

TWC/24/2 Add. ORIGINAL: English DATE: June 19, 2006 INTERNATIONAL UNION FOR THE PROTECTION OF NEW VARIETIES OF PLANTS GENEVA

TECHNICAL WORKING PARTY ON AUTOMATION AND COMPUTER PROGRAMS

Twenty-Fourth Session Nairobi, June 19 to 22, 2006

ADDENDUM TO DEVELOPMENTS IN UPOV CONCERNING THE USE OF MOLECULAR TECHNIQUES

GENOTYPING OF PLANTS USING MICROSATELLITE POLYMORPHISM

Document prepared by an expert from the Russian Federation











Locus	Primer S 5'	equence > 3'	Length range of PCR- fragments, bp	Repeat unit	Number of observed alleles
STIIKA	F-TTCGTTGCTTACCTACTA;	R-CCCAAGATTACCACATTC	100-250	t _n a _m (at) _p	12
STS 1-2	F-TCTCTTGACACGTGTCACTGAAAC;	R-TCACCGATTACAGTAGGCAAGAGA	200-270	(tatc) _n	9
TOM 8-9	F-GCATTGATTGAACTTCATTCTCGT;	R-ATTTTTGTCCACACCAACTAACCG	120-170	(att) _n	8
POT 47-48	F-AACATTACAACACATTAGCA;	R-AACTTATCTGAAACTCTCGT	150-270	(tg) _n (ag) _m	6
POT 83-84	F-GGGACATCACAGTCT;	R-GGTGCTCCTATTGGTG	100-200	(tg) _n	6
ST 15-16	F-AATTCATGTTTGCGGTACGTC;	R-ATGCAGAAAGATGTCAAAATTGA	200-300	(aag) _n	5
POT 53-54	F-GCAAAATACAGGCTCCATAG;	R-TTCTCAACAACTTCCCATCC	150-250	(ct) _n (ca) _m	4
POT 57-58	F-TTGCGTGAAGCAGCCGTAAA;	R-GCCCAGTAAGTAAAACATTG	100-200	(tg) _n	6
POT 81-82	F-ATAAACCGCATGAGAAGC;	R-ATGGGATAGATTTGTTAG	50-170	$(ag)_n(gt)_m(ag)_p$	8
ST 5-6	F-CTTGCAACTTGTTAGTACCCCC;	R-AAATCCTTTGTGACCTCCCC	100-200	(tc) _n (ta) _m	4
STM 0031	F-CATACGCACGCACGTACAC;	R-TTCAACCTATCATTTTGTGAGTCG	50-200	$(ac)_n(ac)_m(gcac)(ac)_p(gcac)_q$	8
STM 1005	F-ATGCCTCTTACGAATAACTCGG;	R-CAGCTAACGTGGTTGGGG	150-200	(gta) _n	3
STM 1016	F-TTCTGATTTCATGCATGTTTCC;	R-ATGCTTGCCATGTGATGTGT	200-300	(tct) _n	9
STM 1019	F-TAGATTTTATTATTCCCAACAAGCA;	R-CAACTACCTTCTCCCCACATAG	200-250	(atc) _n	4
STM 1057	F-TTATGTTTCGGTTAAAATGTA;	R-AAATTAAATGGAAGACAACC	100-150	(aaat) _n	5
STM 1097	F-TGATTTAGTTGCTTGTTTG;	R-GCTTTCGATCCTAATACACC	100-200	(cgttt) _n	4
STM 2005	F-TTTAAGTTCTCAGTTCTGCAGGG;	R-GTCATAACCTTTACCATTGCTGGG	150-200	(ctgttg) _n	3
STM 2013	F-TTCGGAATTACCCTCTGCC;	R-AAAAAAAGAACGCGCACG	150-200	(tcta) _n	4
STM 1105	F-AAACCTGCTACAAATAAGGC;	R-CAGAAATAATTGGAGGAGATG	70-150	(actc),	9













	Locus	D	T 0C	Length range of PCR-	Repeat unit	Genome-	Number of
JN2	Locus	Primer sequence	1m, °C	fragments, bp	Repeat unit	specificity	observed allele
1	Na10-D09	F-AAGAACGTCAAGATCCTCTGC R-ACCACCACGGTAGTAGAGCG	49	150-170	(GT) _n	ABC	6
2	Na12-A02	F-AGCCTTGTTGCTTTTCAACG R-AGTGAATCGATGATCTCGCC	53	160-218	(CT) _n	ABC	16
3	Na12-F12	F-CGTTCTCACCTCCGATAAGC R-TCCGATGTAGAATCAGCAGC	55	170-190	(CCG) _n	ABC	8
4	Ni2-B02	F-CGCTGCAATTATACGAAAGC R-CCTCATGCTCTCCAAAGACC	49	80-110	(GGC)n	ABC	14
5	Ni2-C12	F-ACATTCTTGGATCTTGATTCG R-AAAGGTCAAGTCCTTCCTTCG	49	112-150	(GA) _n	AC	6
6	Ni2-F02	F-TGCAACGAAAAAGGATCAGC R-TGCTAATTGAGCAATAGTGATTCC	49	165-190	(CT)n	BC	8
7	Ni3-G04B	F-ATACTCGGGATAGGTGTGCG R-CATGTGGCAATCCTACATTTAC	55	80-140	(AG)n	ABC	15
8	Ol12-A04	F-TGGGTAAGTAACTGTGGTGGC R-AGAGTTCGCATACTCTGGAGC	55	110-150	(CT) _n	ABC	8
9	Ra2-E12	F-TGTCAGTGTGTCCACTTCGC R-AAGAGAAACCCAATAAAGTAGAACC	55	125-165	(GA)n	ABC	10
10	BRMS-006	F-TGGTGGCTTGAGATTAGTTC R-ACTCGAAGCCTAATGAAAAG	51	140-175	(GA) _n	ABC	5
11	BRMS-036	F-GGTCCATTCCTTTTTGCATCTG R-CATGGCAAGGGGTAACAAACAT	55	125-165	(CA) _m (GA) _n	А	7
12	BRMS-042	F-GGATCAGTTATCTGCACCACAA R-TCGGAATTGGATAAGAATTCAA	48	81-136	$(AAT)_k(CT)_m(T)_2(CT)_n$	ABC	8
13	BRMS-042-2	F-AGCTCCCGACAGCAACAAAAGA R-TTCGCTTCCTTTTCTGGGAATG	55	205-235	(GA)m(CT)n	А	8
14	BRMS-043	F-GCGATGTTTTTTTTCTTCAGTGTC R-TTAATCCCTACCCACAATTTCC	48	280-320	$(A)_k(T)_m(GT)_n$	Α	4
15	BRMS-046	F-TTGGCCTTGCTATTACGAGCTG R-ATGCGCAAACCCTAATTTTCAC	48	125-270	(GA) _k (CA) _m (GA) _n	ABC	19
16	BRMS-050	F-AACTTTGCTTCCACTGATTTTT R-TTGCTTAACGCTAAATCCATAT	48	162-178	(AAT) _k (TC) _m (TTC) _n	AB	9
17	BN6A2	F-CTTTGTGTGGACTTTTAGAACTTTA R-CGCAGCTTTTGGCCCACCTG	55	90-210	(GATT) _n	ABC	6
18	BN83B1	F-GCCTTTCTTCACAACTGATAGCTAA R-TCAGGTGCCTCGTTGAGTTC	48	170-230	(GA) _m (AAG) _n	ABC	10



150

100

150

100

D

C







	Locus Na12-A02		
Genome	. _в Ак, (СТ)m, (GAT)n		
BR-212		- :	1
AABB-210	AGCCTTGTTGCTTTTCAACGTCACACTATAACTGTATTCACCTTAAAACCGCCAT GAAACCTTCTTTTTACCC ACACTTTTTCCCCAAGGAAAAAAAAA	- :	1
BBCC-210	AGCCTTGTTGCTTTTCAACGTCACACTATAACTGTATTCACCTTAAAACCGCCCAT GAAACCTTCTTTTTACCCCACGCTTTTTCCCCAAGGAAAAAAAA	- :	1
BB-208	AGCCTTGTTGCTTTTCAACGTCACACTATAACTGTATTCACTTTTAAAAACCGCCAT GAAACCTTCTTTTTACCCACGCTTTTTCCCCAAGGAAAAAAAA	- :	1
AABB-208	AGCCTTGTTGCTTTTCAACGTCACACTATAACTGTATTCACTTTAAAACCGCCCAT GAAACCTTCTTTTACCCCACGCTTTTTCCCCCAAGGAAAAAAAA	- :	1
BBCC-208	AGCCTTGTTGCTTTTCAACGTCACACTATAACTGTATTCACCTYAAAAACCGCCATTGAAGCCTTCTTTTTACCCACACTTTTTCCTCTTTTCCCCAAGGAAAAAAAA	- +	1
BB-212	GAAACCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCGCGATGATGATGATGATGATGATGGCGGCGGAGCAAGTCGAGACTGTGGACAACGGCGAGATCATCGATTCACT	:	2
AABB-210	GAAACCGTCTCTCTCTCTCTCTCTCTCTCTGCGATGATGATGATGATGATGATGATGGCGCGCGGAGCAAGTCGAGACCGTGGACAACGGCGAGATCATCGATTCACT	:	2
BBCC-210	GAAACCGTCTCTCTCTCTCTCTCTCTCTCTCTGCGATGATGATGATGATGATGATGGCGGCGAGCAAGTCGAGACCGTGGACAACGGCGAGATCATCGATTCACT	:	2
BB-208	GAAACCGTCTCTCTCTCTCTCTCTCTCTCTGCGATGATGATGATGATGATGATGATGATGACGCGCGGGGCGAGCAAGTCGACAACGGCGAGATCATCGATTCACT	•	2
AABB-208	GAAACCGTETETETETETETETETETETETETETETETETETET	•	2
Genome	A		
A A 176	and the second		
	AGCCTTGTTGCTTTCAACGTCACACTCTATAACTGTATTCACCTTAAAAACCGCCATTACACTTTCCTCTTTCCCAAG-AAAAA	т:	8
AA-170	AGCCTTGTTGCTTTTCAACGTCACACTCTATAACTGTATTCACCGTAAAAACCGCCAT AGCCTTGTTGCTTTTCAACGTCACACTCTATAACTGTATTCACCGTAAAAACCGCCAT	т: т:	8
AA-172 AABB-172	AGCCTTGTTGCTTTTCAACGTCACACTCTATAACTGTATTCACCTTAAAACCGCCATT	т: т: т:	8 8 8
AA-172 AABB-172 AACC-172	AGCCTTGTTGCTTTTCAACGTCAACATCTATAACTGTATTCACCTTAAAAACCGCCATT	T : T : T : T :	8 8 8 8
AA-170 AA-172 AABB-172 AACC-172 AA-168	AGCCTTGTTGCTTTTCAACGTCAACATCTATAACTGTATTCACCTTAAAAACCGCCATT	T : T : T : T : T :	8 8 8 8 8
AA-170 AA-172 AABB-172 AACC-172 AA-168 AA-176	AGCCTTGTTGCTTTTCAACGTCAACATCTATAACTGTATTCACCTTAAAAACCGCCATT	T : T : T : T : T :	8 8 8 8 1
AA-172 AABB-172 AACC-172 AA-168 AA-176 AA-172	AGCCTTGTGCTTTICAACGTCAACTCTATAACTGTATTCACCTTAAAACCGCCAT	T : T : T : T : T :	8 8 8 8 1 1
AA-172 AABB-172 AACC-172 AA-168 AA-176 AA-172 AABB-172	AGCCTTGTGCTTTCAACGTCAACTCTATAACTGTATCACCTTAAAACCGCCAT	T : T : T : T : T : :	8 8 8 8 1 1
AA-172 AABB-172 AACC-172 AACC-172 AA-168 AA-168 AA-176 AA-172 AABB-172 AACC-172	AGCCTIGTGCTTICAACGTCAACCTCTATAACTGTATTCACCTTAAAACGCCATT	T : T : T : T : : :	8 8 8 1 1 1 1
AA-172 AABB-172 AACC-172 AA-168 AA-176 AA-172 AABB-172 AACC-172 AACC-172 AA-168	AGCCTIGTGCTTICAACGTCAACTCTATAACTGTATTCACCTTAAAACGCGCAT	T : T : T : T :	8 8 8 1 1 1 1 1
AA-172 AABB-172 AACC-172 AA-168 AA-176 AA-172 AABB-172 AACC-172 AA-168 Genome	AGCCITIGTECTITICAACGICAACICITATAACIGIATICACCITAAAACGCCATI	T : T : T : T :	8 8 8 1 1 1 1 1
AA-172 AABB-172 AACC-172 AA-168 AA-176 AA-176 AA-172 AABB-172 AACC-172 AA-168 Genome CC-160	AGCCITIGTECTITICAACGICAACICITATAACIGATIAACIGATIAAAACCGCCATI	T : T : T : T : T : T : T : T :	8 8 8 1 1 1 1 8
AA-172 AABB-172 AACC-172 AA-168 AA-176 AA-176 AA-172 AABB-172 AACC-172 AA-168 Genome CC-160 AACC-160	AGCCTTGTGCTTTCAACGTCAACTCTATAACTGTATCACCTTAAAACCGCCAT AGCCTGTGGCTTTTCAACGTCAACTCTATAACTGTATCACCTTAAAACCGCCAT AGCCTGTGGCTTTTCAACGTCAACCGCCACCTCATAACTGGTATCACCTTAAAACCGCCAT TTCCTTGTGCTTTTCAACGTCAACCGCCACCTCATAACTGGTATCACCTTAAAACCGCCAT AGCCTGTGGCTTTTCAACGTCAACCGCCATCATAACTGGTCACCTTAAACGGCCAT AGCCTGTCGCTGCTCCCCCTCCCCTCCCCAG AGCCTGTCCCCCGCCCCCCCCCCCCCCCCCCCCCCCCCC	T : : T : : T : : T : : : : : : : : : :	8 8 8 8 1 1 1 1 1 8 8
AA-172 AABB-172 AACC-172 AA-172 AA-172 AA-172 AA-172 AABB-172 AACC-172 AA-168 Genome CC-160 BBCC-160	AGCCTTGTGCTTTTCAACGTCAACTCTATAACTGTATCACCTTAAAACCGCCAT AGCCTTGTGCTTTTCAACGTCAACCTCTATAACTGTATCACCGTAAAACCGCCAT AGCCTTGTGCTTTTCAACGTCAACCGTCAACGTCATAACTGTATCACCGTTAAAACCGCCAT AGCCTTGTTGCTTTTCAACGTCAACGTCACTCTATAACTGTATCACCGTAAAACCGCCAT AGCCTTGTTGCTTTTCAACGTCAACGTCACTCTATAACTGATCACCGTAAAACCGCCAT AGCCTTGTCTCTCTCTCCCCAGCAACGGCGAAGTCGTGGACAACGGCGAAGTCGTGGACAACGGCGAAGTCACCGATCACT CAAACCATCTCTCTCTCTCTCTCTCCCCAGCACGCCAT AGCCATCTCTCTCTCTCTCTCCCCAGCACGCCAT AGCCATCTCTCTCTCTCTCTCCCAGCAACGGCGAAGTCGTGGACAACGGCGAAGTCACCGATCACT CAAACCATCTCTCTCTCTCTCTCTCCCCCGCCCCTCTCTCCCCAGCAACGGCGAAGTCACCGATCACTCCATCCA	T : . T : . T : . T : .	8 8 8 1 1 1 1 8 8 8 8 8
AA-172 AAB-172 AAC-172 AAC-172 AA-168 AA-176 AA-172 AABB-172 AACC-172 AA-168 Genome CC-160 BBCC-160 CC-160	AGCCTTGTGCTTTTCAACGTCAACTCTATAACTGTATCACCTTAAAAACCGCCAT	T : : T : : : : : : : : : : : : : : : :	8 8 8 8 1 1 1 1 1 1 8 8 8 8 1







Our team:



Ilya A. SHILOV - Head of Genome Analysis Group

Nazife S. VELISHAEVA - Researcher Yulia V. ANISKINA - Researcher Anna V. DEMCHINSKAYA - Researcher Olga V. VANYUSHEVA - Junior Researcher Marina S. KUNDA - Junior Researcher Marina E. KARZANOVA - Junior Researcher Natalia E. SHARAPOVA - Junior Researcher

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