



## SSR marker-based DNA fingerprinting of *Sub1* introgressed lines in the background of traditional rice varieties of Assam India

Ashish Gautam<sup>1\*</sup>, SK Chetia<sup>1,2</sup>, Vinay Sharma<sup>3</sup>, Rahul K Verma<sup>3</sup>, Munmi Phukon<sup>2</sup>, Monalisa Kalita<sup>2</sup>,  
MK Modi<sup>3</sup> & T Ahmed<sup>2</sup>

<sup>1</sup>Department of Plant Breeding and Genetics; & <sup>3</sup>Department of Agricultural Biotechnology,  
AAU, Jorhat-785 013, Assam, India

<sup>2</sup>Regional Agricultural Research Station, AAU, Titabar-785 630, Assam, India

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### Supplementary Data

Suppl. Table 1 — List of 68 SSR markers used for DNA fingerprinting with their properties

Chromo. no.	Primer name	Repeat motif	Annealing temperature (°C)	Expected PCR size in (bp)	Primer (5'-3')
1	RM151	(TA)23	55	197	F= Forward, R= Reverse F-GGCTGCTCATCAGCTGCATGCG R-TCGGCAGTGGTAGAGTTTGATCTGC
1	RM9	(GT)15 (GA)2	55	136	F-GGTGCCATTGTCTCCTC R-ACGGCCCTCATCACCTC
1	RM237	(CT)18	55	130	F-CAAATCCCGACTGCTGTCC R-TGGGAAGAGAGCACTACAGC
1	RM10719	(CGG)8	55	163	F-GAGGACGAAGGAGAAGGACAAGG R-CGAGCCCATCTGATGTGAGACC
1	RM3825	(GA)21	55	147	F-AAAGCCCCAAAAGCAGTAC R-GTGAAACTCTGGGGTGTTCG
2	RM324	(CAT)21	55	175	F-CTGATTCCACACACTTGTGC R-GATTCCACGTCAGGATCTTC
2	RM327	(CAT)11 (CTT)5	55	213	F-TTATAGCTCTCTCGCCGAGG R-GAGGCCTTCCCCTTCTTC
2	RM341	(CTT)20	55	172	F-CAAGAAACCTCAATCCGAGC R-CTCCTCCCGATCCCAATC
2	RM424	(CAT)9	55	239	F-TTTGTGGCTCACCAAGTTGAG R-TGGCGCATTTCATGTCATC
2	RM482	(AT)9	55	188	F-TCTGAAAGCCTGACTCATCG R-GTCAATTGCAGTGCCCTTTC
3	RM231	(CT)16	55	182	F-CCAGATTATTTCTGAGGTC R-CACTTGCATAGTTCTGCATTG
3	RM517	(CT)15	55	266	F-GGCTTACTGGCTTCGATTTG R-CGTCTCCTTTGGTTAGTGCC
3	RM232	(CT)24	55	158	F-CCGGTATCCTTCGATATTGC R-CCGACTTTTCTCCTGACG
3	RM251	(CT)29	55	147	F-GAATGGCAATGGCGCTAG R-ATGCGGTTCAAGATTTCGATC
3	RM16030	(AG)11	55	99	F-GCGAACTATGAGCATGCCAACCC R-GGATTACCTGGTGTGTGCAGTGTCC
3	RM55	(GA)17	55	226	F-CCGTGCGCGTAGTAGAGAAG

3	RM186	(CGG)5	61	124	R-TCCCGGTTATTTTAAGGCG F-TCCTCCATCTCCTCCGCTCCCG
3	RM520	(AG)10	55	247	R-GGGCGTGGTGGCCTTCTTCGTC F-AGGAGCAAGAAAAGTCCCC
3	RM468	(TAT)8	55	265	R-GCCAATGTGTGACGCAATAG F-CCCTTCCTTGTTGTGGCTAC
4	RM335	(CTT)25	55	104	R-TGATTCTGAGAGCCAACCC F-GTACACACCCACATCGAGAAG
4	RM518	(TC)15	55	171	R-GCTCTATGCGAGTATCCATGG F-CTCTTCACTCACTCACCATGG
4	RM3742	(GA)17	55	76	R-ATCCATCTGGAGCAAGCAAC F-CTCTTCATCCCCAAGCC
4	RM5709	(AAT)22	55	163	R-GAGAAGAAGAACAGAGCTGCG F-CTGAATTTATTATAGGACGGAAG
4	RM3648	(GA)14	55	186	R-CATAGTATTGGATTGGACACG F-TACCCTTTCTTCCCCAAACC
4	RM280	(GA)16	55	155	R-ACCTCCTCCTCCACTTCTCC F-ACACGATCCACTTTGCGC
5	RM5361	(TC)13	50	138	R-TGTGTCTTGAGCAGCCAGG F-GCACGTGACTCCATCATCTC
5	RM413	(AG)11	55	79	R-ATGCAGATGATAGCCCAAGG F-GGCGATTCTTGATGAAGAG
5	RM169	(GA)12	67	167	R-TCCCCACCAACTTGTCTTC F-TGGCTGGCTCCGTGGGTAGCTG
5	RM31	(GA)15	55	140	R-TCCCGTTGCCGTTTCATCCCTCC F-GATCACGATCCACTGGAGCT
5	RM334	(CTT)20	55	182	R-AAGTCCATTACTCTCCTCCC F-GTTCAGTGTTTCAGTGCCACC
6	RM170	(CCT)7	55	121	R-GACTTTGATCTTTGGTGGACG F-TCGCGCTTCTTCTCGTCGACG
6	RM19629	(TTA)30	55	331	R-CCCCTTGCAGAGGAAGCAGCC F-CAATTTGGAAGTTGAGCCATCG
6	RM204	(CT)44	55	169	R-GAGTAGCTTGGCCCATAATTTGC F-GTGACTGACTTGGTCATAGGG
6	RM402	(ATA)7	55	133	R-GCTAGCCATGCTCTCGTACC F-GAGCCATGGAAAGATGCATG
6	RM253	(GA)25	55	141	R-TCAGCTGGCCTATGACAATG F-TCCTTCAAGAGTGCAAAACC
6	RM276	(AG)8A3 (GA)33	55	149	R-GCATTGTCATGTGCAAGCC F-CTCAACGTTGACACCTCGTG
6	RM6836	(TCT)114	55	240	R-TCCTCCATCGAGCAGTATCA F-TGTTGCATATGGTGCTATTTGA
6	RM527	(GA)17	55	233	R-GATACGGCTTCTAGGCCAAA F-GGCTCGATCTAGAAAATCCG
6	RM3827	(GA)21	55	160	R-TTGACACAGTTGCGATAGAG F-GGACGGATTGTAGGTAGGAC
6	RM340	(CTT)8T3 (CTT)14	55	163	R-CCTTTCTTCAATCTGCATTC F-GGTAATGGACAATCCTATGGC
7	RM346	(CTT)18	55	175	R-GACAAATATAAGGGCAGTGTGC F-AAAGTCTCCCTGTTGTAGCC
7	RM320	(AT)11GTAT (GT)13	55	167	R-CATGAACGTAAAGCAAACG F-CAACGTGATCGAGGATAGATC
7	RM118	(GA)8	67	156	R-GGATTGCTTACCACAGCTC F-CCAATCGGAGCCACCGGAGAGC
7	RM172	(AGG)6	55	159	R-CACATCCTCCAGCGACGCCGAG F-TGCAGCTGCGCCACAGCCATAG

8	RM152	(GGC)10	55	151	R-CAACCACGACACCGCCGTGTTG F-GAAACCACCACACCTCACCG
8	RM25	(GA)18	55	146	R-CCGTAGACCTTCTGAAGTAG F-GGAAAGAATGATCTTTTCATGG
8	RM149	(AT)10	55	253	R-CTACCATCAAAACCAATGTTC F-GCTGACCAACGAACCTAGGCCG
8	RM281	(GA)21	55	138	R-GTTGGAAGCCTTTCCTCGTAACAG F-ACCAAGCATCCAGTGACCAG
9	RM316	(GT)8- (TG)9(TTTG)4	55	192	R-GTTCTTCATACAGTCCACATG F-CTAGTTGGGCATACGATGGC
9	RM3769	(TG)4 (GA)18	50	103	R-ACGCTTATATGTTACGTCAAC F-TGCATGCTTCGTTTCAGCTAG
9	RM205	(CT)25	55	122	R-GTCTCCGAGCTCCTCAGGTC F-CTGGTTCTGTATGGGAGCAG
10	RM222	(CT)18	55	213	R-CTGGCCCTTCACGTTTCAGTG F-CTTAAATGGGCCACATGCG
10	RM5348	(TC)13	55	183	R-CAAAGCTCCGGCCAAAAG F-AATCCGATAGGAGTACCGCC
10	RM216	(CT)18	55	146	R-AAGTGTATGGGCTGGAATGG F-GCATGGCCGATGGTAAAG
10	RM225	(CT)18	55	140	R-TGTATAAAACCACACGGCCA F-TGCCCATATGGTCTGGATG
10	RM258	(GA)21(GGA)3	55	148	R-GAAAGTGGATCAGGAAGGC F-TGCTGTATGTAGCTCGCACC
10	RM304	(GT)2(AT)10(GT) 33	55	160	R-TGGCCTTTAAAGCTGTCGC F-TCAAACCGGCACATATAAGAC
10	RM333	(TAT)19(CTT)19	55	191	R-GATAGGGAGCTGAAGGAGATG F-GTTCAGTGTTCAGTGCCACC
10	RM496	(TC)14	55	267	R-GACTTTGATCTTTGGTGGACG F-GACATGCGAACAACGACATC
10	RM474	(AT)13	55	252	R-GCTGCGGCGCTGTTATAC F-AAGATGTACGGGTGGCATTTC
10	RM171	(GATG)5	55	328	R-TATGAGCTGGTGAGCAATGG F-AACGCGAGGACACGTACTTAC
11	RM167	(GA)16	55	128	R-ACGAGATACGTACGCCTTTG F-GATCCAGCGTGAGGAACACGT
11	RM287	(GA)21	55	118	R-AGTCCGACCACAAGGTGCGTTGTC F-TTCCCTGTTAAGAGAGAAATC
11	RM21	(GA)18	55	157	R-GTGTATTTGGTGAAAGCAAC F-ACAGTATTCCGTAGGCACGG
11	RM206	(CT)21	55	147	R-GCTCCATGAGGGTGGTAGAG F-CCCATGCGTTTAACTATTCT
12	RM28166	(CT)12	55	194	R-CGTTCCATCGATCCGTATGG F-TGCTTGCAAACATTGCTTCTGG
12	RM28519	(TGC)7	55	141	RACTGATGTACTGAACACGGGAAGG F-TTCAGAGCATGTATGTGAGTGAGC
12	RM519	(AAG)8	55	122	R-AAGCTCGGAAACAATCAAGAGG F-AGAGAGCCCCTAAATTTCCG
					R-AGGTACGCTCACCTGTGGAC