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Supplementary

Isolation and characterization of microsatellite markers from *Garcinia morella* using next generation sequencing technology and cross-species amplification

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Supplementary Table 4 : Genetic analysis of microsatellite markers developed for *G. morella*

Locus name	Forward sequence 5' - 3'	Reverse Sequence 5' - 3'	Repeat Type	Number of Allele (k)	Expected size Range (bp)	Observed Heterozygosity (Ho)	Expected Heterozygosity (He)	Polymorphic Information Content (PIC)	Probability of Identity (PI)
GM_KVRw990	AAAAAGCCCAGTGAGTGGGGGA	TTGGATGGTATGTGTGGCTTTGGTT	$(TG)_6$	4	219-234	0.192	0.649	0.577	0.128115
GM_KVRx003	AAAAGAGGGGGTGGGACGCAGA	TTCTCATCATTCCCTAGGCCGACA	$(GA)_{10}$	2	384-386	0.000	0.127	0.117	0.774341
GM_KVRx004	AAAAGATCATGCACGGGAAGGCA	TCCTCCTCCTTCACACCTCCCA	$(GA)_{18}$	9	226-292	0.074	0.855	0.82	0.035163
GM_KVRx022	AAAAGGGGGTACTGGTGCCGGA	TGGGCCACTTCTCTCTTTAGCTGC	$(AG)_{13}$	2	286-384	0.000	0.127	0.117	0.774341
GM_KVRx038	AAACCCAGTGAGCAAATGAGCAGT	TCGTGCAGTATAGGCCGGGTGT	$(AT)_7$	4	243-301	0.000	0.685	0.611	0.168956
GM_KVRx045	AAACGCCCGGTCGTCCGATTTC	AGCCACTTTCTCTCTCTAGCCCTCT	$(AG)_6$	2	156-161	0.071	0.07	0.067	0.674141
GM_KVRx046	AAACGCGAGGGAAAGAGACGGG	TGGACCTTGCTTCTCCTCGTCA	$(AG)_7$	8	110-144	0.76	0.858	0.821	0.034871
GM_KVRx047	AAACGCGTCGCTCTCTCGGAAG	ACCCACCCCCACTACTTTCCCT	$(AG)_6$	5	108-116	0.48	0.723	0.671	0.082382
GM_KVRx048	AAACGCTGAAACGAGGAGGCCG	TGGGCCTCATTCTGGGACTTTCT	$(AG)_8$	6	102-141	0.12	0.822	0.777	0.047679
GM_KVRx049	AAACGCTGAAACGAGGGAGCCG	GCCAAGATTCAAGCCTCCCCTTGC	$(AG)_7$	19	210-298	0.207	0.926	0.903	0.012982
GM_KVRx075	AAAGCCCTGGTGGGCTGAGTGT	TGACACATGCAAAAACACATCCTTGC	$(AC)_{11}$	18	250-340	0.25	0.892	0.866	0.021273
GM_KVRx076	AAAGCCGACGGGTGAAAGAGCC	TGTCAAGTTGCAAAGCTGGTCATGGT	$(AT)_7$	20	366-474	0.259	0.943	0.921	0.009272
GM_KVRx077	AAAGCCGAGAGGAAGGCCGAGA	ATCTCCTCGTTGCCATGGTCGT	$(GA)_7$	21	101-188	0.37	0.941	0.919	0.009473
GM_KVRx090	AAAGCTTGAGGTGGGGTGGGGA	TCTTTGTGTGTTTGAGAGAATGGACCC	$(TA)_7$	19	125-214	0.107	0.936	0.914	0.010235
GM_KVRx091	AAAGCTTGGGGCCCAGAAAGCC	TGGGTCGATTTGTGTGTGCTCAA	$(AT)_7$	22	177-299	0.111	0.92	0.899	0.012498
GM_KVRx092	AAAGGAAATCGAGGGACCGGCA	CCATCTTTGCACTTCACAAGCATCCA	$(AC)_{21}$	24	110-196	0.286	0.959	0.939	0.005915
GM_KVRx093	AAAGGAAATGATGGGGATGTTGTGGAA	CCACCCACTCATTCTTGCCATCCC	$(AT)_{12}$	13	102-157	0.321	0.892	0.865	0.021749
GM_KVRx094	AAAGGAAGGTCCGGCGATGGAG	TACGCTCGGTCGTCTGCTGGTT	$(AG)_7$	21	208-296	0.593	0.942	0.92	0.009415
GM_KVRx095	AAAGGAATGTCCGTACGTATGAGAGGA	TCGAGTCCTGGGCATTCACCAA	$(TA)_6$	15	212-282	0.069	0.906	0.881	0.019508

GM_KVRx133	AAAGTCACTCTAGGGACGCCCG	AGGGAGTGGCATCATTGGCTTGT	$(GA)_7$	10	175-199	0.04	0.706	0.671	0.078668
GM_KVRx134	AAAGTCAGTTCCCAGCGTGGCG	TCTCCTGCAGTACGACATGTTTGC	$(AT)_6$	11	124-199	0.071	0.67	0.636	0.120535
GM_KVRx135	AAAGTCAGTTCCCAGCGTGGCG	AGAAAGGGGTGCATAGGGTGTATCC	$(AT)_8$	10	100-176	0.000	0.711	0.681	0.106519
GM_KVRx432	AAGACTTGTGGTGCGGCTGACG	GTCGGGGAGGACCAACCTATTGT	$(AT)_8$	9	403-495	0.034	0.69	0.625	0.149528
GM_KVRx433	AAGAGAAACCCAGCAGAGTTGCGTA	ACGTCTGATTAGGCTAGCCACCATT	$(AT)_6$	10	99-146	0.103	0.701	0.657	0.113342
GM_KVRx434	AAGAGACCTTGATGTGGTGGGGA	TCTCATGCCACTCCTTAGAGTGTGT	$(TA)_6$	15	114-204	0.08	0.885	0.858	0.024016
GM_KVRy205	ACACACCTACGGGTGGCATGGA	AGTAGACCGTGGCCGTTCGTAGT	$(AT)_7$	11	100-176	0.074	0.763	0.726	0.064490
GM_KVRy206	ACACACCTACGGGTGGCATGGA	AGACTGTGGCCGTTCGCAGTTG	$(TA)_{10}$	9	100-177	0.222	0.744	0.695	0.079501
GM_KVRy207	ACACACCTACGGGTGGCATGGAATCT	AGCCCGTAGGCTCTTGCC	$(AT)_7$	12	113-177	0.241	0.886	0.859	0.025804
GM_IIHRb888	AGAGGGTGAGCATTCAACAGGCT	AGGGATGCCCAAGGGATGGGAT	$(TG)_9$	10	322-409	0.000	0.891	0.863	0.23059
GM_IIHRb889	AGAGGGTGAGCATTCCACGAGC	TTGGCATGACGGCCAATGTGGT	$(GT)_6$	18	276-421	0.259	0.926	0.902	0.12854
GM_IIHRg191	CCCGTAGGCCTAGGCATTCATGTAGT	TCCCCACCTGAGAGGGACCTTGAT	$(TA)_6$	20	292-401	0.241	0.954	0.934	0.006721
GM_IIHRg192	CCCGTAGGTGCCCTACATGTCT	TGGAAGCCTACGGGCTACACGA	$(TA)_6$	15	294-389	0.12	0.827	0.8	0.037676
GM_IIHRt169	TGTTGAAAGAAAGCCCAGAAAGGCT	ATCTCATCTCAATAGGCCCCCGGC	$(AG)_6$	6	156-174	0.3	0.627	0.565	0.198126
GM_IIHRx419	NCGCGTTAAGAATGAGGAATCGGC	GGTGTTTTTGTGAGGACCCATGGTTGT	$(ATA)_5$	10	286-386	0.31	0.854	0.822	0.038323
GM_IIHRx420	NCGGAATTAGTGCGATTTTGGTTGT	TGGGTGTTTGAGGGTAATTCCTGCG	$(TTG)_5$	9	182-309	0.148	0.822	0.782	0.047074
GM_IIHRx421	NCGTATTTGTTGAACCACACTTGGG	TCGGGCTCAAAGTCACGGACCA	$(GAT)_5$	11	355-442	0.571	0.882	0.852	0.026273
GM_IIHRx536	TCAACCCGTCCTGCTTCTGGGA	AGAGCCCACTGCGCCTGCTTTA	$(GGT)_5$	11	115-161	0.231	0.493	0.474	0.184013
GM_IIHRx537	TCAACCGGGCCCTTGATGGAAC	GGTGTCATCTGATTGGGGCATGCTT	$(CAC)_5$	18	374-474	0.667	0.939	0.916	0.010224
GM_IIHRz510	TTTCCCATGCCATCCCCACCTC	AAGTAGGCTATTGGGACACCACCA	$(TGA)_5$	15	329-369	0.32	0.887	0.858	0.024175

GM_IIHRz511	TTTCCTCCACTACACGGTAGCCCC	CCAAGGAGGGCCATGAATGCGT	(TCA)$_5$	15	371-447	0.552	0.915	0.891	0.016250
GM_IIHRz512	TTTCTCACGCCTTGCCTCACGC	TTTGGTGGTGCTGGAACATTGGA	(TAT)$_7$	18	101-153	0.241	0.911	0.887	0.017023
GM_IIHRz572	ACACATGTCGCACACCATGCACT	TGACATGACCAGTTTAGGTGGGTGG	(AATG)$_5$	20	101-204	0.286	0.94	0.918	0.009237
GM_MRDa479	GAAGTCGACAAAGGCAACGCGG	CCCACCCGTGGAAGTGTTACTTGG	(AGAAA)$_5$	16	351-484	0.107	0.672	0.651	0.099727
GM_MRDa828	AGGGACCCTCCAACGCTCAAGT	AACTCTCAGGCAAACTCTCTCACTCT	(GTGAGA)$_5$	18	209-298	0.071	0.928	0.906	0.011589
GM_KVRa040	AACCACCAGACAACGTTCATCAAAGA	CAGCGATGGTCCAGTGATGGGT	(TC)6taacctctttctctctttctttctctaa(CT)$_7$	15	228-300	0.034	0.758	0.734	0.067187
GM_KVRa041	AACCACGGGGTTGGGGTCTCAT	ACCGTCTGGCAATGGGGACAGT	(ATTC)5ggtctttcttcttttttttcctttttttttctttttttt(TC)$_6$	14	431-535	0.000	0.828	0.8	0.043133
GM_KVRa042	AACCAGTGGGACCCCTGACCAA	TTTCATAAATGAGCACAGAGCCCCC	(TA)6cataggtatatatatgtatatatatg(TA)6c(AT)6ctatatgtatatataca tatagatacatatg(TACATA)5tgtatatacatatgtatatatg ttcatatacatacatac(AT)7aa(AT)8(GT)$_{13}$	15	225-318	0.033	0.816	0.79	0.051826
GM_KVRa325	ACATCCGCATAACACATAGCATCAACA	GGTGAGAGGTTTGTTGTGTGTGCC	(AT)7ctac(AT)$_9$	19	102-171	0.1	0.893	0.869	0.023720