Online Resource 1

EST-SSR marker characteristics in six *F. pennsylvanica* populations.

Cross amplification of 15 EST-SSR markers in the genus *Fraxinus*

Conservation genetics Resources

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EST-SSR marker[a]	Accession number	Forward sequence 5' - 3'	Reverse sequence 5' - 3'	Size range (bp)	T_a[b]	H_o[c]	A_r[d]	PIC[e]	Motif[f]
Fp6985	KJ626346	GCTTCCCAATACTAAACTCAGACG	TGGATGAATGCTATGGGTCC	153-186	62	0.720	23	0.724	$(ca)_{10}$
Fp12353	KJ626347	TCGAGGCAAGATGTGAAGG	TTATTATGGGTCACGTTTCGG	224-248	62	0.642	6	0.596	$(taat)_5$
Fp12378	KJ626348	TCTTCAATGCCTCTACTCAGTAACC	TGGAGAGATTTAGCAGCAAGC	166-208	65	0.755	28	0.826	$(tc)_8$
Fp14665	KJ626349	AGTAGCCCACTGCCACTAGC	GGACCCAAACACACTGTCG	262-312	62	0.735	25	0.734	$(ct)_8$
Fp17710	KJ626350	ATTGGCAATTTGGACAGACC	TTCCCTTTCGTGCAGTCG	289-319	62	0.611	19	0.642	$(gt)_8$
Fp18437	KJ626351	ATAGGATGCCATACATGCCG	GATTGAGGTAAGAGACTGAAATGG	294-335	65	0.552	19	0.690	$(ct)_{10}$
Fp18801	KJ626352	AGTCTTCTCGCCATTTGTGC	CAAATTCAGATGCTAATGCAGC	314-341	65	0.474	21	0.546	$(tc)_{10}$
Fp19299	KJ626353	TACCATTCTTGTGAATGCCG	TTTCTGATCCATGCTCTATGC	217-233	62	0.417	6	0.562	$(ac)_8$
Fp19681	KJ626354	TTATTCTAATACCTCTTCTTCTTACCC	AAATTTCAAAGAACTTCACGAGC	209-236	62	0.500	14	0.576	$(ct)_8$
Fp20239	KJ626355	TGCCACTATCAGCTATACGCC	CACTTTGAGTCGAACCCAGG	292-314	62	0.583	10	0.593	$(ggctg)_4$
Fp20456	KJ626356	ATTGGAGACTGCTATTAGGGC	CTTCGCGAATTCATCATCC	170-196	60	0.604	10	0.534	$(tttcc)_4$
Fp21064	KJ626357	CTACATACCCTCAGGAGCCC	CTAAGGAGAACAAGCCTGCG	222-246	62	0.527	12	0.705	$(gcc)_7$
Fp21068	KJ626358	ACAGAGGTTGAAGTGGCAGG	CACTCCACAAGCTAAAGAGGG	236-271	65	0.546	14	0.562	$(ttggt)_4$
Fp81073	KJ626359	CATGGGACATGTTATCAGCC	GAGCTTCGAGTTTCTGCTCG	133-171	62	0.667	17	0.701	$(gagcc)_5$
Fp104136	KJ626360	TGTCCCACCAGTCAAACG	AAACCCTGCTTCTCGATACC	150-168	60	0.427	9	0.470	$(ag)_8$

[a]Contig names with accession number at NCBI. [b]Annealing temperature. [c]Observed heterozygosity across sites. [d]Allelic richness. [e]Polymorphism information content. [f] Repeattype and number in sequenced EST-SSR.