

Supplementary data:

Database of predicted SCAR markers in five fruit and three vegetable crops

Balakrishnan Vasanthakumari Premkrishnan and Vadivel Arunachalam

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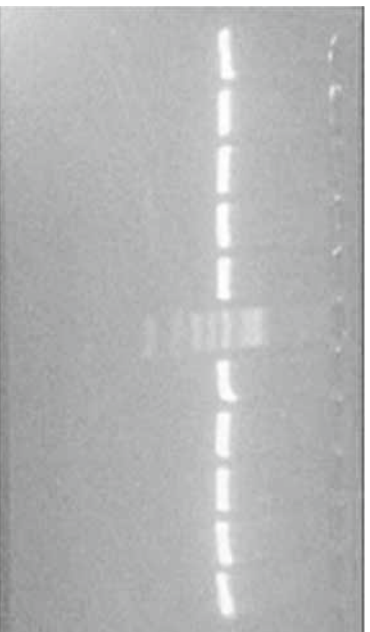


Figure 1. Multiplex PCR with SCAR primer designed based on OPJ-04 along with 16S rRNA- specific primers with genomic DNA of banana (lanes 1–5 and 7–11). Lane 6, 100-bp ladder.

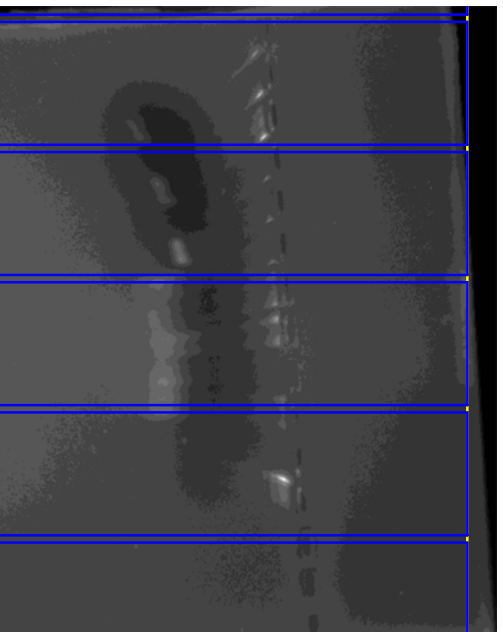


Figure 2. PCR with primer OPA-02SCAR266 (Pr032359362) and banana genomic DNA (lanes 1–5), and with primer OPA-02SCAR272 (Pr032359363) and banana genomic DNA (lanes 6–10). Lane 12, 500-bp ladder Chromous.

Table 1. Predicted SCAR markers for published RAPD/ISSR reports on diversity/marker-trait association.

Crop	Sequence ID	Sequence type	Primer name	Primer type	Product size	Forward SCAR from database
Apple	>gi 226776745 gb GO532532.1 GO532532	Expressed Sequence Tags	OPA-14	RAPD	282	TCTGTGCTGTATGTTTTCT
Apple	>gi 46596786 gb CN495474.1 CN495474	Expressed Sequence Tags	OPA-14	RAPD	348	TCTGTGCTGGAGCAGATTTA
Apple	>gi 48111823 gb CN856321.1 CN856321	Expressed Sequence Tags	OPB-06	RAPD	237	TGCTTGCCCTGCTCTGCTT
Apple	>gi 226769287 gb GO525682.1 GO525682	Expressed Sequence Tags	OPB-10	RAPD	539	CTGCTGGGACACTGCTGGGC
Apple	>gi 312234423 gb CM001031.1	Whole Genome Sequences	UBC-817	ISSR	1329	GTGTGTGTGTGTGTGTGTAGAGAG
Banana	>gi 197650080 gb FL661587.1 FL661587	Expressed Sequence Tags	OPA-02	RAPD	274	ACGGCTCGAGCTACGTGCA
Banana	>gi 400271321 emb HE813981.1	Whole Genome Sequences	OPA-02	RAPD	266	ACGGCTCGAAAGTTGCGCC
Banana	>gi 401022641 emb HE813975.1	Whole Genome Sequences	PRI-21	RAPD	1063	GCGACAGGGCGTTTCGTCT
Banana	>gi 400265855 emb HE813978.1	Whole Genome Sequences	OPJ-04	RAPD	1662	GGCTTGTGCTGCTGGGTTG
Banana	>gi 400265857 emb HE813984.1	Whole Genome Sequences	OPC-15	RAPD	1475	GACGGATCCCGTCGAGTC
Banana	>gi 415426079 emb HE813983.1	Whole Genome Sequences	OPB-01	RAPD	992	GTTTCGCTATTAGAGGTT
Cacao	>gi 215518074 gb CU604411.1 CU604411	Expressed Sequence Tags	OPP-15	RAPD	545	GGAAGCCAAGGGGCAAAC
Cacao	>gi 312265536 emb FR720988.1	Whole Genome Sequences	UBC-840	ISSR	566	GAGAGAGAGAGAGAGAGATATTTT
Cacao	>gi 312265421 emb FR720873.1	Whole Genome Sequences	UBC-812	ISSR	227	GAGAGAGAGAGAGAGAAAGTGTGTGTG
Melon	>gi 326219265 gb JG473016.1 JG473016	Expressed Sequence Tags	OPD-13	RAPD	440	CCCCACTGCAGTCGCATGG
Melon	>gi 393370789 gb CAJI01004850.1	Whole Genome Sequences	ISSR-7	ISSR	845	GAGAGAGAGAGAGAGAATGAGAGTGAG
Papaya	>gi 187567578 gb DS982520.1	Core nucleotide	UBC-856	ISSR	1741	TGTGTGTGTGTGTGTGTGTTATGTTT
Papaya	>gi 187563212 gb DS984615.1	Core nucleotide	UBC-815	ISSR	277	CTCTCTCTCTCTCTGAGCTTTTAAC
Papaya	>gi 187567585 gb DS982516.1	Whole Genome Sequences	UBC-836	ISSR	1656	AGAGAGAGAGAGAGAGAGAGAGATTGA
Potato	>gi 215745479 gb AC233439.1	Core nucleotide	UBC-811	ISSR	577	GAGAGAGAGAGAGAGAGAGAGATATA
Potato	>gi 347326306 gb JH137946.1	Whole Genome Sequences	UBC-864	ISSR	619	TACTACTACTACTTCTTCTCTCT
Potato	>gi 257153506 gb AC237597.1	Core nucleotide	UBC-857	ISSR	987	ACACACACACACACTCACATTCAT
Potato	>gi 347326394 gb JH137858.1	Whole Genome Sequences	UBC-857	ISSR	1037	ACACACACACACACTTAGAAATTT
Potato	>gi 347326324 gb JH137928.1	Whole Genome Sequences	UBC-822	ISSR	1056	TCTCTCTCTCTCTTTCTTTTGTG
Strawberry	>gi 315422320 gb CM001057.1	Core nucleotide	CA-d8	ISSR	694	CACACACACACACACGCGCGCGCGC
Strawberry	>gi 31542236 gb GG775245.1	Core nucleotide	UBC-844	ISSR	474	GAGAGAGAGAGAGAGAATGAAGAT
Strawberry	>gi 315422320 gb CM001057.1	Core nucleotide	UBC-817	ISSR	721	GTGTGTGTGTGTGTGTATATATATAT
Tomato	>gi 322718800 gb CM001071.1	Whole Genome Sequences	GA-d8C	ISSR	523	CTCTCTCTCTCTGTGTGTGTGTG
Tomato	>gi 322718799 gb CM001072.1	Whole Genome Sequences	UBC-815	ISSR	532	CTCTCTCTCTCTCTCTCTCT
Tomato	>gi 322718800 gb CM001071.1	Whole Genome Sequences	HB-14	ISSR	372	GAGGAGGAGCGCTTGGAGCGT
Tomato	>gi 322718798 gb CM001073.1	Whole Genome Sequences	CT-d8	ISSR	1667	CTCTCTCTCTCTCCCTCATCTCC
Tomato	>gi 322718805 gb CM001066.1	Whole Genome Sequences	UBC-823	ISSR	1672	AGAGAGAGAGAGAGAGAGTGTGATGG

Table 1 (contd)

Crop	Reverse SCAR from database	Accession	Reference	Primers used in the reference	Primers found useful in the reference
Apple	CCAGCACAGAGTTCCACCCA	Pr032359357	Ur-Rahman <i>et al.</i> (1997)	OPA-01 to OPA-20	OPA-01, 02, 08, 09, 10, 12, 13, 14, 16, 18 and 20 helped to identify apomictic seedlings
Apple	CAGCACAGAACATCTTGGG	Pr032359358	Sharma <i>et al.</i> (2012)	OPA-01 to OPA-20; OPB-01 to OPB-20	OPB-12, OPA-14, OPB-10, OPB-06, OPA-13, OPA-08 and OPA-11 were found highly polymorphic
Apple	GGGCAGAGCACGGAGGGGTG	Pr032359359	Sharma <i>et al.</i> (2012)	OPA-01 to OPA-20; OPB-01 to OPB-20	OPB-12, OPA-14, OPB-10, OPB-06, OPA-13, OPA-08 and OPA-11 were found highly polymorphic
Apple	TCCCAGCAGAATGAAAGCC	Pr032359360	Sharma <i>et al.</i> (2012)	OPA-01 to OPA-20; OPB-01 to OPB-20	OPB-12, OPA-14, OPB-10, OPB-06, OPA-13, OPA-08 and OPA-11 were found highly polymorphic
Apple	ACACACACACACACTGCATACATA	Pr032359361	Pathak and Dhawan (2012)	15 UBC primers	UBC-818 gave 7 bands not on outlier and useful for verification of clonal fidelity
Banana	CGAGCCGTGGCGCTGGTC	Pr032359362	Miri <i>et al.</i> (2009)	OPA-01 to OPA-11 OPA-13; OPAA-14, OPD-07	OPA-02-250 helped to identify salinity tolerance
Banana	CGAGCCGTCCACATGCAG	Pr032359363	Miri <i>et al.</i> (2009)	OPA-01 to OPA-11 OPA-13; OPAA-14, OPD-07	OPA-02-250 helped to identify salinity tolerance
Banana	CCTGTGCGGCCTCCACC	Pr032359364	Javed and Chai (2004)	OPA-01 to OPA-20; PRI-21 to PRI-28	PRI-21-1000 found to identify fusarium resistant
Banana	CACAAGCCTCGACAATGT		Damasco <i>et al.</i> (1996)	OPA-06, OPH-09, OPH-13, OPJ-04, OPA-10, OPA-13 OPS-04	OPJ-04-1600 discriminated tall and dwarf banana
Banana	CTGATCCGTCCTTATGTGAC	Pr032359365	Bairu <i>et al.</i> (2006)	OPJ-04, OPC-15	OPC-15-1500 discriminated the tall and dwarf
Banana	AGCGAAACTCAGGGTGCC	Pr032359366	Vidal and Garcia (2000)	OPA-01, OPA-02, OPA-04, OPA-12, OPA-17, OPA-19, OPB-01, OPB-05 to OPB-07	OPB-01-9-947 identifies yellow sigatoka disease resistant
Cacao	TTGGCTTCTCAAACCTCT	Pr032359367	N'Goran <i>et al.</i> (1994)	OPD-01 to OPD-20, OPK-01 to OPK-20, OPL-01 to OPL-20, OPM-01 to OPM-20, OPP-01 to OPP-20, OPQ-01 to OPQ-20)	OPO-15-600 one among the polymorphic
Cacao	TCTCTCTCTCTCTCTATATATATA	Pr032359368	Rivas <i>et al.</i> (2013)	UBC-807 to UBC-809, UBC-811, UBC-826 to UBC-827,834, 835,840,844,855,873,889	UBC-840 highly polymorphic among species and populations
Cacao	TCTCTCTCTCTCTCTGCCTGCTTT	Pr032359369	Charters and Wilkinson (2000)	UBC 812, 827, 834, 841, 857, 888 and 890.	UBC-812 one among the polymorphic with 10 bands
Melon	GCAGTGGGGCGTGCGCGGC		Erdinc <i>et al.</i> (2013)	A04, A18, B06, D02, D13, E07, E14	OPD-13 highly polymorphic
Melon	TTCTCTCTCTCTCTATCTATATG		Yildiz <i>et al.</i> (2011)		ISSR-7 is polymorphic 12 bands on Turkish melons
Papaya	CACACACACACACATATATATATA	Pr032359370	Carrasco <i>et al.</i> (2009)	UBC814, UBC836, UBC834, UBC841, UBC844 and UBC856	UBC856 polymorphic with 15 bands of 310–1800 size on Chilean highland papayas <i>Vasconcellea pubescens</i>

Table 1 (contd)

Crop	Reverse SCAR from database	Accession	Reference	Primers used in the reference	Primers found useful in the reference
Papaya	AGAGAGAGAGAGAGAGGTCCATTGTT	Pr032359371	Dinesh <i>et al.</i> (2007)	UBC807, UBC810, UBC815, UBC817, UBC856, UBC861	UBC 807, 810, 815 and 861 useful, UBC 815 three amplified male specific bands confirming hybridity in intergeneric hybrids
Papaya	CTCTCTCTCTCTCTCGTACACGTA	Pr032359372	Sudha <i>et al.</i> (2013)	24 ISSR primers	UBC-836 polymorphic with 212 bands
Potato	TCTCTCTCTCTCTCTTTTCTCTCTC		Marczewski (2001)		UBC811-660- to detect the Ns Resistance gene
Potato	AGTAGTAGTAGTAGTAATAGAAGAAG		Marczewski <i>et al.</i> (2004)		UBC864-600 was linked to the resistance to potato leafroll virus and UBC864 linked to susceptibility
Potato	GTGTGTGTGTGTGTTTTTTTTTTTT		Flis <i>et al.</i> (2005)	UBC-857-900 and RFLP markers	UBC-857-980 was linked to potato virus resistance
Potato	GTGTGTGTGTGTGTTGGTGTGGGT		Flis <i>et al.</i> (2005)	UBC-857-900 and RFLP markers	UBC-857-980 was linked to potato virus resistance
Potato	AGAGAGAGAGAGAGAGGATCAGTGC		Marczewski <i>et al.</i> (2006)	Other RAPD, ISSR and RFLP markers in the locus GP250, GP283, GP38, OPH18-480, UBC822-1079 and UBC864-816	UBC822-1079 closely linked to Potato virus M resistance at Rm locus on Chr XI
Strawberry	TGTGTGTGTGTGTGTGGGGCTCCTCT	Pr032359658	Arnau <i>et al.</i> (2002)	(AC)7, (CA)7, (CT)7, (TC)7, (AG)7	17 polymorphic bands useful in identifying 30 cultivars by (CA) 7 primer
Strawberry	CTCTCTCTCTCTCTACCTTCCAG	Pr032359659	Carrasco <i>et al.</i> (2007)	UBC811, UBC841, UBC844, UBC847, UBC850, UBC855	UBC844 gave 15 polymorphic bands of size 450–1500 bp
Strawberry	ACACACACACACACATGAGAAGCG	Pr032359660	Debnath <i>et al.</i> (2008)	UBC 801 to UBC900	UBC817 gave 19 polymorphic bands of size 400- 3800 bp
Tomato	CAGAGAGAGAGAGAGAGAGAGTAGT	Pr032359661	Shahlaei <i>et al.</i> (2014)	(CT)8A, (AG)8G, (GT)8T, (TC)8AGG, (GA)8A and (AT)8T,	(AG)8C one among the polymorphic loci
Tomato	AGAGAGAGAGAGAGAGTAGTAGTAGT	Pr032359662	Rai <i>et al.</i> (2013)	45 ISSR markers	UBC-815-564 discriminated tomato leaf curl virus resistant
Tomato	CGCTCCTCCTCATCAGCAATC	Pr032359663	Edris <i>et al.</i> (2014)	814, 844A, 844B, HB8 to HB12, HB14	HB-14 highly polymorphic
Tomato	AGAGAGAGAGAGAGAGATTTTGAGTC	Pr032359664	Levin <i>et al.</i> (2000)	Two modified ISSR primers with CT repeats	MS6 -(TC)7CCT amplified a fructose glucose ratio locus in tomato and wild relative
Tomato	CTCTCTCTCTCTCTATATATATAT	Pr032359665	Tikunov <i>et al.</i> (2003)	14 ISSR primers for <i>Lycopersicon</i> sp	(AG)8YC 4 bands for L Penneli substitution lines

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