

Variation in the grain morphology among the dwindling indigenous rice biodiversity

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Abstract

Rice is one of the very few crop species endowed with rich genetic diversity which account over 100,000 landraces and improved cultivars and makes it one of the most researched crop. This genetic wealth is being silently eroded due to neglect and over-exploitation. Thousands of valuable allelic variations of traits of economic significance still remain unutilized in this crop plant. A better knowledge of genetic aspects of rice will also aid in genetic improvement and conservation programs of landraces of West Bengal. The rice genotypes used in the study comprised of aromatic and non-aromatic rice landraces of West Bengal specifically adapted to varied climatic and edaphic conditions of West Bengal. A total of 10 grain morphological and 6 different measurements of grains and kernels were used for the assessment of genetic diversity.

Success in any breeding programme depends largely on the extent of genetic variability present at different levels. The continuous selection among crosses of genetically related cultivars has led to a narrowing of the genetic base of the crops. Dwindling genetic wealth erodes the capacity to maintain and enhance agricultural productivity. The concern is not the loss of a

single species like wheat or rice, but the loss of diversity within species of the same population. Sufficient knowledge about genetic diversity in the gene pool is a pre requisite to adopt efficient and valuable breeding approach⁶. Utilisation of diverse parents in hybridisation programmes has been observed to yield better hybrids⁸. Indigenous rice biodiversity conservation is now seen as a necessity rather

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than a luxury¹. The farm level choice of cultivating a modern variety versus landrace for any one crop is driven by a set of supply and demand side factors. Grain morphology is one such trait which is important quality for consumers worldwide.

Rice is one of the very few crop species endowed with rich genetic diversity which account over 100,000 landraces and improved cultivars and makes it one of the most researched crop. These landraces constitute a conspicuous source of variation for crop improvement¹⁰. Long grain *geng/japonica* rice has a higher market preference due its excellent appearance quality. The *dense and erect-panicle 1 (dep 1)* gene has been widely used in the breeding of high-yielding *geng/japonica* rice cultivars in China. This gene causes short and round grain shape thus making it less attractive in global rice markets. So breeding of high-yielding long-grain *geng/japonica* rice cultivars by incorporating *dep1* with major-effect grain shape gene is of high priority in rice industry⁷. In China the breeding of high-yielding long-grain *geng/japonica* rice cultivars by incorporating *dep1* with major-effect grain shape genes is of high priority in rice industry⁹.

According to Chang² the greatest diversity of cultivated rice is found in a belt from North East India to South East China. Over 62,000 landraces of the Indian rice (*Oryza sativa* var *indica*) have been recorded from the Indian subcontinent alone³. West Bengal, a state of India in this belt has rich rice genetic wealth³. The major breeding efforts in the twentieth century have been a strong force in the reduction of crop genetic

diversity⁴. The Green Revolution introduced high-yielding varieties of rice to the developing world, replacing farmer's traditional crop varieties. The rice genetic wealth is being silently eroded due to neglect and over-exploitation.

The main objective of this study was to study grain morphological variation in some of the still extant landraces of West Bengal and selected cultivars of rice using grain morphological data. This information on the existing genetic diversity will be useful for selecting parents for future rice breeding programs attempting to improve the grain quality of rice varieties.

Plant material :

The rice genotypes used were adapted to varied climatic and edaphic conditions of West Bengal. 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.

Experimental design :

The rice genotypes were grown in a randomized block design (RBD) with three replicates of 40 plants each. Insects, pests and diseases were controlled as and when necessary by appropriate chemical sprays. Harvesting was done at 85% maturity of the seeds.

3. Assessment of genetic diversity :

A total of **16 traits** were measured

at various growth stages using the Standard Evaluation System (SES) for rice developed by the International Rice Research Institute, (IRRI, 2002). This trait characterization was divided into the following groups viz. 10 grain morphological trait characterization using descriptive codes and 6 measurements of grain and kernel dimensions using actual measurements.

Methodology for the ascertaining the grain/kernel dimensions :

The length and breadth of grains and kernels of 10 grains per landrace was measured under a dissecting microscope (Olympus).

Even though most of the rice genotypes belonged to *Oryza sativa* L. an enormous amount of variation was reflected during the characterization. The study confirmed the existence of a wealth of phenotypic divergence in the local rice germplasm. This variation reflects the capability of the indigenous farmers for developing and sustaining diverse landraces.

The 10 grain morphological trait characterization used in this study was viz. 1) Awning (An), 2) Awn Color (AnC), 3) Apiculus colour (Apc), 4) Aroma (Aro), 5) Lemma and Palea Colour (LmPC), 6) Lemma and Palea Pubescence (LmPb), 7) Sterile Lemma Colour (Slmc), 8) Sterile Lemma Length (Slml), 9) Sterile Lemma Actual Length (SlLt), 10) Seed Coat (bran) Color (SCC). The grain morphology trait characterization was carried out mostly using the following methodology of Descriptive codes: These codes are used for traits that have more or less discontinuous genetic variation (*e. g.*

lemma and palea pubescence) or for traits whose nature of expression is not easily translated into numerical units (*e.g* lemma and Palea Colour). There were some characterization that relied on the actual measurements viz. Sterile Lemma Actual Length (SlLt).

Assessment by grain morphological characterization :

The 10 grain morphological characters taken and the genetic diversity of the 15 rice genotypes estimated as shown in Table-2. Awning (An) was found in only 4 genotypes, Jalkamini, Jugal, Tulaipanja and Pusa Basmati-1. The Awn Color (AnC) colour however was the same in all varieties viz. straw colour. 2 types of Apiculus colour (Apc) observed in the 15 varieties. Tulsibhog, Mohonbhog and Tulasimanjari 14-2 had purple apiculus colour and the rest had straw colour. There was considerable variation in Lemma and Palea Colour (LmPC), In 9 genotypes (60%) the lemma and palea colour (LmPC) score was 0 (straw coloured), in 2 genotypes (13.33%) the score was 1 (Gold and gold furrows on straw background), Scores 2, 6, 9 and 10 denoting straw coloured lemma and palea with brown spots, purple spots on straw, blackish/greyish furrows in majority of the grains and black respectively were observed in 1 variety each. The Seed Coat (bran) Color (SCC) was white for most varieties, light brown for 1 viz. Jugal, the dual seeded landrace. Agniban had brown SCC. Red SCC was observed in Valki.

This baseline data based on the descriptor codes and actual measurements can be exploited in many ways to strengthen the long-term conservation, to rationalize the maintenance of the collections and to improve

accessibility to the conserved germplasm to support its use. This study would help in the documentation of the rich rice genetic wealth of West Bengal. The detailed characterization of genotypes, especially the west Bengal landraces would be an important documen-

tation for posterity.

The authors thank the indigenous farmers who provided the indigenous rice varieties.

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	ORIGIN	TYPE OF CULTIVAR
1	KOBIRAJSAI	MIDNAPUR	CL,SF	NA WBL
2	TULSIBHOG	COOCHBEHAR	CL, SF	NA WBL
3	KHEJURCHARI	24 PGS (SOUTH)	CL, SF	NA WBL
4	VALKI	COASTAL MIDNAPUR	CL, SF	NA WBL
5	JALKIMINI	GOTRA, NADIA	CL, SF	NA WBL
6	AGNIBAN	RANGABELIA, GOSABA	CL, SF	NA WBL
7	MOHANBHOG	RANGABELIA, GOSABA	CL,SF	A WBL
8	JUGAL	PURULIA	CL,SF	MS WBL
9	SWARNA	BANKURA	CL, SF	HYV INA
12	TULAI PANJA	MALDA	CL, SF	NA WBL
11	IR68305	BCKV, NADIA, WB, INDIA	CD from several crosses	HYV NA
12	PUSA BASMATI-1	IARI, NEW DELHI, INDIA	Pusa 150/Karnal Local	EB
13	TULASIMANJARI-14-2	India	Pure line	IA
14	AZUCENA	IRRI, Philippines	CL, SF	EA
15	PATNAI 23	CRRS, WB, India	CD from several crosses	HYV INA

Table 1. A WBL = Aromatic West Bengal landrace, BCKV= Bidhan Chandra Krishi Viswavidyalaya, CD = complex derivative, CL = collection line, CRRS= Chinsura Rice Research Station, EA = exotic aromatic, EB = evolved Basmati, HYV = high yielding NA =non-aromatic, IA = indigenous aromatic, INA = indigenous non-aromatic, MS WBL = multiple seeded West Bengal landrace, IRRI= International Rice Research Institute, NA WBL = Non aromatic West Bengal landrace, SF = self-fertilized.

Table-2. Grain morphological trait characterization

Sl No.	CULTIVAR	An	AnC	Apc	Aro	LmPC	LmPb	Slmc	Slml	Sllt	SCC
1	KOBIRAJSAI	0	0	2	2	0	4	1	5	3	1
2	TULSIBHOG	0	0	7	1	10	4	4	5	2.9	1
3	KHEJURCHARI	0	0	2	2	0	1	1	3	2	1
4	VALKI	0	0	2	2	9	4	1	3	2	5
5	JALKIMINI	9	1	2	2	0	4	1	5	3.3	1
6	AGNIBAN	0	0	2	2	1	5	1	3	2	4
7	MOHANBHOG	0	0	7	1	0	4	4	3	2	1
8	JUGAL	1	1	2	2	0	4	1	3	2.1	2
9	SWARNA	0	0	2	2	1	4	1	3	2.1	1
12	TULAI PANJA	9	1	2	2	0	5	1	5	3.5	1
11	IR68305	0	0	2	2	0	4	1	3	1.9	1
12	PUSA BASMATI-	9	1	2	1	0	4	1	5	3.5	1
13	TULASIMANJARI-14-2	0	0	7	2	6	4	4	3	1.8	1
14	AZUCENA	0	0	2	2	0	4	1	5	2.8	1
15	PATNAI 23	0	0	2	2	2	4	1	5	2.9	5

Table 2. Awning (An), Awn Color (AnC), Apiculus colour (Apc), Aroma (Aro), Lemma and Palea Colour (LmPC), Lemma and Palea Pubescence (LmPb), Sterile Lemma Colour (Slmc), Sterile Lemma Length (Slml), Sterile Lemma Actual Length (Sllt), Seed Coat (bran) Color (SCC).

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