African Journal of Biotechnology Vol. 10 (4), pp. 499-506, 24 January, 2011
Available online at http://www.academicjournals.org/AJB
DOI: 10.5897/AJB10.413
ISSN 1684–5315 © 2011 Academic Journals

Full Length Research Paper

Improvement of Basmati rice (*Oryza sativa* L.) using traditional breeding technology supplemented with molecular markers

D. Singh*, A. Kumar, A. Sirohi[4], P. Kumar[1], J. Singh[2], V. Kumar, A. Jindal, S. Kumar, N. Kumar, V. Kumar[3], V. Sharma, S. Gupta[4] and S. Chand

Molecular Biology Laboratory, Department of Genetics and Plant Breeding,
[1]Department of Biochemistry & Physiology,
[2]Department of Immunology& Defense Mechanism,
[3]Department of Ag. Biotechnology, AAU, Gujrat, India (Present address)
[4]Department of Molecular Biology & Genetic Engineering, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut-250 110, UP (India).

Accepted 17 September, 2010

The present study was undertaken to combine dwarfism (*sd-1*) from Pusa-1121 and aroma and resistance against diseases from Khalsa-7 into basmati background (Type-3). The dwarf segregants of the cross (Khalsa 7 X Pusa 1121) with Type-3 were screened under artificially created epiphytotic conditions in order to select plants free from common diseases of rice. Data recorded for yield and physical standards of quality acceptable in the global trade measured in All India Coordinated Trial Research Project (AICRP) trials were used for demonstration. In addition, two separate polymerase chain reaction (PCR) studies were conducted for detection of resistance against blast. PCR products using random amplified polymorphic DNA (RAPD) and sequence characterized amplified regions (SCAR) markers detected resistance against blast in the genotype Vallabh Basmati-21. The Basmati type, disease resistant and promising selections were assessed for lineage with traditional varieties of basmati rice. The resultant genotype VB-21 expressed close molecular lineage with traditional varieties of basmati rice as well. The present study indicated substantial utility of molecular markers to supplement traditional methods of breeding for improvement of basmati rice.

Key words: Basmati rice, random amplified polymorphic DNA, sequence characterized amplified regions, molecular lineage, Vallabh Basmati- 21.

INTRODUCTION

Due to the demand of basmati rice in the domestic as well as global market at premium price, the total traditional basmati growing area under the Geographical Indication (GI) of India has been designated as Agri Export Zone for Basmati rice by the Government of India in order to promote production of the commodity and enhance the improvement of socio-economic conditions of the farmers living in the area (Singh and Sirohi, 2005).

Traditional varieties of basmati rice are durable, photosensitive (Singh et al., 2000) and susceptible to all rice diseases prevalent in the area. These varieties are also tall with weak stem and therefore, they lodge under high input agriculture resulting into yield loss and inferior quality. Therefore, development of short duration, dwarf, photo-insensitive and disease resistant varieties of basmati rice requires special considerations. In view of

*Corresponding author. E-mail: devisingh11@gmail.com. Tel: +91 1212888536 or +919358918146. Fax: +91 121 2888505

Abbreviations: ASV, Alkali spreading value; **BLB,** bacterial leaf blight; **CTAB,** cetyltrimethyleammoniumbromide; **DNA,** deoxyribose nucleic acid; **ER,** elongation ratio; **PCR,** polymerase chain reaction; **RAPD,** random amplified polymorphic DNA; **SCAR,** sequence characterized amplified regions.

this, the present study involving traditional breeding strategy assisted with molecular markers (Khush, 2007; Brar and Khush, 2007) was initiated with the following objectives: (a) Development of high yielding, photo insensitive and dwarf varieties of basmati rice by skilful visual selection (Allard, 1960); (b) evaluation of disease reactions to detect disease resistant families under artificially created epiphytotic conditions and by using marker aided selection; (c) estimation of the molecular lineage of such promising genotypes with traditional basmati varieties based on adequate random amplified polymorphic DNA (RAPD) markers (Raghunathachari et al., 1999). In the present communication, a case study of the development of improved variety of basmati rice involving accomplishment of the above three objectives is discussed.

MATERIALS AND METHODS

Plant material and field trials

For combining dwarfism from Pusa1121 (semi dwarf) and aroma and disease resistance from Khalsa7 into basmati background (Type-3), segregating populations of the cross (Khalsa 7 X Pusa 1121) with Type-3 were evaluated phenotypically for target characters. Simultaneously, artificial inoculation of susceptible spreader variety PB-1 for blast, bacterial leaf blight (BLB) and sheath rot were used in F_6 generation. Thus, screening for disease resistance was made under artificially created epiphytotic conditions at the research farm at Meerut (North West Plains Zone, India, 28°N and 77°E) in rainy crop season. Approximately, 25 - 30 plants of each genotype were grown in a plot that comprised three rows of 3 m length and 25 cm apart. Variety PB-1, a highly susceptible rice genotype to the pathogens of all the rice diseases was planted in alleys and borders to enhance the spread of inoculums. Standard levels of agronomical management were followed to raise a good crop. Inoculums for blast were prepared from infected leaf samples having conidia and mycelium of pathogens. Inoculums having concentration of 10×10^4 to 50×10^4 conidia per ml were used for the inoculation of plants in the field in alternate seasons. Fields were frequently irrigated to induce environmental conditions conducive to pathogens of the above diseases prevalent in the area in order to create epiphytotic conditions. Leaves were harvested from 15 days old seedlings of randomly selected 10 plants from each family that comes from field trial during *Kharif* (rainy season). Then, leaf samples were packed into poly bags and stored at -80°C for isolation of genomic DNA, using cetyltrimethylea mmoniumbromide (CTAB) method (Moller et al., 1992).

Evaluation of grain and cooking quality

Seeds harvested from individual plants in the F_6 generation were analyzed for quality characters viz., kernel length, breadth of milled and elongation of cooked rice, aroma and alkali spreading value (ASV). For determination of the length breadth ratio (L/B ratio), twenty fully developed wholesome milled rice kernels were measured for their length and breadth. The kernel elongation ratio (ER) was estimated as ratio of length of the cooked kernels to that of uncooked kernels. Determination of aroma was based on panel reports. The strength of the sample size aroma was scored. ASV was estimated based on visual rating of starchy endosperm (Subdaiah, 2005). Twenty rice kernels were incubated in 1.7% potassium hydroxide solution in Petri dishes for 23 h at 3°C. Then, starchy endosperm was visually rated (Table 1). The popular varieties, Tarori and Pusa Basmati-1, were used as standards.

Field data analysis for area under disease progress curve (AUDPC) estimation of diseases

Disease severity (%) was recorded (Jeger, 2004) at three different stages such as late anthesis, late milking and dough stages. AUDPC was scored based on disease severity over time as estimated using the formula:

$$\text{AUDPC} = \sum_{i=1}^{i} [\{(Y_i + Y_{(i+1)})/2\} \times (t_{(i+1)} - t_i)]$$

Where, Y = Disease level at time t_i, $t_{(i+1)} - t_i$ = Duration (days) between two disease scores.

DNA amplification and gel electrophoresis

The 520 resistant families selected under artificially created epiphytotic conditions were subjected to screening for confirmation of transfer of the resistance genes against blast with the help of ten RAPD and two SCAR primers. Each reaction mixture (30 µl), used for RAPD and SCAR amplification, consisted of assay buffer (10 mM Tris Hcl, pH 8.0, 50 mM KCl), 3.0 mM $MgCl_2$, 1 U of *Taq* DNA polymerase, 1.0 mM each of dATP, dTTP, dCTP and dGTP, 10 µm of primer (Bangalore Genei) and approximately 50 and 250 ng of genomic DNA for RAPD and SCAR, respectively. The PCR amplification was followed by 45 cycles of denaturation at 95°C for 1 min, primer annealing at 30°C for 1 min, elongation at 72°C for 2 min, extension step at 72°C for 7 min and then, final hold at 4°C till electrophoresis. For SCAR analysis, the number of cycles was 35 and annealing temperature was 50°C. PCR products were mixed with 5 µl of gel loading dye (1x buffer, bromophenol blue, 0.1%; xylene cyanol 0.1% and glycerol in water, 50%). The amplification products were electrophoresed on 1.5% agarose gel at 3 - 5 volts/cm in 1x TBE buffer. Genomic DNA was quantified by UV absorbance at 260 and 280 nm, using BIO-RAD Smart Spac™ plus spectrophotometer. The ratio of OD 260/280 was also calculated to estimate the purity of nucleic acid. Genomic DNA was also quantified by agarose gel electrophoresis as the size of genomic DNA was quite big. A 0.8% gel was used to visualize the genomic DNA, as it can resolve DNA molecules in the range of 0.7 - 8.5 kb. Ten RAPD and two SCAR primers based on previous studies (Sandhu et al., 2003; Naqvi and Chattoo, 1996) were used to detect polymorphisms among the promising genotypes developed in the present study.

Data analysis and detection of genetic diversity

This study involved 5 varieties of traditional basmati rice namely, Type-3, Basmati 370 and Basmati 385, and Ranbir Basmati and Tarori Basmati. Also, 5 evolved varieties and five strains of premium quality rice *Kalanamk* that are popular in areas adjoining to Nepal and 3 varieties of non-basmati *indica* rice popular in Northern India were used in the study (Table 2). Polymorphic products from RAPD assays were calculated qualitatively for presence (1) or absence (0) of amplification bands. The proportion of bands of RAPD primers shared between any two varieties that are averaged over all loci, was used as the measure of similarity between varieties of the pair. Clustering pattern was based on distance matrices by using the unweighted pair group method analysis

Table 1. State wise superiority of Vallabh Basmati-21 in the Agri Export Zone (Basmati rice) over PB-I (Yield check) and Tarori basmati (Quality check). Report 2005(1) Varietal Improvement AICRP, DRR (ICAR) Hyderabad, India.

State	% yield superiority of Vallabh Basmati-21 over	
	PB-I (yield check)	Tarori Basmati (quality check)
U.P.	36.74	69.84
Haryana	17.52	51. 98
Punjab	4.52	13.80
UttaraKhand	4.79	26.56
Jammu & Kashmir	-	13.0

Results are cited from the Progress Report 2005 (1) Varietal Improvement AICRP, DRR (ICAR) Hyderabad, India.

Table 2. Brief description of rice varieties used in the present study.

S/N	Variety	Source/Origin	Character			
			50% flowering (Days)	Plant height (cm)	No. of tillers (per sq.m)	Grain yield (Q/ha)
1	Haryana Basmati -1 (EB)	CCSHAU, Kaul,India	120	107	173	44.20
2	Vallabh Basmati -21 (NP)	SVBPUA&T, Meerut UP, India	83	110	231	57.36
3	Ranbir Basmati (TB)	DRR, Hyderabad, India	97	140	330	31.70
4	Pusa-1121 (EB)	IARI, New Delhi India,	101	110	264	41.80
5	PB-1 (EB)	IARI, New Delhi India,	110	102	276	37.71
6	Basmati-385 (TB)	PAU, Ludhiana, Punjab, India	101	105	248	45.40
7	Kalanamak-1 (NB quality rice)	Local collection, Basti,U.P., India	124	169	110	30.20
8	Kalanamak-2 (NB quality rice)	Local collection, Basti, U.P., India	128	141	279	31.82
9	Kalanamak- 3 (NB quality rice)	NDA Uni, Faizabad, UP, India	123	154	246	33.07
10	Kalanamak-4 (NB quality rice)	NDAU,Faizabad, UP, India,	125	153	251	29.16
11	Kalanamak-5 (NB quality rice)	NDAU, Faizabad UP, India	126	154	254	35.41
12	Type-3 (TB)	SVBPUA&T,Meerut,UP, India	119	168	214	37.00
13	Super Basmati (EB)	PAU,Ludhiana, Punjab, India	1o5	150	215	26.29
14	NDR-359 (NB)	NDAU, Faizabad,UP, India	95	103	256	62.14
15	Tarori (TB)	CCSHAU,Kaul, Haryana,India	112	135	309	30.84
16	CSR-30 (EB)	CSSRI,Karnal, Haryana,India	114	131	272	27.48
17	Ramkajra (NB)	Local collection, Basti,UP, India	NA	NA	NA	NA
18	Sathi (NB)	Local collection, India	60	78	528	18.40

(UPGMA) program in WINBOOT software (Yap and Nelson, 1996). The genetic diversity between varieties is given in the form of dendrograms (Figure 1). Analysis of variance for AUDPC and the disease severity (%) at dough stage was performed using SAS software (SAS Institute Inc; CaryNC 1997). The purpose of statistical analysis was to test the level of significance of disease reactions in comparison to highly susceptible genotypes.

RESULTS AND DISCUSSION

Now, application of molecular markers merits special considerations in crop improvement. However, traditional breeding methods seem to have potential for crop improvement towards food security at least for the next two decades. Molecular markers are of great value for the selection, particularly of polygenic traits. For the fact that such markers are independent of Genotype x Environment effect, they have no epistatic effects and can easily pick up desired homozygous plants. Such molecular tools are capable of distinguishing with greater reliability the homozygous lines from others at an early stage and/or an early generation. However, application of molecular markers cannot be a substitute of traditional methods of breeding, but can enhance their efficiency by providing more reliable results at faster rate, low costs and space. Presently, two separate molecular studies for (a) detection of blast resistance and (b) assessment of genetic similarity of the new product with the traditional varieties of basmati rice were conducted to confirm findings of traditional breeding methodology used.

The segregating population of the cross (Khalsa-7 X Pusa 1121) xType-3 was screened for days to flowering,

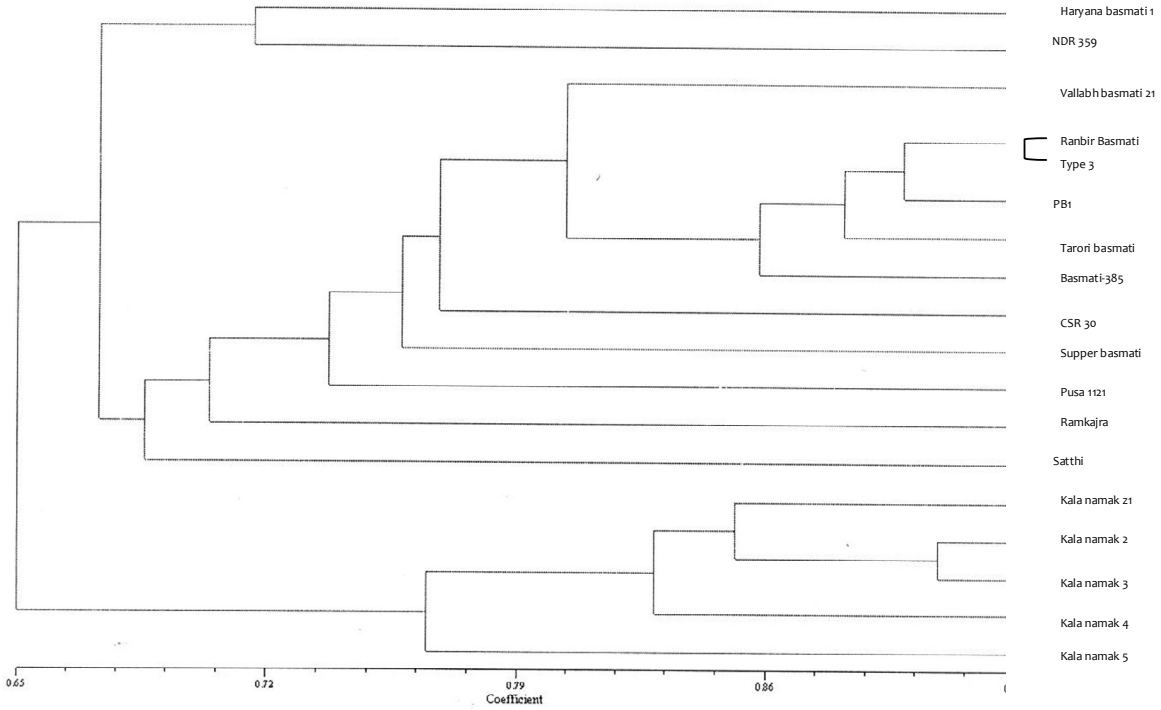

Figure 1. Dendrogram showing clustering pattern of 18 rice genotypes based genetic similarity values obtained from the RAPD data.

Table 3. Yield performance of the variety Vallabh Basmati-21 pooled over the SVTs and AICRP trials and percent superiority over all the check varieties used.

Variety	Yield (q /ha)	Percent superiority over the check
Vallabh Basmati-21	37.59	-
PB 1 (Yield check)	34.29	9.62 (The check was used both in AICRP trials and SVTs)
Basmati-370 (Quality check)	29.92	36.10 (The check was used in SVTs)
Tarori Basmati (Quality check)	30.84	27.43 (The check used in AICRP trials)

Yield comparisons were made at corresponding locations where the check variety was included in the trial.

dwarfism, aroma, disease resistance and yield as per pedigree method (Allard, 1960). The populations were subjected to artificial inoculation of susceptible spreader varieties for blast, bacterial blight and sheath rot in alternate seasons to screen the population for disease resistance under artificially created epiphytotic conditions. The analysis indicated that only 520 lines, out of about 4,000 lines tested, expressed resistance against BLB), blast and sheath rot diseases of basmati rice under artificially created epiphytotic conditions conditions.

Considering comparatively higher yield loss in basmati rice due to blast disease (*Pyricularia oryzae* pv.), resistance against this disease was confirmed at the molecular level in promising genotypes in separate PCR studies using ten RAPD and two SCAR primers. The PCR studies indicated resistance for blast in only 325 selections. For the sake of brevity, photographs of the gel consisting of only 48 improved lines are given (Figure 2). Out of these 325 selections, two hundred promising dwarf with early maturity and resistant to diseases blast, sheath rot and BLB, basmati type families were selected and isolated in F_6 generation. Such selections with confirmed resistance against blast disease were evaluated for yield. The 53 lines expressed yield potential significantly higher than that of traditional varieties of basmati. The 40 lines were irresponsive to photoperiods and therefore, could be suitable for multiple cropping systems practiced in high input agriculture areas of *Indo-Gangetic* plains under the geographical indication for Basmati rice in India. The rest 13 photosensitive lines were of little interest in the present context (Singh and Sirohi, 2005).

The highest yielding entry, Vallabh Basmati-21 (Table 3), was further assessed for molecular lineage with traditional basmati varieties for confirmation of ancestral basmati background, represented by DNA sequences within limited efficiency of the molecular markers used.

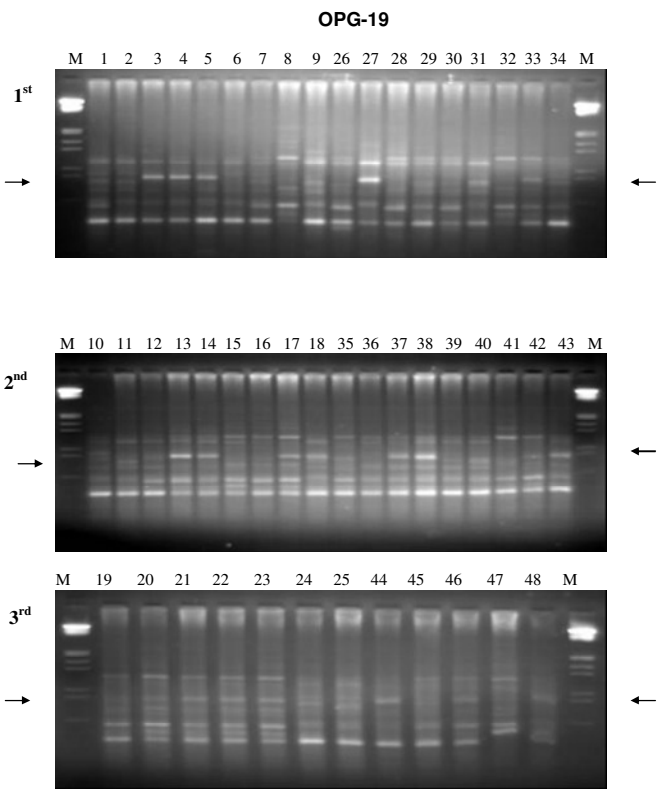

Figure 2. RAPD profile of 48 rice genotypes (resistant genotypes; 1 to 9 in 1st gel, 10 to 18 in 2nd gel and 19 to 25 in III gel; susceptible genotypes; 26 to 34 in 1st gel, 35 to 43 in 2nd gel and 44 to 48 in 3rd gel). M is the molecular marker DNA/*Eco*RI+Hind-III. Arrow shows the polymorphic band (500 bp), present in resistant genotypes. Vallabh basmati-21 is indicated at 14. Susceptibility and resistance was observed under artificially created epiphytotic condition. Genotypes tested are indicated by numbers 1 to 48.

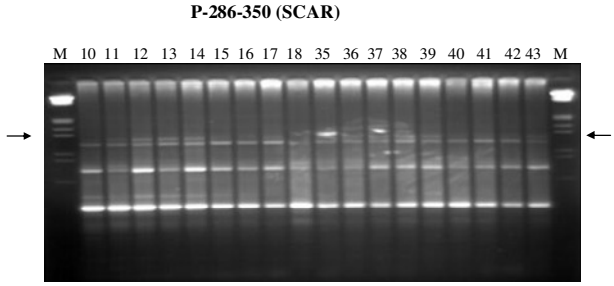

Figure 3. Vallabh basmati -21 is indicated at 14 positions with SCAR primer.

Ten RAPD and two SCAR primers (Sandhu et al., 2003; Naqvi and Chattoo, 1996) were used to detect polymorphisms among genotypes used. Out of these, eight RAPD and two SCAR markers produced distinct, reproducible and polymorphic profiles and displayed linkage in coupling phase to blast resistance genes (Sandhu et al.,

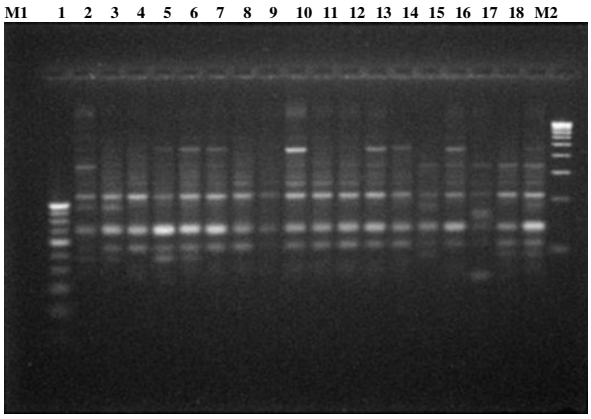

Figure 4. DNA banding pattern of 18 genotypes of rice for primer OPF-14. M1, 100 bp ladder; M2, 500 bp ladder.

2003). The approximate size range of the RAPD products was 40 bp to 4.2 kb. Reproducibility of the amplification pattern was determined by repeating each reaction at least thrice using the same protocol. Although, a number of species-diagnostic RAPD bands were noted, however, most of them were either rather faint or not repeatedly found in all the resistant genotypes (Raghunathachari et al., 1999). Therefore, such bands were not taken into account. The rate of polymorphism was highest in the case of RAPD primer OPF-06 (Shivpriya and Hittallmani, 2006), followed by OPA-05 and OPH-18. However, no amplification was observed in the case of OPF-19. Comparing between resistant and susceptible genotypes, eleven fragments produced by OPA-05 (1000 and 1200 bp), OPF-06 (4000 bp), OPF-09 (600 bp), OPF-17 (700 bp), OPF-19 (no band), OPG-17 (100 bp), OPG-18 (550 bp), OPG-19 (500 bp) (Figure 4), OPH-18 (100 and 500 bp) and OPK-12 (900 bp) were identified to be linked with blast resistant and thus, considered as potential markers for identification of the blast resistant genes (Table 4). The SCAR primer (P-286-350) linked with blast resistance gene (Sandhu et al., 2003) had also exhibited amplification in Vallabh Basmati-21 that indicated presence of the linked gene responsible for blast resistance (Figure 3). Resistance for rice blast could not be confirmed at the molecular level in 195 lines out of 520 lines which were, however, observed to be resistant under controlled conditions in the present study. Such misleading results could be obtained due to genotype x environment interactions. Only application of molecular markers may assist the breeder under such circumstances.

Basmati rice is an export quality commodity and a fetch premium price in the global market. Therefore, maintenance of purity of export commodity also linked with the national credibility that warrants no chance for adulteration should be left. This is why the best selected lines, despite having all quality characteristics of basmati rice (Singh, 2008) acceptable in the global trade with

Table 4. A comparative analysis of size of amplified products of ten random primers (RAPD), two SCAR primers and size of polymorphic bands present in resistant and susceptible genotypes.

S/N	Primer	Primers sequence	Size of amplified product *(bp)*		Polymorphic bands *(bp)*	
			Resistant genotype	Susceptible genotype	Resistant genotype	Susceptible genotype
RAPD primer						
1	OPA 5	5'AGGGGTGTTG3'	40 bp - 1.2 kb	40 bp - 1.9kb	1 and 1.2 kb	-
2	OPF 6	5'GGGAATTCGG3'	40 bp - 4.2 kb	40 bp - 4.2 kb	4000 bp	-
3	OPF 9	5'CCAAGCTTCC3'	70 - 1000 bp	70 - 947 bp	600 bp	-
4	OPF 17	5'AACCCGGGAA3'	90 - 1300 bp	-	700 bp	-
5	OPF19	5'CCTCTAGACC3'	-	-	-	-
6	OPG 17	5'ACGACCGACA3'	40 – 1600 bp	40 - 1200 bp	100 bp	-
7	OPG 18	5'GGCTCATGTG3'	80 - 850 bp	30 - 900 bp	550 bp	-
8	OPG 19	5'GTCAGGGCAA3'	80 - 1400 bp	80 - 1400 bp	500 bp	-
9	OPH 18	5'GAATCGGCCA3'	40 - 950 bp	40 bp - 950 bp	100 and 500 bp	-
10	OPK 12	5'TGGCCCTCAC3'	70 - 947 bp	70 - 2000 bp	900 bp	-
SCAR primer						
1	P 265 550(F) (R)	5'CAGCTGTTCAGTCGTTTG3' 5'CAGCTGTTCATACAAGAAAT3'	45 bp – 1 kb	40 bp - 1 kb	850 bp	-
2	P 286-350 (F) (R)	5'GCTCCGCATTAACGGGAAG3' 5'AGCCGGCTCCGGAGGTGA3'	80 - 900 bp	80 - 900 bp	900 bp	-

Table 5. Sequence of primers used for estimation of molecular similarity in the present study.

S/N	Primer	Sequence (5'-3')	Total no. of bands	No. of polymorphic fragments	Polymorphism (%)	MW (bp)
1	OPC-07	5'GTCCCGACGA3'	5	5	100	800 - 1800
2	OPC-15	5'GACGGATCAG3'	6	5	83.33	400 - 3500
3	OPC-07	5'GTGTGCCCCA3'	9	4	44.44	350 - 2000
4	OPD-08	5'GGGAATTCGC3'	7	4	57.14	500 - 3000
5	OPF-06	5'GGCTGCAAGG3'	9	7	77.77	450 - 2800
6	OPF-13	5'TGCTGCAGGT3'	10	7	70.00	400 - 2500
7	OPF-14	5'AACCCGGGAA3'	7	7	100	450 - 2500
8	OPF-17	5'CCACACTACC3'	4	2	50	350 - 2500
9	OPJ-13	5'AATGCCCCAG3'	4	2	50	380 - 3000
	OPK-11		61	43	70.29	

Table 6. Quality standards accepted in the global trade measured at DRR, Hyderabad (Results cited from Progress Report, 2005, Varietal Improvement, AICRP, DRR, GOI, Hyderabad, India pp. 1.301).

Parameter	Required quality standard (accepted in the global trade)	Quality standard expressed By Vallabh Basmati 21	Superiority of variety Vallabh Basmati- 21over the check varieties used
Milling (%)	65.0% (Minimum)	66.20%	-
Head rice recovery (%)	45.0% (Minimum)	51.00%	-
Kernel length	6.61 mm (Minimum)	7.64 mm	PB-l and Tarori Basmati
Kernel breadth	2 mm (Maximum)	1.79 mm	PB-l
Length breadth ratio	3.5 (Minimum)	4.27	PB-l and Tarori Basmati
Grain calkiness	10% (Maximum)	VOC	-
Volume expansion ratio	3.0 (Minimum)	4.70	Tarori Basmati
Water uptake	250 ml (Minimum)	310 ml	PB-l and Tarori Basmati
Kernel length after cooking	12.0 mm (Minimum)	13.20 mm	-
Elongation ratio	1.70 (Minimum)	1.73	-
Alkali spreading value	4 - 5	7.00	At par with that of Pusa Basmati-l
Amylose content	20 - 25%	24.48	PB-l
Aroma	3.0	3.0	At par with that of Pusa Basmati-l and Tarori Basmati

confirmed resistance against blast disease, were further evaluated for molecular lineage with traditional varieties of basmati rice. Presently, only one genotype, Vallabh Basmati-21, expressed ancestral similarities with traditional varieties of basmati rice. However, such molecular similarity for quality and other characteristics between one such genotype Vallabh Basmati-21 and traditional varieties will be within limits of efficiency of primers used in the present study (Table 5). Thus, the similarity among basmati varieties observed herein was accounted for within limits of regulation of the target characteristics by the genes represented by the DNA sequences that were randomly spread over the entire genome. These sequences were represented by the molecular markers used.

Estimates of similarity (Singh, 1985) and dissimilarity or divergence (Singh and Gupta, 1984; Mahalanobis, 1936) based on several morphological characters between promising genotypes, generally have been exploited long ago in different ways for improvement of crops; but then, there was no consideration for molecular aspects of the problem. In the present context, nine random decamer primers were used for estimation of similarity/dissimilarity or divergence based on PCR amplification scores. Selected nine RAPD primers generated an adequate amount of polymorphism (Figure 4). Analysis of PCR amplifications of genomic DNA revealed that, significantly, exploitable polymorphism existed among the banding patterns obtained. The molecular diversity among the varieties Type 3, Ranbir Basmati, Pusa Basmati-1, Tarori Basmati, Basmati-385 and Vallabh Basmati-21 seems to be in order of consumers' preference based on quality of these varieties. Clustering pattern indicated that the newly developed variety Vallabh Basmati-21 (Singh, 2008) expressed closeness (Figure 1) with traditional varieties and also with popular evolved basmati varieties CSR-30 and PB-1 (Nagaraju et al., 2002). On the basis of evaluation in replicated trials for yield, quality, duration and resistance against diseases, the genotype was observed to be excellent (Singh, 2008). This genotype was included in the AICRP trials coordinated by directorate of rice research (DRR), ICAR Government of India and in station varietal trial (SVTs) conducted by the regional agricultural training and demonstration station (RATDS) centers of State Department of Agriculture for formal evaluation of target characters. The variety, Vallabh Basmati-21, out yielded all qualifying varieties and checks used in AICRP trials in U.P., Haryana, Punjab and UttraKhand states under Agri Export Zone (Basmati) (Subaiah, 2005) and in SVTs for three years under irrigated conditions (Table 1). Vallabh Basmati-21 (MAUB-21) also expressed all the quality parameters when tested in the National Quality Laboratory (Subbaiah, 2005) at DRR, Hyderabad (Table 6). The variety fulfilled all the quality standards (Table 6) approved by the Government of India and was acceptable to the global trade (Anonymous, 1998). It was concluded from PCR studies that the variety expressed general resistance (Kumar, 2007) against blast disease (Figure 2). The variety, Vallabh Basmati- 21, got excellent

overall acceptability ratings for rice quality on account of its acceptability for appearance, cohesiveness, tenderness on touching and chewing, aroma, taste, elongation and flaky texture on cooking in the penal test scores at DRR, Hyderabad (Subaiah, 2005).

ACKNOWLEDGEMENTS

The authors are greatly thankful to scientists working in All India Coordinated Trial Research Project (AICRP), Directorate of Rice Research (DRR), Indian council of agricultural research (ICAR) Hyderabad and the Regional Agricultural Training And Demonstration Station (RATDS) centers of Uttar Pradesh, India, for conducting the experiments successfully and providing data required for present communication.

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