

Phylogeography of *Toona ciliata* (Meliaceae) complex in China inferred from cytonuclear markers

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Table S1. Twenty pairs of primers from mitochondrial DNA tested in *Toona ciliata* complex

Primer pair	Forward and reverse primer sequences	Annealing temperature	Reference
<i>atp9F-atp9R</i>	CCAAGTGAGATGTCCAAGAT CTTCGGTTAGAGCAAAGCC	50	Duminil <i>et al.</i> , 2002
<i>ccb203F-ccb203R</i>	ASGTTCTACGGACCGATGCC CACGGGGAGGGAGCRGGCGA	56	Duminil <i>et al.</i> , 2002
<i>ccb206F-ccb206R</i>	TCAATCTTGTRAACTAATCG CYYCTCCACACCAATCACGA	62	Duminil <i>et al.</i> , 2002
<i>ccb256F-ccb256R</i>	GGAAGTTAGCAAAGTTAGAC TTGTTCTTAACAGCGATGGC	56	Duminil <i>et al.</i> , 2002
<i>cox2/1-cox2/2</i>	TTTTCTTCCTCATTTCTKATTT CCACTCTATTGTCCACTTCTA	50	Dumolin-Lapegue <i>et al.</i> , 1997
<i>cox3F-cox3R</i>	CCGTAGGAGGTGTGATGT CTCCCCACCAATAGATAGAG	58	Duminil <i>et al.</i> , 2002
<i>orf25F-orf25R</i>	AAGACCRCCAAGCYTCTCG TTGCTGCTATTCTATCTATT	50	Duminil <i>et al.</i> , 2002
<i>rpl5F-rpl5R</i>	AGTGGTAAAGTCTCATCT ATYGTGTGAAATAAGAGTAG	50	Duminil <i>et al.</i> , 2002
<i>rps4F-rps4R</i>	CSTTTCYGCTCCGAAGAG TCTCCGAAGATTGAGG	58	Duminil <i>et al.</i> , 2002
<i>rps12-1-nad3-2</i>	TTTCTTCTCTACCATGACGA TGATCCYACTCGGTSTTCCT	50	Duminil <i>et al.</i> , 2002
<i>rrn5-rrn18-1</i>	GAGGTCGGAATGGGATCGGG GGGTGAAGTCGTAACAAGGT	58	Duminil <i>et al.</i> , 2002
<i>mh44_F-mh44_R</i>	ATGACTGGAAGAATTGCTCAC TTCACCTGATACTCACCCCC	55	Duminil <i>et al.</i> , 2002
<i>nad1/B-nad1/C</i>	GCATTACGATCTGCAGCTCA GGAGCTCGATTAGTTTCTGC	57.5	Demesure <i>et al.</i> , 1995
<i>nad4/1-nad4/2</i>	CAGTGGGTTGGTCTGGTATG TCATATGGGCTACTGAGGAG	57.5	Demesure <i>et al.</i> , 1995
<i>hc_mt1F-hc_mt1R</i>	AGGGTGGCTATTTCTCGCTC CGAGAAAGAATAGAATCAAGGG	52	This study
<i>hc_mt2F-hc_mt2R</i>	TGCTACTGCTGCTACCATGA GCACCAGCAAAGCAAAGCT	50	This study
<i>hc_F3-hc_R3</i>	AACATAGAACTGAGGTAATG ATTACGCCAAAAGTATGCT	50	This study
<i>26SrRNA-tRNA-Leu</i>	AACATAGAACTGAGGTAATG ATTACGCCAAAAGTATGCT	50	This study
<i>26SrRNA-tRNA-Leu</i>	ACGGATACTTTGTCATTAGA TTTATGTGGTTCCGACTGTA	50	This study
<i>cox1-nad1</i>	ACAAACAGTTAGTAAGGTCA TTTCCAGTCTTCAAATCGGT	50	This study

Table S4. Estimates of parameters of mismatch distribution and statistical tests #

Population	θ_0	θ_1	$\tau(t)$	SSD (P-value)	Rag (P-value)
JX	7.794	16.549	1.977	0.059 (0.20)	0.121 (0.11)
YF	1.995	23.125	2.125	0.014 (0.44)	0.042 (0.48)
XL	1.552	37.285	3.131	0.002 (0.84)	0.013 (0.86)
LD	0.028	14.214	4.205	0.003 (0.94)	0.020 (0.92)
CH	0.171	122.344	5.359	0.004 (0.51)	0.020 (0.51)
WM	1.872	50.859	2.607	0.005 (0.53)	0.023 (0.55)
XY	-	-	-	-	-
JL	0.021	12.109	3.418	0.043 (0.07)	0.136 (0.04)
DC	2.164	41.680	3.867	0.003 (0.69)	0.010 (0.87)
HD	0.002	15.073	4.576	0.007 (0.61)	0.023 (0.76)
YR	0.011	15.264	4.773	0.001 (0.95)	0.010 (0.99)
SM	0.068	42.802	3.582	0.002 (0.90)	0.022 (0.84)
XJ	-	-	-	-	-
TL	-	-	-	-	-

#: SSD: the sum of squared deviation (SSD); Rag: Harpending's raggedness index; $\theta_0=2N_0\mu$, $\theta_1=2N_1\mu$, where N_0 and N_1 are the population sizes before and after population expansion; $\tau(t)$: the time elapsed since a sudden expansion. "-": appropriate estimates were not derived from sequence data. Populations XJ and TL: Estimates were not available.

Table S2: Five hundred samples of alignment sequences each of which was a concatenated sequence of *cox1-nad1* and *26S-rRNA-tRNA-Leu* segments

Table S3: Four hundred and sixty-seven samples of ITS alignment sequences