Population Structure and Marker-Trait Association in Indigenous Aromatic Rice

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Abstract: Joha rice of Assam is a class of rice with aroma, good cooking qualities and excellent palatability, which are grown in different places of Assam with their adaptability to local situations. A total of 143 simple sequence repeat markers were used in this study to reveal sufficient genetic variations among the 40 Joha and 14 non-Joha rice genotypes. Polymorphism information content of these markers were from 0.17 to 0.88, where the average of 3.7 alleles were observed. The model-based population assignment and dendrogram analysis identified three distinct groups in the 54 rice accessions, which established a clear identity of Joha accessions from the Basmati accessions, indicating high diversity and strong population structure in Joha rice. Furthermore, a total of 29 significant marker-trait associations ($P < 0.05$) for 10 characters were detected. The QTLs related with yield and grain quality can be used effectively in crop improvement programs and for further fine mapping and validation of specific genes to develop gene-based perfect markers in rice breeding and for mining of better alleles of these genes in Joha rice collections.

Key words: Joha rice; genetic diversity; association mapping; population structure; quantitative trait locus; aroma

Rice is the world's most important food crop and a major source of nutrition for about two thirds of populations. Different rice genotypes across the world have some special uses which are termed as 'Specialy Rice' (Grist, 1983). Such specialty rice includes the group of Basmati type, aromatic non-Basmati type, non-aromatic Basmati type and non-aromatic special purpose rice type (Shenoy and Kalagudi, 2004). Among these, aromatic rice is the most prominent one. India abounds with a wealth of specialty rice, the prominent among which are the aromatic rice including both Basmati and the short grain indigenous types which have become part of our heritage and are considered as national treasure. Among these categories, the aromatic rice of Assam is a unique class under Sali rice traditionally known as 'Joha'. The Joha rice cultivars are known for its unique aroma, superfine kernel, good cooking quality and excellent palatability (Das et al, 2010). The area under Joha rice, however, is nominal owing to its poor productivity, long duration and high susceptibility to diseases and insects. Due to negligence, over-emphasis on high yield and trade-driven promotion of longer grain types, most of the genetic variation in Joha rice is under threat from extinction. Despite having high degree of genetic variability in specialty traits as well as other agronomic traits, few attempts have been made to commercially exploit these materials for developing high-yielding aromatic rice suitable for this region to boost up the production of Joha rice to an economically viable culture. Therefore, an accurate identification of genetic variability among Joha rice landraces of Assam, using

DNA-based markers, is regarded as the need of hour for measuring the extent of genetic variability among landraces (Shaktivel et al, 2009).

Population genetic analysis of particular class of rice landraces collected from a region is essential in understanding the complex interaction between rice diversity and human cultivation practices and culture, as the cultivar classification is shaped by the interplay between adaptation to the local environment and artificial selection imposed by the farmers (Roy et al, 2015).

Genetic diversity is a key factor for breeders to enhance success rate in the breeding by exploiting the variability. Joha rice of Assam is such class of rice with aroma, which is grown in different places of Assam with their adaptability to local situations. Despite their low-yielding potential, these cultivars are grown for their high market and social values. The Joha rice improvement requires the proper characterization of genetic diversity and highly polymorphic molecular markers, which in turn can be effectively utilized for the mapping of genes/QTLs for economically important traits and their subsequent use in molecular breeding. Hence, the present study is

initiated to know the genetic base of the Joha germplasm in comparison with some other non-Joha aromatic rice accessions.

The major objective of this study was to estimate the molecular relationship in natural population, and then to detect the loci controlling the target traits by association analysis, so as to lay a theoretic foundation for the effective improvement of Joha rice and the heightening of breeding efficiency.

MATERIALS AND METHODS

Rice materials

The experimental materials (Table 1) for the investigation comprised of 54 rice genotypes, among which 40 were Joha aromatic accessions collected from different parts of Assam and the remaining were Joha non-aromatic accessions. The field experiment, conducted in Jorhat, Assam, India, was laid out in a completely randomized block design with three times and observations were recorded for 15 characters, length of leaf blade (mm), width of leaf blade (mm),

Table 1. Genotypes used in this study.

No.	Genotype	Parent	Date of heading (d)	Yield per plant (g)	Aroma score [a]	No.	Genotype	Parent	Date of heading (d)	Yield per plant (g)	Aroma score [a]
1	Kunkuni Joha-1	IJR	123	32.780	3	28	Bor Joha	IJR	125	42.640	1
2	Kamini Joha	IJR	131	41.487	4	29	Bhugri Joha	IJR	131	43.510	3
3	Ronga Joha-2	IJR	131	47.810	3	30	Bhaboli Joha	IJR	131	36.873	4
4	Tulsi Joha	IJR	132	39.880	2	31	Boga Joha-1	IJR	120	21.300	1
5	Monipuri Joha-2	IJR	132	60.610	3	32	Kharika Joha	IJR	121	44.467	3
6	Kon Joha-3	IJR	129	36.103	3	33	Koli Joha-2	IJR	120	21.117	1
7	Kola Joha-2	IJR	123	51.923	4	34	Siali Joha	IJR	123	42.033	1
8	Konbogi Joha	IJR	129	41.940	4	35	Kunkuni Joha-2	IJR	120	36.047	4
9	Goalporia Joha-2	IJR	127	47.763	3	36	Maniki Madhuri Joha	IJR	118	32.480	2
10	Joha	IJR	124	24.060	3	37	Monipuri Joha-1	IJR	120	35.147	1
11	Koli Joha	IJR	120	36.643	3	38	Kolajoha new	IJR	120	30.330	1
12	Joha Bora	IJR	127	53.510	3	39	Jeera Joha	IJR	120	22.560	3
13	Kon Joha-1	IJR	120	38.560	4	40	Kon Joha	IJR	120	34.700	1
14	Ronga Joha-1	IJR	122	31.920	3	41	Keteki Joha	H	136	21.993	3
15	Kola Joha-1	IJR	120	39.807	2	42	NDR6330	B	120	20.807	3
16	Goalporia Joha-1	IJR	127	42.880	3	43	Dehradun Basmati Selection-13	D	110	19.307	1
17	Chufon Joha	IJR	128	35.510	3	44	13-Selection Kamal	L	90	18.850	3
18	Cheniguti Joha	IJR	131	31.817	4	45	15-Selection Kamal	L	86	24.970	3
19	Bor Sal Joha	IJR	122	38.573	2	46	Bishnubhog	PV	130	29.793	1
20	Boga Tulsi Joha	IJR	121	24.570	4	47	Tulsi Phool	PV	131	24.430	2
21	Boga Joha	IJR	121	42.843	2	48	Kala Namak	PV	117	46.997	1
22	Bengoli Joha	IJR	122	37.060	2	49	Indrobhog	PV	120	17.817	2
23	Badshabhog	IJR	119	21.387	2	50	Jowar Pool	PV	124	27.980	4
24	Arab Joha	IJR	133	25.050	3	51	Kalijeera	PV	128	21.357	2
25	Bokul Joha	IJR	119	41.663	1	52	Harinarayan	PV	128	29.680	2
26	Boga Maniki Modhuri	IJR	120	28.780	3	53	Saheb Sali	PV	120	41.020	3
27	Bogi Joha	IJR	100	37.055	1	54	Ranjit	NH	128	24.614	1

IJR, Indigenous Joha rice; H, High-yielding aromatic rice of Assam developed from Savitri × Badshabhog; B, Selection from Bishnuparag; D, Selection from Dehradun Basmati; L, Selection from local Kamal; PV, Pure line variety; NH, Non-aromatic high-yielding variety of Assam developed from Pankajb × Mahsuri. Nos. 1–40 are Joha aromatic rice accessions, and Nos. 41–54 are Joha non-aromatic rice accessions.
[a] Based on Sood and Siddiq (1978).