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The complete mitochondrial genome of the Bristletail *Songmachilis xinxiangensis* (Archaeognatha: Machilidae)

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Abstract
This study determined the complete mitochondrial genome of the bristletail *Songmachilis xinxiangensis* (Machilidae: Machilinae). It is a circular molecule of 15,473 bp long, and contains 37 genes typically found in other insects, with 13 protein-coding genes, 2 ribosomal RNA subunits genes, and 22 tRNA genes. The mitochondrial genome arrangement of *S. xinxiangensis* was similar to *Pedetontus silvestrii* (Machilidae: Petrobiinae) and *Nesomachilis australica* (Meinertellidae), but different from *Trigoniophthalmus alternatus* (Machilidae: Machilinae) in position of $tRNA^{Ala}$ and *Petrobius brevistylis* (Machilidae: Petrobiinae) in the position of $tRNA^{Tyr}$. The A + T content of total nucleotide and control region is 73.6% and 86%, respectively.

Keywords: *Microcoryphia, Mt genome, Bristletail,* Songmachilis xinxiangensis

Archaeognatha is a primitive Order in Insecta, and useful to discuss the origin of Insecta. There are nearly 500 described bristletail species divided into two major families Machilidae (including three subfamilies: Machilinae, Petrobiellinae, and Petrobiinae) and Meinertellidae (Sturm and Machida 2001; Mendes 2002). Four mitochondrial genomes of bristletails have been sequenced which included two species in Petrobiinae (Podsiadlowski 2006; Zhang et al. 2008), one species in Machilinae (Carapelli et al. 2007), and one species in Meinertellidae (Cameron and Miller 2004). The mt genome arrangement of *Petrobius brevistylis* was not the same as most insect mitochondrial genomes in position of $tRNA^{Tyr}$, and *Trigoniophthalmus alternatus* in position of $tRNA^{Ala}$.

The sample of *S. xinxiangensis* (No. XX120-YTS) was collected at Yuntai Mountain in Henan Province, China, preserved in 100% ethanol and stored at −70°C for DNA extraction. Whole genomic DNA extraction from a single individual was carried out using DNeasy Blood & Tissue Kit (50) (Qiagen, Hilden Germany), and was used as template for PCRs. We amplified overlapping fragments of *S. xinxiangensis* mt genome by normal PCR and LA-PCR methods. All PCRs were performed using a MJ Mini thermal cycler (BioRad, Hercules, CA, USA).

The mtDNA sequences were proofread and assembled by the program SeqMan in Lasergene version 5.0 (DNASTAR, Inc., Madison, WI, USA). The locations of protein coding genes and ribosomal RNA genes were determined by comparison with the published bristletail mitochondeial sequences. Seventeen of the tRNA genes were using tRNA-scan SE 1.21 (Lowe and Eddy 1997) to identify their cloverleaf secondary structure and anticodon sequences. The sequences of five tRNA ($tRNA^{Ile}$, $tRNA^{Gly}$, $tRNA^{Arg}$, $tRNA^{Ser1}$, and $tRNA^{His}$) genes were determined by DNASIS v2.5 Demo (Hitachi Software, Yokohama, Japan). Nucleotide ratios and the codon frequency were calculated in Mega 5.0 (Tamura et al. 2011).

The complete mitochondrial genome of *S. xinxiangensis* is a circular double molecule 15,473 bp in length and has been deposited in GenBank (No. JX308221). The genome contains 37 genes typically found in other insects, consisting 13 protein-coding genes

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Table I. Organization of *S. xinxiangensis* mitochondrial genome.

Gene	Strand	Position	Length (nuc.)	Anticodon	Start codon	Stop codon	Intergenic nucleotides
tRNA ^{Ile}	+	1–67	67	GAT			−3
tRNA ^{Gln}	−	65–132	68	TTG			−1
tRNA ^{Met}	+	132–201	70	CAT			0
ND2	+	202–1233	1032		ATA(M)	TAA	−2
tRNA ^{Trp}	+	1232–1297	66	TCA			3
tRNA ^{Cys}	−	1301–1366	66	GCA			0
tRNA ^{Tyr}	−	1367–1433	67	GTA			−8
COI	+	1426–2970	1545		ATT(I)	TAA	−5
tRNA $^{Leu2(UUA)}$	+	2966–3030	65	TAA			7
COII	+	3038–3725	688		ATG(M)	T	0
tRNA ^{Lys}	+	3726–3797	72	CTT			6
tRNA ^{Asp}	+	3804–3870	67	GTC			0
ATP8	+	3871–4032	162		ATT(I)	TAA	−7
ATP6	+	4026–4703	678		ATG(M)	TAA	−1
COIII	+	4703–5485	783		ATG(M)	TAA	1
tRNA ^{Gly}	+	5487–5551	65	TCC			−3
ND3	+	5549–5905	357		ATA(M)	TAA	2
tRNA ^{Ala}	+	5908–5971	64	TGC			1
tRNA ^{Arg}	+	5973–6035	63	TCG			−1
tRNA ^{Asn}	+	6035–6103	69	GTT			0
tRNA ^{Ser1}	+	6104–6170	67	ACT			0
tRNA ^{Glu}	+	6171–6234	64	TTC			7
tRNA ^{Phe}	−	6242–6307	66	GAA			−1
ND5	−	6307–8049	1743		ATT(I)	TAA	−8
tRNA ^{His}	−	8042–8109	68	GTG			0
ND4	−	8110–9459	1350		ATG(M)	TAG	−7
ND4L	−	9453–9752	300		ATG(M)	TAA	2
tRNA ^{Thr}	+	9755–9820	66	TGT			0
tRNA ^{Pro}	−	9821–9885	65	TGG			0
ND6	+	9886–10,395	510		ATT(I)	TAA	−1
Cyt b	+	10,395–11,531	1137		ATG(M)	TAA	0
tRNA ^{Ser2}	+	11,532–11,595	64	TGA			27
ND1	−	11,623–12,543	921		ATT(I)	TAA	21
tRNA ^{Leu1}(CUA)	−	12,565–12,631	67	TAG			0
16S rRNA	−	12,632–13,952	1321				0
tRNA ^{Val}	−	13,953–14,024	72	TAC			0
12S rRNA	−	14,025–14,848	824				0
CR		14,849–15,473	625				0

(*ATP6*, *ATP8*, *COI-III*, *ND1-6*, *ND4L*, and *Cyt b*), 2 genes encoding for ribosomal RNA subunits (*12S rRNA* and *16S rRNA*), 22 tRNA genes, and non-coding regions (Table I).

All of the 13 protein coding genes start with the usual standard ATN, 6 of them start with ATG (*ND4*, *ND4L*, *COII*, *COIII*, *Cyt b,* and *ATP6*), 5 genes start with ATT (*ND1*, *ND5*, *ND6*, *COI*, and *ATP8*), and 2 genes start with ATA (*ND2* and *ND3*). 1 (*ND4*) of 13 protein coding genes ends with TAG as stop condon, one gene (*COII*) ends with a single T, and other genes end with TAA.

The β-strand encodes both *12S rRNA* and *16S rRNA* genes and both genes are separated by *tRNA ^{Val}*. The *16S rRNA* gene (1321 bp in length) is located between *tRNA ^{Leu1}* and *tRNA ^{Val}* genes, and the *12S rRNA* gene (834 bp in length) is located between *tRNA ^{Val}* and control region.

Control region is the major non-coding region, and it has 625 bp sequence located between *12S rRNA* and *tRNA ^{Ile}* gene. There are two longer non-coding sequences found between *tRNA ^{Ser2}* and *ND1* (27 bp), between *ND1* and *tRNA ^{Leu1}* (21 bp), respectively. The A + T content in the total genome of *S. xinxiangensis* is 73.6%, whereas AT content of control region is 86%.

Nucleotide sequence accession number. The complete genome sequence of *S. xinxiangensis* has been assigned GenBank accession number JX308221.

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