

表 1 候选 32 个桉树 EST-SSR 的引物以及对细叶桉(P₂)的 PCR 序列确认

Table 1 Primer pairs and sequence validation for the 32 candidate EST-SSRs of *Eucalyptus*

序号 No.	EST-SSR 标记 EST-SSR locus	EST 号 GenBank accession	引物对(5'-3') Primer pair (5'-3')	EST 设计长度 (bp) EST target size (bp)	PCR 产物长 度 ^a (bp) PCR product size ^a (bp)	EST 的重复单位 Repeats in EST	测序确认的 P ₂ 的重复单位 Repeats in P ₂ as revealed in sequencing		序列一致 性(%) Sequence identity (%)
							PCR 产物直接测序 ^b Direct PCR product sequencing ^b	混合克隆测序 ^c Pool cloning of PCR products ^c	
1	EUCeSSR1085	CU403532	F:GTTGTA CTCTGCCCTAA R:CAGCCTCGGATTGTTCA	118	111 (113)	(CT) ₈	(CT) ₆	(CT) ₅ : [16]	97.30
2	EUCeSSR1078	CU402447	F:GTGGCATT CACAAGAGCA R:GGAAGCCTTTCGGGATAA	126	129	(CAA) ₅	(CAA) ₅	(CAA) ₅ : [32]	100.00
3	EUCeSSR0984	CU395760	F:TCTTACGCACCGTCTCT R:AGCCATTCGCTCCTCC	130	139	TCGTCA (TCG) ₆	(TCG) _(2+n) T(C/A)T (TCC) ₂	(TCG) ₈ (TCT) (TCC) ₂ : [32]	97.69
4	EUCeSSR1110	GO247750	F:ATCTCCGCACCCACTCTT R:TGTCATTCTCGTT CAGC	185	173	(CCAATC) ₃	CCAATT	CCAATT: [24/16/8]	90.23
5	EUCeSSR0925	CU402880	F:GAAGGCAGAGGCTTACGA R:CTATTTTCTCTCCCCCAA	222	209	(ATC) ₁₁	(ATC) ₆		99.32
6	EUCeSSR1135	CU402600	F:GAAGTGTCTGCTGCCGAATG R:TGAAGCCCAAGGAAATGC	217	205	(CT) ₁₄	(CT) ₈	(CT) ₈ : [32/24/16/8]	100.00
7	EUCeSSR0980	EW688281	F:TGACCCTTCGGCTTCTT R:GGGCTCGCCAATCTCCAT	217	214	(GAG) ₆	(GAG) ₅	(GAG) ₅ : [24]	99.07
8	EUCeSSR0985	CU396018	F:CTTGTTCCGGTTTCTTTCA R:CACTGAGTAACAGGCAAG	264	242/244/246	(AG) ₂₀	(AG) _{(8+n)(9+n)}	(AG) _{9/10} : [32/24/16/8]	99.19
9	EUCeSSR0955	GO248042	F:CATTGGAGTAGCACGAGAA R:ACTCCATACTCTCTGTGTCTCT	257	263	(GAC) ₇ + (GA) ₇	(GAC) ₇ + (GA) ₁₀		99.04
10	EUCeSSR1046	CU396352	F:TCAAACCCAGCGATACCC R:AGCCCGATGATCCAAATAA	264	266	(TGC) ₅	(TGC) ₅		98.61
11	EUCeSSR1049	CU397549	F:GGTGATGAGGTGGACAG R:GAGTGGAGTTTCTTATGG	294	312/314	(GA) ₇	(GA) _{11/12}		94.76
12	EUCeSSR1075	CU402010	F:TGCGTGTGCTCAGGAT R:TGACATTGCCCTTCGAT	379	368	(GA) ₁₈	(GA) ₅ (GGGA) ₂ GAGGACAA	(GA) ₅ (GGGA) ₂ GAG GACAA: [32]	96.73
13	EUCeSSR0946	CU403671	F:ACTCCGTCTACATAGCATC R:CCAAGACCACCAAACATA	372	366/370	(TC) ₁₀	(TC) _{7/9}	(TC) _{7/9} : [32/16]	98.92
14	EUCeSSR1002	CU395531	F:GAGGAGGATGACGAGATGAG R:CGCAGATAAGTAAGAAGGCTAA	370	370	(CAC) ₅	(CAC) ₅		93.15

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							Repeats in P ₂ as revealed in sequencing		
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15	EUCeSSR1014	CU395155	F:GGGACTGAGCTCTGATCCTACT R:GACCGCTGGTACTTGGCTG	235	396/402	(AG) ₃ AA(AG) ₃ G AAGCAAGAGA T(AG) ₁₅ GAAAG	AC(AG) _{9/12} : [24/8/32]	97.42	
16	EUCeSSR1083	CU403250	F:CGGGGTCTCTCGAAGCGTCT R:CCGACGGCATCGTAAACC	314	435	(GGAAGC) ₃	(GGAAGC) ₃ : [24/16]	97.45	
17	EUCeSSR1136	CU396171	F:GATGGCAGGACATAAAGA R:GCTAAACAAACCAGGAAA	373	490/492	(GA) ₈ AA(GA) ₉	[(G/A)A](GA) ₅ [(G/A)A](GA) _{20/21}	98.79	
18	EUCeSSR1091	CU404650	F:GTTTCATCCGCCCTTACAG R:ACCCTTGCTCCTTCTTCG	402	~490	(TGTTT) ₃ +T ₁₄ G ₃	TGTT(TGTTT) ₂ + (T ₉ G ₁₇)/(T ₈ G ₁₂ A ₃ G ₄)	97.51	
19	EUCeSSR0894	EW688426	F:AGTCCTTCAGCAGGTCA R:CCGCCGGTATAGTAGTTG	145	518	(CAC) ₆	(CAC) ₆	92.78	
20	EUCeSSR0961	CU396545	F:CCCCTTCACTGCTCTTCT R:ACCAACCGCGAGTATGTC	242	547	(GCT) ₆	(GCT) _{n/(n+1)} (GCT) ₃ [(G/A)CT] (GCT) _{2/3} : [32/24/16]	98.76	
21	EUCeSSR1087	CU403690	F:TGAGGCACAACAAGGTAA R:CTGGCTGTAGATTGAAGAGT	439	~650	(AGC) ₁₀			
22	EUCeSSR1054	CU398509	F:CTTCTCGTCTTCTTCTGC R:TAAGGTCACCCAAGTTCTG	241	665/671	(CTG) ₂ (CCG) (CTG) ₆ : (CTG) ₆	(CTG) _{(n+3)/(n+5)} (CTG) _{1/2} (CCG) (CTG) _{9/10} : [32/16/8]	99.59	
23	EUCeSSR1122	GO248349	F:ACAACAATCTTGCCTTCT R:TCACAATAAACGAGTCCC	361	687	(CTG) ₆	(CTG) ₆ (CTG) ₆ : [32/24/16]	99.59	
24	EUCeSSR1011	CU396518	F:GCAGAGGAGCGGAAACTA R:GCTACTTTGGGTGIGTCTT	440	~850	(TC) ₉			
25	EUCeSSR1150	CU397973	F:ACCCTCCTCCTCCGTATT R:CACATCCCATCTCCTTCC	440	~850	(TC) ₆			
26	EUCeSSR0970	CU402791	F:GGCCCGCCTTTCCAATTC R:TTGTCTCGGTTGGGTCTT	225	997	(TC) ₁₀	(TC) ₁₀ : [32/16/8]	91.11	
27	EUCeSSR0914	CU397331	F:CCGGGGGCTTTGCTTICA R:TACCTCCATTGCTTCCTT	220	~1200	(AG) ₁₀	(AG) ₁₀ : [32]	96.36	
28	EUCeSSR1069	CU400565	F:ACCTCCATCCTAAGACGA R:ATCCCAAGACCCATT	318	1175	(GA) ₅ CA(GA) ₄ (CA)(GA) ₅ CA (GA) ₃	(GA) _{15/16} (GA) ₁₅ : [32/24]	97.36	
29	EUCeSSR1102	EW688317	F:TTCTTCTTGGGTTTCAGT R:ACAAGCAATGCTTTTCTC	371	~1300	(GG) ₂ (AG) ₇ AA(A G) ₃	GG(GA) _{10/12} : [32/24/16]	98.36	

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30	EUCeSSR1060	CU398944	F:CTCAGCTTCCGTATCTTG R:TTGATTACTGCGATTTAGAG	420	1274	GG(GA) ₇		(GG) ₂ (GA) ₁₃ : [24]	98.57
31	EUCeSSR1034	CU399256	F:CGGGGGCGTTTCGGAGATT R:CCACTCTGACAGCCCTTT	240	1450	(AGAAG) ₃			97.62 (部分序列)
32	EUCeSSR1028	GO248406	F:GCCATTGGGTATTCTTCT R:CTCGCTTCCTTTCACT	299	1500	(GA) ₇			

注: a: PCR 产物长度优先根据克隆测序的结果确定, 次则根据 PCR 产物直接测序与源 EST 的比对结果推测, 测序未成功者根据图 1 确定; b: PCR 产物直接测序中, 因部分 SSR 的重复单位靠近(前向)测序引物, 只有部分重复单位可见, n 表示未知的重复单位数; c: 混合克隆测序中, 中括号内数字表示成功测序的混合克隆的 PCR 产物数量
Note: a: PCR product size was determined sequentially with pool cloning of PCR products, direct sequencing of PCR products or manually estimated from Figure 1; b: n denotes an unknown number of SSR motif repeats missed in sequencing due to the closeness of SSR motifs to the (forward) sequencing primer site; and c: Numerals in the brackets show the number of EST-SSRs pooled for cloning in which the marker was successfully sequenced