Performance of Rice Landraces Under Salt Stress at the Reproductive Stage

2 Using SSR Markers

3 ABSTRACT

Rice is the staple food crop of half of the world population and salinity is the most significant causes of rice yield reduction. The aim of this study was to screen 24 rice genotypes including 20 landraces to find out potential germplasm source for salt tolerance breeding program. Screening was performed at reproductive stage by evaluating the yield and yield attributes in sustained water bath maintaining the salinity level at 8 dS/m. Three microsatellite markers linked with salt tolerance quantitative trait loci *viz.* RM234, RM134 and RM9 were selected in response to salinity in rice landraces. At the reproductive stage, four landraces *viz.* Kute Patnai, Kashrail, Bazra Muri and Tal Mugur were identified as salt tolerant on the basis of phenotypic evaluation but SSR based marker, eight rice genotypes *viz* Binadhan-8, Patnai, KutePatnai, BazraMuri, Tal Mugur, Pokkali, Kashrail and FL 378 were found as tolerant. Combined assessment of morphological and SSR marker, four genotypes were considered as true salt tolerant lines. These identified landraces could be a potential germplasm sources for future salt tolerance rice breeding program.

Keywords: *Rice*, *landrace*, *salt tolerant*, *microsatellite marker*

Introduction

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Rice (Oryza sativa L.) is an important crop that feeds more than half of the world's population. Asian farmers contribute about 92 % of the total world's rice production [1]. But it is very sensitive to salinity stress and is currently listed as the most salt sensitive cereal crop with a threshold of 3 dS/m for most cultivated varieties [2]. Salinity is most important abiotic stress that directly regulates the plant growth and development [3-5]. It affects all the growth stages of rice from seedling to maturation [6] but reproductive stage is more sensitive for grain yield production [7]. Rice yield in salt-affected land is significantly reduced with an estimation of 30-50% yield losses annually [8]. Due to natural salinity and human interferences, the arable land is continuously transforming into saline that is expected to have overwhelming global effects, resulting in up to 50% land loss by 2050 [9,10]. In Bangladesh, 11.37 million hectares of land produces 34.53 million tons of rice [11] and about 1.8 million ha of coastal land is affected by different degrees of salinity. Most of the southern districts of the country are under saline zones which cover an area of 25-30% of the total cultivable land [12]. The population of Bangladesh is still growing by two million every year and may increase by another 30 million over the next 20 years. Thus, Bangladesh will require about 27.26 million tons of more rice for the year 2020 (http://www.knowledgebankbrri.org/riceinban.php). To increase the production it needs development of salt tolerant variety and utilization of salt affected areas. Methods for salinity tolerance screening are important for the success of a breeding program. As improving yield of plants undergoing salinity stress is one of the main targets of plant breeding, salinity tolerance screening based on agronomical parameters such as growth, yield and yield components has become the method of choice by labs worldwide [13-16]. A number of genomic tools, such as molecular markers can greatly improve the efficiency of breeding programs. The use of molecular markers has been increasing considerably because

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of their reliability and helps in deciding the distinctiveness of species [17]. Among the molecular marker technologies, microsatellite or simple sequence repeats (SSRs) are widely used in rice genetic studies because of their availability, widespread distribution in the genome, high allelic diversity and have been found to be efficient in identification of rice cultivars [18-20]. Microsatellite or SSR markers are proved to be ideal for making genetic maps [19,21] assisting selection [20] and have been applied to analyze diversity [22,23]. SSR markers are playing important role to identify genes and quantitative trait loci [24,25] that can be helpful for plant breeders to develop new cultivars. Landraces are currently being used as preferred potential donors of salt tolerance traits because of their local adaptation. Due to genetic similarities between cultivated rice species, the transfer of useful genes from one to another is possible. The presence of markers tightly linked to resistance genes will allow selection and maintenance of the desirable resistant genotypes in breeding process [26,27]. Thus, the evaluation of rice landraces could provide valuable information for genetic improvement of salt tolerant rice variety. The objective of this study was to identify the salt tolerant geneotypes based on phenotype and molecular markers linked to the salt tolerance which can be used further for marker assisted selection in rice breeding program.

61 Materials and methods

- 62 Plant Materials
- A total of 24 rice lines including 20 landraces, 2 BINA developed high yielding varieties and
- 2 advanced lines were collected from the germplasm center of Bangladesh Institute of
- 65 Nuclear Agriculture (BINA). BINA developed salt tolerant variety Binadhan-8 was used as
- tolerant control and HYV Binadhan-7 as susceptible control.
- 67 Plant growth condition and phenotypic evaluation under Salinity

68 IRRI standard protocol [13] was followed to assess the genotypes for their tolerance to 69 salinity in sustained water bath. Completely randomized design (CRD) with three replications 70 was followed for experimental design. Both Normal and salinized setups were maintained. 71 The seeds were kept in the convention oven for 5 days at 50°C for breaking the seed 72 dormancy. The oven treated seeds were soaked with tap water for 24 hours for pre-73 germination. The pre-germinated seeds were sown on the soil surface in perforated pots (3/4) 74 seeds/pot) which were kept in the tray with water. After 2 weeks, the seedlings were thinned 75 to two per pot and the water level was raised up to 1 cm above the soil surface. The water 76 level was maintained daily and the plants were protected from pests and diseases. After 3 77 weeks of sowing the pots were salinized at EC 8 dS/m by dissolving crude salt and EC was 78 monitored in every week till maturity. Data were recorded on plant height (cm), days to 79 flowering, number of effective tillers/plant, number of field grains and unfilled grains, 80 percent fertility and grain yield (g). 81 Percent fertility was calculated using the following formula. 82 % fertility = {(No. of filled grains/ (No. of filled grains+ No. of unfilled grains)} x100 83 Percent reduction was calculated using the following formula: 84 % reduction= {(traits in normal - traits in saline)/Traits in normal} x100 85 DNA extraction, PCR amplification and molecular marker analysis 86 Modified CTAB mini prep method was followed for genomic DNA extraction from 25-day-87 old seedling leaf sample [28]. Ten primers were surveyed and among them three primers 88 showed polymorphism and clear bands (Table 1). Each PCR reaction carried out with 13.0µl 89 reactions containing 1.5 µl 10x buffer, 0.75 µl dNTPs, 1µl primer forward, 1µl primer 90 reverse, 0.25 μl taq polymerase, 8.25 μl ddH₂O and 1.0 μl of each template DNA samples. 91 PCR analysis was performed according to our previous study by Akter et al. [29] with little 92 modifications. PCR profile was maintained as initial denaturation at 94°C for 5 min.,

followed by 34 cycles of denaturation at 94°C for 30 second. annealing at 55°C for 30 second and polymerization at 72°C for 1min., and a final extension of 7 min. at 72°C. Primer pairs were optimized for PCR to amplify microsatellite loci. Parental varieties were used to identify SSR polymorphism associated with the salt tolerance gene. Finally, we used the three polymorphic SSR markers (Table 1) for genotyping the 24 rice landraces. The amplified PCR products were separated in a 2.5 % agarose gel and then stained in 0.1 g/ml ethidium bromide containing water. Banding patterns were visualized with ultraviolet gel documentation system. The banding patterns of 24 genotypes were scored by comparing with tolerant and susceptible controls and similar banding pattern with Binadhan-8 were considered as tolerant and Binadhan-7 as salt susceptible.

Table 1. The sequence and size of the microsatellite markers used for screening salt tolerant rice

106 lines

Primer	Expected		Annealing				
name	PCR product size (bp)		Primer sequence				
RM234	156	For.	ACAGTATCCAAGGCCCTGG	55			
ICVI231	150	Rev.	CACGTGAGACAAAGACGGAG	. 33			
RM134	93	For.	ACAAGGCCGCGAGAGGATTCCG	55			
KWI154	93	Rev.	GCTCTCCGGTGGCTCCGATTGG	33			
RM9	136	For.	GGTGCCATTGTCGTCCTC	55			
KWI9	130	Rev.	ACGGCCCTCATCACCTTC] 33			

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110 **Results and discussion** 111 Phenotypic performance of rice landraces at reproductive stage 112 A wide range of phenotypic variation was observed at reproductive stage among the rice 113 germplasms under 8 dS/m salinity stress. Normal plant growth and development was 114 observed in normal setup but in salinized setup growth and development was retarded. 115 Different adverse symptoms, such cracked and dried leaves, stunted plant growth and early 116 flowering & maturity were observed in saline condition. Rice genotypes showed significant 117 difference in reduction of plant height, panicle length and number of filled grains. 118 119 The percentage of plant height reduction ranged from 6.55 to 29.24 and highest reduction rate 120 was observed in Volanath (29.24%) followed by Rupessor (28.59%), Binadhan-7 (27.42%) 121 and Koicha binni (26.88%). On the other hand, Pokkali (6.55%) followed by Binadhan-8 122 (6.61%), Kashrail (7.54%), FL-378 (8.17%), Tal Mugur (8.84%), Bazra Muri (8.96%), FL-123 478 (9.43%), Kute Patnai (10.63%), Nona Bokra (10.74%), Jamai naru (12.44%) and Patnai 124 (12.77%) showed comparatively lower reduction rate (Table 2). This reduction may be due to 125 the inhibition of cell division or cell enlargement for salt stress. Reduction in plant height due 126 to salt stress was also reported by Rubel et al. [30], Bhowmik et al. [31] and Choi et al. [32]. 127 Percent reduction in panicle length was ranged from 6.88 to 22.61. Considering the panicle 128 length, Volanath (22.61%), Binadhan- 7 (21.91%), Rupessor (21.35%) and Koicha Binni 129 (21.56%) showed heigher reduction. Besides, Kashrail (6.88%), Pokkali (7.11%), Binadhan-8 130 (7.20%), FL-478 (7.43%) Patnai (7.69%), FL-378 (8.19%), Bazra Muri (8.72%), Nona Bokra 131 (8.99%), Kute Patnai (9.13%), Tal Mugur (9.40%) and Jamai Naru (9.60%) showed lower 132 reduction in panicle length (Table 2). 133

Table 2. Effects of salinization (EC 8dS/m) on plant height, panicle length and number of filled grains at reproductive stage of the rice germplasm grown in sustained water bath at BINA

GY YY	G	P	lant height (cm	n)	Pa	nicle Length (c	m)	No. of filled grains/ panicle				
SL No.	Genotypes	Non-salinized (mean)	Salinized (mean)	% Reduction	Non-salinized (mean)	Salinized (mean)	% Reduction	Non-salinized (mean)	Salinized (mean)	% Reduction		
1.	Jamai Naru			9.60	89.30 39.20		56.10					
2.	Patnai	134.70	117.50	12.77	20.80	19.20	7.69	112.10	81.20	27.56		
3.	Kute Patnai	136.40	121.90	10.63	20.80	18.90	9.13	102.70	58.30	43.23		
4.	Holde Gotal	125.50	105.50	15.94	22.63	20.03	11.49	99.20	47.30	52.32		
5.	Bashful Balam	138.60	111.70	19.41	22.90	20.10	12.23	122.20	64.10	59.56		
6.	Bazra Muri	129.40	117.80	8.96	19.50	17.80	8.72	78.10	51.20	34.44		
7.	Ghunshi	141.10	116.40	17.51	21.10	18.50	12.32	88.20	44.80	60.54		
8.	Chinikani	123.20	100.30	18.59	18.60	15.40	17.20	101.30	41.20	59.33		
9.	Binadhan 7	100.30	72.80	27.42	17.80	13.90	21.91	99.70	27.80	72.12		
10.	Volanath	139.20	98.50	29.24	23.00	17.80	22.61	122.20	28.90	76.35		
11.	Rupessor	147.60	105.40	28.59	21.87	17.20	21.35	146.90	44.20	69.91		
12.	Kalo Mota	138.50	118.90	14.15	23.17	20.40	11.96	116.30	48.40	58.38		
13.	Nona Kochi	141.50	118.00	16.61	23.50	21.00	10.64	106.20	46.60	56.12		
14.	Tal Mugur	123.30	112.40	8.84	23.40	21.20	9.40	104.10	57.20	45.05		
15.	Ghigoj	146.33	115.50	21.07	23.40	19.20	17.95	114.20	57.40	49.78		
16.	Fulkainja	138.00	105.40	23.62	17.50	13.89	20.63	99.70	37.60	62.29		
17.	Koicha binni	138.40	101.20	26.88	21.80	17.10	21.56	114.60	35.60	68.94		
18.	Nona Bokhra	131.30	117.20	10.74	22.03	20.05	8.99	98.80	53.70	45.65		
19.	Binadhan 8	87.70	81.90	6.61	21.12	19.60	7.20	131.20	74.60	43.14		
20.	FL 378	83.20	76.40	8.17	21.13	19.40	8.19	135.40	75.20	44.46		
21.	Kashrail	131.30	121.40	7.54	21.23	19.77	6.88	112.30	67.70	39.72		
22.	Jolkumri	134.00	116.20	13.28	22.30	19.80	11.21	133.20	69.60	47.00		
23.	Pokkaly	131.20	122.60	6.55	23.48	21.81	7.11	120.20	74.90	37.69		
24.	FL 478	85.90	77.80	9.43	20.20	18.70	7.43	103.50	53.90	47.92		

139 Considering the number of filled grains per panicle, Volanath (76.35%), Rupessor (69.91%), 140 Binadhan-7 (72.12%) and Koicha Binni (68.94%) showed higher reduction and Patnai 141 (27.56%), Bazra Muri (34.44%), Pokkali (37.69%), Kashrail (39.32%), Binadhan-8 142 (43.14%), Kute Patnai (43.23%), FL-378 (44.46%), Tal Mugur (45.05%) and FL-478 143 (47.92%) showed lower reduction in filled grains per panicle (Table 2). Under salt stress condition, about 80 unfilled grains panicle⁻¹ was found in Volanath, 144 145 Rupessor, Koicha Binni, and Holde Gotal whereas Kashrail, Pokkali, Binadhan-8, FL-478, 146 Patnai, FL-378, Bazra Muri, Kute Patnai, Tal Mugur and Nonabokra produced less than 50 147 unfilled grains per panicle (Table 3). But under normal growth condition, the range of 148 unfilled grain was found about 15 to 35 per panicle except Binadhan-7 and Bashful Balam. Considering the effective tiller plant⁻¹ Bashful Balam, Chinikani, Volanath, Rupessor and Fulkainja 149 150 showed higher (>30) reduction. But Kashrail, Pokkali, Nona Bokra, Kute Patnai, Patnai, Bazra 151 Muri, Kalo mota, Binadhan-8 and Kashrail showed lower reduction (< 20) (Table 3). 152 Under salinized condition, the rice genotypes Binadhan-8, Kashrail, Pokkali, FL-478, Nona Bokra, 153 Kute Patnai, Tal Mugur, Patnai, FL-378 and Bazra Muri showed higher fertility (> 60%) and 154 Rupessor, Koicha Binni, Volanath, Jamainaru, Ghunshi and Holde Gotal showed lower 155 fertility (< 45%) (Table 4). All the genotypes showed more than 70% fertility under normal 156 condition. Under normal condition all the genotypes produced about 10 g or more yield plant⁻¹. But under 157 158 salt stress all the genotypes produced less than 10 g yield plant⁻¹ proved that yield has been 159 reduced due to salt stress in all tested lines. Jamai Naru, Kute Patnai, Holde Gotal, Bazra Muri, 160 Kalo Mota, Tal Mugur, Binadhan-8, FL-378, Kashrail and Pokkali produced more than 8 g yield plant⁻¹ and Ghunshi, Volanath, Binadhan-7, Rupessor and Jolkumri produced less than 5 g yield 161 plant⁻¹ (Table 4). This result supported by Asch et al. [33] who worked with 80 rice cultivars 162 163 and found that cultivars differed in their salt uptake and tolerant cultivars had lower salt

- effect on yield and yield components than susceptible. Filled grain weight and total dry
- matter weight contributed much variation in grain yield under salinity stress.

Table 3. Mean values of number unfilled grain/plant, effective tiller/plant, days to flowering of studied rice germplasm under
 salinized (EC 8dS/m) and non-salinized condition at reproductive stage

SL No.	Genotypes	No. of unfi	lled grain	No. o	of effective tiller	Days to flowering			
		Non-salinized	Salinized	Non-silanized	Salinized	% Reduction	Non-salinized	Salinized	
1.	Jamai Naru	25	74.23	12	9	25.00	133	123	
2.	Patnai	30	42.78	10	8	20.00	118	115	
3.	Kute Patnai	33	36.45	12	11	8.33	108	105	
4.	Holde Gotal	26	91.45	11	8	27.27	114	108	
5.	Bashful Balam	70	78.4	11	6	45.45	113	107	
6.	Bazra Muri	18	28.34	12	10	16.67	126	123	
7.	Ghunshi	22	54.68	7	5	28.57	128	123	
8.	Chinikani	20	51.09	10	7	30.00	116	111	
9.	Binadhan 7	45	69.2	9	6	33.33	106	101	
10.	Volanath	25	101.6	11	7	36.36	126	121	
11.	Rupessor	30	99.1	12	8	33.33	103	97	
12.	Kalo Mota	17	68.3	11	9	18.18	131	127	
13.	Nona Kochi	30	54.3	11	9	27.27	128	124	
14.	Tal Mugur	29	44.34	10	8	20.00	92	89	
15.	Ghigoj	38	56.34	7	5	28.57	108	105	
16.	Fulkainja	25	67.45	12	8	33.33	98	92	
17.	Koicha binni	42	88.45	11	8	27.27	96	90	
18.	Nona Bokhra	28	41.23	10	9	10.00	103	99	
19.	Binadhan 8	30	48.98	12	10	16.67	91	88	
20.	FL 378	28	43.8	13	9	25.00	93	89	
21.	Kashrail	31	46.7	9	8	11.11	94	91	
22.	Jolkumri	32	54.3	10	8	20.00	93	90	
23.	Pokkaly	26	35.78	13	11	15.38	96	93	
24.	FL 478	25	41.45	14	11	27.27	95	92	

SSR marker survey for salt tolerance rice genotypes

In this experiment, initially ten primers namely, RM314, RM140, RM1594, RM9, RM407, RM510, RM51, RM121, RM134 & RM234 were used for polymorphism survey of twenty four rice landraces. Of them, three SSR markers *viz.*, RM19, RM134 and RM234 showed highly polymorphism and that were selected to evaluate 24 rice germplasms for salt tolerance. According to the phenotypic performance, Binadhan-8 was considered as tolerant and Binadhan-7 was considered as susceptible. The genotypes having similar banding pattern to Binadhan-8 were considered as tolerant and similar to Binadhan-7 were considered as salt susceptible (Table 5).

Table.4 Fertility (%), yield/plant of rice landraces under salnized (EC 8dS/m) and non-salinized condition at reproductive stage

SL No.	Genotypes	Fertilit	y (%)	Yield/plant (g)				
	July 19 Fire	Non-salinized	Salinized	Non-salinized	Salinized			
1.	Jamai Naru	78.13	45.99	10.34	8.45			
2.	Patnai	78.89	60.16	16.95	7.36			
3.	Kute Patnai	79.18	69.88	18.97	8.34			
4.	Holde Gotal	79.23	43.81	17.34	8.87			
5.	Bashful Balam	72.89	56.08	16.19	6.19			
6.	Bazra Muri	81.27	64.28	13.99	9.95			
7.	Ghunshi	80.04	47.16	11.75	4.77			
8.	Chinikani	83.51	56.07	9.80	5.83			
9.	Binadhan -7	68.90	57.61	6.32	2.34			

SL No.	Genotypes	Fertility	y (%)	Yield/plant (g)				
	71	Non-salinized	Salinized	Non-salinized	Salinized			
10.	Volanath	81.78	44.68	15.34	4.23			
11.	Rupessor	83.04	50.35	13.67	4.89			
12.	Kalo Mota	87.25	51.46	18.72	8.38			
13.	Nona Kochi	77.97	56.53	19.17	5.12			
14.	Tal Mugur	78.21	51.54	17.34	8.05			
15.	Ghigoj	77.93	61.87	16.42	5.06			
16.	Fulkainja	79.95	47.73	11.41	5.59			
17.	Koicha binni	58.89	43.98	17.35	5.27			
18.	Nona Bokhra	77.92	64.25	13.35	7.96			
19.	Binadhan -8	81.39	64.62	19.38	8.11			
20.	FL 378	69.29	58.70	15.61	8.13			
21.	Kashrail	70.06	61.79	15.86	8.97			
22.	Jolkumri	82.44	65.61	10.92	4.67			
23.	Pokkali	82.22	73.43	14.43	9.33			
24.	FL 478	69.70	55.90	14.08	6.96			

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Table 5. Genotypic performance of twenty four rice germplasm using SSR markers

Genotypes	Salt tolerance with SSR markers						
	RM9	RM134	RM234				
Binadhan-8, Patnai, KutePatnai, BazraMuri, Tal Mugur,	Т	Т	Т				
Pokkali, Kashrail and FL 378							

Binadhan-7, Bashful, Balam, Volanath, Rupessor, Nona Kochi and Koichabinni	S	S	S
HoldeGotal, KaloMota, Nona Bokra and FL- 478	S	T	S
Ghunshi	Т	S	Т
Chinikani	T	S	S
Ghigoj	T	T	S
Fulkainja and Jolkumri	S	S	T
Jamai naru	S	Т	T

Where, S=Susceptible and T=Tolerant

As compared to Binadhan-8, genotypes Patnai, Kute Patnai, Chinikani, Tal Mugur, Ghigoj, Bazra Muri, Ghunshi, Kashrail, Pokkali and FL-378 were found tolerant when samples were amplified with RM9 because they positioned in the same level of Binadhan-8. In the same reaction, Holde Gotal, Bashful Balam, Volanath, Rupessor and FL 478 were found susceptible as they positioned in the same level of Binadhan-7 (Fig. 1).

In case of RM134 primers, BazraMuri, Patnai, Kute Patnai, Holde Gotal, Nona Bokra, Kashrail, Pokkali and FL 378 were found tolerant and Volanath, Rupessor, and Jolkumri were identified as susceptible (Fig. 2). Regarding to RM234 primers, KutePatnai, BazraMuri, Tal Mugur, Kashrail, Pokkali and FL-478 were identified as tolerant. Patnai, Ghunshi, Chinikani, Volanath Nona Bokra and Rupessor were found susceptible (Fig. 3). These three primers (RM109, RM7134 and RM234) showed polymorphisms in studied genotypes because they showed different banding pattern and discriminate tolerant genotypes from susceptible in relation to Binadhan-8 (tolerant) and Binadhan-7 (susceptible). These markers were reported as highly polymorphic for tagging salt tolerant genes [19,21].

But the rice genotypes, Kute Patnai, Bazra Muri, Kashrail, Tal Mugur, FL-378, and Pokkali were found as tolerant and Bashful Balam, Nona Kuchi, Rupessor, Volanath and Koichabinni were found as susceptible in all the tested markers. Based on Phenotypic observation, Binadhan-8, Kute Patnai, Kashrail, FL-378, Tal Mugur, Bazra Muri were found as tolerant while Binadhan-7, Rupessor, Koicha Binni, Volanath were found as susceptible. This phenotypic observations support the genotypic findings for identification of salt tolerant rice genotypes.

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BINA dhan-7 Bina dhan-8 patnai

Basful balam Holde gotal Bazra muri

Kute patnai

Nona kochi Kalo mota Rupessor Chinikani Volanath Ghunshi

Koicha binni Tal mugur Ghigoj fulkainaj

Ghigoj fulkainaj

Jami naru Nona

Jolkumari Kashril

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.00bp Ladder

BINA dhan-8 3INA dhan-7

oatnai

Fig. 1. Banding profiles of 24 rice germplasm using RM9 primer

Holde gotal Basful balam

3azra muri

(ute patnai

Chinikani Ghunshi

Nona kochi Rupessor Kalo mota Fal mugur Volanath

Koicha binni Nona bokhra Jami naru

olkumari kashril

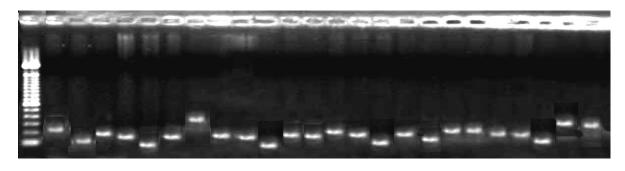


Fig. 2 Banding profiles of 24 rice germplasm using primer RM134

bp Lado	⋖ ・	BINA dhan-7 patnai	Kute patnai Holde gotal Basful balam	Bazra muri	Ghunshi	Chinikani	/olanath	Rupessor Kalo mota	Nona kochi	Tal mugur	Ghigoj fulkainaj	Koicha binni	Nona bokhra	Jami naru	FI 478	Jokashril	Jolkumari	Pokkali El 378	-L-3/8
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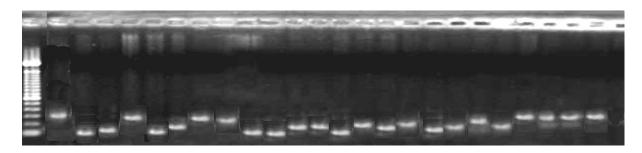


Fig. 3 Banding profiles of 24 rice germplasm using primer RM234

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