

Screening of microsatellite loci and analysis of polymorphism in *Triplophysa hsutschouensis* based on RAD sequencing

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Table S1 Sample RAD-Seq library quality assessment results

Sample	Qubit concentration (ng/ μ L)	Volume (μ L)	Total amount (μ g)	Test result	Remarks
J1	118	100	11.8	Qualified	slight contamination
J2	124.4	100	12.44	Qualified	slight contamination
J3	95.6	100	9.56	Qualified	no contamination
J4	86	100	8.6	Qualified	slight contamination
J5	332.8	100	33.28	Qualified	slight contamination
J6	270.4	100	27.04	Qualified	slight contamination

Table S2 Microsatellite loci and PCR primer information for *T. hsutschouensis*

Locus	Primer (5' to 3') f	Primer (5' to 3') r	Repeating unit	T ($^{\circ}$ C)	Length (bp)
J1	ACAGACATCAGCTTCTTGAATTG	AACATTAGTAGGCCTAAATGAAAATG	(AAT) 10	49.4	160~170
J2	CAGTATTACCAGCATTACACGGG	GATTTGTACAGACGGACTGAAGC	(TCA) 9	53.0	125~310
J3	ATGTCCAGAAGCATCAAACCTT	AGAAGAATCACACCAGCAAAGAG	(GAT) 9	50.3	138~269
J4	GCAAACCTACCTAAGAGCCATTT	ACCAATACAACCATTTGACCAAG	(ATT) 8	51.3	102~159
J5	ACCAATACAACCATTTGACCAAG	GCAAACCTACCTAAGAGCCATTT	(AAT) 8	50.3	159~298
J6	GGGTTTCAGCTATGGTACACACTC	GTCAATTCAGACGGATTGATCTC	(ATC) 8	53.0	129~172
J7	CAGGACACAACTGGAGACCTAC	TCTTCATGAGTCTTCTGGACACA	(TAA) 8	53.0	144~207
J8	CACATCAACGGAATTTAAAGAGC	GTTTCTGTGGATTCAATTTTCAGC	(AAC) 8	50.3	112~155
J9	GTGTAATGGTGTAACCTCCCAAGC	GACCGGTTTTATGGCAGAATAAT	(TTC) 8	52.1	131~145
J10	TATGTATGCTTTGGCCCTTCATA	TTCGGGCTACAATCATCTAAAAA	(GAT) 8	49.4	129~257
J11	GAGTCTCAGCTCTGTCTGGTCTTA	TGCAGCTATATTAGGGTTTCGAG	(AAT) 8	53.0	142~238
J12	GCAAACCTACCTAAGAGCCATTT	ACCAATACAACCATTTGACCAAG	(ATT) 7	50.3	156~250
J13	CCAGACCTCATAGCTCAGGTAAT	TCCCTGTAAATCTGCTTTGAAAC	(TTA) 7	53.0	148~194
J14	GCAAACCTACCTAAGAGCCATTT	AGTCACAGCTCTGTCTGGTCTTAC	(ATT) 7	53.0	138~107
J15	CGAAGGGCTAGAAACCTATTGTAT	CAAGGACTACTACCATCTGACCG	(TTC) 7	53.0	136~145
J16	GCAAACCTACCTAAGAGCCATTT	ACCAATACAACCATTTGACCAAG	(TAT) 7	50.3	156~250
J17	TGCGACTGCATTAGTAGAGTCAT	TCTTAAACAACCTGAACCATAAACAA	(TAAAA) 6	49.4	120~199
J18	CCTAGCGTGTGTTTTCTGTCTCT	GAAGAACAATGCGTTTCAATTC	(GTCT) 6	52.1	147~228
J19	ACCACAAACTCTGAATCTCTCCA	TACCATCTGTCATCCTCTCGTCT	(ATCC) 8	52.6	154~180
J20	GAGAAGACAGATTGTTGAGGTGG	CAATCATTGAGTTTCACTTTTGA	(TTGT) 7	52.6	126~366
J21	GTTATTTTGAAAACGGCACTCTG	TCGCAAATAGAAAAACAGACA	(GTCT) 7	49.4	141~156
J22	AATTTGCACTTTTCACACCTCAT	TATCTGTGTGTGTGGGAGTGTGT	(CACG) 7	52.1	129~259
J23	ATAGCAAGGAAATTGGACACTG	TTCTTTCTCTTTCTTTTCGTT	(GAAA) 7	49.4	105~119
J24	TTGGTCTTGAGCTCCTAAATGTC	ACGAATGAAGTCGAATTAGAAA	(ATTG) 6	49.4	122~136
J25	GAGATTACTGAGGTGGCCAGT	ACGAAATGCCCATTAAATAAACAC	(TCCA) 6	52.1	98~284
J26	AGGAAATGAGATGGAGTAGAAGC	TGGAGTCTCAACACATCTCTGAA	(CAGA) 6	52.1	116~128
J27	CCACATAAACGGTTAAAAGGACA	TTTGGTGTAGTGGTTATTGTCACAT	(GATA) 6	50.3	122~132
J28	CTCACTACTGATCCGCTGGAA	TTCAGATCTCACAGCAGAAAACA	(AGAC) 6	52.1	148~167
J29	AGCAGTTTTTTAAAGAAGGCATCC	AGGCACCTACAGCACACTAAAAC	(TTAT) 6	52.1	138~287
J30	CATTGGAAGAAGTGGGTGAATA	GACATGATGAATGAATTTGCTGA	(AATA) 6	49.4	113~144
J31	AATGCTCACATGGACTGAGAAAT	ACACACACACACACACAGAAA	(TCAT) 6	49.4	109~209
J32	TAATTGGAACAGAGGTGCATGAT	TTCAGGACATTAGGACACAAGGT	(TG) 15	50.0	156~181

J33	TAATTTGTTCCCTTCCCAAATA	TTTTCTCAAAATCGCTGAATAGTG	(AT) 15	48.0	130~169
J34	AACGGACGTGACTTTACAATGTT	GGACTTGTGTGTGAATGACTCAA	(CT) 16	50.0	151~179
J35	TACAGTAATGACAAACAGCAGCG	AGCTGCTGTACATGTCAACCTTC	(AG) 15	52.0	108~121
J36	AGAAAAAGAGCTAAAGTGCTCC	TCTATGCTTTAGTGTAGCTGGCA	(TC) 16	52.0	151~160
J37	ATGTGAAATCCATACGCAAAATC	TGACAGAACATGCAAAATGAAGAG	(CT) 16	48.0	105~138
J38	ATAAAACAAGCAGTTTGACCAGG	GCTGTGAAAGCTGTTCAAGTGTA	(CA) 15	50.0	149~260
J39	GCTATAACTTGTGCGTGTGTGAG	GTGTGTGCCATAATCACCTCC	(AC) 16	53.0	153~160
J40	GTGGTGAAGTGAAGTGTGTGTC	TTCACAAACGAAGGGATGTAGAC	(TC) 16	53.0	137~249
J41	GACTTAGCCCTCACTAAACAGCA	CGAGACATGTCAACACAAAGAGA	(TC) 15	52.0	146~149
J42	GATTTATTGTCTTATCCTCCGGG	ATTCTCTCTCCATCTCCATCTCC	(GA) 16	52.0	107~110
J43	GCCTACAACCATTAAGTGTCTG	CACACTTGCAATCCTCAAAATAA	(AG) 16	50.0	136~224
J44	ACACAGGTCATTACAGCAACACA	AGTACGGCTCTTTGAAAATCCTC	(AG) 16	52.0	102~233
J45	GCATCCACCACACTGATAACATA	TTACACATTACAGCGTTCTGGG	(CT) 15	52.0	127~150
J46	AGTTTGCCATTTTGAGTGTGAAT	GCTGGTGTACGGACATATGATT	(TC) 16	50.0	160~178
J47	AGTTGGTGTGCATTGAGTTTT	CATGAACAGTATTCTACCGGAT	(CA) 16	50.0	113~238
J48	TGACATCAGTCACAAACAACACA	TGCTGCATTACATTAGTCAGACG	(CA) 15	50.0	136~140
J49	CATTTAGCAGATGCTTTTATTACA	CCGATGATGTGTTGAGTAATGA	(TC) 16	50.0	143~147
J50	CGCAAAAACACAAACATTTACAA	TTTTCAGACATGTTTACCTGCC	(GA) 15	48.0	131~213
J51	CAAGTCTGATTTCTGGGTCTGAG	CCTGGAGTGTGTAATCAAGGAC	(AC) 16	48.0	107~122
J52	TGAGAGGATAAGGCTTTGAAAT	TTACAAAATCAGCAGGAGATCAAA	(TA) 12	50.0	119~152
J53	AAACACAAGATGTATTGAAGAGGC	TGAGAAATTCACATGTTTGGACC	(TA) 15	50.0	137~156
J54	AAACTGTCACGTCACGTGCTATAAA	TTTCATTGTTTTCTCAGCCATCT	(TA) 13	50.0	118~172
J55	CAAAAACAACAGCAGTGATGAAC	AATGGTAATTAAGGGGGAAAAA	(AT) 14	48.0	149~196
J56	TCACACACAGATTCCATTTTGTGTC	CACAAAGGGACTTCTCTTTCCTT	(AG) 15	50.0	149~155
J57	CTCTCGAAAAGAACAGTGTCTGTC	GATGTGTGAGCTATATTGGGAGC	(AC) 15	53.0	127~158
J58	ATTCTATCTGTGGAGTGTGAG	GCATTAAACCTTCTGCTGAGTCT	(TC) 15	52.0	124~370
J59	GTGCCTTTCCCTGAGCTTACTAT	CGTCTTCTGGAGCTTCAGTACTTC	(AC) 16	53.0	159~299
J60	GTGAAGAACCCTTTAAAGCACCT	AGGTGTGCTTATGTGCAGGATAC	(CA) 16	52.0	109~112
J61	TTTAATGTCTGTCTGTCGGTCC	GAATGATAATGAAGCAAACCTGGG	(TC) 15	50.0	141~164
J62	CTTTTCTTCATCTCCCTCACTCC	ATCCGCCATAATGATAAATGACA	(CT) 15	50.0	109~128
J63	TTGCGTCATTGTACGTTCTACAC	GATACACTTGACACACTTGCTGC	(TG) 15	52.0	141~169
J64	AATGATTGGATGTTTTTCACAGC	AACAATGTTTGGATGCTTCATTT	(TG) 15	48.0	146~171
J65	ATAAGATCTCAGAACCACACCGA	CTTTTGCTTGTATCACTGTGTC	(AG) 15	52.0	113~144
J66	CATGGCAAAAAGTACACACACAT	CGAAAGAACTTTACCTTCTTTGATT	(AT) 16	50.0	159~179
J67	CTGAGGGTCTACACACAAACA	GAGCGAATATCTCTGGTGATCTG	(AC) 15	53.0	144~271