Mitochondrial DNA

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MITOGENOME ANNOUNCEMENT

Complete mitogenome of the ixodid tick *Ixodes pavlovskyi* (Acari: Ixodida)

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Abstract

Here, we present complete mitochondrial DNA sequence of *Ixodes pavlovskyi* Pom., 1946 for the first time. The mitogenome is 14,575 bp in length and contains 13 protein-coding genes, 2 *rRNA* genes, 22 *tRNA* genes and a control region. The overall base composition is 40.1% T, 13.8% C, 37.9% A and 8.1% G. Four protein-coding genes are initiated by ATT codon, three genes – by ATA codon and ATG start codon is found for six genes. Only *tRNA-Lys, tRNA-Ile, tRNA-Arg* are folded into the cloverleaf secondary structure, other tRNA have atypical structure with reduced T- or D-arms.

Keywords

Complete mitochondrial genome, *Ixodes pavlovskyi*, tick, tick-borne infections

History

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Ixodes pavlovskyi Pom., 1946 ticks were found in southern regions of Siberia, Russia (Bolotin et al., 1977). In the recent years, these ticks spread out considerably and now dominate the largest Siberian cities (Malkova et al., 2012; Romanenko, 2011). *Ixodes pavlovskyi* ticks are a vector for tick-borne infections (TBIs), such as tick-borne encephalitis, Lyme disease and other TBIs within natural and urban foci (Chausov et al., 2009, 2010, 2011; Mikryukova et al., 2014). Our study contributes to taxonomy, evolution and molecular probes for ixodid ticks.

Here, we report the first complete mitochondrial DNA sequence of *I. pavlovskyi*. We collected adult ticks in Tomsk, Russia in 2011 as previously described (Moskvitina et al., 2008). The entire *I. pavlovskyi* mitogenome was amplified by PCR from tick DNA isolated from tick homogenate using RIBO-sorb kit (AmpliSens, Moscow, Russia). Primers for PCR were designed based on sequences of related tick *I. persulcatus* (AB073725). PCR products were gel-purified using S.N.A.P.^{TM} kit (Invitrogen) and directly sequenced on Applied Biosystems 3130XL sequencer four times. Sequences were aligned using Vector NTI Suite 10.0 (www.invitrogen.com), Lasergene 7.0 (www.dnastar.com) and MEGA 5 (Tamura et al., 2011). Annotation of the protein coding genes and *rRNA* genes was achieved by comparing sequences with citrus red and brown dog ticks (Liu et al., 2013; Yuan et al., 2010). The *tRNAs* were virtually folded using MS fold WEB server (Zuker, 2003).

The complete mitogenome of the tick *I. pavlovskyi* is 14,575 bp in length encoding 13 protein genes, 2 *rRNA* genes, 22 *tRNA* genes, and a control region (KJ000060). The order of genes and transcriptional direction in *I. pavlovskyi* mitogenome is identical to mitogenomes of *I. persulcatus* and *I. ricinus* ticks (AB073725, JN248424) but different from brown dog tick (Liu et al., 2013). The overall base composition of the mitogenome is 40.1% T, 13.8% C, 37.9% A, and 8.1% G. The ratio A + T for ATP8 is high 85.2% and low in G 3.8%. The homology of *I. pavlovskyi* mitogenome compared to *I. ricinus* and *I. persulcatus* is 89 and 91%, respectively. Four protein coding genes (*COX1*, *ATP8*, *NAD3* and *NAD5*) are initiated by ATT start codon, three genes (*NAD2*, *ATP6* and *NAD6*) by ATA codon and six genes by classical ATG codon (Table 1). Most of the protein coding genes are terminated with TAA and four genes are stopped by incomplete stop codon T. The *12S rRNA* and *16S rRNA* genes were 723 and 1220 nucleotides long, respectively.

Twenty two *tRNA* genes ranged in size between 58 (*tRNA-Ser*) and 69 (*tRNA-Gln*) nucleotides (Table 1). *tRNA* sequences potentially fold into the atypical cloverleaf secondary structure lacking T- or D-arms with the exception of *tRNA-Lys, tRNA-Ile, tRNA-Arg,* which have typical cloverleaf secondary structure. The 354 bp control region of *I. pavlovskyi* mitogenome is located between the *12S rRNA* and *tRNA-Ile* genes.

We identified 67 noncoding nucleotides in 14 unassigned intergenic and 77 bp short overlaps at five gene junctions, with the largest one (57 bp) at junction *tRNA-Ser-NAD1*.

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Table 1. Organization of the mitochondrial genome in *Ixodes pavlovskyi.*

Gene	Direction	Position	Size (bp)	Intergenic spacer	Protein-coding genes		tRNA genes	
					Start codon	Stop codon	Codon	Anticodon position
tRNA-Met	+	1–61	61	1			AUG	31–33
NAD2	+	63–1034	972	0	ATA	TAA		
tRNA-Thr	+	1035–1099	65	−7			UGA	1064–1066
tRNA-Cys	−	1093–1156	64	14			UGC	1120–1122
tRNA-Tyr	−	1171–1234	64	−7			UAC	1200–1202
COX1	+	1228–2766	1539	8	ATT	TAA		
COX2	+	2775–3450	676	0	ATG	T−−*		
tRNA-Lys	+	3451–3519	69	0			AAG	3484–3486
tRNA-Asp	+	3520–3582	63	1			GAC	3552–3554
ATP8	+	3584–3739	156	−4	ATT	TAA		
ATP6	+	3736–4398	663	6	ATA	TAA		
COX3	+	4405–5182	778	0	ATG	T−−		
tRNA-Gly	+	5183–5248	66	0			GGA	5214–5216
NAD3	+	5249–5584	336	0	ATT	TAA		
tRNA-Ala	+	5585–5645	61	0			GCA	5616–5618
tRNA-Arg	+	5646–5707	62	0			CGA	5678–5680
tRNA-Asn	+	5708–5775	68	3			AAC	5743–5745
tRNA-Ser (AGA)	+	5778–5835	58	0			AGA	5797–5799
tRNA-Glu	+	5836–5900	65	−2			GAA	5867–5869
tRNA-Phe	−	5899–5963	65	0			UUC	5926–5928
NAD5	−	5964–7632	1669	0	ATT	T−−		
tRNA-His	−	7633–7693	61	3			CAC	7660–7662
NAD4	−	7697–9013	1317	1	ATG	TAA		
NAD4L	−	9015–9282	268	2	ATG	TAA		
tRNA-Trp	+	9285–9347	63	0			ACA	9316–9318
tRNA-Pro	−	9348–9412	65	2			CCA	9374–9376
NAD6	+	9415–9843	429	3	ATA	TAA		
COB	+	9847–10,927	1081	0	ATG	T−−		
tRNA-Ser (UCA)	+	10,928–10,990	63	−57			UCA	10,958–10,960
NAD1	−	10,934–11,929	996	0	ATG	TAA		
tRNA-Leu (UUA)	−	11,930–11,994	65	12			UUA	11,959–11,961
tRNA-Leu (CUA)	−	12,007–12,067	61	0			CUA	12,034–12,036
rrnL (16S rRNA)	−	12,068–13,287	1220	0				
tRNA-Val	−	13,288–13,349	62	0			GUA	13,320–13,322
rrnS (12S rRNA)	−	13,350–14,072	723	0				
Control region		14,073–14,426	354	0				
tRNA-Ile	+	14,427–14,494	68	6			AUC	14,456–14,458
tRNA-Gln	−	14,501–14,569	69	6			CAA	14,536–14,538

*TAA stop codon is completed by the addition of 3′A.

Declaration of interest

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

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