ผนวก ก

เครื่องหมาย EST-SSR ที่ผ่านการวิเคราะห์หาหน้าที่ของยีนด้วยโปรแกรม Blast2Go จำนวน 374 คู่ไพรเมอร์จากทั้งหมด 1,570 EST-SSR โดยกำหนดชุดซ้ำของ mono- , di- , tri- , tetra- , penta- และ hexa nucleotide ให้มีจำนวนซ้ำ 10, 5, 5, 3, 3 และ 3 ตามลำดับ

Marker	motif	Forward Primer (5'-3')	Reverse Primer (5'-3')	Tm (ºC)	Size (bp)	Function	E-value	Parent genotypes	Segregation ratio
PESTM4	(A)18	ATTCAAGTTTGTGACTTCGGGT	AGGCGATTAAGTTGGGTAACG	60	258	alpha peptide	6.79E-26		
PESTM11	(T)10	GAATCCTGATGCTGAGTGTTCA	GGGGTTAGAACTAGCGACACAG	60	250	---NA---			
PESTM13	(T)18	AACTGCTTGAGTTTGGGGC	GTTCCTGAAAATAGACGGCAAG	56	215	---NA---	-		
PESTM22	(A)18	TCTGTCTTCGCTCCACAAGTTA	AAATTACAGGCTCTGCCACATT	60	111	thioredoxin-related protein 14	7.31E-34		
PESTM31	(GA)9	CCGCCGAGAGAGCGAGAG	TCGGTCAACAAAGTCCCCTAGAA	64	287	protein phosphatase	6.19E-61		
PESTM40	(CT)21	TCCACTCCTCTCTTTCGTTCTC	TTTCTGTTCCACCTCCAAAACT	60	304	nucleosome assembly protein family	4.54E-27		
PESTM43	(AG)8	CGCTCTTCTCTTCTTCTCCATC	AAAGTGATAGGTAACGGCGAAA	60	306	ormdl family protein	9.80E-59	aa X ab	1:1
PESTM50	(CGC)7	GCGACGGAAGTACAAGAACTC	GTTGTCCCACTCCCTCTTTTC	60	145	---NA---	1.03E-23	aa x ab	1:1
PESTM51	(GCA)5	AAGAACCAGAAAAGATCCACCA	AGAGTATTGCCTGTGCTGTTGA	60	125	nhl repeat-containing protein	6.91E-28		
PESTM54	(GA)12	TCTCGATCACATCAATCTTTGG	CTCCGGTACTCATTCTTATGGC	60	124	proline-rich protein	1.61E-24		
PESTM58	(GAA)6	AGTTGCTGAGTCTGGGGAATTA	TAACATGCTCTGGTTGCCTATG	60	371	eukaryotic translation initiation factor 2 beta subunit	1.18E-75		
PESTM60	(CGC)6	TCTGACGTGGGGCGAAGG	CTCAACCGCAGGCAAAGGATAG	65	231	udp-n-acetylglucosamine pyrophosphorylase	3.04E-31		
PESTM61	(AAT)5	AAGCATCTTGTTGATGGTGATG	TTGTGTGATTAAGCTGACTGGG	60	295	gdsl-motif lipase hydrolase family protein	4.56E-17	aa x ab	1:1
PESTM62	(TTC)7	ATCCTTTGAACGAAGATCCAGT	TAGGAGGAGAACAGCATTGTGA	60	193	---NA---	2.05E-40		
PESTM64	(CAG)7	CTACAACCCTCCGGCCAT	CATAAGCACTCCACTCCCTGA	60	365	---NA---	7.18E-37		
PESTM68	(GCA)4, (GA)10	GGTTTAGAAAGTGAGACGGTGG	CCTCTGATGAAAACATGCTCAA	60	150	small nuclear ribonucleoprotein sm d3	7.91E-48		
PESTM72	(CTT)5	GAAAATGGGCGGTGGAAT	TGCCAAAGAGCAGAGAATGTTA	60	274	at5g10780 t30n20_50	2.28E-54		
PESTM73	(TGC)5	ACACCTTTACCAAATAGGCTGG	CACCTTCCATGAATGACACACT	60	331	---NA---	3.74E-26	aa x ao	1:1

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Marker	motif	Forward Primer (5'-3')	Reverse Primer (5'-3')	Tm (ºC)	Size (bp)	Function	E-value	Parent genotypes	Segregation ratio
PESTM73	(TGC)5	ACACCTTTACCAAATAGGCTGG	CACCTTCCATGAATGACACACT	60	331	---NA---	3.74E-26	aa x ao	1:1
PESTM74	(ACC)5	CAAACCCTTGCTAAACATCCTC	TCTGTGGTGTAAAATCTCGGTG	60	282	leucine zipper protein	1.94E-14		
PESTM75	(AAG)5	AGATGGTTGGAGATTTCATGGT	AACTTGAGGGTGCCATTACAAG	60	253	zinc finger (c3hc4-type ring finger) family protein	1.59E-32		
PESTM76	(AGC)5	AACTACTTCAGCATTTACGGGC	TCCTCAGTAACAACTCCTGGCT	60	340	zinc finger c-x8-c-x5-c-x3-h type familyexpressed	4.93E-50		
PESTM77	(GCA)5	GCCTCCCAATGTATGCAGATAG	TGACTGGACAGCAACAATTAGC	60	231	mrna cappingc-terminal domain containingexpressed	4.23E-17		
PESTM78	(GCA)5	AGGTACTCCTCTCGGACTGTTG	GTCACAATCATGCAGTGGTAGG	55	277	copper chaperone	6.96E-28		
PESTM79	(GCG)6	TTTCCCTCCCTCCATAAACC	ATCTCCGTTGCCAGTATTGTCT	60	142	60s ribosomal protein l9	1.77E-15		
PESTM79	(AAG)5	CGCTGAGAAGTTTGATGACAAG	TTGGAGGGAAAAGGGTTAAGAT	54	284	60s ribosomal protein l6	2.69E-24		
PESTM80	(GCG)6	CCATTTCCAAAACCCTAACCTT	GGGATGGTACTTGTCGAAGAGA	54	221	60s ribosomal protein l27a	4.06E-58		
PESTM81	(GGT)6	AAATTAAAGCTACAGCCCACCA	CTTCCTCTACCCTTTCCATCCT	60	342	developmentally regulated gtp-binding protein	4.20E-50		
PESTM82	(GCT)5	CCCTCGACACCCATAGTTATTT	CTCGATTTCTGGCCTCTCATAC	60	188	plastid ribosomal protein cl15	2.49E-25		
PESTM83	(GAC)5	CAGTACCGTTGCTCCTCTGGT	CTGCACACGCAATGAGAGATAG	61	283	hypersensitive-induced response protein	2.03E-43		
PESTM84	(TCGA)4	CCTTCTTCGTTTTCGATCATTC	CTCCTTAGCCTTCTCAACCTCA	57	266	charged multivesicular body protein 4b	6.63E-47		
PESTM84	(GGT)6	CATACCCAAGTGCAATCAAAGA	CTGACCACCATTCCTGCC	60	197	---NA---	3.74E-42		
PESTM85	(ATG)5	ATCCCTGCCATTGAAGAAGTTA	CTCTCCTGCCACAAGCTCA	60	285	transcription factor btf3	1.51E-51		
PESTM87	(GCT)5	AACTTTATGCAACCCGATGAAG	GCATCCAAACATCAACTACGAA	60	267	mediator of rna polymerase ii transcription subunit 18	2.70E-24		
PESTM87	(AAAAT)4	ACGGTCGTTTTCTCTTTGTTTC	CTTCCCCTTGCTAATGAACATC	60	345	type 2 proly 4-hydroxylase	5.49E-41	ao x ao	1:2:1
PESTM88	(CTT)5	TCTTGACTACCTTCGCCTCTTC	ATAACCACATAACGCGATCCA	60	331	---NA---	4.14E-41		
PESTM88	(AGC)4	CCTAAAGATTTTCGCCCGAT	GCAACAATATCCTCCTCTCCAC	56	258	at5g20650 t1m15_50	1e-27		
PESTM91	(GAA)7	ACCCCAACCACATAATAACCAA	AGGGTCTTCTGATATGCTCTCG	60	308	---NA---	6.83E-36		
PESTM93	(GA)15	CCGGCACAGAGAAGACAG	GGCTTAGGCTTTGGAAGATG	59	328	ribosome biogenesis regulatory proteinfamily protein	2.74E-40		

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Marker	motif	Forward Primer (5'-3')	Reverse Primer (5'-3')	Tm (ºC)	Size (bp)	Function	E-value	Parent genotypes	Segregation ratio
PESTM94	(GGCGCC)3, (GCAG)3	CTCCATCTCTAACTCCACGCTT	AGTTCTTGTCGGGCACCTT	56	219	protease inhibitor-like protein	1e-30		
PESTM96	(GCG)6	TTTCCCTCCCTCCATAAACC	GAAGTCGAGGTTGAGGTGCTT	56	251	60s ribosomal protein l9	1e-15	aa x ab	1:1
PESTM97	(TTC)9	AAAATTCCCTCATCGTCTCCTT	CTTCCTCAAATCCTCCTTCAAA	60	131	syntaxin	3.10E-20		
PESTM98	(GA)14	CCATTGCTCGCTGTCGAA	CTCATCTTCACCTCCAGCTCAC	61	157	pp2ac-2 - phosphatase 2a isoform 2 belonging to family 2	1.11E-33		
PESTM99	(T)10	GCGCTTTTCTAACCCTTCTTTT	ATAGCTGTTGTCCTTGCTCTGG	61	282	betaine aldehyde dehydrogenase-like	6.32E-29		
PESTM101	(A)12	TACCTCCTCTTTCCTCTTTCCC	CACCAACAAACTCAGCATCTTC	60	327	growth-on protein gro10	1.77E-23	aa x ab	1:1
PESTM108	(CATC)4	ACTGTTTGCCATGTGGATGTAG	CTCGACCATTTATTCCCAATTC	53	283	ubiquitin-conjugating enzyme	4.29E-46		
PESTM110	(GCA)6	AAATAAACAGCCACAGCAGGAT	GGACAAGATACAATGCAGGTCA	60	332	rna binding protein 45	3.15E-28		
PESTM111	(GAGGGC)4	CAAAGAAAAGAAAGAGCGAAGC	ACTAGGGTCTTCAGGTCCATCA	60	196	tonneau 1b	7.43E-38		
PESTM113	(TTC)5	TTCCCAGTTCGATAATGTTTCC	GAGAGGAGGAGGAGGAAGAAAG	60	195	at5g53800 mgn6_19	1.28E-29		
PESTM116	(T)11	TCAACAAGCTGAAAGAGGATGA	ATATTTTCGCAAGCACCAGAGT	60	386	pdi-like protein	2.79E-15		
PESTM119	(A)13	GTCCCCTCACCACGAAAA	TTGTTTAGAGCAATTACACGCC	59	360	ribosomal biogenesis gtpase	4.50E-43		
PESTM121	(AT)9	AACTTGTGGATTCTGGTGCTTT	ACCCAGGAGAGGTCTAAGGTTC	60	139	atp synthase cf0 subunit iv	2.16E-24		
PESTM123	(AG)5	TTCTCCCTCTCGTACTCTCTCG	GAACGTCCTCCACTCCGAC	58	236	transcription factor iib	1e-53		
PESTM124	(TATG)5	AGAAGGTAAAGGAGGAGGAGGA	TACCATAGCAGGCAACACTCTC	59	285	chaperone	5.24E-25		
PESTM126	(A)19, (TC)7, (T)11	AAAAGCTACTGCCTCCACCTC	ACTCCAAGAAAACTTGAGGCAG	58	720	translation initiation factor 2 alpha	1e-33		
PESTM129	(GAT)5	AAGGTGCTGGTGTGAAAATTG	AGACCCCTCCAGATGCTTTAAC	55	201	elongation factor 1-delta 1	1.85E-28		
PESTM130	(GCT)7	GGCCCTTTCCTACCCTACTTTA	GGCTGAAACCCATATCCTCAT	55	266	60s ribosomal protein l36	2.44E-49		
PESTM131	(CT)5	TCGCCTACTTCTCTACCACCTC	ACACCACCTACTCCTCGTCTTC	57	595	dna-binding protein mnb1b	8.33E-33		
PESTM132	(A)18, (TC)5	CAAAATGGTCTCGATTAGTACCTC	TGAGTCCTTCCTATTCCCATAA	55	251	60s ribosomal protein l24	7.76E-57		
PESTM134	(GA)12	TCTCGATCACATCAATCTTTGG	CTCCGGTACTCATTCTTATGGC	60	124	proline-rich protein	1.61E-24		
PESTM136	(T)17	GCACGAGGAGAGAGAGAGAGAG	CATGATAAGAGCCATCAACCAA	57	284	glutaredoxin i	6.10E-40		
PESTM139	(GA)10	GGTTTAGAAAGTGAGACGGTGG	CCTCTGATGAAAACATGCTCAA	57	276	small nuclear ribonucleoprotein sm d3	7.91E-48		

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Marker	motif	Forward Primer (5'-3')	Reverse Primer (5'-3')	Tm (ºC)	Size (bp)	Function	E-value	Parent genotypes	Segregation ratio
PESTM140	(T)12	GGCTGTTATGAATGCCCAGATA	CAACTGGCTTATACTGCACCAA	60	367	serine threonine protein kinase	1.03E-30		
PESTM141	(AG)11	CAATCCTCCTCTCCTCACACTC	GGAGTTACGATCCATCCTGAAG	60	207	zinc finger ccch-type containing 14	6.38E-26	aa x ab	1:1
PESTM142	(AAG)5	ATCCTATCTCCCTGTGGACTGA	CTTGGTGATCTCTTCAGGCTTT	58	224	bet1 sft1-related snare	8.52E-50		
PESTM144	(AT)7	TGGCTATCAAGCAAGAGATGAA	GGATAACATGCAATGAAGGGAT	60	170	---NA---			
PESTM145	(GCGA)3	TTATGAGGGAGAGAGAGAGGGA	GATGACGGTGGAGATGCC	55	250	spermidine synthase	1e-25		
PESTM150	(CAG)5	GAGCATTGGCTTCAGCTCTT	AAACACACCACAAAACCATCTG	60	387	---NA---			
PESTM152	(GA)10	GGTTTAGAAAGTGAGACGGTGG	CCTCTGATGAAAACATGCTCAA	56	276	small nuclear ribonucleoprotein sm d3	7.91E-48		
PESTM304	(AG)6	CAAGGAACTCAACGAGAGAGG	GCCATACCACGCTCCACTA	60	115	---NA---			
PESTM305	(AG)6	CAATCCTGTTAGAAGCAGAGGG	GCTAGTGTTGGGTTCTCCCTTA	60	195	---NA---			
PESTM308	(AG)7	GCATGTCTGTGGGTGTATGAAA	GGAGAGTGTTGAAAGGGAGAGA	60	128	---NA---			
PESTM311	(TA)10	GGAATGCCGCTAATGAATG	AGCTTCAGCAACCAACCATA	58	154	---NA---			
PESTM314	(AT)7	AAATAGATGGAACGGAACGTGT	TCTGACCGAAATAGGCTTTGAT	60	224	ribosomal protein s18	4.47E-44		
PESTM315	(TC)9	ACCAAAGGACAAGGAATGCTAA	AGAACCAACCGGATAAAAGGAT	60	163	---NA---			
PESTM317	(AT)7	GTGGAGCATGTTTCCTCTCACT	GAACTTGTGATGTCGTCCTCTG	60	172	---NA---			
PESTM328	(CT)6	GACAAGGATCGCATGATTAGTT	ATATGTTGAGATGAGAGAGGGG	53	215	---NA---			
PESTM331	(AT)6	TTCATCATATTTGGGCTCCATC	AGTATGTTTTCCAATCGGCATC	60	150	---NA---			
PESTM332	(AT)6	AGTTAATGTGTCAGGGCCAGTT	CTTGGTTCACTTGGGTGTGTC	56	222	retrotransposon gag protein	2.23E-10		
PESTM336	(ATA)8	ATAGGATACAGCCCACGACTCT	AAGAAAGGAAAGAGCAGCACC	60	140	---NA---		ab x bc	1 : 1 : 1 : 1
PESTM337	(CAT)5	AAACAGTGGAGATGAAGGCAGT	GCCTCAGAAAATCAACCTCAAA	61	149	---NA---			
PESTM338	(AAG)5	CATCACATGGGGAGAGAAATTG	TCAAGATGGGGAAGAATGAAGA	61	144	---NA---			
PESTM340	(AT)6	TTGGGACACCTATGTATTCAGTC	TCTACTCTCCCTCATTATAGCAATC	57	216	---NA---			
PESTM341	(TC)6	CAGAAATTGAGTACCACATGCC	TTGAACAACAAACTTCAGCCTC	59	101	---NA---			
PESTM342	(AG)6	GAGGAGAAGGGGAGAGAAAATC	CAAAAGAAGGATGAAAGGATGG	60	151	---NA---			
PESTM343	(GA)6	GTCTTCGACCATGAGTTGCAT	TGTTGGTTTGGTGAGAAATGAG	60	201	---NA---			
PESTM343	(CCA)5	CGCTATCATCACCAGCATTATT	CTCTTTTCATATTCCCGTCACC	60	155	---NA---			
PESTM344	(TCT)5	GCCTCAAGAACATTTTGCAGAT	CCTAAATTGCATGGGAGATTGT	54	191	---NA---			

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Marker	motif	Forward Primer (5'-3')	Reverse Primer (5'-3')	Tm (ºC)	Size (bp)	Function	E-value	Parent genotypes	Segregation ratio
PESTM349	(ATT)5	TCACCTTTATCTCTGTTCTCCTCC	GGAATGAACCAATCTCCAAAGA	60	194	---NA---		ab x ab	1:2:1
PESTM351	(GAG)6	ACACAGAGAAGTCAATCGTGGG	ATCAAGATACGCTCCCTCCTTC	61	162	---NA---		ab x ab	1:2:1
PESTM353	(AGG)6	GATCAACTCGAAAGGGAAAATG	GGTTCCATCACCACCGTTAT	60	100	---NA---			
PESTM354	(TTC)5	CATCCTTCTTTAGCCTGCTCTC	CTATTCTCGCTGTGGAGTGAAC	59	109	---NA---			
PESTM359	(ATC)5	ATTGTTCCAACTCCTCTCCAAC	TTTCTCCACTTGTATCTGCCAA	60	195	---NA---			
PESTM363	(AAGA)4	TCATTTTGCAGCTACTGGATTG	GGTCTTCTCTTTTGGGGACTTT	60	171	---NA---			
PESTM381	(AACA)5	ACCCGCAGCACTTGTCCA	CGCCCTCACCCACCAGTAG	60	188	---NA---			
PESTM386	(TGCG)4	CCGTCCACTTCTCAGTAACCTC	CATGACACACACATCGAAGAAA	60	167	---NA---			
PESTM394	(ATAC)4	TTGGCATAGCAGTCAAAGTGAA	TGCGTGCATGTCTGTGTGTAT	61	104	---NA---			
PESTM403	(AAAAG)5	ACGTGGTCTTGCACCATTTA	GACCCTACGCCCTTTCTCT	58	145	---NA---			
PESTM405	(AAAAT)5	CATCGCAAATCCCAGAGG	TCTGTTCCAACTCCAAGTCTCA	60	276	---NA---			
PESTM413	(TTCTT)4	CTTCGAGACCCTCATCTCCTAC	GGAAAGTAACAGGACCCAGAAT	59	129	---NA---			
PESTM421	(ATTTTT)4	GAGGGTATAGTCTGCGGTTGTC	GCTCCAGCCATTCAGAGTTC	60	191	---NA---			
PESTM427	(A)11	GATGAGAGGGAAGAGACAATGC	GGTGCTGATGGTAAATCCTGA	60	179	---NA---			
PESTM428	(CAAA)5, (A)11	TGCATAAAACTTCCCTACGTGA	ACGGAAAACCAACCCAAATA	59	177	---NA---		ab x ab	1:2:1
PESTM429	(TTTTC)4	GGAAGAGAAAAGGAGAAAGAGGA	CGGGAAGAAGAAGGAAAAGAA	60	149	---NA---			
PESTM432	(ACCG)4	GATCGACCCCACTCATATTGAC	AAAGGTCTACCCGACTGACGTA	60	165	---NA---			
PESTM435	(A)15	GCAGTCATTCAACCCCTTGT	GCTTTATGTATTTGCTTGGGGA	60	180	---NA---			
PESTM436	(GA)8, (AC)6, (GA)6	GTCCGATTCTCTAATACCCACG	CATTCTGTCTCTCCTGCTTCCT	60	342	---NA---			
PESTM437	(A)12, (AACA)5	CTCCTGCAACCAAACCATTATT	TGTCTTGATCTTTTGCTGTTGG	60	188	---NA---			
PESTM447	(AC)6	TGTTGCCTCTTTCTTTCTCCAC	CCCAAACCCCAACCAAAA	62	175	---NA---			
PESTM457	(GA)12	TCTCGATCACATCAATCTTTGG	CTCCGGTACTCATTCTTATGGC	60	124	proline-rich protein	1.61E-24		
PESTM458	(CT)10	TCTAATCCCCTTCTCCACCTC	CCTATCTCCAAGAAAAGAGCGA	60	149	---NA---			
PESTM459	(AG)11	ACAGTCGAAAGATGGGGAGATA	CTCGGCCTTGTGACGTATG	60	139	---NA---			
PESTM460	(TC)10	ACAAATATCCCAATCCATGCC	CGTAAGAAAAGGGAAAGTAGAAGACAC	61	223	cellulose synthase-like protein	4.90E-13		

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Marker	motif	Forward Primer (5'-3')	Reverse Primer (5'-3')	Tm (°C)	Size (bp)	Function	E-value	Parent genotypes	Segregation ratio
PESTM461	(GA)8	CAAAATTGTATGCGGGTGC	CAGTCTCCGCCAAGAAAACTAC	60	108	---NA---			
PESTM462	(TA)8	AAGTCGCCCTACGATAGAATAA	GGAGGAGAAAGAAGAAACCCT	58	164	---NA---			
PESTM463	(AC)10	TGAATCCACTCAAGGGGC	CTATGGTTTGAATAGGGTGGGA	60	189	---NA---			
PESTM464	(AT)8	GGCTGAGGTTTTGATTTATCTCC	TATGTCCGCTATATGTGCCGT	60	205	---NA---		ab x aa	1:1
PESTM465	(GA)8	CAAAATTGTATGCGGGTGC	CAGTCTCCGCCAAGAAAACTAC	60	108	---NA---			
PESTM466	(CT)9	CCTCCATTCAAAAGAAGATGGT	GGTATAACCTTAAAACTCCAACCTG	59	112	---NA---			
PESTM467	(AG)11	CACATTTTCATGGGTAAGACCA	AACAATGCAAGGAAGAGTAGGG	60	102	---NA---			
PESTM468	(AT)8	GCTATCCGAAGTAGACCAATCG	TTCTTGTGAAGGGAACCAAACT	60	188	---NA---			
PESTM469	(TA)8	ATGTTGTTGGAAGATGTTGTCG	CCACGGCATTCTTTTAATCTG	60	124	---NA---			
PESTM470	(GT)8	GCTTACATGGAGCAACACTTGA	ATGCTTTGATATGGAACCCAGT	60	131	---NA---		aa x ab	1:1
PESTM471	(CT)9	TTGCCCTTCTATAAACCGTCTC	GCTCTCCTTTCTTCGTCTTCTC	59	107	---NA---		ab x ab	1:2:1
PESTM472	(AG)13	ATCCTGATTTTGTCCAGGCTT	TGTGTTCTTGAGGTGCCTAATC	59	166	---NA---		ab x aa	1:1
PESTM473	(TG)8	CTCAATATGAAGCAGTGAGCGT	CGTTTCGCGTTTCCCTAC	59	112	---NA---			
PESTM474	(CT)12	AGTTTAAGAAGTGGGGAAAGCG	GGAGAGGAAGGGAGGGTCTAA	61	198	---NA---			
PESTM475	(GA)12	TCTCGATCACATCAATCTTTGG	CTCCGGTACTCATTCTTATGGC	60	124	proline-rich protein	1.61E-24		
PESTM475	(CA)8	TTCCCTTTTATCACTTGGCATC	TACGTCAGCTTAGGATTTCCGT	60	178	---NA---		ab x ab	1:2:1
PESTM476	(AG)10	GAGTTTTCCTTTTGTTTCGCC	TGCGCTTACCTAATAAGAGAGGA	60	221	---NA---			
PESTM477	(CT)8	AAGTCAAGGTCATCATAGAACGG	GTCTTTACGTTTGTTGGCACAG	60	216	---NA---			
PESTM478	(CT)10	TGGGCTTGCCACTATGATTTA	GTTAAGATTGTTCCCTGGCTTG	60	207	---NA---			
PESTM479	(TA)11	TGGTGATACAAGGGTGATCTGT	TATCTTCTGGCATGGGTTATTG	59	175	---NA---			
PESTM480	(AG)8	GAGGTAAGAGGACGGCTCG	CGGAGTAGACGAGAAGAGCG	60	200	---NA---			
PESTM481	(GCT)7	GCTGTGTATGACAATGGGTCAG	AGCTGGCTCCTCTTTCTTCTCT	60	350	nod18 protein	3.25E-38		
PESTM482	(GGT)6	AAATTAAAGCTACAGCCCACCA	CTTCCTCTACCCTTTCCATCCT	60	342	developmentally regulated gtp-binding protein	4.20E-50		
PESTM483	(GCG)6	TTTCCCTCCCTCCATAAACC	ATCTCCGTTGCCAGTATTGTCT	60	142	60s ribosomal protein l9	1.77E-15		
PESTM484	(GGT)6	CATACCCAAGTGCAATCAAAGA	CTGACCACCATTCCTGCC	60	197	---NA---	3.74E-42		

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Marker	motif	Forward Primer (5'-3')	Reverse Primer (5'-3')	Tm (ºC)	Size (bp)	Function	E-value	Parent genotypes	Segregation ratio
PESTM485	(CGC)6	TCTGACGTGGGGCGAAGG	CTCAACCGCAGGCAAAGGATAG	65	231	udp-n-acetylglucosamine pyrophosphorylase	3.04E-31		
PESTM486	(AAT)9	ACCTTGGCAGTTAGGAGCTGT	GATCCGACACCCTTCTCTACAA	60	187	---NA---			
PESTM487	(AGA)6	CATGCGCTAGTCAAACATTAAG	AGTTATGAAACCCCTTGCTTG	58	169	---NA---			
PESTM488	(ATA)6	TGAGATCAAGATAGGCTCCCTC	AGCTGAGATGACAAAGCACAAG	60	136	---NA---		ab x ab	1:2:1
PESTM489	(CCA)6	ATCTCCACCAACATCACTACCA	CGTCTGAAGCAATAAAACCACT	58	198	---NA---			
PESTM490	(CTT)6	AGAAGGAAGGCGAACCAACTAC	TGGACGATTTTACCTGGGATTA	61	235	---NA---			
PESTM491	(GAC)8	GATTCTTCCACCCCTTCCTG	GAAATAGTAACGGCGGCGA	61	159	---NA---			
PESTM492	(CGG)9	CGGAAGTCGAACGAAAGATACT	GTAGTGCATCTCCCTCAGCTCT	60	131	cytochrome p450	4.33E-22		
PESTM493	(GGA)7	AAGAGGAGGAAGAGAGAAGAAGG	TCTCCGACGACTTCACCC	60	105	---NA---			
PESTM494	(GCG)6	AGGAAGAAGAAGAGATGGAAGACA	GGGACAATCATAGCAGCAGTTT	61	213	---NA---		ab x aa	1:1
PESTM495	(AAAT)5	AAAACCCTCACCCTAACACAAA	GGACTGGAGATTTTCAACAAGG	60	148	---NA---			
PESTM496	(TAAT)5	GACGGCATTAGCGATGGT	TACGCCCAGATCCCATATTT	59	216	---NA---			
PESTM497	(AAAT)5	ATGGGTTGGAATTAAGAGTGGT	ACGGAACCATCCATTTTCTT	58	253	---NA---			
PESTM498	(TAAA)5	TCCTCAATTCCGCTAGAAAGAG	CCTTGATGCGATGTTATAGAAGTG	60	164	---NA---			
PESTM499	(TTTA)7	GGACTTTTCCTTCCGTGC	TTTACCTTTCACTCTCCCCAA	59	124	---NA---			
PESTM500	(ATTT)7	GCGCTAATGAATGTAGATGGAA	TACCACTGATTTGGTCTCATGG	60	164	---NA---		ab x ab	1:2:1
PESTM501	(ATTT)5	TAAATCCTCCCACTGACTTCGT	TTCCTCACTCCCCAACAAAA	60	263				
PESTM502	(AAAAAT)5	GGAGGACTTCTTCAACAGGACA	TTGCTTCTTCTTCTTATTCGGC	60	227	---NA---			
PESTM503	(CGATTT)5	AGTGGAATGGGAATGGGTTAAT	GGATCGAAATCGGAATAGTCAA	60	146	---NA---			
PESTM504	(GGTTAG)5	GGCCCATCAAACCCGAAT	TGCAACCCCACTATAACCCTAACT	62	273	---NA---			
PESTM505	(CCGA)6, (CCGA)6	CCGCTCGTGCCGACTTAT	GGGAGAGTGGAAAAGGTCTGTC	61	223	---NA---			
PESTM506	(TA)7, (TG)9	GTAAGAGATCCCAAACACGATG	CATCCCACCTGCCTCTATAACT	60	175	---NA---			
PESTM507	(T)16	AAAACGCAGTAGCTGTCCCTT	AGCGAAGGAGATCAAGACCAT	60	180	---NA---			
PESTM508	(T)16	GAGTACACCTTTTCTTGGTGGG	AGAGCACAACCCCAAACTACC	60	103	---NA---			
PESTM509	(A)16	CCACCCAGACTCATAAGGTACA	CATCTTCAGGGGAAGGAAAATA	59	168	---NA---			
PESTM510	(A)16	TGGGGATGAATCTCGGTAGTAG	GATCGGTCTTCTCCTCCTTTG	60	183	---NA---			

ผนวก ก (ต่อ)

Marker	motif	Forward Primer (5'-3')	Reverse Primer (5'-3')	Tm (ºC)	Size (bp)	Function	E-value	Parent genotypes	Segregation ratio
PESTM511	(T)16	TCAATCCTCTCAATTACAGCCA	TCTGTGAGCAACCTACTACCTCTC	59	149	---NA---			
PESTM512	(A)16	CCCCAACCCCACCTAGAC	TTCTCCATGTGTTTCATGCTCT	60	113	---NA---			
PESTM513	(A)16	TCCTTTGTATCTCCTCTCTGCG	ACCTTGTTTTATGTGACTCGAACTC	60	140	---NA---		ab x ab	1:2:1
PESTM514	(A)16	ATGTAAAGCTAGGCCGCGA	GTGTTTCATGGACAAGCCATCT	61	132	---NA---			
PESTM515	(A)16	ATGCAAGTTCAGCATGAGTGTT	TAGAGGACCCAAAATGTCCAAT	60	168	---NA---		aa x ab	1:1
PESTM516	(A)16	TTTCACAGACGTGGCAGATG	TCTACAAATACTGGCAACTCAGACA	60	134	---NA---			
PESTM517	(A)16	ATTGGCCGAAGGAGGCTT	GCACATTCTTATGGAGCCAGATT	62	291	---NA---			
PESTM518	(A)16	TCCATTTGTACTGTTGGGCATA	GCTTAATCTTTTCGTCACAGCA	60	102	---NA---			
PESTM519	(A)16	ACCAACAAGATGTGCAGTATCG	ACCTCACAATTCTCCAACGAAG	61	145	---NA---			
PESTM520	(A)16	TTCCTGAGCCCATAAAATTGAG	GGCAGGTTAGCAGTCTTTGAGT	60	163	---NA---			
PESTM521	(A)16	CTGTCTTCTTCCAAACCCCATA	GGCCATGAAGCCTAGATTTGTA	60	200	---NA---		ab x aa	1:1
PESTM522	(A)16	AGTAGGGCATGGATGAGAGCTT	CCGTGGTTTTGTCAGGATTAAC	61	194	---NA---			
PESTM523	(A)16	TAGGTTTCGTTATTTGTTCCCG	AGCCATATAGGATGTTATCTAGTCAGC	60	128	---NA---		ab x aa	1:1
PESTM524	(A)16	AAAACCGCTCCTCTTGATATTG	TTTGCCCCTTCTTTCTTGG	60	202	---NA---		ab x ab	1:2:1
PESTM525	(A)16	CTACAGGGCAACCACAACAATA	TGAGGAGCAGAGACGAAGAAAT	61	176	---NA---			
PESTM526	(A)16	TCTCTCTTTCCTTCCCTCCTCT	TGGTTCTGCTAACTCTTCTGGA	59	236	---NA---		aa x ab	1:1
PESTM527	(A)16	CCAACCAAACGATTAGAATGGA	CACCACAATCACTACGACAAATTC	61	278	---NA---		aa x ab	1:1
PESTM528	(A)16	GATTGTAGGCGGTAATCAGGTC	ATGTGAAACCAGCGAAGCA	60	153	---NA---			
PESTM529	(T)17	GTTCTTTCCTGGTATCCAAACG	GCAGCAATTACAGTGGACTCAT	59	104	---NA---			
PESTM530	(A)17	GTCCTGATATGTGTTGCTGACC	GAGAGAGAGGGAGAGAGATTTTGT	59	101	---NA---			
PESTM531	(A)17	ATGATTGATGTAGTCTGCGTGG	GTTAGCTTCCGGTTTTGCTCTA	60	201	---NA---			
PESTM532	(A)17	CGTTAGCATGGTCTGTGAAGATT	CAGCCTCAAGTCTAGGATCGTT	60	248	---NA---			
PESTM533	(A)17	TGCTAACGTGGTAGAACAATCC	AATCGCAATAGTGTCTGCATGT	60	141	---NA---		ab x ab	1:2:1
PESTM534	(A)17	CGAGAGGACGTGATGTATGTGT	TCTAAAGGGAGGGGAAGAGAGT	60	286	---NA---			
PESTM535	(A)17	TTGCCATACTGGTTGATACTGG	TCATCGGAGAAGAAGACTCCC	61	130	---NA---			
PESTM536	(T)18	GGATGGGCAACCTTACTACTGA	TGACATAGCTTATTGTTGTCTGAGG	60	258	flotillin domain protein	3.97E-23		
PESTM537	(A)18	ATTCAAGTTTGTGACTTCGGGT	AGGCGATTAAGTTGGGTAACG	60	258	alpha peptide	6.79E-26		

ผนวก ก (ต่อ)

Marker	motif	Forward Primer (5'-3')	Reverse Primer (5'-3')	Tm (ºC)	Size (bp)	Function	E-value	Parent genotypes	Segregation ratio
PESTM538	(A)18	TCTGTCTTCGCTCCACAAGTTA	AAATTACAGGCTCTGCCACATT	60	111	thioredoxin-related protein 14	7.31E-34		
PESTM539	(T)18	GCACGAGGAGAGAGAGAGAGAG	GTTGCCATGTTTTGGGTCTTAT	60	117	annexin p35	5.73E-22		
PESTM540	(A)18	TAGACTGCGAGAGTAGCACAGG	GGTTTATATGAGATGGGTCGTCA	60	114	---NA---			
PESTM541	(A)18	TGAAAGATCACCACTAACCCCT	GAATGCTGGCTTTATAGGGAAA	60	164	---NA---			
PESTM542	(A)18	ATATAACCGCAATTCCTTGCTC	CAAAGAGTGCATATAAGGCGTG	60	150	---NA---			
PESTM543	(T)18	CCGAAGAAGAAAACAATGGAAC	GAAGGAAGGGGAAGCAAAAC	60	178	---NA---			
PESTM544	(A)18	GGGAAATAAGGAGATCAGAGGG	TGCGTTCCATTCATTCAGATAG	60	166	---NA---			
PESTM545	(A)18	ATCAGAAGGGTCACAAGAATCC	GGACAAGGTATGGTTCGGTCT	60	180	---NA---			
PESTM546	(A)18	GCTTCCTCAATTCTGACCAGTT	ATTTTGCCACGAAAAGTTGG	60	291	---NA---			
PESTM547	(A)18	CAATCAAGCATTCACCTCTTCA	CCGATCTTATGTTCTATTTGGTTCC	61	179	---NA---			
PESTM548	(G)18	TTTGTCTGCTGCTGTGGTTT	GCATCTCTCTCAATGCCTTTCT	60	209	---NA---			
PESTM549	(A)18	GTTCAAAAGAAGTGCCATACCC	AGAAAGTTGATGTTTTCGGAGC	60	244	---NA---		ab x ab	1:2:1
PESTM550	(A)18	TTTCCAAACAGGACGTTGTCT	CATAATTCAAGGGATCACACCA	60	162	---NA---			
PESTM551	(A)18	TTATGTCCAAAAGGCCATGTCT	GGTACGGGGAGGAGGGTC	62	185	---NA---			
PESTM552	(T)19	GATCTTGTAGAGCATGGTTCCC	ACTTGTTAAGGCAACGGAAAGA	60	227	---NA---			
PESTM553	(A)19	ATAAATTGTGCGAGGGGAAAAC	AGATCCGCGACAGGTCTTAAC	61	173	---NA---			
PESTM554	(A)19	ATATCGGCAGGTGCAAGAAA	TTCAGCTACTCCTTCCCTTCAG	60	154	---NA---			
PESTM555	(A)19	GAGGGATGCAAATCTCAGC	CTTAATGGAGACAAGCAGCAAG	59	154	---NA---		ab x ab	1:2:1
PESTM556	(A)20	CCTGCTTCTTCCTTCTCTTCAC	CCACGATGCTCAAACAAAGAT	60	165	---NA---			
PESTM557	(A)20	GCAGCGATTACCTCCTACTCTC	GATGATTGCCACACCAGTATTT	59	201	---NA---		ab x ab	1:2:1
PESTM558	(A)21	CAAGAGCACAATCATCCATCA	GGTTTGTCTAGCTTTGAGGTTACA	59	191	---NA---			
PESTM559	(A)23	GGAGTAGAATGAGCAAATATACAGG	GCTCGTCCATGTTGTGTGTA	58	245	---NA---			
PESTM560	(A)23	ACAGTTGCGGATGGAAAGAAT	GGCCTTGTAGTGTTGAATGGTC	61	271	---NA---			
PESTM561	(CT)7	CCGAACTCAACCTTCAACTTCT	ACATCGAGACGACAAACAAGG	60	289	ribosomal protein s13	2.75E-61		
PESTM562	(CT)7	GCTCTTCTCTCTCTCTCTCGC	GATGTCGTTCCGGTTGTAGA	59	298	reversibly glycosylated polypeptide	5.59E-46		
PESTM563	(TC)7	ATATTTTGGACTCGGTTGTGGT	GAAGGAAGCAATCTCCAGTCAG	60	349	---NA---			

ผนวก ก (ต่อ)

Marker	motif	Forward Primer (5'-3')	Reverse Primer (5'-3')	Tm (ºC)	Size (bp)	Function	E-value	Parent genotypes	Segregation ratio
PESTM564	(GT)7	CGCCCCAACCTGTCCATATTAC	GCCTCCTCTCCGCCTACGTTA	65	129	---NA---			
PESTM565	(AC)7	GGGTAGGGTCACAAAGCACT	TTGATTTTCCTGATGACTGGTG	60	117	---NA---		ab x ab	1:2:1
PESTM566	(AG)7	GTGTCATCAAATTCGGTCCTTT	CGGTTCTTCTGCTGCTCTACTT	60	204	---NA---			
PESTM567	(GA)7	CAGGAAGAGAAAATACCTTTTAGGG	GGAAAGAGGAACGGGGAA	60	122	---NA---		ab x ab	1:2:1
PESTM568	(CT)7	ATGACGGCTATCCAGCAAATAC	CTTCCACGGCCCAGTTATC	60	138	---NA---			
PESTM569	(TC)7	TGTTCAAACTCAAAGAACGGAG	TCACCTATTCGCTGTAGAACCA	60	105	---NA---			
PESTM570	(AG)7	GTCCTTCTTGGTTTCTTCATGG	CTAGAGGCGTTCCCTTTCCT	60	238	---NA---	7.17E-09		
PESTM571	(AG)7	GACCGTTATAGTGACCTTGGCT	TCTTTCCTTTCCTGCCTTCTC	60	195	---NA---			
PESTM572	(TA)7	AATATCACTCCTGCACATCACG	CCCATACTAAAACCGAGAGGAA	59	182	---NA---			
PESTM573	(AT)7	GGACCTCTCCATCTACCTACGA	TTGATTGATCGTGCTACAAAGC	60	159	---NA---			
PESTM574	(CT)7	AGACCTCTCTCCATCTTCCCTC	GGTAGAATTGTCCTGAGCCACT	60	190	---NA---			
PESTM575	(GA)7	CCTCATCCCCAAACAAGAGA	TTTGTACCATCAGGAGTCAAGG	59	127	---NA---			
PESTM576	(AT)7	ACAAAAGCAAGAGCAACTGTGA	GAAAGGGCGGCTAAGAAAAC	60	146	---NA---			
PESTM577	(TC)7	TCATCACTTTCTCCTCTCTTGTTC	CTTCGCTAGGATTGATATTGGG	60	220	---NA---			
PESTM578	(AT)7	TATAAATGCACAACCAACCGTC	TGATTTTCCCCTTGTCTTCCT	60	142	---NA---			
PESTM579	(TA)7	GGTAGCAATTAAGAAGGCAAGAGA	CGACCCGACTCATCCTATTCTA	60	197	---NA---			
PESTM580	(TA)7	ATCATGTTTTGCACATATCCCC	GTTGTAATTCGTTTTGGGCCT	60	137	---NA---		ab x ab	1:2:1
PESTM581	(TC)7	ATTTTGCATCTGGCACTTGAC	GGAGTCAGCTTCAGACCTACCA	61	200	---NA---			
PESTM582	(AT)7	AATGTGTCGAGCTTTGGATTCT	GTGAGCATCTGTGAGAGTTTGG	60	103	---NA---			
PESTM583	(AT)7	ATAGGTCCAAACCAAATCCAATCC	GAAACTAACTTGAAACACACACACGC	63	100	---NA---			
PESTM584	(CT)7	TGTGCTGTCCAGTTAAGGAGAA	GGGATGAGGTTCTGAGTTTGAC	60	116	---NA---			
PESTM585	(TA)7	ACCAATAGGCTTACCAGCAGAC	GATTGCTACTTCTTGTCCAGGG	60	234	---NA---			
PESTM586	(AC)7	TTAATGCACCCCTTCCTCC	TACTGCACCTCGATATGATTGG	60	222	---NA---			
PESTM587	(CT)7	CTTCCCACCTTACAAAATGACC	AAGAACCATAAAACCCTAGCCA	59	157	---NA---			
PESTM588	(AT)7	CAAAGAGAGCAGTAGGAAGGGA	CTTCTCAATCGACCGGCTT	60	243	---NA---			
PESTM589	(CT)7	GCACCCACTCTTCTTTATTTCAC	CAACAACGATGCTAGAGGGAG	60	133	---NA---			
PESTM590	(TC)7	ATTAGCTTGCGAGGGTTTCAT	GGAGAGGGAGAAGGAAAAGAAG	60	210	---NA---			

ผนวก ก (ต่อ)

Marker	motif	Forward Primer (5'-3')	Reverse Primer (5'-3')	Tm (ºC)	Size (bp)	Function	E-value	Parent genotypes	Segregation ratio
PESTM591	(AT)7	CGGTTGCAGACGTTTCTCTAAT	GGGAAGTCCACACCAAACATA	60	136	---NA---			
PESTM592	(CT)7	GATCGCATCAAGAACTCACCTT	TTTTCCCACAGAGAGAGAGAGG	60	217	---NA---			
PESTM593	(AG)7	CATCACTCTTCTTATTTGGGGC	GTAGCCAACACTTCCTCGTCAT	61	125	---NA---			
PESTM594	(TC)7	CAATCACAACCCTACTCTCCCT	GACTTTTGGGCAGAACAATCA	60	219	---NA---			
PESTM595	(AG)7	GTAGGGACGACCAGCGTAAAT	GAGAGGGAGAGAGGGAAGAGAG	60	162	---NA---		ab x ab	1:2:1
PESTM596	(AT)7	AAGAACGAGCAGGTAGGTAGG	GAATGGCGTTTTGCTTTTAG	58	153	---NA---			
PESTM597	(AT)7	GTCAGGAATCATACTCAGGGTC	CTCAAAGCCGGTGAAACTACT	59	121	---NA---			
PESTM598	(AC)7	GCCAAACTGTCTCCCTGGTAT	CATGCCTTCAATCTCTCTTTCC	60	145	---NA---			
PESTM599	(AT)7	CGACTCAACTCAACTCGAATATCA	AGCTTGTGAGCCAACTCGAA	61	149	---NA---			
PESTM600	(TA)7	TTTCACCCCTGATACTTGTTGA	TCACATGGAAGGCATGATTTAG	60	116	---NA---			
PESTM601	(TC)7	ATGAGGCTGGTACTGAGGGAT	CAGTGATGGTGATCTGCCTTTA	60	164	---NA---		ab x ab	1:2:1
PESTM602	(TA)7	GGTTTTAGCGGGTTAGATTTTG	AATGAAAGCCCACCTTATGAGA	60	207	---NA---			
PESTM603	(TC)7	TCCTTCTAACCTCATCCATTCTCT	TCTTTCCAAATTCCATCCCTC	60	214	---NA---		aa x ab	1:1
PESTM604	(AT)7	CAATCCAACCTCTTCATTCCAT	TGTATCTTTTGCCCCTGAAAGT	60	139	---NA---		ab x aa	1:1
PESTM605	(TA)7	GGAGGTTGGTTGTCTCCACA	GCAACAGCAAAGAACTTGGATT	61	205	---NA---		ab x ab	1:2:1
PESTM606	(TA)7	GACCAAAGTCACCAAATCCAAT	GAGCATTCCCATTCACTCTTTC	60	181	---NA---			
PESTM607	(GC)7	GGGCTTTGTGTTGGGTCTTTAT	TAAAATTCGGGGTGGATATGG	61	173	---NA---		ab x aa	1:1
PESTM608	(TG)7	ATTTTGAGGGTCAGGCCAA	TAGTCACAAGCGGTCAGAAACA	61	108	---NA---			
PESTM609	(GA)7	AGGCGGTGATGAAGATGAAG	CTCCTCTCAAACAGAGTGGGAT	60	151	---NA---			
PESTM611	(AT)8	TGTGAGAGAAAGAGAAGAGGGC	AACCGATCACTTGTTTGATGG	60	167	---NA---			
PESTM612	(GA)8	TCAGGATGCACCGAACTAGAC	CTCCCTCTCCCTCTCCCTCT	61	187	---NA---			
PESTM613	(TC)8	TAAATCACATCCAACAACTCGG	TACACACACACACGCGCA	61	141	---NA---			
PESTM614	(TA)8	GGATTGAGTTCGGATAGTGACC	ACTAAGCCACAAAGGGCATAAG	60	153	---NA---		ab x ab	1:2:1
PESTM615	(GT)8	AAGGCATTGTAAAGAGGGATGA	GCTTTTAGGTAAGTTTCGTGCG	60	146	---NA---			
PESTM616	(CT)8	GAAGACCGAGTGCTTTCCTTC	CAGGATGTGCATACGTGAGAGA	61	165	---NA---		ab x aa	1:1
PESTM617	(AT)8	CAAGAAGCACCTGATTTACCAT	TTTTGGGTTCCTGGGATTT	59	173	---NA---			
PESTM618	(AT)8	TGTGCAGACATTTAGCCAGGT	AAAGAGTGAAAGGACAAAGGACTTC	61	201	---NA---		ab x ab	1:2:1
PESTM619	(AT)8	AGCTATGATTGTTCTGTACTGCTG	ATACCCTGAAATGCTCCAATAG	57	208	---NA---		ab x aa	1:1

ผนวก ก (ต่อ)

Marker	motif	Forward Primer (5'-3')	Reverse Primer (5'-3')	Tm (ºC)	Size (bp)	Function	E-value	Parent genotypes	Segregation ratio
PESTM620	(TC)8	TTAATTCCATGTCCCTTGTTCC	GGGTTTTGATGATGATGTGATG	60	129	---NA---			
PESTM621	(TG)8	TAGCCTTTGCAGTTTAGGTTCG	AAACGTGTAGTAGCTTGCACCA	60	145	---NA---			
PESTM622	(TA)8	GCTTCTTGTGGCCTCTTTTCT	ATTGGAGTAACGGATTTTCACC	59	136	---NA---			
PESTM623	(GA)8	ACGACTCCACCTCCTACTTTCA	CCATTCTTTCCCACTTCTTCTG	60	193	---NA---			
PESTM624	(TC)8	GAACCCGTTTGACGTATCTACA	TCAGGATTGATTGATTTACCCC	60	142	---NA---			
PESTM625	(AG)8	TTCTCTCTTCTTTGGTGCTGTG	TCTTCCTCTTCCTTCCTCCTCT	60	207	---NA---			
PESTM626	(CT)8	AGTATATCCGAGCCGCCCT	AGAAGAGAGAAGAGGTGGGGTG	61	100	protein	1.28E-21		
PESTM627	(TA)8	ATCATATTTGTCCACGAGCCTT	GCCAATCTCATTCTGTCGTTTA	59	182	---NA---			
PESTM628	(AT)8	TGGTTTCGGTGCATGATAATAG	CAACACCACCATGAGTTATACCA	60	156	---NA---		ab x ab	1:2:1
PESTM629	(AG)8	AAGGAAGGCGGCTACTACAAG	AACCAAGAACTCTCTGCTCGAT	60	221	---NA---		ab x ab	1:2:1
PESTM630	(AT)8	TTTTCACCCCTGACACCTTC	GGGATGGAGCAAAATAAGCA	60	113	---NA---			
PESTM631	(TA)9	TTTTATGGGACTCTTGTCGGAT	AACTAACTTGCCACCAGCTTTC	60	214	---NA---			
PESTM632	(TC)9	ACTCTAATCTGAAGCCCAACGA	CGGATTTCGTCAAGTTTGGTTA	61	149	---NA---		ab x ab	1:2:1
PESTM633	(GA)9	GTACTCTAGTCCGCTGGTTTGC	TCCTGTGAGTGCATAGCATGT	59	139	---NA---			
PESTM634	(GA)9	GGTTGTAGGTGGTTCCAAAAGT	TAGGTTACGTTTCTCCTCCCTC	59	156	---NA---			
PESTM635	(TG)9	CAGGTTGGGATTGGTTTAGTTC	CAACACACACACACACACAAAA	59	108	---NA---			
PESTM636	(AC)10	AGGTGATCTTTCCTAGTGACATTC	ATGCTATGGGAGTTCCTTTATG	57	134	---NA---			
PESTM637	(AG)10	CAGTGAGTGAGTGAGTGAGTGAGT	GGCCATCTTGTTGAGTTCCTA	59	159	---NA---			
PESTM638	(GA)10	CCTTCTCCTCTCCTTCTTCCAT	AAACCCTTCGTGTTCATCTGAC	60	158	---NA---		aa x ab	1:1
PESTM639	(GA)10	CCCAAAATAAGGGATAAACAGC	CTTACTCTCCTCCCCTCTCCTC	60	121	---NA---			
PESTM640	(AT)11	AAGTAAATCAAATGACCCGTCC	TTTAGAGGCAAATCAAAGTCCC	60	223	---NA---			
PESTM641	(CA)11	TGACTTCATTGTTTCTCCCCAC	GCACAACATGCTCAAATGGTAG	61	130	---NA---		ab x bc	1 : 1 : 1 : 1
PESTM642	(TC)11	TCTGACCCTTGATCTCTGACCC	GACAGCAGGGCGAGTTGG	63	149	---NA---			
PESTM643	(AG)11	ATTTGCAGCCTTACTCCTGTTT	CAGGGCCAATTTTGTATCTCAT	60	140	---NA---			
PESTM644	(TG)11	CTTTCCCACTGATGGTGAGATT	AGCTCAATTTTCTACAGCCAGC	60	197	---NA---			
PESTM645	(GA)11	ACAGTGAAGGTCTTGGGGTGT	TTAATGCCTCTTCTCCCTCTCTT	60	100	---NA---			
PESTM646	(GA)12	GTTAAAATCCGCCATAGTGAGC	AAACCCTAAACCGTAACAATCG	59	137	---NA---			

ผนวก ก (ต่อ)

Marker	motif	Forward Primer (5'-3')	Reverse Primer (5'-3')	Tm (°C)	Size (bp)	Function	E-value	Parent genotypes	Segregation ratio
PESTM647	(TA)12	CTGGTTTCCTTGAGCAGATGTA	CACAAGATTACGCAGAAGCAAG	60	203	---NA---			
PESTM648	(TG)12	TGCTCAACTCTTACCACAAGGA	CTTTTACACCCCGACCCC	60	127	---NA---			
PESTM649	(GA)13	GTACCCTTGATGCAAACTGAAA	ACAGGCTTGGCTCCATCTAAT	60	137	---NA---		ab x ab	1:2:1
PESTM650	(AG)14	GCCTTTTCTGGTTAATGGACTG	GTTTGTCTATGGATGATTGTGAGG	60	214	---NA---			
PESTM651	(TTA)6	TCATTCTTGGGTATCGTCCATT	ACAGTTTTGATGGGGTTCAGAT	60	203	---NA---		ab x ab	1:2:1
PESTM652	(GAG)6	CATACCGTCACCACTCAGAAAC	GCCGTCATTCTACCAGTTGAG	60	148	---NA---			
PESTM653	(TCC)6	AAAGAGACAGCAGCAGAAGAGG	AATGGTGAGAGCAGTAGCAACA	60	105	---NA---			
PESTM654	(AAG)6	AGCTCTCTCCTCTCTTCCCTTC	TGCTCGCAACCATATAAAAGTG	60	193	---NA---			
PESTM655	(AGG)6	TACTATGCGATGTGTGCAAGG	CCTCCTCCTTCTGTTCCTCTAA	59	205	---NA---			
PESTM656	(GAA)6	TTCAGCTACCTCCTAGCCTTTG	TCCCTTAGCCACAGGTTCTCTA	60	134	---NA---			
PESTM657	(AGA)6	ACAACATTGGACAACACCGAG	CGATCTGTGCTTTGGATCACT	60	147	---NA---			
PESTM658	(AAT)6	TCGACCAACTCCTTTGCC	CCTTCTGATTGGAGGTTTCTGT	60	202	---NA---		aa x ab	1:1
PESTM659	(TGC)6	AGCCAATGCTTCAGATATGCCC	GCATCCACTGCTGCCGAA	65	141	---NA---			
PESTM660	(TTA)7	GCCGCTTCTAAATATCAAACTG	TGGGTCCACACTAACAACTACA	58	164	---NA---			
PESTM661	(AAT)7	ACCGAATTGATTAGAGACCCCT	TCTCCCTCCCTACCCGAC	60	160	---NA---			
PESTM662	(GAT)7	AGTCTGGCTACTGCCTGCTC	ACTTCTCAATGGCCTCTACTGC	60	220	---NA---			
PESTM663	(AAT)7	TATGAATTGAGGCCAGAACCTT	CGGCATACAGGAAACAAGAAAT	60	119	---NA---		ab x aa	1:1
PESTM664	(GTG)7	GTGGTGAAGGAGGAGATGGT	GATTCAGAGGTGTGATGGAAAA	59	188	---NA---			
PESTM665	(AAT)7	AGGGTGGACGGTGATTTTAGA	GTTGTTGATGCTTGTAGGCTTG	60	163	---NA---			
PESTM666	(GGA)7	AGATAAGGGAAGAAGGGCCAC	CCTCCATCTATTTTACCACCTCC	60	227	---NA---			
PESTM667	(AAT)7	CTCCCATCACCGATCAAATAA	GATTTCCGGCCTCTCACC	61	169	---NA---			
PESTM668	(GCC)7	GAATCCATTTGTTTTCGGGTAG	CCACCAGCGGCAATACTC	60	175	---NA---			
PESTM669	(ATT)7	GTAGCCCACCCCAAACAC	TGGTATAACCTCCCACTTCATC	58	178	---NA---			
PESTM670	(ATA)7	GAGAAACACTGAAGCGTGAAGA	ATATTGACGGGTTTATGGATGG	60	141	---NA---		aa x ab	1:1
PESTM671	(ATT)8	CCCGGATTTTATTTAGCACAAC	TTTAATTCCCTGACCCCAAAC	52	229	---NA---			
PESTM672	(CAC)8	CCTCCCTCTTATGCACCATC	GCATGTTGTCGAGATTGAGAGA	60	109	---NA---			
PESTM673	(TTC)5	AAGTCACCCATGTTTTCTCCTG	CATGCCCTGTTTGTTGATAGAA	60	133	---NA---		ab x aa	1:1
PESTM674	(CAG)8	ATCAGCTCCTATTCAGCAGGTT	AATCTTGCTCCTCTTTCTCCAG	59	167	---NA---			

ผนวก ก (ต่อ)

Marker	motif	Forward Primer (5'-3')	Reverse Primer (5'-3')	Tm (ºC)	Size (bp)	Function	E-value	Parent genotypes	Segregation ratio
PESTM675	(GGC)9	TTTCGCCTTCTGATGCTCTATT	TTCCTCCTCCTACTACCAGACG	60	214	---NA---			
PESTM676	(AAT)9	TATGAGTGCAAACTCCAACAGG	CATGTCCCCTTCCTTGATAAAC	60	176	---NA---			
PESTM677	(GAT)9	CGTGATGCTTATGATGTGCC	TTGTTCTTGTTCCTCTTGTTGG	59	111	---NA---		aa x ab	1:01
PESTM678	(TAT)11	CCCGGTCGTCCACTACTACTAC	CTCTAAACACCCTTATGCCAAGA	60	106	---NA---		ab x bc	1 : 1 : 1 : 1
PESTM679	(TAAT)5	ACCTATGATTTGAGACAGGGGA	ACAGCAACAGCAACAACAACA	60	107	---NA---			
PESTM680	(TTAT)5	GACCCAATCCAAAATATCCAGA	TTGTTCTCCTCCTGTCTTCACA	60	181	---NA---			
PESTM681	(AAAT)5	TCTGAATTGTCGGAGTGGC	CATCCTTGCGTAAACAAAAGAG	59	193	---NA---			
PESTM682	(TTAT)5	GGGGAATTTTCTATCATCCAAC	AAGCTCATAGTAGGCCGTGTAAA	59	160	---NA---			
PESTM683	(ATGT)5	AGTCCACAAAAGCACCAAATG	GTACGGCAAACCATGATACCTC	61	226	---NA---			
PESTM684	(AAAT)5	TGAAGGAACAAGAGGAAAGGAA	TCAGATTGAAGGGAGAGAGAGAA	60	153	---NA---			
PESTM685	(CAAA)5	GATTAAGACCATCCAGCGGT	TTGGTGATAGAAGGGGAATAGC	59	201	---NA---		ab x ab	1:02:01
PESTM686	(GAGG)5	CTAGGGCATCTAAGGGGAATG	ACAACACTCTCTCCTCTCCACC	60	230	---NA---			
PESTM687	(AAAT)6	AGAGAACTACGACAGTGGCAAA	AACTTCTACTTTGTTGGTGCCC	60	127	---NA---		ab x ab	1:01
PESTM688	(TTTA)6	AAGATTAGGTGCAGGGAAGTCA	AACCAACAAAACTGCTCGAACT	60	187	---NA---			
PESTM689	(CGAC)7	TTGAGATATACCGACTGACCGAT	GTCCAACCGACATACCTTCG	60	182	interferon-alpha beta receptor alpha chain	1.48E-09	ab x bc	1 : 1 : 1 : 1
PESTM690	(TCTCT)5	GCCATCCAATCCGTTACTTCTA	CGCCAGAAATCAAATTATCAGC	61	130	---NA---		ab x aa	1:01
PESTM691	(TGGGG)5	ACCTGACCCACTCATAGAAAGC	TACCTACCACCAAACCAACCTC	60	230	---NA---			
PESTM692	(CTTTT)5	CCCTTCATCTTTCCTTTCCTTT	CATGATTGATCCAACCGAGAT	60	145	---NA---		ab x aa	1:01
PESTM693	(TCTTT)5	ATACTGCCGCTTCCTATCGTC	CACTGAAAAGAAAAGAAAGGCG	60	130	---NA---			
PESTM694	(AAATA)5	CATGGTTTGATCTGCTCCTACA	TCCCAGGTTCTCAAGATAATGAC	59	150	---NA---			
PESTM695	(TCTCCT)4	ATCGACCGAGCACAAAAGATA	GGCCTAAGAACCTCTCTCTCCT	60	194	---NA---			
PESTM696	(GGTCTC)4	GCAAGAGAGAACGAGAGAGAAGA	ATCCAACCCACCCATCCT	60	215	---NA---		ab x aa	1:01
PESTM697	(AATTTG)5	CGATGCCCTTGTGATTTTCT	TAATGGAATGTCTATGATGGCG	60	143	---NA---			
PESTM698	(GCGAGG)5	GCGAGAGAGAGGGAAGCATAC	AACATTAAGCCACGGCCTC	60	194	---NA---			
PESTM699	(GCGGAG)5	TCTACCTCCTCGTCCACCAC	CATCGAGATCGGAAGCGT	60	180	---NA---			
PESTM700	(GTGGGA)5	TTCTCGCAATATACCACGGAG	ACATTCCCTTGCTCTTGTGAA	60	233	---NA---			
PESTM701	(A)12, (CT)7	AATAGGAGCAAAACGCCAAAG	GGAAGAGGAAAGAGAGAGGAGG	60	197	---NA---			

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Marker	motif	Forward Primer (5'-3')	Reverse Primer (5'-3')	Tm (ºC)	Size (bp)	Function	E-value	Parent genotypes	Segregation ratio
PESTM702	(A)18, (A)13	AACCCAGTTTCACCTTGTCTGT	CCTGTTGCGTTGTCTCTTTAGTT	60	191	---NA---			
PESTM703	(GA)6, (GA)7	AAGAACAGATGGAATCACGAGC	ATAACAAACGATAGAACGGCGA	61	188	---NA---			
PESTM704	(GA)6, (GA)7	AAGAACAGATGGAATCACGAGC	ATAACAAACGATAGAACGGCGA	61	188	---NA---			
PESTM705	(A)11, (T)17	AGACTACGCATATCAAGGGTGA	TTGCCACGATACCATAAGTACC	59	275	---NA---			
PESTM706	(A)17, (A)13	GCATCGTCTTCCATATTTACCC	ATTTCTCTCCTCGCATAACCTC	59	163	---NA---			
PESTM707	(AG)6, (GA)7	GAGATCCTGACGGACTTCAAAA	AGGTACGACTCTCTCCCTCTCC	60	145	---NA---			
PESTM708	(A)19, (T)13	TTTTGGTAGTGAGCTGGTTTGA	GGGATTTTGTATCCTTCTCCGT	61	220	---NA---			
PESTM709	(A)13, (A)18	CCCAACAATATCGGAACAAAAG	CCTCTCCACCTATGCTCTGC	60	204	---NA---			
PESTM710	(A)10, (A)16	AGCATGGATTCTGTTTCCCATA	AAGCCTCTCATGTTGTTGCTCT	60	193	---NA---			
PESTM711	(A)19, (A)12	CTTGCCTTTCAATCGCTCAT	AAGAGAAACACGAGGAATACGG	60	181	---NA---			
PESTM712	(C)10, (A)16	TACTAACAGAAACGCCCGCT	CAGAGTGATGCTCTTCCAGTTG	60	260	---NA---			
PESTM713	(TTC)6, (T)12, (T)10, (A)14	GGGGCTATCTGTGTCTGTTTT	CCATTTGATGAGGTCTTATGCT	58	265	---NA---			
PESTM714	(TTAT)5, (AATA)5	AACCACCTTAGCCAGTTGTTTG	TGGCCCTCATCTTCTTCCTT	61	187	---NA---		ab x ab	1:02:01
PESTM715	(A)16, (A)10, (G)10	TGAAGGAACAGTCGATTAGTGA	CTAAATCAGGCAGCATACGTG	58	191	---NA---			
PESTM716	(TTC)6, (T)12	CTTAACCCTGCCGGTATCTCT	CTTGTCTCTTCTGTCCTGGCTT	60	232	---NA---			
PESTM717	(AG)9, (GT)7	GTGTGACTGCTGGATTGTACC	GCAGACTTGCTGGCATTTA	58	177	---NA---		ab x ab	1:02:01
PESTM718	(GAA)5, (AGG)6	GCATTTTGTGAGGATGATGATG	TTCTTCTTGTCCCTCGTTCTTC	60	129	---NA---			
PESTM719	(AGG)6, (AGG)7	CTCCTCCGCCTCAACCTTA	TTGGAGATGTAGTGGTCAATGC	60	225	---NA---			
PESTM720	(A)10, (CT)9	GCTTCTCGTGGGAGCAAC	CACAACACACACACGCACAC	61	246	---NA---			
PESTM721	(A)11, (AAT)6	TCTTGGACTGTTTCAGGCATTA	GAAATTAGGTTTCCTGCCCTTT	60	254	---NA---			
PESTM722	(A)14, (AAG)6	AAAAGGAACATAACACCGCTTC	AGGCTTACATCCCATCTGCT	59	123	---NA---			
PESTM723	(A)13, (AT)8	AATCCAATAGCTTCATCACCTC	GCTAGACCAGGAGAGTTTGGT	58	116	---NA---			
PESTM724	(TA)8, (TCGC)4	CCATCATCGGAGCTAAAAGATT	AGAGAGGGGAGGAGAGAGAGAG	60	167	---NA---			