

SUPPLEMENTARY MATERIAL

The complete nucleotide sequence and gene organization of the mitochondrial genome of *Triatoma boliviiana* (Hemiptera, Reduviidae, Triatominae) and phylogenetic comparisons

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Table S1. Annotation of the complete mitogenome of *Triatoma boliviana*. Negative numbers in the “intergenic spacers” column indicate genes overlaps.

Gene	Strand	Nucleotide Number	Intergenic Spacers	Start Codon	Stop Codon
(I) <i>tRNA-Ile</i>	H	1–63	–3	–	–
(Q) <i>tRNA-Gln</i>	L	61–129	–1	–	–
(M) <i>tRNA-Met</i>	H	129–196		–	–
<i>nd2</i>	H	197–1195	5	ATT	TAA
(W) <i>tRNA-Trp</i>	H	1201–1267	–8	–	–
(C) <i>tRNA-Cys</i>	L	1260–1322		–	–
(Y) <i>tRNA-Tyr</i>	L	1323–1387		–	–
<i>coI</i>	H	1388–2921		ATG	T(aa)
(L) <i>tRNA-Leu</i> (1, UUR)	H	2922–2988		–	–
<i>coII</i>	H	2989–3667		ATA	T(aa)
(K) <i>tRNA-Lys</i>	H	3668–3737	–1	–	–
(D) <i>tRNA-Asp</i>	H	3737–3801		–	–
<i>ATPase8</i>	H	3802–3957	–7	ATC	TAA
<i>ATPase6</i>	H	3951–4634	–14	ATG	TAA
<i>coIII</i>	H	4621–5404		ATG	T(aa)
(G) <i>tRNA-Gly</i>	H	5405–5467	–3	–	–
<i>nd3</i>	H	5465–5820		ATA	TA(a)
(A) <i>tRNA-Ala</i>	H	5821–5884	5	–	–
(R) <i>tRNA-Arg</i>	H	5890–5954	8	–	–
(N) <i>tRNA-Asn</i>	H	5963–6029	–1	–	–
(S) <i>tRNA-Ser</i> (1, AGN)	H	6029–6097		–	–
(E) <i>tRNA-Glu</i>	H	6098–6160	4	–	–
(F) <i>tRNA-Phe</i>	L	6165–6229		–	–
<i>nd5</i>	L	6230–7941		ATT	TA(a)
(H) <i>tRNA-His</i>	L	7942–8009		–	–
<i>nd4</i>	L	8010–9340	–7	ATG	TA(a)
<i>nd4L</i>	L	9334–9627	2	ATG	TAG
(T) <i>tRNA-Thr</i>	H	9630–9691		–	–
(P) <i>tRNA-Pro</i>	L	9692–9755	3	–	–
<i>nd6</i>	H	9759–10259	–1	ATG	TAA
<i>cytB</i>	H	10259–11395		ATG	TAA
(S) <i>tRNA-Ser</i> (2, UCN)	H	11396–11463	767	–	–
<i>nd1</i>	L	12231–13160	–6	ATA	TAA
(L) <i>tRNA-Leu</i> (2, CUN)	L	13155–13219		–	–
<i>lrRNA</i>	L	13220–14480		–	–
(V) <i>tRNA-Val</i>	L	14481–14552		–	–
<i>srRNA</i>	L	14553–15335		–	–
Control region		15336–16719		–	–

Table S2. Codon usage of *Triatoma boliviana* mitogenome protein coding genes.

Codon	n	%	RSCU	Codon	n	%	RSCU
UUU(F)	282	7.62	1.67	UAU(Y)	148	4.00	1.7
UUC(F)	56	1.51	0.33	UAC(Y)	26	0.70	0.3
UUA(L)	348	9.40	3.95	UAA(*)	12	0.32	1.85
UUG(L)	47	1.27	0.53	UAG(*)	1	0.03	0.15
CUU(L)	68	1.84	0.77	CAU(H)	52	1.40	1.41
CUC(L)	8	0.22	0.09	CAC(H)	22	0.59	0.59
CUA(L)	52	1.40	0.59	CAA(Q)	50	1.35	1.67
CUG(L)	5	0.14	0.06	CAG(Q)	10	0.27	0.33
AUU(I)	348	9.40	1.77	AAU(N)	129	3.48	1.61
AUC(I)	46	1.24	0.23	AAC(N)	31	0.84	0.39
AUA(M)	240	6.48	1.8	AAA(K)	79	2.13	1.56
AUG(M)	27	0.73	0.2	AAG(K)	22	0.59	0.44
GUU(V)	106	2.86	2.27	GAU(D)	65	1.76	1.86
GUC(V)	6	0.16	0.13	GAC(D)	5	0.14	0.14
GUA(V)	65	1.76	1.39	GAA(E)	70	1.89	1.54
GUG(V)	10	0.27	0.21	GAG(E)	21	0.57	0.46
UCU(S)	120	3.24	2.62	UGU(C)	47	1.27	1.74
UCC(S)	22	0.59	0.48	UGC(C)	7	0.19	0.26
UCA(S)	87	2.35	1.9	UGA(W)	84	2.27	1.7
UCG(S)	3	0.08	0.07	UGG(W)	15	0.41	0.3
CCU(P)	66	1.78	2.03	CGU(R)	22	0.59	1.63
CCC(P)	18	0.49	0.55	CGC(R)	1	0.03	0.07
CCA(P)	46	1.24	1.42	CGA(R)	26	0.70	1.93
CCG(P)	0	0.00	0	CGG(R)	5	0.14	0.37
ACU(T)	89	2.40	1.85	AGU(S)	32	0.86	0.7
ACC(T)	28	0.76	0.58	AGC(S)	6	0.16	0.13
ACA(T)	73	1.97	1.52	AGA(S)	93	2.51	2.03
ACG(T)	2	0.05	0.04	AGG(S)	4	0.11	0.09
GCU(A)	63	1.70	1.91	GGU(G)	77	2.08	1.42
GCC(A)	21	0.57	0.64	GGC(G)	9	0.24	0.17
GCA(A)	42	1.13	1.27	GGA(G)	104	2.81	1.92
GCG(A)	6	0.16	0.18	GGG(G)	27	0.73	0.5

A total of 3702 codons were analyzed.

RSCU: relative synonymous codon usage.

* =termination codon.

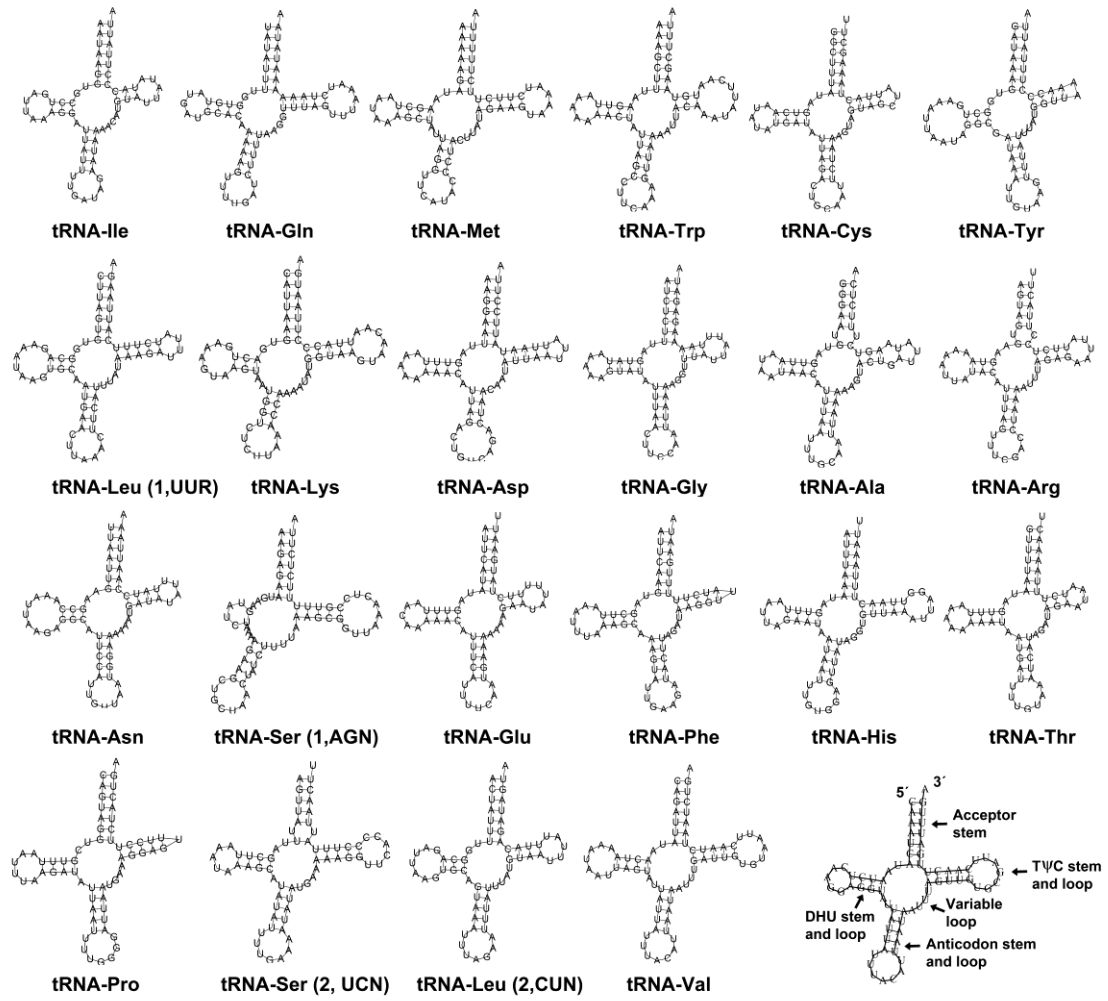


Figure S1. Secondary structure of tRNAs in *Triatoma boliviana* mitogenome.

TCGCAAAAAAAAAATCATTAGGTTGACCTAA
AATATATTTAATTCACCTAAAATAATGCAATAAACATTATAGTAACTCCAGAAAAAGGATATAACTATCCTTATAACTAAGTGCCTAATTTATAACAGTAACGGGGCAAAGTCCCTTAAATTCAAAATAAACATTCAAAGTTTATACTT
AATATATTTAATTCACCTAAAATAATGCAATAAACATTATAGTAACTCCAGAAAAAGGATATAACTATCCTTATAACTAAGTGCCTAATTTATAACAGTAACGGGGCAAAGTCCCTTAAATTCAAAATAAACATTCAAAGTTTATACTT
AATATATTTAATTCACCTAAAATAATGCAATAAACATTATAGTAACTCCAGAAAAAGGATATAACTATCCTTATAACTAAGTGCCTAATTTATAACAGTAACGGGGCAAAGTCCCTTAAATTCAAAATAAACATTCAAAGTTTATACTT
AATATATTTAATTCACCTAAAATAATGCAATAAACATTATAGTAACTCCAGAAAAAGGATATAACTATCCTTATAACTAAGTGCCTAATTTATAACAGTAACGGGGCAAAGTCCCTTAAATTCAAAATAAACATTCAAAGTTTATACTT

Figure S2. Sequence of the intergenic spacer located between *tRNA-Ser* (UCN) and *nd1* genes. Repeat sequences are underlined.

		10	20	30	40	50	60	70	80	90	100
AF301594	T dimidiata	CCGGTACATTATCAA	TATAT	CCCCCCTCCGTATAGCCTCCCCT	GAGGT	GCCCACC	CGGAACGG	CGACT	CTCAAGATTTTTC		
MT757851	T dimidiata		G								
MT733872	T dimidiata	T	TG								
MT757849	T dimidiata	T	TG								
MT757850	T dimidiata	T	G			A					
MT556666	T dimidiata		TG								
MT556656	T dimidiata										
MT757848	T dimidiata										
MT733873	T dimidiata	T	TG								
MT556657	T dimidiata										
MT757852	T dimidiata	N	NN		N	N					
NC 050325	T huehuetenanguensis		CAG	G		C G T		TG T		C	
NC 050324	T mexicana	T		G							
MT556660	T phyllosoma	TT	AG								
NC 050327	T mazzottii	TT	AG								
MT556658	T longipennis	TT	AG								
MT556663	T recurva	TT	AG						T		
MT556661	T picturata	T	GG								
MT556659	M pallidipennis	TT	G								
NC 050329	T sanguisuga	T	GG		N		G		T	G C	
MT556662	T protracta	T		T		CA	C	T C	TCGG G A	A A T	A
MT556655	T barberi	T			A		CA	C	T C	GG G A	A G T
NC 050326	T lecticularia	A		G	T	C C C T	GC C	C	TC G T	GG G	T G
MT556654	D maximus	A		G		C CCG T	CA A	CA	TC	TCCGG G	T G
NC 042881	T migrans	GT	AG	T		T C G	T CC T GC CAGC	AT	TT TC A	T	AC A
MH934953	T rubrofasciata	TT	A	ATAT		A T C		CCTT C AGC	AT G T A AG T	A C A G C	
MT556664	T rubida	TT		G T		ATAGT	G G		CCT T C	G GT GAA G	C C
NC 042682	P rufotuberculatus	T	AG							G T A	C
MT561168	T infestans		A	G		T C G	AA	CTT G	A	T	A TC
KY640305	T infestans		A	G		T C G	AA	CTT G	A	T	A TC
MT556665	T vitticeps	T		T	G T	T CCT	G G	TA	A	ATC G	G C
T boliviana			AGG AATAC C		T T G	G	TA C	TG	CC CA A A	CC A	
BK013130	R pictipes	TT		G	G T	CT TCCGGCT	ACGC G	CGTGGC A	T CT TC G T	TGTC ACT	TTCTC G A
NC 043846	R pictipes	TT		G	G T	CT TCCGGCT	ACGC G	CGTGGC A	T CT TC G T	TGTC ACT	TTCTC G A
NC 050328	R prolixus	T	C			TC T	CT TCGG C	ACGC G	CGTGGC T	CT TCGG	CGTC ACT TTTAC G A

		110	120	130	140	150	160	170	180	190	200
AF301594	T dimidiata	C ATGAATAGTT	ATATTAGATATTAACATATTATTAATATTTTGTATAGTTAAACCATTACC	TATATAAATCTAGTTGCCGTATCTCATATA	ATA						
MT757851	T dimidiata	T									
MT733872	T dimidiata	T									
MT757849	T dimidiata	T									
MT757850	T dimidiata	T									
MT556666	T dimidiata	T									
MT556656	T dimidiata	T									
MT757848	T dimidiata	T									
MT733873	T dimidiata	T									
MT556657	T dimidiata	T									
MT757852	T dimidiata										
NC 050325	T huehuetenanguensis	AT							G	A T	
NC 050324	T mexicana	AT							C	G C	
MT556660	T phyllosoma	AT							T C	G CT	A
NC 050327	T mazzottii	AT							T C	G CT	A
MT556658	T longipennis	AT							T C	G CT	A
MT556663	T recurva	T							T C	G CT	A
MT556661	T picturata	AT							T		
MT556659	M pallidipennis	TT							G	A	
NC 050329	T sanguisuga	AT							TT C	G CT A	C
MT556662	T protracta	TT	T C		A	TA C	A G	TT C	T	TCG TAC	TTA G
MT556655	T barberi	TT	T C		G T C		A G	TT C	T	TCG C AT	TTA GG
NC 050326	T lecticularia	ATG	TG A		G T C		A G	TC C	T	TCG C G	TTA T GG
MT556654	D maximus	ATG	T T		G T C		A GA	TG C	C	CTCG CG	TACG T GG CG C
NC 042881	T migrans	A T A T A CCA		TA	T C		A A	T CTT	C	GA A	GA
MH934953	T rubrofasciata	A T ACT CCA	G	TG T AT C		AC	TA	T CGT	CG	A A A	GG T
MT556664	T rubida	A T A T T A G	C	G		CAC	G	TC	T	G C ATAG ATTA	T TC
NC 042682	P rufotuberculatus		TG TA C		TA T C		A	T C		GTC GA A ATT G T	CG T
MT561168	T infestans	AT	T T A CA		GG		A G		A	AC GC AA GA	TTAC GTC TACA
KY640305	T infestans	AT	T T A CA		GG		A G		A	AC GC AA GA	TTAC GTC TACA
MT556665	T vitticeps	AT	TG TA T A	C	C		AC GA	TC C TA	AC	AA GA A AACTCA TCATACA	
T boliviana		A T ACT	A AG		TA G TATAC		A G	TT CG A	AG	A A AAG	TAGTAT
BK013130	R pictipes	AT	T G TAGG	A TG	TAC		AC G	TG AT A G	AT	C AT A G GG	CG
NC 043846	R pictipes	AT	T G TAGG	A TG	TAC		AC G	TG AT A G	AT	C AT A G GG	CG
NC 050328	R prolixus	AT	T G TGGG	A TG	TAC		AC G	TG AT TA A	GAT	C	G G C

		210	220	230	240	250	260	270	280	290	300
AF301594	T dimidiata	CAACT ACCATCTCGATATA GTTAGAATTAAAGTTTCAGATGTCATT	CCCTC	ATTCTACT	CAACGTAGAAATGACGT	CTGGCT	TTGCCG				
MT757851	T dimidiata										
MT733872	T dimidiata										
MT757849	T dimidiata										
MT757850	T dimidiata										
MT556666	T dimidiata										
MT556656	T dimidiata										
MT757848	T dimidiata										
MT733873	T dimidiata										
MT556657	T dimidiata										
MT757852	T dimidiata										
NC 050325	T huehuetenanguensis			A		T C	T		TC	T G	
NC 050324	T mexicana									GT	
MT556660	T phyllosoma	T									
NC 050327	T mazzottii	T									
MT556658	T longipennis	T									
MT556663	T recurva	T									
MT556661	T picturata	T									
MT556659	M pallidipennis										
NC 050329	T sanguisuga										
MT556662	T protracta										
MT556655	T barberi	T									
NC 050326	T lecticularia										
MT556654	D maximus										
NC 042881	T migrans	G A G G	A	TACGA C	C	AG	C A CA CG	T		C AACC	A G
MH934953	T rubrofasciata	G AC T	G C A A	CAACA	G	A	ACA CA AG			C	CCAG AC G
MT556664	T rubida	T T G T	G T A	G C		G ATC A C	T			T T A	GA A
NC 042682	P rufotuberculatus										
MT561168	T infestans										
KY640305	T infestans										
MT556665	T vitticeps										
T boliviana		G TC T		G G A		G	A A CC A	CG	T		
BK013130	R pictipes	TTCA TT	AC A A A	CTT	CG		A TGA	T ATA	TATATGC		T G
NC 043846	R pictipes	TTCA TT	AC A A A	CTT	C T G		A TGA	T ATA	TATATG		TTG

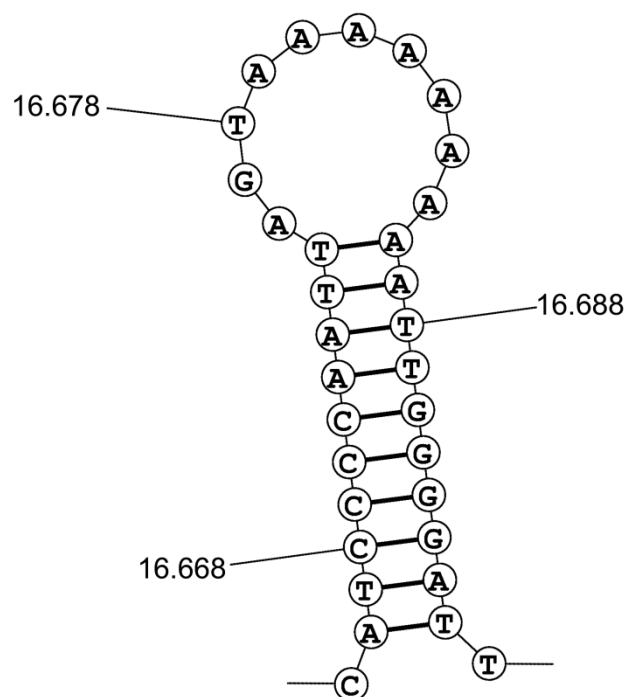


Figure S5. Stem-loop structure on last part of the control region. Some nucleotide positions are indicated.