

Table S1. Gene order, gene position, intergenic regions, gene overlap and DNA transcription direction strand in the mitochondrial genome of *Nothoaspis amazoniensis*.

Genes	Gene position and intergenic regions*		Gene size and intergenic regions (pb)	Strand direction
//* tRNA-Met	1	61 ^b	61	Positive
NAD2	32 ^b	1021	990	Positive
tRNA-Trp	1020	1082 ^b	63	Positive
tRNA-Cys	1075 ^b	1135	61	Negative
tRNA-Cys / tRNA-Tyr ^a	1136 ^a	1137 ^a	2	-
tRNA-Tyr	1138	1199 ^b	62	Negative
COX1	1192 ^b	2730	1539	Positive
COX1 / COX2 ^a	2731 ^a	2733 ^a	3	-
COX2	2734	3483 ^b	750	Positive
tRNA-Lys	3410 ^b	3475 ^b	66	Positive
tRNA-Asp	3474 ^b	3533	60	Positive
tRNA-Asp / ATP8 ^a	3534 ^a	3551 ^a	18	-
ATP8	3552	3689 ^b	138	Positive
ATP6	3683 ^b	4351 ^b	669	Positive
COX3	4303 ^b	5130 ^b	828	Positive
tRNA-Gly	5130 ^b	5189 ^b	60	Positive
NAD3	5187 ^b	5525	339	Positive
tRNA-Ala	5526	5587 ^b	62	Positive
tRNA-Arg	5587 ^b	5644	58	Positive
tRNA-Asn	5645	5706 ^b	62	Positive
tRNA-Ser	5704 ^b	5754	51	Positive
tRNA-Glu	5755	5815 ^b	61	Positive
tRNA-Phe	5814 ^b	5874	61	Negative
NAD5	5875	7537 ^b	1663	Negative
tRNA-His	7535 ^b	7594 ^b	60	Negative
NAD4	7593 ^b	8909 ^b	1317	Negative
NAD4L	8903 ^b	9181	279	Negative
NAD4L / tRNA-Thr ^a	9182 ^a	9188 ^a	7	-
tRNA-Thr	9189	9247	59	Positive
tRNA-Pro	9248	9308	61	Negative
tRNA-Pro / NAD6 ^a	9309 ^a	9336 ^a	28	-
NAD6	9337	9756 ^b	420	Positive
CYB	9756 ^b	10859	1104	Positive
CYB / tRNA-Ser ^a	10860 ^a	10861 ^a	2	-

tRNA-Ser	10862	10924 ^b	63	Positive
NAD1	10872 ^b	11849 ^b	978	Negative
tRNA-Leu	11847 ^b	11906	60	Negative
tRNA-Leu / tRNA-Leu ^a	11907 ^a	11910 ^a	4	-
tRNA-Leu	11911	11975 ^b	65	Negative
16S rRNA	11975 ^b	13195	1221	Negative
tRNA-Val	13196	13258	63	Negative
12S rRNA	13259	13949	691	Negative
12S rRNA / tRNA-Ile ^a (CR)	13950 ^a	14290 ^a	341	-
tRNA-Ile	14291	14353 ^b	63	Positive
tRNA-Gln //*	14351 ^b	14416	66	Negative

^a Intergenic regions; ^b Gene overlapping; Control Region (CR); //*: Circular link.

Table S2. Cleavage sites for restriction enzymes in the mitogenome of *Nothoaspis amazoniensis*.

Cleavage sites	Position of the cleavage between bases	Type of cleavage	Gene/Intergenic Interval
EcoRV	4592-4593	B	COX3
EcoRV	5381- 5382	B	NAD3
XbaI	8385-8386 / 8389-8390	A	NAD4
BglIII	9255-9256 / 9259-9260	A	tRNA-Pro
XhoI	10048-10049 / 10052-10053	A	CYB
BglIII	10433-10434 / 10437-10438	A	CYB
HindIII	11515-11516 / 11519-11520	A	NAD1
EcoRI	11855-11856 / 11859-11860	A	tRNA-Leu
HindIII	11871-11872 / 11875-11876	A	tRNA-Leu
EcoRV	11921-11922	B	tRNA-Leu
HindIII	12825-12826 / 12829-12830	A	16S rRNA
EcoRV	12915-12916	B	16S rRNA
HindIII	13821-13822 / 13825-13826	A	12S rRNA
BglIII	14051-14052 / 14055-14056	A	12S rRNA / tRNA-Ile (CR)

A: symmetrically located around the axis of symmetry; B: in the axis of symmetry; CR: Control Region.

Table S3. Gene overlaps for the mitogenome of *Nothoaspis amazoniensis*.

Genes	Overlapping passages	bp
tRNA-Met / NAD2	32-61	30
NAD2 / tRNA-Trp	1020-1021	2
tRNA-Trp / tRNA-Cys	1075-1082	8
tRNA-Tyr / COX1	1192-1199	8
COX2 / tRNA-Lys	3410-3475	66
tRNA-Lys / tRNA-Asp	3474-3475	2

COX2 / tRNA-Asp	3474-3483	10
ATP8 / ATP6	3683-3689	7
ATP6 / COX3	4303-4351	49
COX3 / tRNA-Gly	5130	1
tRNA-Gly/ND3	5187-5189	3
tRNA-Ala / tRNA-Arg	5587	1
tRNA-Asn / tRNA-Ser	5704-5706	3
tRNA-Glu / tRNA-Phe	5814-5815	2
NAD5 / tRNA-His	7535-7537	3
tRNA-His / NAD4	7593-7594	2
NAD4 / NAD4L	8903-8909	7
NAD6 / CYB	9756	1
tRNA-Ser / NAD1	10872-10924	53
NAD1 / tRNA-Leu	11847-11849	3
tRNA-Leu / 16S rRNA	11975	1
tRNA-Ile / tRNA-Gln	14351-14353	3

Table S4. Non-coding intergenic regions in the mitogenome of *Nothoaspis amazoniensis*.

Genes	Intergenic regions intervals	bp
tRNA-Cys / tRNA-Tyr	1136-1137	2
COX1 / COX2	2731-2733	3
tRNA-Asp / ATP8	3534-3551	18
NAD4L / tRNA-Thr	9182-9188	7
tRNA-Pro / ND6	9309-9336	28
CYB / tRNA-Ser	10860-10861	2
tRNA-Leu / tRNA-Leu	11907-11910	4
12S rRNA / tRNA-Ile ^(CR)	13950-14290	341

CR: Control Region.

Table S5. Distance matrices and identity of the complete mitogenome of tick belonging to Argasidae family.

p-distance matrix		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
Family Argasidae	Subfamily Ornithodorinae	1 <i>Nothoaspis amazoniensis</i>																	
		2 <i>Antricola mexicanus</i>	0,229																
		3 <i>Carios faini</i>	0,231	0,219															
		4 <i>Carios capensis</i>	0,240	0,233	0,227														
		5 <i>Ornithodoros brasiliensis</i>	0,266	0,262	0,265	0,261													
		6 <i>Ornithodoros rostratus</i>	0,266	0,263	0,261	0,257	0,225												
		7 <i>Otobius megnini</i>	0,276	0,267	0,270	0,278	0,269	0,261											
		8 <i>Ornithodoros savignyi</i>	0,288	0,291	0,295	0,296	0,268	0,274	0,293										
		9 <i>Ornithodoros moubata</i>	0,289	0,284	0,281	0,282	0,269	0,270	0,278	0,223									
		1 <i>Ornithodoros porcinus</i>	0,290	0,283	0,283	0,281	0,266	0,269	0,282	0,227	0,172								
	Subfamily Argasinae	1 <i>Ornithodoros costalis</i>	0,290	0,288	0,280	0,284	0,271	0,275	0,279	0,299	0,288	0,293							
		1 <i>Ornithodoros compactus</i>	0,291	0,288	0,282	0,285	0,270	0,271	0,279	0,223	0,035	0,171	0,287						
		1 <i>Argas striatus</i>	0,294	0,291	0,289	0,295	0,295	0,287	0,290	0,321	0,297	0,302	0,298	0,300					
		3 <i>Argas walkerae</i>	0,302	0,300	0,296	0,300	0,294	0,292	0,292	0,316	0,306	0,308	0,298	0,306	0,251				
	Subfamily Argasinae	1 <i>Argas sp. SpringbokSA-QMS95171</i>	0,303	0,301	0,296	0,306	0,305	0,297	0,293	0,320	0,314	0,310	0,304	0,314	0,256	0,236			
		5 <i>Argas miniatus</i>	0,305	0,301	0,294	0,302	0,298	0,291	0,296	0,322	0,310	0,307	0,302	0,310	0,253	0,160	0,235		
		6 <i>Argas lagenoplastis</i>	0,308	0,306	0,299	0,309	0,303	0,296	0,299	0,319	0,309	0,316	0,304	0,308	0,255	0,229	0,232	0,231	
		7 <i>Argas</i>	0,309	0,304	0,303	0,307	0,304	0,299	0,295	0,319	0,313	0,312	0,304	0,313	0,255	0,234	0,133	0,238	0,233

[illegible]

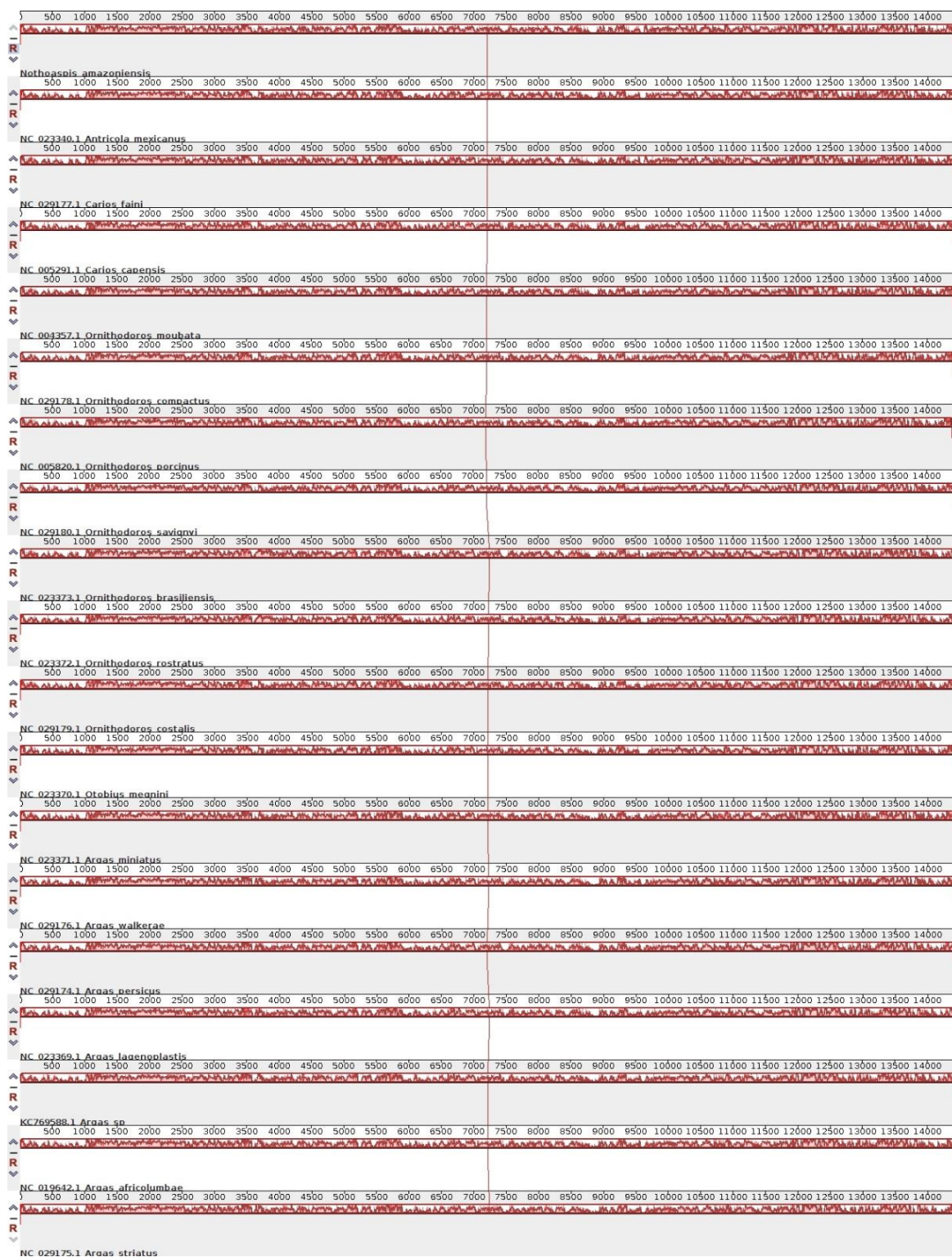


Figure S1. Comparative and organizational alignment of complete mitochondrial genomes of the Argasidae family. Red connects conserved blocks.