

Table S1. The tested primers status for *Commiphora gileadensis*.

Marker		Ta(°C)	SSR motif	Size of PCR product s	References
Prot02	F: ATAAACCCTCTTACGGTGAG R: GGGATTTGTTGACTTTGAAC	60/45	(ACAT) ₆	170–230	[19]
Prot08	F: TATGTCCCACAATGATCCTC R: TTTATAGGAGCGCTCTGATC	60/45	(ACAT) ₇	186–242	
Prot13	F: TGATTTCCTTGTCCTCAAAGAG R: AGCCACATACCGATAAACTC	60/45	(AAAG) ₇	309–311	
Prot22	F: TAACCCTTGACAAGCATTTTC R: AAATTACGGCTTCAGAATTG	60/45	(AGAT) ₉	326–360	
Prot28	F: CGCAGTTTCAGAAATATCAG R: GCATGATTTCGATGTTATAGG	60/45	(ACAT) ₈	238–261	
Prot29	F: TGAAGTACCTTTGCATGAC R: AAGAGGGTGGTCTGAACTG	60/45	(AAAG) ₁₅	128–172	
Prot67	F: TCATGCTGTAATTCCTGTC R: GAGAAGAGCAAAGATTCGATAG	60/45	(ACAT) ₇	191–239	
Prot70	F: CCATTATTAAGCATGCAAAC R: CAATGGCCTGTTCATATAAAG	60/45	(AAG) ₉	111–255	
Prot71	F: CCATCCTCAGCTCTTACTTTC R: GATCGGTCACAGATTCAATG	60/45	(AAG) ₈	398–422	
Prot78	F: CACACCAGGAAAGACTCAAG R: TTGGAAGGAGGATTTATAGG	60/45	(AAG) ₈	139–148	
Prot83	F: CGTCTGGATGGAAGATAAAG R: TCCTCGTTCTCCACTACAAC	60/45	(AAC) ₁₀	161–189	
Prot97	F: ATTCCGATTAAACCTCATTC R: GGGTATGAGCTTGAATTAGG	60/45	(AG) ₁₃	166–196	
Prot99	F: ATGCTATGATAATCGGTTCC R: GAAATGGTTGCACTTCACTC	60/45	(AG) ₁₂	149–209	
Prot100	F: ATCTCTCGTTCCAACCTCAAC R: CGTCGAAGTACTCACCCTC	60/45	(AC) ₁₀	178–190	
Prot101	F: CATTTAGGGACCACGTTTAC R: ATTGTTCCAGGATCTAGGTG	60/45	(AG) ₁₁	288–292	
Prot102	F: GTCGACCAAATAATGTCACC R: ATGGACACACAGGACCTATC	60/45	(AG) ₁₅	370–388	
Prot104	F: TAACCGCAATATCAACTCTC R: ACACCACGACTAAAGACTGG	60/45	(AC) ₁₁	281–299	
BS6	F: CTACGTATTGATGAGGCGGC R: GAGATCGATGGAATTGCTGGT	60	(GA) ₁₄	178–239	[20]
BS8	F: CGCCTCAGCTCACCAGTAAT R: CTGCCAGAGTATGAGAAGCAA	52	(CAAAA) _{4... (CAA)₄}	180–210	
BS10	F: ACACGGGTCTGAACTCCAAC R: GGATGATTCATTCCTGGAAAA	60	(AAG) ₂₀	198–222	
BS11	F: AACAACCAACCCATCTCACTC R: GGTCGGTTGAGGATGGAATA	54	(TC) ₇	182–216	
BS12	F: ATCGGGTGATTCTGCTATCG R: GCAGAATCGCTACTCGATGA	58	(AG) ₉	170–199	
BS13	F: TTCCTTGACATAGCCAAATCT R: GTAGACCTAGCATCTTCAGCTG	58	(AG) ₁₁	278–303	
BS14	F: CCGGCGCAACTTCAATAATA R: ATCAGCAAGTCCGTCTGTCC	58	(AAC) ₄	192–222	
BS16	F: CGCTTTCTATTTTCCTTTTGG R: GCTAACGATTGACAACCTGCTG	50	(CT) ₁₅	112–144	

BS18	F: CAACGAGAGGAGGCAGTGAT R: TTAAGGCCTGGCTAGCAGAA	58	(TC) ₃₀	188-202	
BS19	F: GGATCCAGCCGCACTATATC R: TCGACAGCTCAAGGAATGTG	56	(TG) ₃₂	212-233	
BS21	F: CAGCCTTCCTCAATCGGATA R: AAGTCGGTCACCTCATTGGA	52	(TGT) ₁₂	211-233	
BS23	F: CACGATGACGTGATTCTGCT R: CAAGCTTGACACACAGGAAAA	52	(CA) ₉	191-266	
BS25	F: TCAAGCCGTTGTAGTTGGTG R: TGGAAGCACAGAAAGAAGCA	52	(TC) ₁₅	200-244	
BS28	F: CCAGCATTTTTCTTTCTTTTT R: TTGCTCACGAAATCCTTCCT	56	(AAG) ₁₃	154-181	
BS29	F: CACGATGACGTGATTCTGCT R: CTTACACCATCTCCCTCTGC	52	(AG) ₉	178-238	
BS32	F: CTGCCAGGCCTTAAACAAAA R: GCAGTGGATGGGGTAGAATC	60	(TG) ₁₇	240-277	
Santri04	F: AGCAGTGTTGGTTCAGGAGAA R: AGCTTCTGCTCCACCTGATG	63.7	(TG) ₉	133-148	[21]
Santri07	F: CAGCATGAGGTTGATTGGAC R: CAACCTTGCTACTGTTTCG	62.4	(CA) ₈	188-233	
Santri10	F: Q4-AAGAGAAGCATGGATGACGG R: TGAGGTGGTCCAGACTTTCC	63.7	(AG) ₁₁	202-247	
Santri15	F: TTCATCTGGGTCAGCCGTAT R: CTCACAATCCCGCTTCTC	62.3	(GAA) ₈	267-288	
Santri16	F: Q3-GAATCCATCTTCCCTTAGCAG R: CCATTGAGTTGCCTCCAAAT	61.8	(TTC) ₈	266-322	
Santri20	F: GCCCTTCTAAGAAATCACCCA R: CATTACACGAGCATTACATT	61.7	(CA) ₈	370-412	
Santri26	F: Q3-CTTGATTCTTCTTGACGG R: CACGAGGGATGAGAGCAACT	64.9	(TC) ₁₀	152-168	
DaE-14	F: GGCGGCCATGTTTGTGAAAT R: TACGTAACGGCGATTCACTTT	53	(AT) ₈	122-139	[22]
DaE-24	F: AGGCGTAGAAATCCCATCCA R: ATCTCCAGGAACGGTTGACT	53	(AT) ₈	150-163	
DaE-34	F: TGTGTTTCTCCGCCTCACA R: ATGAACTGCAGCCTCAAACG	53	(AT) ₇	169-190	
DaE-5 ^c	F: AGGATGTTGGTCTGTTGGTGG R: TGGCAGAGGAGAGGATAAGCA	53	(AT) ₈	101-152	
DaE-7	F: AAGAAGGCAAGGCAACACC R: CAGAGCACACTGTAAGGCA	53	(AG) ₈	110-163	
DaE-28	F: CAGAGGTGGAATCTTAA GCCA R: AACACTGCTTCAGCTTTCAGA	53	(AG) ₁₅	151-172	
DaE-39	F: ACCCATTTGAGCTCATTTGACA R: TGCCACTGGGAGTAGAAGAGT	53	(AT) ₁₆	169-216	
DaE-13	F: ATGGCCATTCTCACACCTGG R: ACAGTTGATTTCCATTCCACCC	53	(AT) ₇	138-169	
DaE-19	F: GCAAGATTGTGGTGTGCTGT R: GTGACTCGGAGAAAGCGGT	53	(AAC) ₉	118-157	
DaE-27	F: TTCAATATTGTGGCTGGTCCCA R: TCAGCTCTCAGACAAAGGCA	53	(AG) ₁₅	150-213	
DaE-36	F: TCATTGAGCCACAAGGGAAC R: ACAGAGGAGTGTGATCGAAGA	53	(AT) ₁₀	160-223	
DaE-41	F: TGGTTACTTCAAGCACAGAGAC R: CTGCAATATCGATGCCCTCTCT	53	(AT) ₁₁	199-252	
DaE-16	F: CTAATCGTACTGCTCTTGC R: GGAATGACCGTGTGTTTGGG	53	(AG) ₂₀	115-166	

DaE-20	F: AGATCCCTCTGAATCCCTGATT R: TCATGTCTTCCCTCTTTAGGCT	53	(AT) ₉	130–191
DaE-23	F: CAGCGAACCCATGTCAAACG R: TCCTCAAAGCTACCCTATCCCA	53	(AG) ₁₃	133–248
