriculture system, because improvement in existing variety depends upon desirable genes which are possibly present in landraces and wild varieties only (Shiva, 1991).

Biological poverty in the rice genepool

This wealth of genetic resources as found in rice may provide the base for future progress in rice improvement in the face of shrinking resources both biological and physical (Chang, 1984). The widespread adoption of high-yielding rice varieties (HYVs) has led to the biological poverty of rice germplasms, as local rice varieties are abandoned for modern varieties. (Pant, 2010). At present significant numbers of the West Bengal rice landraces are on the verge of being eroded (Deb, 2000, 2005). Plant genetic resources are among the most vulnerable of all non-renewable natural resources. Once lost, they are lost forever.

Qualitative assessment using descriptor codes

Qualitative characters are important for plant description and mainly influenced by the consumers preference, socio-economic scenario and natural selection (Hien *et al*., 2007). Some morphological characters could be grouped into distinct classes on the basis of each of these characteristics. Descriptive codes were used for traits that have more or less discontinuous genetic variation (e.g. Collar colour, Culm internode colour etc) or for traits whose nature of expression is not easily translated into numerical units.

Objective of the investigation

For many morphological features often more than two character states are observed. Descriptor codes are then used for qualitative assessment. Documentation and awareness of the ecological, agronomic and cultural importance of the still extant West Bengal folk rice varieties is necessary as many of the indigenous folk rice varieties are on the verge of extinction due to rampant cultivation of modern, high yielding varieties (HYVs). The aim of the present study was to characterize 20 accessions of landraces rice (*Oryza sativa* L.) varieties of West Bengal, based on qualitative agro-morphological descriptors.

Methodology

Plant Material: Rice germplasm used in this study consisted of 20 folk rice varieties of West Bengal collected from different districts of West Bengal. Both aromatic and non aromatic landraces were chosen. As a check a high yielding indigenous non aromatic was taken. One multiple seeded landrace was taken in the sample. These accessions were collected from different agro-climatic belts of West Bengal, studied under field conditions for two consecutive years.

The details of the rice genotypes are given in Table 1.

Table 1. The rice genotypes used in this study: genotype name, place of adaptation/source and type of cultivar**.**

SL No.	Genotypes	Place of adaptation / Source District	Origin	Type of Cultivar
1	CHINIATAP	Hilli, Cooch Behar	CL, SF	A WBL
2	JUGAL	Purulia	CL SF	MS WBL
3	LATASAIL	Purulia	CL, SF	NA WBL
4	KHIRABICHI	Purulia	CL, SF	NA WBL
5	LALBADSHAHBHOG	Purulia	CL, SF	NA WBL
6	MANIKKALMA	Purulia	CL SF	NA WBL
7	MURGIBALAM	Bankura	CL, SF	NA WBL
8	NYATA	Purulia	CL, SF	NA WBL
9	PADMASAIL	Bankura	CL, SF	NA WBL
10	PANCHALI	Purulia	CL, SF	NA WBL
11	PAAN	Bankura	CL SF	NA WBL
12	PATNAI	Purulia	CL, SF	NA WBL
13	SWARNA	Bankura	CL, SF	HYV INA
14	TIKARNADI	Purulia	CL, SF	NA WBL
15	RADHUNIPAGOL	Chakdah, Nadia	CL SF	A WBL
16	KATARIBHOG	Chakdah, Nadia	CL, SF	A WBL
17	BADSHAHBHOG	Chakdah, Nadia	CL, SF	A WBL
18	SWAPANDALI	Siliguri, Darjeeling	CL, SF	NA WBL
19	TULAIPANJA	Malda	CL, SF	NA WBL
20	SONAJHULI	Dinhata, Coochbehar	CL SF	NA WBL

Table 1. A WBL = Aromatic West Bengal landrace, CL = collection line, HYV = high yielding NA =non-aromatic, INA = indigenous non-aromatic, MS WBL = multiple seeded West Bengal landrace, NA WBL = Non aromatic West Bengal landrace, SF = self-fertilized.

Experimental design

The rice genotypes were grown in a randomized block design (RBD) with three replicates of 40 plants each. Seeds were sown in the seed bed on the last week of June and one healthy seedling/hill was transplanted after 30 days at a row x plant spacing of 25cm x 15cm. Normal agronomic practices were followed.

Descriptor Codes used for the qualitative assessment

Qualitative characterization was done following the Standard Evaluation System (SES) for rice developed by the International Rice Research Institute (IRRI, 2002). Morphological characters and their respective descriptor codes used for the qualitative evaluation of genetic diversity among the 20 rice genotypes are given in Table 2. A total of 9 (nine) morphological characters which can be evaluated by descriptor codes were taken. The results are shown in table 3.

Table 2. List of Descriptor codes used for the qualitative evaluation of genetic diversity among the 20 rice genotypes.

SL. No.	Trait	Abv.	Growth stage	Method of scoring	code	Description
1	**Auricle Colour**	**AC**	Stem elongation to booting stage	Ocular inspection	1	Light green
					2	Purple
2	**Basal Leaf Sheath Color**	**BLSC**	Early to late vegetative stage	Visual observation	1	Green
					2	Purple lines
					3	Light purple
					4	Purple
3	**Collar Color**	**CC**	Stem elongation	Ocular inspection.	1	Light Green

			to booting stage		2	Green
					3	Purple
4	**Culm Angle**	**CmA**	Milk stage to mature grain stage	Visual observation. Readings are based on majority of plants grown in the entire plot	1	Erect (<30^0)
					3	Intermediate (~45^0)
					5	Open (~60^0)
					7	Spreading (>60^0)
					9	Procumbent (the culm or its lower part rests on ground surface)
5	**Culm Internode Colour**	**CmIC**	Milk stage to mature grain stage	Visual observation of the outer surface of the internodes of the culm is recorded.	1	Green
					2	Light gold
					3	Purple lines
					4	Purple
6	**Flag Leaf Angle**	**FLA**	Stem elongation to booting stage	Visual observation. Sample size = 5.	1	Erect
					3	Intermediate
					5	Horizontal
					7	Descending
7	**Leaf Angle**	**LA**	Stem elongation to booting stage	Visual observation.	1	Erect
					2	Nearly erect, acute angle formed.
					3	Angular
					4	Wide angular to horizontal.
					5	Horizontal
					9	Droopy
8	**Leaf Blade Colour**	**LBC**	Stem elongation to heading stage	Visual observation. Readings are based on majority of plants grown in the entire plot	1	Light green
					2	Green
					3	Dark Green
					4	Purple tips
					5	Purple margins
9	**Leaf Blade Pubescence**	**LBP**	Booting to heading stage	Ocular inspection, then fingers were rubbed from the tip down on the leaf surface. Presence of hairs on the blade surface were classified.	1	Glabrous
					2	Intermediate
					3	Pubescent

Results and Discussion

The rice genotypes selected for this study belonged to the indica group of *Oryza sativa* L. These rice landraces were collected from different districts of West Bengal where there are distinct eco-geographic variations. Though all the rice genotypes belonged to *Oryza sativa* L. the present study revealed sufficient genetic divergence for various qualitative traits (Table 3). This variation reflects the capability of the indigenous farmers for developing and sustaining diverse landraces.

Table 3. Qualitative evaluation: Use of descriptor codes to estimate genetic diversity among the 20 rice landraces.

Sl. No.	**Rice Land-race Name**	**AC**	**BLSC**	**CC**	**CmA**	**CmIC**	**FLA**	**LA**	**LBC**	**LBP**
1	CHINIATAP	1	1	1	5	1	3	5	2	**2**
2	JUGAL	2	3	2	1	1	3	3	2	3

3	LATASAIL	2	4	3	3	2	5	5	2	3
4	KHIRABICHI	2	3	3	3	1	3	3	2	3
5	LALBADSHAHBHOG	1	1	1	1	2	5	5	2	3
6	MANIKKALMA	1	1	1	3	1	1	3	2	3
7	MURGIBALAM	1	1	2	3	1	1	3	2	3
8	NYATA	1	1	1	5	1	1	3	1	3
9	PADMASAIL	1	1	1	3	1	5	5	1	3
10	PANCHALI	1	1	2	5	1	5	4	2	1
11	PAAN	1	1	1	3	1	5	3	2	1
12	PATNAI	1	1	1	1	1	1	3	2	3
13	SWARNA	1	1	1	1	1	1	3	2	3
14	TIKARNADI	1	1	1	5	1	1	3	7	3
15	RADHUNIPAGOL	2	1	1	3	1	5	5	2	3
16	KATARIBHOG	1	1	2	1	1	3	4	2	3
17	BADSHAHBHOG	1	1	2	1	1	5	5	2	3
18	SWAPANDALI	2	1	1	1	1	1	3	2	3
19	TULAIPANJA	1	1	2	3	1	5	5	2	3
20	SONAJHULI	1	1	1	1	1	1	3	2	3

Conclusion

The basic diversity data of landraces has been found important to monitor the dynamics of crop genetic resource management. Rice (*Oryza sativa* L.) diversity data generated in time and space have been valuable to communities, scientists and policy managers to formulate and implement conservation strategies of *in situ*, on-farm as well as *ex situ* conservation and management of genetic resources (Li *et al.*, 2000, Hien, 2007, De, 2014a). West Bengal has rich rice genetic wealth. But this genetic wealth is being silently depleted due to the onslaught of the high-yielding varieties (HYVs) and neglect (De, 2014b). There is an urgent need to document, characterize and conserve these varieties.

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