International Journal of Advanced Biotechnology and Research
ISSN 0976-2612, Online ISSN 2278–599X,
Vol 3, Issue 3, 2012, pp 711-719
http://www.bipublication.com

SIMPLE SEQUENCE REPEATS MARKERS AND GRAIN QUALITY CHAR ACTERSTICS FOR GENETIC DIVERGENCE AND SELECTIVE IDENTIFICATION OF AROAMTIC RICES

Yogendra Singh[1*] and U.S Singh [2]

[1] Scientist (Biotechnology) , Marker Assisted Selection Laboratory, Department of Plant Breeding & Genetics, College of Agriculture , J.N.K.V.V, Jabalpur- 482004 (M.P) India

[2] South Asia Regional Project Coordinator, IRRI-India office, NASC complex, New Delhi-110012, India.

[*]Corresponding author: Email: yogendrasinghbt@gmail.com Tel: + 91 9407274826 (Cell)

[Received-17/09/2012, Accepted-29/09/2012]

ABSTARCT:

Aromatic rices are preferred by consumers all over the world due to its flavour and palatability. A large number of these collections are available but there is still scope for systemic analysis on grain quality and genetic divergence front. During the present investigation comparative analysis of grain quality characters was done and attempt were made to correlate these grain quality characters with genetic distance and relatedness obtained with forty five SSR markers. Possibility of finding exclusive loci in specific germplasm was also targeted. In the dendrogram constructed by SSR markers all genotypes were grouped in two major and nearly equal clusters having 22 and 23 genotypes at 50 % similarity coefficient. On other hand 18 SSR markers amplified 21 exclusive loci in 14 genotypes. These can be used as a tool for quick and reliable detection of specific genotype. Over all a lot of divergence was detected among all genotypes. The selective genotypes from these clusters may be used as potential donors for future hybridizations programme to develop varieties with more grain as well as kernel length.

Key words: Aromatic rice, Dendrogram, Genetic divergence, Grain quality, SSR markers

INTRODUCTION: Rice (*Oryza sativa* L) is the most important human food crop in the world. Rice is known as the grain of life, and is synonymous with food for Asians. More than 90% of the world's rice is grown and consumed in Asia, where 60% of the calories are consumed by 3 billion Asians [1] **.** Aromatic rices form a separate group among rice and are nature's gift exclusive to Indian sub continent [2] India possesses an immense wealth of aromatic rice germplasm and land races exhibiting a wide variability with respect to their morpho-physiological, agronomic, grain and cooking characteristics. Among aromatic rices Basmati is accepted as best scented longest and slenderest rice in world. India is leading country in the export of Basmati rice and due to its importance the Basmati rice is considered as *Scented pearl* [3] **.**The Basmati types are characterized by a harmonious combination of minimum kernel dimensions (kernel length ≥ 6.5 mm; length (L) to breadth (B) ratio (L/B ratio) ≥ 3), intensity of aroma (medium to strong), texture of cooked rice, high volume

expansion during cooking made up by linear kernel elongation (elongation ratio ≥ 1.80) with minimum breadth-wise swelling, fluffiness, palatability, easy digestibility and longer shelf life [4] **.** Many farmers in India still grow local germplasm under different names and they also bring some varieties from distant places and start cultivating them with local names. A number of medium to long-grained aromatic rice varieties in our country are named after Basmati. These are grown and traded as Basmati which is not fair and hamper the credibility of original Basmati in national as well as in International market. There is lack of the absolute knowledge due to some missing links about these genotypes that how related they are from each other. Therefore there is an urgent need to establish linkage between different Basmati lines and this can be done in reliable manner based on their grain quality traits as well molecular markers (SSR) analysis.

In present study, Characterization of forty two medium to long grained aromatic rice genotypes and three control lines (two small-grained non-Basmati scented rices and one long grain non-scented rice) was performed for various grain quality characters .Diversity was also assessed at molecular level using forty five SSR markers. Attempts were made to correlate these grain quality characters with genetic distance and relatedness obtained with forty five SSR markers. Possibility of finding exclusive loci in specific germplasm was also targeted.

MATERIALS AND METHODS: SSR analysis was completed in four steps. The first step of this process was isolation of genomic DNA. For this the method describe by Mukherjee (1999) with slight modifications was followed [5]. The second step was PCR amplification of SSR markers. It was performed in a volume of 20µl reaction set up having 30 ng of template DNA, 800µM of dNTPs mix, 1.0U of Taq DNA polymerase, 1X Reaction buffer, 0.3 µM each of forward & reverse Primer and rest of deionized water. The PCR amplification was achieved in M.J Research Thermocycler (PTC 200), The PCR conditions were initially 5 min denaturation step at 94^0C, followed by 41 cycles having denaturation at 94^0C for 1 min, annealing 55^0C for 1 min, & polymerization 72^0C for 2 min and at last Polymerization at 72^0C for 7 min. A set of 18-29 mer nucleotides SSR primers (forward &reverse) was employed for PCR amplification. Primer sequences were obtained from IRRI (courtesy Dr. G.S. Khush). They were got synthesized from Bangalore Genei Pvt. Ltd., Bangalore The details of RM-code, chromosome position, sequence of the primers are given in **table no. 01**. In Third step Horizontal submerged gel electrophoresis for amplified product was done at 80 V for 4 h in 1xTAE electrophoresis buffer using 2.0% Metaphore gel [6] and finally in fourth step Dendrogram was prepared using Dice's coefficient of similarity and UPGMA cluster analysis using Gel Compar-II, version 3.5 (Applied Maths. U.S.A).

For grain quality characteristics field performance of all the forty five genotypes was evaluated at Seed Production Center (S.P.C) at G.B. Pant University of Agriculture & Technology, Pantnagar, Uttaranchal, India, in two replications, using Randomized Block Design (R.B.D) under organic farming system. During transplanting plant-to-plant distance was 15 cm and row-to-row distance was 20 cm. Observations for fourteen characters were recorded after harvesting seed in 2 replications using five plants of each genotypes. The mean values of two replications were used for data analysis. As standards for evaluation of kernel length and shape of rice germplasm vary among countries and marketing areas. The size and shape classification given in **table no.02,** proposed by Dela Cruz and Khush (2000) was followed during the present study [7]:

RESULTS AND DISCUSSION: High degree of polymorphism was shown by SSR markers **(Fig no. 01).** The details of SSR loci are given in **table no .03**. SSR Dendrogram clustering is represented by fig. no 02 and depicts that at 50 % similarity all genotypes were grouped in two major clusters A & B having 22 and 23 genotypes respectively. The A major group was sub grouped in to A1 & A2 having 03 and 19 genotypes respectively at 63 % similarity. The A2 subgroup was further classified in to A2-a & a2-b having 08 and 11 genotypes. Similarly the B major group was sub grouped in to

B 1 & B2 subgroups having 17 & 06 genotypes respectively at 54 % similarity. The B 2 sub group was further classified in to B 1-a B 1 -b & B1-c sub-sub groups consisting of 02, 03 & 12 genotypes respectively at 60 % similarity. Mean values of fourteen grain quality characters are summarized in **table no. 04.** After study of this we found that among different aromatic rice genotypes paddy length varied from7.25 mm (Kalanamak 3121) to 10.3 mm (Hansraj 3072-2 & Taraori Basmati), similarly the paddy breadth ranged from 1.95 mm (Basmati 3085 & Basmati 127) to 2.35 mm (Basmati 3032 AR 575 U & Pokkali U), while The L/B ratio of grain varied from 3.25 (Tilakchandan 3048) to 4.95 (Taraori Basmati).The hulling recovery ranged from 70 % (Basmati 6129) to 81.70% (Tilak Chandan 3048) and the milling recovery ranged from 55.25% (Basmati 3034) to 67.0% (Basmati107).The kernel length of 20 genotypes was long (> 6.61 mm) and for 23 genotypes it was medium (5.5 to 6.6 mm) and small for 02 genotypes(< 5.50 mm). Among all genotypes the longest kernel was of Basmati 43A (7.5 mm) and smallest was for Kalanamak 3121 and Tilakchandan 3048 (5.25 mm each).The kernel breadth ranged from 1.6 mm (Hansraj 3067 & Basmati 375 A) to 2.0 mm (Basmati 43 A). Except for Tilakchandan 3048 and Kalanamak 3121, grain shape for all other scented rice lines was slender (L: B ratio > 3.0), as L/B ratio of kernel ranged from 2.9 (Tilakchandan 3048, Kalanamak 3121) to 4.20 (Basmati 375 A).Among different aromatic rice genotypes cooked kernel length ranged from 9.35 mm (Tilakchandan 3048) to 14.55 mm (Basmati Sathi).The cooked kernel breadth varied from 2.0 mm (Basmati 136, Basmati Nepal, Basmati1-1A, Basmati 5836, Basmati 5875, Basmati375 A, Kalanamak 3121)) to 2.45 mm (Pokkali U). The kernel elongation ratio ranged from 1.7 (Basmati 5836, Basmati Uzearpka) to 2.20 (Basmati 3317-1). Gel consistency of most of the aromatic rice genotypes was soft. Medium gel consistency (GC) was shown by Type 3, Hansraj 3067, Hansraj 3074, Basmati 127, Basmati 1-1A, Basmati 134 and Basmati 5836. The gel length varied from 31.5 mm (Basmati375 A) to 92.5 mm (Basmati Sathi & Basmati 6129). Among all aromatic rices gelatinization temperature varied from low to high. The alkali digestion score varied from 1.25 (Basmati1-1 A) to 6.9 (Hansraj 3078).Amylose content was intermediate to high-intermediate and it ranged from 20% (Basmati Nepal) to 30 % (Hansraj 3086, Basmati 3032 AR 575 U). Except for Pokkali U aroma content varied from moderate to strong.

The rice quality is one of the most important characters as it exerts large effect on the market value and consumer's acceptance. Grain quality of rice is determined by many factors such as grain appearance, nutritional value, cooking and eating qualities [8] Among the quality traits the grain length, grain breadth kernel length and milling recovery may be used as selection parameter in the segregating generations as these characters play crucial role in genetic divergence.DNA markers are useful tools for assessing genetic diversity among germplasm [9,10]**.** Compared with pedigree information, DNA marker based diversity estimates reflect actual DNA differences.In present study SSR markers were selected for analysis of genetic divergence as they were reported earlier for satisfactory work [11,12].The structure and length of simple sequence repeats are considered to be the major factors affecting microsatellite variability[13]**.**In rice the SSRs have been used to assess the genetic diversity of both wild and cultivated species [14,15,16] **.** Recently Usefulness of microsatellite markers for molecular characterization and diversity analysis in rice has been reported by several workers. [17,18,19, 20]

In present study we found that different indigenous varieties named after Basmati vary widely in their grain quality traits and molecular characteristics. However, a number of Dehradun Basmati and Hansraj selections show high degree of similarity indicating that Hansraj, which was once grown widely in district Bijnore, Pilibhit and Bareilly of U.P. and Udham Singh Nagar of Uttaranchal is a Basmati. Probably Basmati lines grown in these districts were called as Hansraj. The present study provided an overview of the genetic diversity of the rice genotypes carrying good quality traits. The use of SSR markers in genetic diversity analysis enabled to group the similar genotypes at one place.

The results further indicated that since the SSR markers are neutral and Co- dominant they are powerful tools to assess the genetic variability of the genotypes under study. The information regarding genetic diversity of these genotypes may be useful for proper identification and selection of appropriate parents for further crop improvement programmes. The exclusive loci amplified by specific primers may be used as a tool for quick and accurate preliminary identification of respective genotypes after standardization the protocol accordingly.

FINANCIAL DISCLOSURE: Author is thankful to G. B. Pant University of Agriculture & Technology, Pantnagar, Uttarakhand, India for this research work.

REFERENCES:

[1] Khush G S. [1997] Origin, dispersal, cultivation and variation of rice. *Plant Mol. Biol.* 35: 25-34.

[2] Glaszman JC. [1987] Isozyme and classification of Asian rice varieties. *Theor.App.Gene*t.74:21-30.

[3] Siddik E A. [1996] The Hindu survey of Agriculture.47-58.

[4] Singh V P. [2000] The Basmati Rice of India in: *Aromatic Rices* (Singh RK, Singh U S, and Khush G S, Eds.). Oxford & IBH Publishing Co., New Delhi. 135-153.

[5] Mukherjee P K. [1999] Rapid extraction of plant genomic DNA suitable for restriction analysis and PCR amplification. *Asian Pacific J. Mol. Biol. Biotechnol*. **7:** 95-96.

[6] Sambrook J, Fritsch E F, Maniatis T. [1989] Molecular cloning: A Laboratory Manual, 2nd edition, Vol. 3. Cold Spring Harbor Laboratory, Cold Spring Harbor, New York

[7] DelaCruz N, Khush G S. [2000] Rice grain quality evaluation procedures. In: Aromatic Rices (Singh R K, Singh U S, and Khush G S , Eds.). Oxford & IBH Publishing Co, New Delhi. 15- 28.

[8]: Juliano B O, Petrz C M, Ard M K. [1990] Grain quality characteristics of export rice in selected markets. *Cereal chem.* 67: 192-197.

[9] Lee M. [1995] .DNA markers and plant breeding programs.*Adv.Agron*.55: 265-344.

[10] Almanza-pinzone M , Khairallah I M, Fox P N, Warburton M L. [2003] Comparison of molecular markers and coefficients of parentage for analysis of genetic diversity among spring bread wheat accessions. *Euphytica.* 130 (1): 77-86.

[11]Xu Y, Beachell H, Mc Couch S R. [2004] A marker-based approach to broadening the genetic base of rice in USA. *Crop Sci.* 44: 1947-1959.

[12]Jeung J U, Hwang H G, Moon H P, Jena K K.[2005] . Fingerprinting temperate *japonica* and tropical *indica* rice genotypes by comparative analysis of DNA markers. *Euphytica*. 146 (3): 239-251.

[13] Brinkmann B, Klintschar M, Neuhuber F, Huhne J, Rolf B. [1998] Mutation rate in human microsatellites: influence of the structure and length of the tandem repeat. *American J. of Human Genet*.62 (06):1408-1415.

[14] Siwach P, Jain S, Saini N, Chowdhary V K, Jain R K [2004] Allelic diversity among Basmati and non-Basmati long-grain indica rice varieties using microsatellite markers. *J. of Plant Biochem. and Biotech.* 13: 25-32.

[15] Neeraja C N, Hariprasad A S, Malathi S, Siddiq E A [2005] Characterization of tall landraces of rice (*Oryza sativa* L.) using gene derived simple sequence repeats. *Curr. Science*. 88 (01): 149-152.

[16] Cunmin Q, Fuyou F, Liezhao L, Kun L, Jieheng H, Liu X, Xie J, Chen L , Wang R , Zhanglin T, Jiana L. [2012] .Simple sequence repeat (SSR) markers analysis of genetic diversity among *Brassica napus* inbred lines based on correlation between seed quality traits and seed pigments content. *African J.of Biotech.* 11(33): 8202-8211.

[17] Ndjiondjop M N, Cisse F, Girma G, Sow M, Bocco R, Djentin G, Blandine F. [2010] Morpho-agronomic and molecular characterization of *Oryza glaberrima* germ plasm for Mali. *African J.of Biotech*. 09(44): 7409-7417.

[18] Chakravarthi , B K, Naravaneni R. [2006]. SSR marker based DNA fingerprinting and diversity study in rice (*Oryza sativa*. L). *African J. of Biotech*.5 (9): 684-688.

[19] Lapitan V C, Brar D S, Toshinori A, Redona E D. [2007]. Assessment of genetic diversity of Phillipine rice cultivars carrying good quality traits using SSR markers. *Breeding Science*. 57:263-270.

[20] Wong S C, Yiu P H, Bong S T W, Lee H H , Neoh P N P, Rajan A. [2009]. Analysis of Sarawak Bario Rice Diversity Using Microsatellite Markers. *American J. of Agri. and Biological Sci*. 4 (4): 298-304.

Table no.01: SSR primers used in present study:

S.N	SSR primer code	Lab code	Chromo some No	Forward Primer Sequence(5'to 3')	Reverse Primer Sequence (5'to 3')
1	RM 2	SSR 2	7	ACGTGTCACCGCTTCCTC	ATGTCCGGGATCTCATCG
2	RM 3	SSR 3	6	ACACTGTAGCGGCCACTG	CCTCCACTGCTCCACATCTT
3	RM 4A	SSR 4	12	TTGACGAGGTCAGCACTGAC	AGGGTGTATCCGACTCATCG
4	RM 4B	SSR 5	11	TTGACGAGGTCAGCACTGAC	AGGGTGTATCCGACTCATCG
5	RM 7	SSR 8	3	TTCGCCATGAAGTCTCTCG	CCTCCCATCATTTCGTTGTT
6	RM 8	SSR 9	2	CACGTGGCGTAAATACACGT	GGCCAAACCCTAACCCTG
7	RM 9	SSR 10	1	GGTGCCATTGTCGTCCTC	ACGGCCCTCATCACCTTC
8	RM 13	SSR 13	5	TCCAACATGGCAAGAGAGAG	GGTGGCATTCGATTCCAG
9	RM 14	SSR 14	1	CCGAGGAGAGGAGTTCGAC	GTGCCAATTTCCTCGAAAAA
10	RM 17	SSR 16	12	TGCCCTGTTATTTTCTTCTCTC	GGTGATCCTTTCCCATTTCA
11	RM 18	SSR 17	7	TTCCCTCTCATGAGCTCCAT	GAGTGCCTGGCGCTGTAC
12	RM 20A	SSR 19	12	ATCTTGTCCCTGCAGGTCAT	GAAACAGAGGCACATTTCATTG
13	RM 20B	SSR 20	11	ATCTTGTCCCTGCAGGTCAT	GAAACAGAGGCACATTTCATTG
14	RM 21	SSR 21	11	ACAGTATTCCGTAGGCACGG	GCTCCATGAGGGTGGTAGAG
15	RM 22	SSR 22	3	GGTTTGGGAGCCCATAATCT	CTGGGCTTCTTTCACTCGTC
16	RM 23	SSR 23	1	CATTGGAGTGGAGGCTGG	GTCAGGCTTCTGCCATTCTC
17	RM 25	SSR 24	8	GGAAAGAATGATCTTTTCATGG	CTACCATCAAAACCAATGTTC
18	RM 26	SSR 25	5	GAGTCGACGAGCGGCAGA	CTGCGAGCGACGGTAACA
19	RM 27	SSR 26	2	TTTTCCTTCTCACCCACTTCA	TCTTTGACAAGAGGAAAGAGGC
20	RM 29	SSR 27	2	CAGGGACCCACCTGTCATAC	AACGTTGGTCATATCGGTGG
21	RM 30	SSR 28	7	GGTTAGGCATCGTCACGG	TCACCTCACACGACACG
22	RM 32	SSR 30	8	AGTCTACGTGGTGTACACGTGG	TGCGGCCTGCCGTTTGTGAG
23	RM 34	SSR 31	1	GAAATGGCAATGGTGGCG	GCGGGAGAACCCTAGCTC
24	RM 35	SSR 32	1	TGGTTAATCGATCGGTCGCC	CGACGGCAGATATACACGG
25	RM 36	SSR 33	3	CAACTATGCACCATTGTGGC	GTACTCCACAAGACCGTACC
26	RM 38	SSR 34	8	ACGAGCTCTCGATCAGCCTA	TCGGTCTCCATGTCCCAC
27	RM 41	SSR 36	9	AAGTCTAGTTTGCCTCCC	AATTTCTACGTCGTCGGGC
28	RM 44	SSR 38	8	ACGGGCAATCCGAACAACC	TCGGGAAAACCTACCCTACC
29	RM 48	SSR 40	2	TGTCCCACTGCTTTCAAGC	CGAGAATGAGGGACAAATAACC
30	RM 50	SSR 42	6	ACTGTACCGGTCGAAGACG	AAATTCCACGTCAGCCTCC
31	RM 55	SSR 43	3	CCGTCGCCGTAGTAGAGAAG	TCCCGGTTATTTTAAGGCG
32	RM 87	SSR 44	5	CCTCTCCGATACACCGTATG	GCGAAGGTACGAAAGGAAAG
33	RM 101	SSR 45	12	GTGAATGGTCAAGTGACTTAGGTGGC	ACACAACATGTTCCCTCCCATGC
34	RM 105	SSR 48	9	GTCGTCGACCCATCGGAGCCAC	TGGTCGAGGTGGGGATCGGGTC
35	RM 108	SSR 51	9	TCTCTTGCGCGCACACTGGCAC	CGTGCACCACCACCACCACCAC
36	RM 119	SSR 54	4	CATCCCCCTGCTGCTGCTGCTG	CGCCGGATGTGTGGGACTAGCG
37	RM 124	SSR 57	4	ATCGTCTGCGTTGCGGCTGCTG	CATGGATCACCGAGCTCCCCCC
38	RM 131	SSR 60	4	TCCTCCCTCCCTTCGCCCACTG	CGATGTTCGCCATGGCTGCTCC
39	RM 134	SSR 61	7	ACAAGGCCGCGAGAGGATTCCG	GCTCTCCGGTGGCTCCGATTGG
40	RM 147	SSR 64	10	TACGGCTTCGGCGGCTGATTCC	CCCCCGAATCCCATCGAAACCC
41	RM 150C	SSR 67	6	CACGACGACGACGAGCAGCAGC	GCTCGAGGGAGAGCGACCTGCC
42	RM 160	SSR 69	9	AGCTAGCAGCTATAGCTTAGCTGGAGATC	TCTCATCGCCATGCGAGGCCTC
43	RM 171	SSR 72	10	AACGCGAGGACACGTACTTAC	ACGAGATACGTACGCCTTTG
44	RM 183	SSR 74	2	GGAGCGGGAGAGAGAGCGCACG	TGCCGATGAAGGACTGCGACGC
45	RM 184	SSR 76	10	ATCCCATTCGCCAAAACCGGCC	TGACACTTGGAGAGCGGTGTGG

Table No.02: Classification of size & shape rice grain

Size classification			Shape classification		
Scale	Size category	Length (mm)	Scale	Shape	Length/Breadth ratio
1	Very long	>7.50			
3	Long	6.61 to 7.50	1	Slender	> 3
5	Medium or intermediate	5.51 to 6.60	5	Medium	2.1 to 3.0
7	Short	< 5.50	9	Bold	≤ 2.0

Table no.03: The details of SSR loci detected using 45 SSR primers.

S.N	Primer Code	Range of loci scored (b.p)	Total loci	Mono morphic loci	Polymorphism		Exclusive loci		
					No. of loci	%	No.	Germplasm	Mol Size (bp)
1	SSR 2	50-280	7	0	4	100.0	2	Basmati 3034 Basmati 106	220 150
2	SSR 3	160-270	4	0	4	100.0	-	-	-
3	SSR 4	145-310	5	0	5	100.0	1	Hansraj3074 (U)	145
4	SSR 5	310-1400	6	0	6	100.0	1	Basmati uzerpka	330
5	SSR 8	60-1800	11	0	11	100.0	2	Basmati136, Basmati 3067	60 1400
6	SSR 9	50-290	8	0	8	100.0	1	Dehradun Basmati 3020	260
7	SSR 10	70-1850	8	0	8	100.0	-	-	-
8	SSR 13	290-1350	8	1	7	87.5	-	-	-
9	SSR 14	60-800	9	0	9	100.0	1	Dehradun Basmati 3020	405
10	SSR 16	140-340	5	1	4	80.0	1	Basmati 3065 AR 771 (U)	340
11	SSR 17	130-590	10	1	9	90.0	2	Basmati 3065 AR 1409 (U) Basmati Sathi	480 130
12	SSR 19	120-280	6	0	6	100.0	-	-	-
13	SSR 20	410-1850	7	1	6	85.7	-	-	-
14	SSR 21	110-280	5	0	5	100.0	-	-	-
15	SSR 22	80-360	5	0	5	100.0	1	Dehradun Basmati 3020	80
16	SSR 23	100-320	7	0	7	100.0	1	Basmati 3085	130
17	SSR 24	140-320	5	0	5	100.0	-	-	-
18	SSR 25	140-310	6	0	6	100.0	-	-	-
19	SSR 26	140-510	5	0	5	100.0	-	-	-
20	SSR 27	190-810	7	0	7	100.0	1	Hansraj 3072-2	305
21	SSR 28	160-2100	9	2	7	77.7	1	Hansraj 3078	270
22	SSR 30	60-100	2	1	1	50.0	-	-	-
23	SSR 31	60-2080	7	1	6	85.7	-	-	-
24	SSR 32	60-180	4	1	3	75.0	-	-	-
25	SSR 33	140-290	5	1	4	80.0	-	-	-
26	SSR 34	140-400	5	0	5	100.0	-	-	-
27	SSR 36	140-300	5	0	5	100.0	1	Pokkali (U)	140
28	SSR 38	130-590	2	1	1	50.0	-	-	-
29	SSR 40	305-2100	7	2	5	71.4	-	-	-
30	SSR 42	100-315	5	0	5	100.0	-	-	-
31	SSR 43	140-405	5	0	5	100.0	-	-	-
32	SSR 44	150-310	5	0	5	100.0	-	-	-
33	SSR 45	570-1950	5	0	5	100.0	-	-	-
34	SSR 48	605-1050	3	0	3	100.0	-	-	-
35	SSR 51	60-2050	8	0	8	100.0	-	-	-
36	SSR 54	140-280	4	0	4	100.0	-	-	-
37	SSR 57	130-280	4	0	4	100.0	1	Hansraj 3078	130
38	SSR 60	160-280	4	0	4	100.0		-	-
39	SSR 61	160-290	5	1	4	80.0	1	Hansraj 3074 (U)	250
40	SSR 64	150-300	5	0	5	100.0	1	Hansraj3074 (U)	150
41	SSR 67	590-1100	3	0	3	100.0	-	-	-
42	SSR 69	80-360	5	0	5	100.0	1	Dehradun Basmati 3020	80
43	SSR 72	120-280	4	0	4	100.0	-	-	-
44	SSR 74	100-310	6	0	6	100.0	1	Basmati 3085	130
45	SSR 76	140-280	4	0	4	100.0	-	-	-

Table 04: Mean values of grain quality characters of different aromatic rice germplasm

Genotype name	PL (mm) L	PB (mm) B	L/B ratio	HR (%)	MR (%)	KL (mm)	KB (mm)	L / B ratio	CKL (mm)	CKB (mm)	ER	GC		GT		AC		Aroma
												GL (mm)	Cat	AS	GT	%	Cat	
Tilak Chandan 3048	7.45	2.30	3.25	81.70	58.50	5.25	1.80	2.90	9.35	2.20	1.80	90.0	S	5.25	H-I	26.00	H-I	Moderate
Kalanamak 3121	7.25	2.10	3.45	77.00	64.50	5.25	1.80	2.90	10.55	2.00	2.00	91.0	S	2.25	H	23.50	I	Moderate
Pokkali U	9.75	2.35	4.10	74.50	60.00	7.35	1.90	3.90	13.10	2.45	1.80	73.0	S	2.00	H	29.75	H-I	Slight
Basmati 3317-1	8.35	2.10	3.90	74.70	63.25	6.40	1.75	3.50	13.20	2.30	2.20	80.0	S	3.25	H-I	26.50	H-I	Moderate
Basmati 370	9.75	2.10	4.65	74.25	62.00	6.40	1.75	3.80	12.55	2.15	2.00	63.5	S	4.75	I	25.75	H-I	Strong
Basmati 3034	9.80	2.20	4.40	79.15	55.25	6.75	1.80	3.75	13.45	2.10	2.00	62.0	S	3.50	H-I	24.25	I	Moderate
Basmati 3085	9.25	1.95	4.70	74.00	61.50	6.80	1.75	3.90	13.10	2.20	1.90	91.0	S	2.00	H	24.25	I	Moderate
Dehradun Bas.3020	9.76	2.10	4.65	79.00	65.00	7.00	1.80	3.90	13.10	2.25	1.90	84.5	S	2.25	H	29.50	H-I	Strong
Taraori Basmati	10.30	2.20	4.95	72.50	62.50	7.20	1.80	4.00	14.00	2.25	1.90	82.0	S	4.90	I	30.00	H-I	Strong
Basmati 3032 AR 575 (U)	9.50	2.35	4.05	80.00	63.50	6.65	1.80	3.65	12.00	2.25	1.80	91.0	S	4.25	I	30.00	H-I	Moderate
Basmati 3065 AR 1409 (U)	9.65	2.20	4.40	78.00	60.00	6.25	1.75	3.55	11.00	2.10	1.75	62.0	S	2.25	H	23.00	I	Moderate
Dehradun Basmati 3020(U)	9.50	2.20	4.35	81.00	65.50	6.45	1.70	3.80	11.50	2.10	1.80	89.5	S	2.25	H	23.50	I	Moderate
Basmati 217	9.45	2.00	4.75	81.00	64.00	6.60	1.70	3.90	13.20	2.35	2.00	78.5	S	2.90	H-I	21.00	I	Moderate
Basmati 107	9.70	2.30	4.20	80.00	67.00	7.00	1.80	3.90	12.60	2.05	1.80	83.50	S	1.75	H	27.25	H-I	Moderate
Basmati 136	8.50	2.10	4.05	77.50	66.50	6.25	1.65	3.80	11.05	2.00	1.80	84.5	S	3.00	H-I	26.00	H-I	Strong
Basmati UzerpkaU	8.50	2.10	4.05	77.00	65.50	6.75	1.70	3.95	11.70	2.15	1.70	63.5	S	3.15	H-I	22.50	I	Moderate
Basmati 124-10	9.70	2.05	4.75	80.50	64.50	6.45	1.65	3.90	11.90	2.15	1.85	90.5	S	5.90	L	29.25	H-I	Strong
Basmati 127	9.45	1.95	4.85	72.00	59.50	6.75	1.70	3.95	12.2	2.05	1.80	47.5	M	4.90	I	22.50	H-I	Strong
Basmati 3065 AR 771(U)	9.30	2.20	4.20	78.00	65.50	6.60	1.70	3.90	12.05	2.15	1.80	88.5	S	3.75	I	27.50	H-I	Moderate
Basmati 6129	10.05	2.10	4.80	70.00	57.00	6.60	1.65	4.00	13.10	2.15	2.00	92.5	S	4.00	I	23.50	I	Moderate
Basmati Nepal	7.60	2.00	3.80	80.00	61.50	5.25	1.70	3.10	10.70	2.00	2.00	33.5	H	4.15	I	20.00	H-I	Moderate
Basmati 1-1A	9.15	2.10	4.35	76.50	58.00	6.40	1.65	3.90	11.50	2.00	1.80	56.5	M	1.25	H	24.25	I	Moderate
Basmati 433	9.85	2.30	*4.30*	78.00	66.50	7.20	1.80	4.00	13.05	2.10	1.80	69.0	S	4.40	I	24.25	I	Moderate
Basmati 134	9.10	2.10	4.30	78.00	62.00	6.80	1.70	4.00	12.45	2.05	1.80	5.07	M	4.85	I	21.00	I	Moderate
Basmati Mohan 381	9.60	2.10	4.60	76.00	59.00	6.65	1.70	3.90	13.20	2.10	1.95	62.5	S	1.75	H	20.50	I	Moderate
Basmati 43 A	9.15	2.30	4.00	78.00	60.00	7.50	2.00	3.80	13.10	2.25	1.80	90.0	S	2.15	H	22.50	I	Strong
Basmati 106	9.40	2.30	4.10	78.50	59.05	6.45	1.65	3.90	12.15	2.10	1.90	71.5	S	2.00	H	24.25	I	Strong
Basmati 122	8.65	2.10	4.10	78.00	60.00	6.25	1.90	3.30	11.65	2.20	1.90	81.0	S	5.00	H	23.50	I	Moderate
Basmati 5836	9.10	2.15	4.20	78.00	62.00	6.50	1.65	4.00	11.20	2.00	1.70	42.5	M	3.80	I	22.25	I	Moderate
Basmati 5875	8.65	2.10	4.10	78.50	65.50	6.30	1.70	3.70	11.25	2.00	1.80	89.5	S	2.50	H	26.50	H-I	Moderate
Basmati Sufaid 100	9.85	2.10	4.70	79.50	65.50	6.60	1.65	4.00	12.25	2.05	1.85	72.0	S	1.90	H	23.75	I	Moderate
Basmati C-622	9.45	2.10	4.50	75.00	59.50	6.40	1.70	3.80	12.20	2.05	1.90	90.0	S	1.75	H	27.75	H-I	Strong

Basmati 376	9.70	2.10	4.65	76.50	56.75	6.70	1.70	3.90	11.90	2.15	1.80	85.5	S	5.10	I	22.50	I	Strong
Basmati Sathi	9.25	2.10	4.40	77.50	66.50	6.70	1.75	3.80	14.55	2.30	2.15	92.5	S	3.15	H-I	21.00	I	Strong
Basmati 375 A	9.70	2.00	4.85	78.00	63.00	6.80	1.60	4.20	12.75	2.00	1.90	31.5	H	3.20	H-I	24.50	I	Strong
Type-3	9.40	2.00	4.70	75.00	63.25	6.35	1.70	3.75	12.70	2.25	2.00	41.0	M	1.75	H	22.40	I	Strong
Hansraj 3078	10.1	2.10	4.80	76.50	57.50	6.25	1.70	3.65	11.25	2.40	1.80	72.0	S	6.90	L	23.75	I	Strong
Hansraj 3072-2	10.3	2.10	4.85	79.50	58.00	7.15	1.80	3.95	13.65	2.35	1.90	91.5	S	6.75	L	22.75	I	Strong
Hansraj 3072-1	10.1	2.20	4.70	75.50	61.00	7.15	1.75	4.10	13.30	2.05	1.85	39.0	H	6.40	L	22.25	I	Moderate
Hansraj 3067	9.75	2.10	4.65	75.00	60.00	6.45	1.60	4.05	12.50	2.20	1.90	50.0	M	1.95	H	22.75	I	Moderate
Hansraj 3086	9.50	2.10	4.50	76.00	63.50	6.35	1.65	3.85	11.40	2.15	1.80	81.5	S	6.80	L	30.00	H-I	Moderate
Hansraj 3077	9.35	2.00	4.65	75.50	62.75	6.55	1.70	3.85	13.20	2.15	2.00	92.0	S	2.80	H-I	24.50	I	Moderate
Hansraj 3074	10.10	2.10	4.80	76.00	60.00	6.50	1.65	4.00	12.60	2.15	1.95	42.0	M	2.90	H-I	21.75	I	Strong
Hansraj 3072-2 U	10.10	2.30	4.40	78.50	61.00	7.10	1.80	3.95	13.40	2.10	1.90	57.0	S	6.30	L	24.25	I	Strong
Hansraj3074 U	9.95	2.10	4.75	73.50	59.50	6.75	1.70	3.95	13.70	2.20	2.00	71.5	S	6.75	L	29.00	H-I	Strong
CD at 1%	0.28	0.81	0.25	3.44	3.52	0.20	0.10	0.25	0.32	0.16	0.68	5.41	-	0.67	-	1.76	-	-
CD at 5 %	0.21	0.60	0.19	2.57	2.63	0.15	0.79	0.18	0.24	0.12	0.51	4.05	-	0.50	-	1.31	-	-

PL=Paddy length, PB= Paddy breadth, HR= Hulling recovery, MR=Milling recovery, KL=Kernel length, KB=Kernel breadth, L/B ratio= Kernel length/Kernel breadth ratio, CKL=Cooked kernel length, CKB=Cooked kernel breadth, ER=Elongation ratio (after cooking), AS=Alkali score, GT=Gelatinization temperature, GC=Gel consistency, GL=Gel length, AC=Amylose content, Cat.=Category; L=low; I=Intermediate; H-I=High-Intermediate; H=High Amylose content codes: I=intermediate (20-25%), H-I=High-Intermediate (25-30%), H=High (>30%)

Aroma codes: Strong/ Moderate/Slight, CD= Critical Difference

Alkali score codes: **Gelatinizing temperature**

1	H=High
2	H=High
3	H-I=High-Intermediate
4	I=Intermediate
5	I=Intermediate
6	L=Low
7	L=Low

Gel consistency:

Gel Length (mm)	Category
0-40	H= hard
41-60	M=Medium
61-100	S = Soft

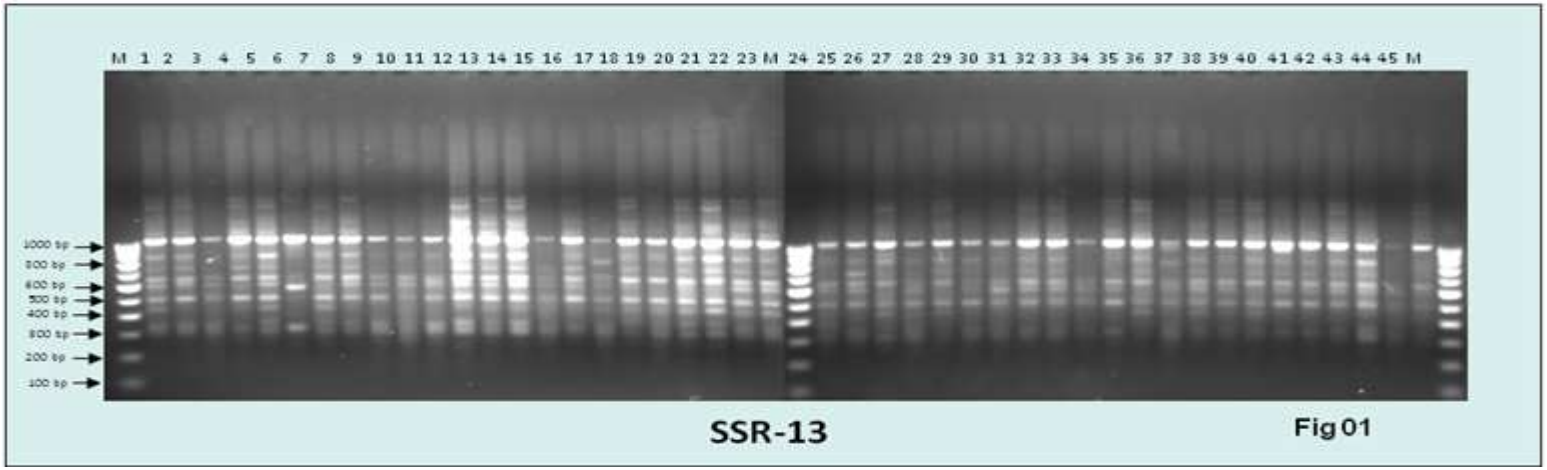

Fig.No.01: Banding pattern of 45 aromatic rice genotypes with SSR primer no 13

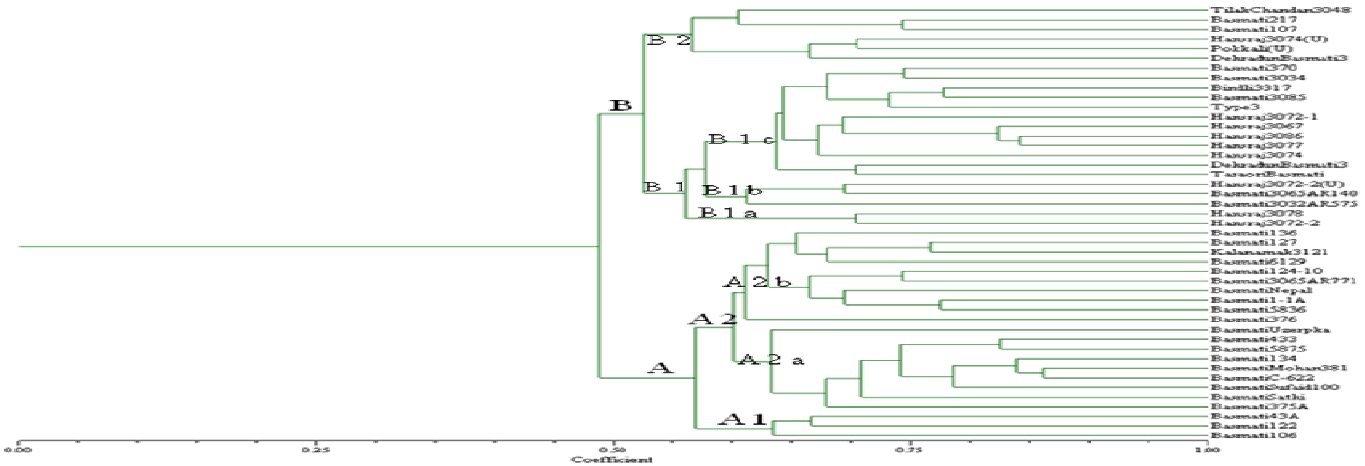

Fig. No. 02: SSR primer based dendrogram