

Table 2 Primer sequences, accession numbers, and characteristics of the 70 SSR markers in 24 *Nicotiana* species

Locus	Repeat motif	Primer sequence (5'-3') Forward/Reverse	GenBank Accession no.	No. of alleles	Allele size range (bp)	H <sub>e</sub>	H <sub>o</sub>	R	PI
TbM1	(ttc) <sub>7</sub>	ttgcttagatctggactatccgtag/cgggttttccctgtatataggtgt	DQ777877	5	150-300	0.32	0.48	-0.12	0.30
TbM2	(tc) <sub>16</sub>	agaataactcaagctatgcatccaac/ ttccttagatctggactatgtgctc	DQ865406	6	200-350	0.24	0.49	-0.01	0.18
TbM3	(ac) <sub>14</sub> (n) <sub>59</sub> (ac) <sub>20</sub> (n) <sub>22</sub> (ac) <sub>52</sub>	agtgattctctgcttagatctgga/gggaattcgattctctgcttagat	DQ865407	6	200-700	0.29	0.40	0.19	0.34
TbM4	(ag) <sub>10</sub>	ttctctgcttagatctggactacc/ccctactgttggttagtaggtgaa	DQ865408	4	150-500	0.17	0.42	-0.09	0.13
TbM5	(tc) <sub>18</sub>	ttagtagcacttaggtcctgcat/attcgattctctgcttagatctgg	DQ865409	5	200-400	0.38	0.43	0.34	0.44
TbM6	(ag) <sub>11</sub>	agagtgtacgcagacctaccctac/atacgactcactatagggcgaattg	DQ865410	5	200-400	0.36	0.46	0.25	0.37
TbM7	(gt) <sub>28</sub>	cttgcttagatctggactatgtgct/cacacacacactcagattttctctt	DQ865411	5	190-300	0.11	0.49	-0.27	-0.04
TbM8	(tc) <sub>20</sub>	tccctgcatagaactatctcaactc/tcatgctcttctgtactccctact	DQ865412	6	180-400	0.18	0.49	-0.14	0.08
TbM9	(ct) <sub>19</sub>	gtttgaataaccgattgctcgt/ggtgtgctcctggcttagat	DQ865413	6	200-500	0.09	0.41	-0.23	0.01
TbM10	(tc) <sub>22</sub>	attgtctgtctgtacagtcttgg/ccattctcccagaatagctctaagt	DQ865414	7	200-400	0.32	0.47	0.17	0.32
TbM11	(ac) <sub>14</sub>	tgattctctgcttagatctggact/attcgattctctgcttagatctgg	DQ865415	6	200-300	0.27	0.47	0.07	0.25
TbM12	(tct) <sub>71g</sub> (ttc) <sub>7</sub>	acacgagcgttatttagcag/tcgaagggttaggagagaagtaac	DQ865416	5	200-400	0.12	0.46	-0.23	0.01
TbM13	(ga) <sub>29</sub>	cagtttaagcatctctagcagggtg/caataaacctcctactctctctctcc	DQ865417	6	200-500	0.34	0.50	0.19	0.32
TbM14	(ag) <sub>16</sub>	atagcaatcaacaccaacctcat/cttatactcgtgccatgcaagt	DQ865418	7	200-300	0.22	0.48	-0.05	0.16
TbM15	(aga) <sub>7</sub>	aaaagcagactctgttctgtgact/cctctgcttagatctgtgctctctt	DQ865419	6	200-400	0.18	0.20	0.16	0.29
TbM16	(tct) <sub>7</sub>	tactctgcttatacttgggaag/gtaaacacagcagcctacaaaat	DQ865420	5	200-300	0.30	0.48	0.12	0.28
TbM17	(ac) <sub>14</sub>	tgattctctgcttagatctggact/atacgactcactatagggcgaattg	DQ865421	6	200-500	0.14	0.49	-0.20	0.02
TbM18	(tct) <sub>9</sub>	gaatatgtccatggttttctcactc/tgcttagatctggactagaagaagg	DQ865422	7	200-400	0.17	0.43	-0.09	0.13
TbM19	(ct) <sub>11</sub>	attcgattctctgcttagatctgg/tggaattagggattgagagatagag	DQ865423	6	150-500	0.00	0.00	0.00	0.00
TbM20	(ga) <sub>11</sub>	gggagcagttttagctgtttat/aaagtgatctcactcctagccatct	DQ865424	6	200-300	0.15	0.15	0.15	0.25
TbM21	(aag) <sub>18</sub>	aagagaacagctttaaaccacaag/agtgattctctgcttagatctgga	DQ865425	6	150-500	0.16	0.38	-0.07	0.15
TbM22	(atc) <sub>5</sub> (aga) <sub>7</sub>	actaggaagccactctcatttcag / caaagtcagagttagagaagtgatg	DQ865426	7	200-500	0.18	0.48	-0.12	0.10
TbM23	(tct) <sub>11</sub>	ctcggaaaaggtcagaagagaaaag/tgattctctgcttagatctggact	DQ865427	7	200-300	0.32	0.49	0.16	0.30
TbM24	(ag) <sub>10</sub>	ctaattcttactcagcccatgt/taggtgccttcttgacatatcttc	DQ865428	5	200-500	0.12	0.31	-0.07	0.13
TbM25	(ga) <sub>11</sub>	atctggactagtgttgcctgtct/aagaatctcactcccagctctttt	DQ865429	5	200-500	0.09	0.46	-0.28	-0.04
TbM26	(tg) <sub>5</sub> (tg) <sub>9</sub> (tg) <sub>5</sub> (tg) <sub>6</sub>	gtaacgactactatagggcgaattg/ctcacacacacatactcacacac	DQ865430	5	150-500	0.13	0.50	-0.24	-0.01
TbM27	(ct) <sub>10</sub>	ctggactacaataaacctcatcacc/ggagtagttcacacagctattctgg	DQ865431	6	200-500	0.21	0.44	-0.03	0.18
TbM28	(ggagaa) <sub>6</sub>	agaggaagagtagagatcgggatag/aagagtgtgtcacctgctgtct	DQ865432	5	200-300	0.26	0.49	0.02	0.21
TbM29	(tc) <sub>11</sub>	tagaagtgaccacctgtcaagtaa/gcagatgaaaagagttagagtagacag	DQ865433	6	200-400	0.16	0.38	-0.07	0.14

Continuing table 2

Locus	Repeat motif	Primer sequence (5'-3') Forward/Reverse	GenBank Accession no.	No. of alleles	Allele size range (bp)	H <sub>e</sub>	H <sub>o</sub>	R	PI
TbM30	(ag) <sub>13</sub>	gacacagatgagatgggattttct/atgtcgacaacctcatcaaaagtag	DQ865434	6	200-500	0.16	0.46	-0.15	0.08
TbM31	(ag) <sub>10</sub>	agtgagaacaagcaagttagaagg/tctccataactttacggctaatacg	DQ865435	6	150-300	0.17	0.39	-0.05	0.16
TbM32	(ga) <sub>15</sub>	cgattctctgcttagatctggact/agaataactcaagctatgcatccaac	DQ865436	7	200-300	0.27	0.49	0.05	0.23
TbM33	(ag) <sub>20</sub>	cgattctctgcttagatctggact/gacctcctgagtaagaaccatttt	DQ865437	6	150-300	0.15	0.31	-0.02	0.18
TbM34	(gaa) <sub>8</sub>	atgtcggatcagcacttttgac/tattctaactcctcgaccattgact	DQ865438	8	200-400	0.04	0.35	-0.28	-0.05
TbM35	(aga) <sub>11</sub>	gattcaatcttacaaccacagtcct/ctcctctgcttcttcttctttt	DQ865439	6	200-300	0.06	0.45	-0.32	-0.08
TbM36-	(ttc) <sub>7</sub>	gtgattctctgcttagatctggac/aggggaaaagaaacgaag	EF375958	6	200-400	0.10	0.45	-0.25	-0.01
TbM37	(ttc) <sub>5</sub> n3 (tc) <sub>3</sub>	ctgtcacccttagccataagc/cgggaattcgattctcttgc	EF375959	6	200-500	0.15	0.38	-0.08	0.13
TbM38	(ag) <sub>9</sub> (at) <sub>5</sub>	caatacactcctcctgttgc/tgatacgcacttatccaatacgg	EF375960	7	200-300	0.24	0.48	-0.01	0.19
TbM39	(ct) <sub>6</sub> n2(tc) <sub>3</sub>	aatcacaccaccaatttcg/cctggtttctatgcgaagg	EF375961	6	200-400	0.11	0.50	-0.28	-0.04
TbM40	(tc) <sub>3</sub> n11(tc) <sub>6</sub>	tagtgattctctgcttagatctgg/ttcttatgagcttttagcccttgc	EF375962	7	150-500	0.18	0.50	-0.14	0.08
TbM41	(ga) <sub>8</sub> n9(ag) <sub>9</sub>	ggactaatgctcttctgtacttcc/ccactcctgagctagaacc	EF375963	6	200-300	0.07	0.47	-0.33	-0.09
TbM42	(ag) <sub>11</sub> (tg) <sub>7</sub>	ttgcttagatctgactaagatac/tctatcacatttcatTTTTgtctgc	EF375964	7	150-300	0.14	0.48	-0.19	0.04
TbM43	(ag) <sub>9</sub> n3(ag) <sub>11</sub>	aatccccctcattcatcagc/cgtcgtaggaggaaatttagg	EF375965	8	200-500	0.12	0.49	-0.25	-0.01
TbM44	(ag) <sub>12</sub>	Gtgtctgagatgtatgaggttcc/acggatacactccaatctttagc	EF375966	7	200-500	0.14	0.49	-0.21	0.02
TbM45	(ctt) <sub>9</sub>	ctcgtagctctcgcagatcg /ggaaagacaagaagcaaaaagc	EF375967	7	200-300	0.30	0.49	0.12	0.28
TbM46	(ctt) <sub>9</sub>	aatctctcggctggaagg/agccccgttacttcaactgc	EF375968	9	200-400	0.26	0.43	0.08	0.26
TbM47	(tc) <sub>9</sub> n2(ct) <sub>6</sub>	cctatagcagaacaaaactcatcc/gaagtgagaggagagaaatgagg	EF375969	7	150-500	0.06	0.49	-0.37	-0.13
TbM48	(ag) <sub>6</sub>	tagtgattctctgcttagatctgg/gttctctcctcactcatcattagc	EF375970	6	150-300	0.10	0.35	-0.14	0.07
TbM49	(tc) <sub>6</sub>	Ccttagccatctgcaatctaatagg / tctcttcttagatctggactatcg	EF375971	6	200-300	0.13	0.48	-0.23	0.01
TbM50	(gt) <sub>7</sub> n9(ag) <sub>9</sub>	gctttgccacaagtggtat/cacaagagaagtccaggttg	EF375972	6	150-300	0.23	0.48	-0.02	0.18
TbM51	(ag) <sub>4</sub> n2(ga) <sub>4</sub>	cactagtgattctctgcttagacc/atcacaatcatccctgacatagc	EF375973	5	200-500	0.14	0.47	-0.19	0.04
TbM52	(ag) <sub>4</sub> n2(ga) <sub>6</sub>	cgcttctgattctgtgccc/gaagatgggcaaatcagagg	EF375974	9	200-300	0.14	0.49	-0.21	0.02
TbM53	(aga) <sub>3</sub> n2(gca) <sub>3</sub>	gtgactcagaagcccagattatcc/tccttcaacttcttcttaacc	EF375975	7	150-500	0.09	0.41	-0.23	0.01
TbM54	(ag) <sub>7</sub> n7(ag) <sub>4</sub>	gggtttgtaggagaagtg/gtcaacccttaatttctgcatcc	EF375976	8	200-300	0.15	0.48	-0.18	0.05
TbM55	(ga) <sub>3</sub> n5(ga) <sub>7</sub>	taccttgggtttgatgtgtgg/aagtattggtttcttcaatctcc	EF375977	7	200-400	0.04	0.24	-0.16	0.03
TbM56	(aga) <sub>11</sub> n4 (agg) <sub>3</sub>	ctgtcggaaatcacgtaatagc/aaagtcagagtgagagaagtgatgc	EF375978	9	200-500	0.06	0.48	-0.35	-0.11
TbM57	(tc) <sub>7</sub> n2(tc) <sub>3</sub>	tgtatattgtctataaccgagttcc/tagtgattctctgcttagatctgg	EF375979	8	200-300	0.17	0.48	-0.14	0.08

Continuing table 2

Locus	Repeat motif	Primer sequence (5'-3') Forward/Reverse	GenBank Accession no.	No. of alleles	Allele size range (bp)	$H_e$	$H_o$	R	PI
TbM58	(ag) <sub>4</sub> n5(ag) <sub>8</sub>	aaatatcggcataaaaactaagc/tctttaattaacacaagattctctcc	EF375980	7	200-400	0.24	0.49	-0.01	0.18
TbM59	(gaa) <sub>5</sub> n2(ga) <sub>4</sub>	caattaaggcattgaacttg/tcacccatctcctctctcc	EF375981	9	200-500	0.24	0.49	-0.02	0.18
TbM60	(gag) <sub>6</sub> (gag) <sub>7</sub>	cgggaattcgattctcttg/ggtgtggcggcttagtcc	EF375982	8	200-300	0.11	0.48	-0.25	-0.02
TbM61	(tc) <sub>9</sub> n(tc) <sub>8</sub>	aactcctcacgatccctcc /tccttttagataagcaacttcacg	EF375983	8	200-300	0.26	0.47	0.05	0.23
TbM62	(gaa) <sub>4</sub>	ggttgctgacggacagtag/ccctccatcctcctcacc	EF375984	6	150-500	0.36	0.45	0.27	0.38
TbM63	(gaa) <sub>5</sub> n9(aga) <sub>5</sub>	ggaagttcctacacccaaacc/cctatctgttcttttcagattcc	EF375985	7	200-500	0.24	0.50	-0.02	0.17
TbM64	(ttc) <sub>3</sub> n30(ttc) <sub>4</sub>	ttaaaggaaatctggtcgaacg/cacaagcatgaaagataagaaagg	EF375986	7	200-300	0.15	0.50	-0.20	0.03
TbM65	(ag) <sub>9</sub>	atgctcctgttccattcc/aacgcggactttctattcc	EF375987	8	150-500	0.07	0.36	-0.23	0.00
TbM66	(ga) <sub>9</sub> n2(ag) <sub>3</sub> N2(ag) <sub>6</sub>	cgggaattcgattctcttg/cactagtttgattagtattggcttgc	EF375988	6	150-500	0.18	0.48	-0.11	0.10
TbM67	(aga) <sub>6</sub> (tga) <sub>3</sub>	catggaagatgatgaaaatgg/ccgggtcacattcaactgc	EF375989	6	200-300	0.11	0.50	-0.28	-0.04
TbM68	(ctc) <sub>3</sub> n6(ga) <sub>3</sub>	gacctgtgccgcaataacc/ctggactaaggacgctttgg	EF375990	6	200-400	0.18	0.20	0.16	0.29
TbM69	(gaa) <sub>4</sub> n82(agg) <sub>6</sub>	ggcgataagaactaagaataaagg/tgaaagtcaccgaaagatgc	EF375991	5	200-500	0.32	0.48	0.16	0.30
TbM70	(ct) <sub>9</sub> n7(tc) <sub>17</sub>	tctccttggcatctgtagc/gtttgagcatccctaacaagg	EF375992	6	200-300	0.18	0.20	0.16	0.29

Note:  $H_e$ , expected heterozygosity;  $H_o$ , observed heterozygosity;  $r$ , frequency of null alleles; PI, probability of identity