

Table S2. PCR amplification results of tetraploid *Th. elongatum* molecular markers.

Specific Markers	DNA Sequences of the Special Primers (5'-3')		Fragments Size (bp)	Annealing Temperatures (°C)	CS	SM482	SM921	8801	PI531718 (E)	PI531750 (EE)	1E (1D)	2E (2A)	3E (3D)	4E (4D)	5E (5D)	6E (6D)	7E (7D)
	Forward	Reverse															
<i>chr6E-2</i>	CAAATCAGCATCCAATCAGC	CGCTCGAGTTGCTAGTAGGC	267	61	0	0	0	1	1	1	0	0	0	0	0	1	0
<i>chr6E-3</i>	GGCAGAGTGGAAATCCAAAT	ATTGGTGTACGGACCTCAC	242	58	0	0	0	1	1	1	0	0	0	0	0	1	0
<i>chr6E-5</i>	CTTGTGCTTGCCATGTGATT	TGACACATTGTTGTACGGGAA	196	58	0	0	0	1	1	1	0	0	0	0	0	1	0
<i>chr6E-7</i>	GTCGCCAGAGTCTCTTCGTT	CCTGGGAGAGCTCAGTTGAC	261	62	0	0	0	1	1	1	0	0	0	0	0	1	0
<i>chr6E-8</i>	AGTTCAAGTGCGGATAACGC	ATGCACTTGTGAGTGGAACG	197	61	0	0	0	1	1	1	0	0	0	0	0	1	0
<i>chr6E-10</i>	ACGAACCCTAAGAAAGGGGA	GGCATGTTGGACTGTAGCCT	217	60	0	0	0	1	1	1	0	0	0	0	0	1	0
<i>chr6E-13</i>	GCCCAGACATGGCCTAGTAA	CACGGCCCGTTTACTTTTT	163	62	0	0	0	1	1	1	0	0	0	0	0	1	0
<i>chr6E-14</i>	TTTTTCTCAGGCCCATGTGT	CTTTACCAAATCAGCCCCCT	241	58	0	0	0	1	1	1	0	0	0	0	0	1	0
<i>chr6E-16</i>	GCTCATCAATTTTGAAGAAAAGG	CCGGTGAACCTTGTTGAAAT	191	56	0	0	0	1	1	1	0	0	0	0	0	1	0
<i>chr6E-17</i>	CCTTCTCCCTTTCTCTGCT	CCACCACACATCTCTCCA	187	59	0	0	0	1	1	1	0	0	0	0	0	1	0
<i>chr6E-21</i>	GCCATAGGACAGACTGGAGC	CCCTCTCATCCCGTATCAA	194	58	0	0	0	1	1	1	0	0	0	0	0	1	0
<i>chr6E-23</i>	ACCTGGGCCATGTTAGTCTG	TCAGTCGATGACCACTTTGC	109	59	0	0	0	1	1	1	0	0	0	0	0	1	0
<i>chr6E-24</i>	GAGCCCTCTTCTGTGTGAC	ATCAACAGGTTTCCTGGACG	219	59	0	0	0	1	1	1	0	0	0	0	0	1	0
<i>chr6E-25</i>	TTAACCCCTGCAGAGCACTT	TTTGATGCATGTAAACACCGA	138	57	0	0	0	1	1	1	0	0	0	0	0	1	0
<i>chr6E-26</i>	ACAGAACCGCGGGTTAATA	AAAACACACCACGACTGCAA	143	57	0	0	0	1	1	1	0	0	0	0	0	1	0
<i>chr6E-27</i>	AAGTGGAGCGGCACATTAC	CGTTGAACATGTTTCCAATACG	276	57	0	0	0	1	1	1	0	0	0	0	0	1	0
<i>chr6E-28</i>	TCACCTACTCGTCTTCGGCT	AGATGCTGGGCTCCTACTGA	280	61	0	0	0	1	1	1	0	0	0	0	0	1	0
<i>chr6E-31</i>	GCCGTTAGATCTGTGTTCC	TAGAGAGAGGCCGTGCATTT	202	59	0	0	0	1	1	1	0	0	0	0	0	1	0
<i>chr6E-36</i>	TTCGCAAACAGAAATGGAGA	TGTGTGTCTTCGGTTATCGC	225	60	0	0	0	1	1	1	0	0	0	0	0	1	0
<i>chr6E-37</i>	ACCACATCCCGCATATAAAA	CTTGTCTCATCCTTCACGCA	214	57	0	0	0	1	1	1	0	0	0	0	0	1	0
<i>chr6E-38</i>	AGGAGGGGCATCACGTTAC	CCCTCCATGTCTCATCATC	180	57	0	0	0	1	1	1	0	0	0	0	0	1	0
<i>chr6E-40</i>	GTCGCTTACCTTGTTCCCT	ATATTTTGGGCGAGTGGAG	142	57	0	0	0	1	1	1	0	0	0	0	0	1	0
<i>chr6E-42</i>	TATTGAGCAACCCCGTTTTTC	TACTCCATCACGTCCCCTTC	187	57	0	0	0	1	1	1	0	0	0	0	0	1	0
<i>chr6E-43</i>	TCTGACCTTAAGCGCCAAGT	AAGGTACCCTACCGCCAAC	101	60	0	0	0	1	1	1	0	0	0	0	0	1	0
<i>chr6E-45</i>	TCTGTGCTGAAACTCGCACT	ACAAGTGAAACAACCCCTGGC	252	59	0	0	0	1	1	1	0	0	0	0	0	1	0
<i>chr6E-46</i>	CCGAACCTTGTTATCGTGGGT	GGCGCCAAATAAGGATTACC	193	57	0	0	0	1	1	1	0	0	0	0	0	1	0
<i>chr6E-47</i>	CTGGCTACGGCAGATGTGTA	AAATTACGGGATTGTACGG	235	57	0	0	0	1	1	1	0	0	0	0	0	1	0
<i>chr6E-48</i>	GACACCAGCCTAACCCEAAA	CGCGCATTTAAAAATGGTTT	239	57	0	0	0	1	1	1	0	0	0	0	0	1	0
<i>chr6E-49</i>	ACGAGAGATTGGTGTGCGAG	GGGCGCAAAATTTTAAAGACA	177	57	0	0	0	1	1	1	0	0	0	0	0	1	0
<i>chr6E-50</i>	ATACATGCCACCAACCAAT	TCCCAACGGCTAGACTGACT	136	59	0	0	0	1	1	1	0	0	0	0	0	1	0
<i>chr6E-51</i>	CAGCGGTATTAATTGGCCTT	TGTGTCTTTGACGATTGGGA	175	58	0	0	0	1	1	1	0	0	0	0	0	1	0
<i>chr6E-59</i>	CATGCCCTGGCTAACTGTTT	CTTCACATCCCAACACACG	136	59	0	0	0	1	1	1	0	0	0	0	0	1	0
<i>chr6E-60</i>	AGCCTGCGAGAGAAGAAGTG	CGCCGTTACAGTATCCTTTGT	122	59	0	0	0	1	1	1	0	0	0	0	0	1	0