

Table S1. Primer pairs used for PCR amplification of *Tetragnatha maxillosa* and *T. nitens* mitogenomes.

Primer(F/R)	Fragment (Region)	Primer sequence (5'-3')
F1/R1	<i>ND2–COII</i>	TGATTTTTATTATGAGTGGGGTTAG/AATTATATTAATTTGATTAAAAGT
F2/R2	<i>COII–COIII</i>	CTTTAATCAAATTAATATAATTC/ AAATTAATAATATTCTAAACAATAT
F3/R3	<i>COIII–ND5</i>	ATATTGTTTAGAATATTATTAATTT/ AACTGACAAGAAATATATGGGC
F4/R4	<i>ND5–ND4</i>	GCCCATATATTTCTTGTCAGTTT/ TTTATAATTCACCTTATGACTCC
F5/R5	<i>ND4–Cytb</i>	GGAGTCATAAGTGAATTATAAA/ CAAATTAACCCTTTAATCAGGCAT
F6/R6	<i>Cytb–rrnS</i>	ATGCCTGATTAAGGGTTAATTTG/ CAGTTAATGTTCTAGAAAGAGCA
F7/R7	<i>rrnS–ND2</i>	TGCTCTTTCTAGAACATTAACCTG/ CCCACTCATAATAAAAAATCA

Table S2. Nucleotide composition of *Tetragnatha maxillosa* and *T. nitens* mitogenomes.

Gene	<i>T. maxillosa</i>			<i>T. nitens</i>		
	A+T (%)	AT skew	GC skew	A+T (%)	AT skew	GC skew
Whole genome	74.5	-0.087	0.246	74.3	-0.055	0.200
Protein-coding genes*	73.5	-0.161	0.052	73.0	-0.149	0.032
First codon position	68.7	-0.053	0.270	68.5	0.001	0.255
Second codon position	67.9	-0.452	-0.141	67.3	-0.444	-0.140
Third codon position	83.9	-0.013	0.016	83.1	-0.034	-0.048
tRNA genes	78.1	-0.012	0.191	79.7	0.031	0.188
16S rRNA	79.0	-0.064	0.088	78.3	-0.005	0.028
12S rRNA	81.2	-0.004	0.031	82.5	0.016	-0.058
A+T-rich region	73.3	-0.055	0.108	71.5	0.037	0.100

* Stop codons were excluded.

Figure legends

Fig. S1. The relative synonymous codon usage (RSCU) of *T. maxillosa* (A) and *T. nitens* (B) mitogenomes. Codon families are provided on the X- axis.

Fig. S2. Organization of the A+T-rich region in the two *Tetragnatha* spider mitogenomes. (A) Structure of control region and its neighborhood. T-stretch is highlighted in shadow box. (B) Predicted secondary structures of the first tandem repeat and flanking junctions in *T. maxillosa* (Tm) and *T. nitens* mitogenomes (Tn).

Fig. S3. Phylogenetic trees from Araneae species based on the dataset PCG12 (A) and the dataset PCG12R (B) using Bayesian inference (BI) and maximum likelihood (ML). *Limulus polyphemus* was used as an outgroup. Numbers above the nodes refer to Bayesian posterior probabilities in percentages (left) and ML bootstrap values (right).

Figure S1



