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A novel fragmented mitochondrial genome in the protist pathogen *Toxoplasma gondii* and related tissue coccidia

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Mitochondrial genome content and structure vary widely across the eukaryotic tree of life, with protists displaying extreme examples. Apicomplexan and dinoflagellate protists have evolved highly reduced mitochondrial genome sequences, mtDNA, consisting of only three cytochrome genes and fragmented rRNA genes. Here, we report the independent evolution of fragmented cytochrome genes in *Toxoplasma* and related tissue coccidia and evolution of a novel genome architecture consisting minimally of 21 sequence blocks (SBs) totaling 5.9 kb that exist as nonrandom concatemers. Single-molecule Nanopore reads consisting entirely of SBs ranging from 0.1 to 23.6 kb reveal both whole and fragmented cytochrome genes. Full-length cytochrome transcripts including a divergent *coxIII* are detected. The topology of the mitochondrial genome remains an enigma. Analysis of a *cob* point mutation reveals that homoplasmy of SBs is maintained. Tissue coccidia are important pathogens of man and animals, and the mitochondrion represents an important therapeutic target. The mtDNA sequence has been elucidated, but a definitive genome architecture remains elusive.

[Supplemental material is available for this article.]

Mitochondria are notable for their incredible diversity in genome content and genome topology (Burger et al. 2003; Flegontov and Lukes 2012; Kolesnikov and Gerasimov 2012). The endosymbiont genome sequence that gave rise to the mitochondrial genome sequence, mtDNA, was likely circular, characteristic of its prokaryotic origins (Lang et al. 1997). However, increasing bodies of literature indicate that this structure is not universal and that considerable evolution of both genome structure and gene content has occurred in eukaryotes (Burger et al. 2003; Gissi et al. 2008). At the time of its discovery, the mtDNA of the apicomplexan *Plasmodium falciparum* was the smallest mtDNA known, at 5967 bp, and among the most unusual with only three protein-encoding genes (cytochrome oxidase subunit I, *coxI*; cytochrome oxidase subunit III, *coxIII*; and cytochrome b, *cob*) and fragmented rRNA genes with many rRNA portions missing (Vaidya and Arasu 1987; Feagin 1992; Feagin et al. 1997, 2012; Wilson and Williamson 1997). At the other end of the size spectrum, the mtDNA of angiosperms ranges from 200 kb to 11 Mb in size and shows a huge variation in structure, content, gene/DNA transfers, and processes such as RNA editing (Gualberto and Newton 2017). Mitochondrial genomes consisting of multiple divergent circular molecules have been noted in the fungus *Spizellomyces* (Burger and Lang 2003), *Columbicola* feather lice (Sweet et al. 2020), and certain cnidarian parasites (Yahalomi et al. 2017). Among the protists, the kinetoplastid mtDNA (called kDNA) consists of multiple gene-encoding

maxicircles and guide RNA encoding minicircles that form a tight physical network, the kinetoplast (Morris et al. 2001). The mtDNA of the symbiotic protist *Amoebidium parasiticum* is comprised of hundreds of distinct linear molecules with a common pattern of terminal repeats (Burger et al. 2003).

The alveolates have their own noncanonical mtDNA sequences and structures (Flegontov and Lukes 2012). The ciliates contain a 47-kb linear mtDNA flanked by telomere-like repeats with a number of ciliate-specific open reading frames (ORFs) of unknown function (Slamovits et al. 2007; Nash et al. 2008; Waller and Jackson 2009; Flegontov and Lukes 2012). The mtDNA of dinoflagellates (sister group to the Apicomplexa) share the reduced gene content and fragmented rRNA genes with the Apicomplexa, but their protein-encoding genes are highly fragmented, highly repetitive, contain multiple nonidentical mtDNA molecules, utilize noncanonical start codons, and have evolved *trans*-splicing and RNA editing (Slamovits et al. 2007; Nash et al. 2008; Waller and Jackson 2009; Flegontov and Lukes 2012).

Whereas all sequenced apicomplexan mtDNAs contain only three protein-coding genes (*coxI*, *coxIII*, and *cob*) and show a high level of rRNA gene fragmentation like the dinoflagellates, the orientation and arrangement of these genes vary across the phylum, as does the genome architecture (Creasey et al. 1993; Hikosaka et al. 2010, 2011, 2012, 2013). The *Theileria* mtDNA is a 7.1-kb linear monomer with telomere-like termini (Kairo et al. 1994). Members of the genus *Babesia* have linear mtDNA monomers with a dual flip-flop inversion system that results in four different sequences

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that are present in equal ratios in the mitochondrion (Hikosaka et al. 2011). The coccidian *Eimeria*, the species closest to *Toxoplasma gondii* with a published mtDNA sequence and structure, is detected as a linear concatenation of a repeating 6.2-kb sequence similar to that of *Plasmodium*, albeit with the genes in a different order.

The mitochondrial genome of the coccidian protist pathogen *Toxoplasma gondii* has been enigmatic and elusive. *Toxoplasma gondii* is an incredibly successful zoonotic generalist pathogen which infects 30%–50% of the human population (Flegr et al. 2014) but primarily causes illness in the immunocompromised, or fetuses as a result of transplacental infections (Montoya and Liesenfeld 2004; Dubey 2010). Attempts to assemble the mitochondrial genome from the various organismal genome projects failed, and efforts to isolate the single mitochondrion organelle and identify the complete mtDNA sequence and structure have faced numerous challenges. Attempts to elucidate the mtDNA sequence using sequenced-based approaches, hybridization probes, PCR amplification, or assembly from Sanger or second-generation short-read genome sequence projects were unsuccessful (Minot et al. 2012; Lau et al. 2016; Lorenzi et al. 2016), presumably due to the large number of nuclear-encoded sequence fragments of mitochondrial origin (NUMTs) present in the nuclear genome. NUMTs are insertions of fragments of mtDNA at the location of a nuclear double-strand DNA break (Minot et al. 2012; Lau et al. 2016; Lorenzi et al. 2016). NUMT sequences (which display a range of degeneration relative to organellar mtDNA because they decay with evolutionary time following insertion) can cross-hybridize and interfere with signals from molecular-based mtDNA isolation and amplification methods. NUMTs also interfere with assembly algorithms for short-read sequences (Sanger and Illumina) that were used to generate the numerous existing *Toxoplasma* genome sequences (Minot et al. 2012; Lau et al. 2016; Lorenzi et al. 2016). Physical attempts to isolate the mitochondrion have also failed thus far (Nishi et al. 2008), but mitochondrial-enriched fractions are obtainable (Miranda et al. 2010).

Despite the community's inability to isolate and determine a mitochondrial genome sequence for this important pathogen, multiple lines of evidence suggest that the *T. gondii* mitochondrion is functional, including cDNAs for *cob* and *coxI*. Mitochondrial membrane-potential markers indicate that the mitochondrion is active (Tanabe 1985; Melo et al. 2000; Weiss and Kim 2007); a complete set of tRNAs are imported into the *T. gondii* mitochondrion (Esseiva et al. 2004); the mitochondrial protein *cob* has been proven as an excellent drug target (Vaidya et al. 1993); mutations in *cob* were found to be associated with atovaquone (McFadden et al. 2000) and endochin-like quinolone (ELQ-316) (Alday et al. 2017) drug resistance; and NUMTs identified in the current *T. gondii* ME49 nuclear genome sequence, even if combined together, cannot functionally encode any of the cytochrome genes in their entirety—thus, they must be encoded in the mitochondrion (Namasivayam 2015). Here, we employ Sanger, Illumina, and single-molecule Oxford Nanopore sequencing technology (ONT) of DNA and RNA together with molecular and bioinformatics strategies to identify the sequence and structure of the *T. gondii* mtDNA.

Results

21 discrete sequence blocks constitute the minimal *Toxoplasma gondii* mitochondrial genome

The *T. gondii* ME49 genome sequence project yielded numerous contigs containing portions of, or in some cases, complete cyto-

chrome genes and mtDNA rRNA gene fragments (Gajria et al. 2008; Lorenzi et al. 2016). These contigs did not assemble into a single mtDNA sequence. However, the sequence information contained in these contigs as well as individual unassembled *T. gondii* genomic and EST reads (Sanger chemistry) that matched mtDNA from related species, served as a template for PCR primer design that carefully avoided NUMTs (Supplemental Table S1). Mitochondria-enriched cell fractions were used as template. The PCR results were puzzling. No amplicon was larger than ~3.5 kb. Primer pairs often generated multiple amplicons that, when sequenced and annotated, revealed a high level of sequence identity to each other in some regions (sequence blocks, SBs) but differed in others (Fig. 1A, B, lanes 6–11; Supplemental Fig. S1; Supplemental Data S1). PCR reactions with only a single primer also generated multiple amplicons (Fig. 1C). With difficulty, we did identify primers that avoided NUMTs and would amplify small regions (100–350 bp) within *coxI*, *coxIII*, and *cob* (Fig. 1B, lanes 2–4; Hikosaka et al. 2013).

As PCR is capable of amplifying rare artifacts or a NUMT capable of annealing to the primers, we abandoned approaches that relied on amplification or sequence assembly and examined individual genomic and EST Sanger sequence reads in the NCBI GenBank (<https://www.ncbi.nlm.nih.gov/genbank/>; Benson et al. 2018) to identify putative mtDNA or mitochondrial cDNA. Like the PCR amplicons, identified mtDNA reads and transcripts could be annotated with discrete, reproducible, sequence blocks with similarity to various regions of known apicomplexan mtDNA (Fig. 1D–E; Supplemental Figs. S2, S3). In total, 21 mtDNA SBs that reproducibly share 100% sequence identity were identified. The 21 SBs were named from A to V (Fig. 2; Table 1; Supplemental Data S2). Three SBs (F, K, and M) were observed to also exist in precise, reproducible, truncated forms, indicated with a “p” for partial, for example, Fp (Table 1). Fifteen of the 21 SBs share significant similarity to regions of *Eimeria tenella* and/or *Plasmodium falciparum* mtDNA sequences (Supplemental Table S2). The SBs range from 40 to 1050 bp, and none encodes a cytochrome or rRNA gene in its entirety (Fig. 2). Following SB identification, annotation of the short-read data sets (PCR, Sanger genomic, EST) revealed that reads contained one or more SBs, one directly after the other, with no intervening sequence, in distinct, nonrandom permutations (Fig. 1). No full-length cytochrome genes were observed, but many fragments of cytochrome genes were annotated in a variety of contexts and orientations. Some SBs were always observed in specific combinations with other blocks. For example, we found block E to always occur between blocks J and A. However, these blocks could not be assembled into a larger (JEA) SB because J and A each occur in other contexts, such as LJQ and NAP.

All SBs including the partial forms of F, K, and M when not located at the beginning or end of a read have the same length and sequence irrespective of the blocks they are flanked by, whether they appear in a PCR product, genomic, or EST sequence read. A full-length block C was not found in the Sanger genomic or EST reads nor in the PCR products, perhaps due to its large size, but it was observed in ONT data described below (Fig. 1F). Exhaustive searches of Sanger and second-generation sequence read data repeatedly identified only the 21 SBs. Occasionally, examination of a read revealed the presence of nuclear sequence, indicating the detected SB(s) was the result of a recent intracellular mtDNA transfer, that is, a NUMT (Ossorio et al. 1991; Lopez et al. 1994; Namasivayam 2015). A NUMT, unlike a SB, can be derived from any mtDNA region and the boundaries of a NUMT usually do not match the boundaries of the identified SBs. NUMTs are usually degenerate relative to mtDNA as a result of evolutionary

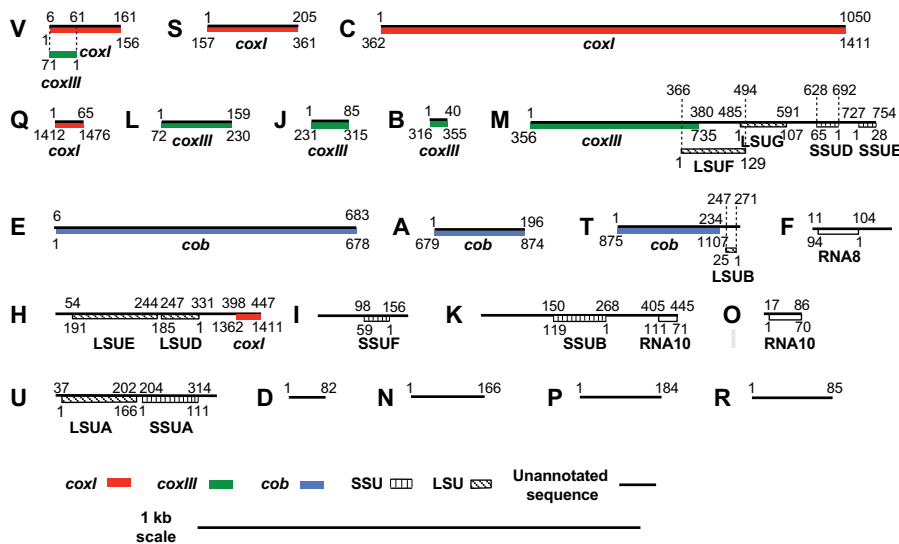


Figure 2. The 21 minimal *T. gondii* mtDNA sequence blocks. The DNA sequence is represented by a black line, drawn to scale and named with 21 alphabet characters, A to V (there is no “G”). The coordinates of an SB that encodes a cytochrome or rRNA gene fragment are indicated above the black line and the corresponding coordinates of the assembled gene or rRNA fragment are indicated below the gene fragment; the fragments are colored as defined in the key. Portions of sequence block V contribute to both *coxI* and *coxIII* but in different orientations.

RNA genes observed in other apicomplexans (Feagin et al. 2012) have not been identified (Fig. 2). Overall, 3333 bp of the SBs are annotated as protein-encoding and 1290 bp are annotated as rDNA. Searches for additional RNA or protein features on each SB and the longest *T. gondii* ME49 ONT read did not reveal any new features.

Full-length cytochrome genes are detected in the ONT reads from both *T. gondii* ME49 and RH (Figs. 1F, 6; Supplemental Fig. S6), and each gene is well supported by Illumina read data (Fig. 3). The encoded *T. gondii* mtDNA cytochrome proteins are comparable in length and sequence to other apicomplexan cytochrome genes, but there is some doubt about the exact beginning of the *cob* open reading frame, as two potential starts are possible, one 9 aa longer than the other. COXI and COB are well conserved, but COXIII is less well conserved. As was observed in the dinoflagellates, *coxI* does not have an ATG start codon. All genes have stop codons. Each sequence begins with a methionine (using mitochondrial translation tables) and ends with a canonical stop codon (Supplemental Fig. S7; Supplemental Data S4). There are no spliceosomal introns located in the full-length CDSs and no indication that RNA editing is required to produce the CDSs.

Cytochrome b is well studied in *T. gondii* (Hikosaka et al. 2011). A partial *coxI* transcript has been reported, but a convincing *coxIII* has not. Using RT-PCR, we were able to generate a nearly full-length *cob* and *coxIII* and a partial *coxI* (Fig. 3; Supplemental Data S5). Full-length sequences for all three cytochrome genes can be assembled from Sanger ESTs as well as Illumina RNA-seq data (Fig. 3; Supplemental Table S4). The RNA-seq evidence is less strong, but we note that poly(A)⁺ RNA was purified for these libraries. *T. gondii* PRU RNA sequence data from ONT (kindly provided by Stuart Ralph), once corrected, revealed a few reads capable of encoding full-length cytochrome transcripts for all three genes (some missing a few bp at read ends) (Fig. 3). The mtDNA transcripts are short ~2.8 kb. Of the 30 longest error-corrected RNA ONT molecules that consisted of

only mtDNA, three reads were capable of encoding *cob*, seven *coxI*, and two *coxIII* (Supplemental Table S5; Supplemental Data S6).

Based on only seven full-length *coxI* ONT transcripts, we observe that all begin at the start of the gene and appear to only encode *coxI* (VSCQ) or *coxI* plus SB J (VSCQJ), whereas the other transcripts encode numerous SBs in addition to the cytochrome CDS. The *coxI* transcripts that are not followed by a nearly full block J are polyadenylated, but the pattern is unusual. An additional 12 nucleotides of sequence, specifically the last 12 nucleotides of sequence block J in the reverse orientation (5'-CACAAATA GAACT), are present following the *coxI* TAA stop codon. These 12 nucleotides are followed by a poly(A) stretch of variable length, suggesting that sequences present in J may serve as a degenerate poly(A) signal because sequence block J contains sequence similar to the canonical AAUAAA poly(A) signal. The remainder of sequence block J is capable of forming a prominent but imperfect

Table 1. Characterization and conservation of the 21 mtDNA sequence blocks in *T. gondii*, *N. caninum*, and *Hammondia*

Block	Block length	100% identity NUMT in nuclear genome?	<i>T. gondii</i> ME49		<i>N. caninum</i> LIV		<i>Hammondia</i>	
			Match to <i>T. gondii</i> block	Match to <i>T. gondii</i> block	Start	Stop	Start	Stop
A	196	N	1	196	1	196	1	196
B	40	Y	1	40	1	40	1	40
C	1050	N	1	1050	1	1050	1	1050
D	82	N	1	82	2	82	2	82
E	683	N	1	683	1	683	1	683
F ^a	179	Y	1	179	1	179	1	179
H	447	N	1	447	1	438	1	438
I	204	N	1	204	1	204	1	204
J	85	Y	1	85	1	85	1	85
K ^a	445	N	1	445	1	445	1	445
L	159	Y	1	159	1	159	1	159
M ^a	754	N	1	754	104	560	104	560
N	166	N	1	166	1	166	1	166
O	86	Y	1	86	1	86	1	86
P	184	N	1	184	1	184	1	184
Q	65	Y	1	65	1	65	1	65
R	85	Y	1	85	1	85	1	85
S ^b	205	Y	1	205	1	205	1	205
T	279	N	1	278	1	276	1	276
U	354	N	1	354	26	354	26	354
V	161	Y	1	161	1	161	1	161

^aBlocks F, K, and M also occur in partial forms; Fp (89–179), Kp (1–112), and Mp (1–104), in *T. gondii* and *N. caninum*. Occurrence of partial forms in *Hammondia* is unknown.

^bBlock S occurs as a partial form in *N. caninum*, S (1–52).

Block background colors indicate SBs that contribute to: *cob* = blues; *coxI* = reds; *coxIII* = greens; grays encode rRNAs; yellows have no annotated features.

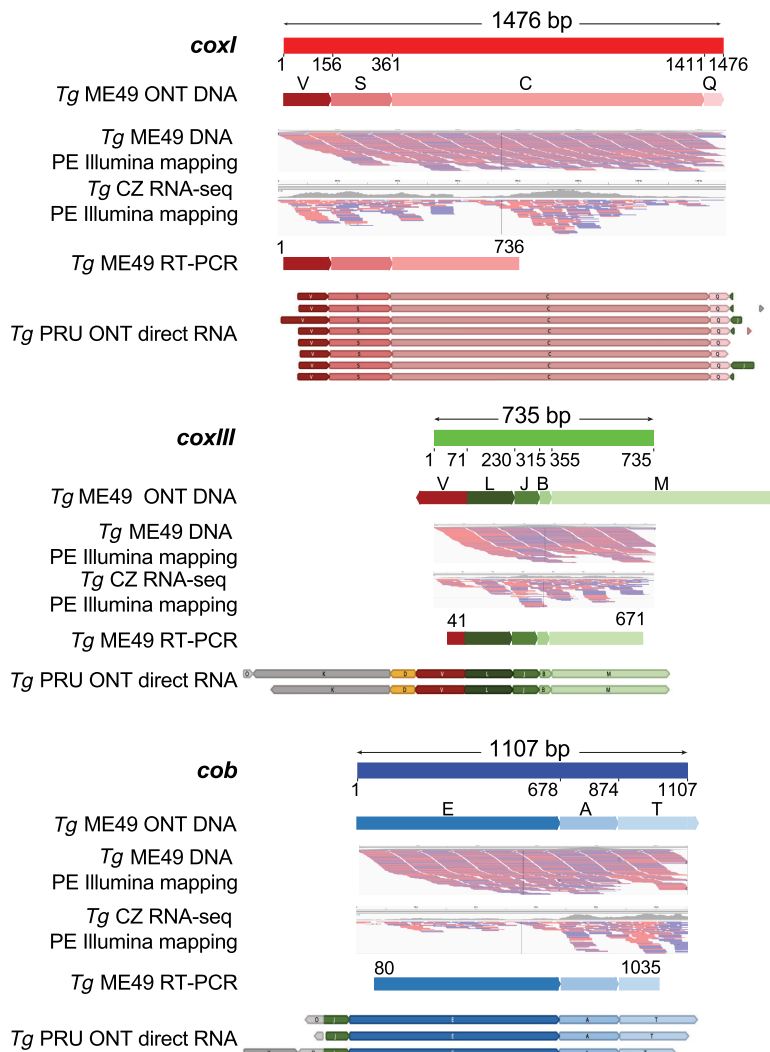


Figure 3. Full-length protein-encoding genes and their expression in the *T. gondii* mt genome are supported. Segments of an ONT read that can encode a full-length cytochrome gene are annotated with their SB name and shown *below* the schematic of each gene. Numbers *below* each gene schematic represent nucleotide start/stop positions of a SB on the gene. All blocks are in the forward orientation except block V in *coxIII*. Only a portion of SBs V, M, and T is included in the CDS. MtDNA-specific PE-150 Illumina DNA (SRR9200762) and RNA-seq (SRR6493545) reads were independently mapped to each of the cytochrome gene sequences. Red and blue lines *below* each gene indicate mapped Illumina paired-ends. Both ends were required to map. RT-PCR products and ONT RNA reads with full-length CDSs are shown.

stem-loop (Supplemental Fig. S8), but the rest of the SBs do not appear to contain long runs of obvious hairpin structures, as evidenced by the dot plots (Fig. 4). There is no evidence of polyadenylation of any other transcripts based on the few available sequences (Supplemental Table S5).

Homoplasmy of sequence is maintained

Comparative analyses of the multiple copies of the 21 SBs revealed that all internally located SBs, that is, blocks not at the end of a sequence read (where incomplete blocks are often present), are identical in sequence, barring a few SBs that contain small aberrations characteristic of rearrangement artifacts (Supplemental Tables S5, S6). To assess homoplasmy in the context of this unusual fragmented and redundant genome architecture, a *T. gondii* RH N-ethyl-N-

nitrosourea (ENU) *cob* mutant named ELQ-316 (Alday et al. 2017) was sequenced with Oxford Nanopore technology (Supplemental Table S3). This strain has a point mutation in SB “E” which encodes a Thr222→Pro substitution. SB “E” is only found flanked by SBs “J” and “A” arranged as (JEA) (Table 2). If homoplasmy exists, we expect this mutation to be present in all copies of SB “E.” To avoid bias, only uncorrected Nanopore reads from an early passage of this mutant were analyzed. Seven hundred seventy-nine mtDNA reads were identified (Supplemental Table S3). Of the 138 SB “E” identified in these reads that contained the mutated region, 132 contained the point mutation (Supplemental Fig. S9), indicating homoplasmy is maintained. The six blocks that did not show the mutation are well within the ~5% error rate of ONT.

mtDNA sequence blocks are evolutionarily conserved in the Toxoplasmatinae but not *Eimeria*

We analyzed available genomic and transcriptomic data for the closely related *Neospora caninum*. All 21 mtDNA SBs are highly conserved between the two species in sequence and length (Table 1; Supplemental Table S2; Supplemental Data S7). However, *N. caninum* does contain an additional partial SB, block Sp, relative to *T. gondii*. Analysis of *N. caninum* Sanger genomic and EST reads using the 21 *N. caninum* SBs revealed the presence of nonrandom arrangements similar to those identified in *T. gondii* (Supplemental Figs. S2, S3). We generated low-coverage ONT genome data for *N. caninum* strain Nc-1. mtDNA reads of 0.374–15.6 kb, some of which are capable of encoding cytochromes, were detected (Supplemental Fig. S10; Supplemental Table S3; Supplemental Data S8). *N. caninum*

ESTs encoding mtDNA SBs, which if assembled could encode each of the cytochromes, were also detected (Supplemental Table S4; Supplemental Data S9).

Examination of available sequences from another closely related Toxoplasmatinae, *Hammondia* (Walzer et al. 2013), also revealed the presence of all 21 mtDNA SBs. The ends of a few blocks could not be detected likely due to the sparsity of data available for this species (Table 1; Supplemental Table S2). However, we were not able to conclusively determine the nature of the mtDNA in the more distantly related *Sarcocystis neurona*, a member of the Toxoplasmatinae separated by ~250 million years (Su et al. 2003). We identified hits to a number of the 21 mtDNA SBs, but the block boundaries were rarely conserved (Supplemental Table S2) and we were unable to detect similar permutation patterns. An examination of the more distant coccidian *E. tenella* (Su et al.

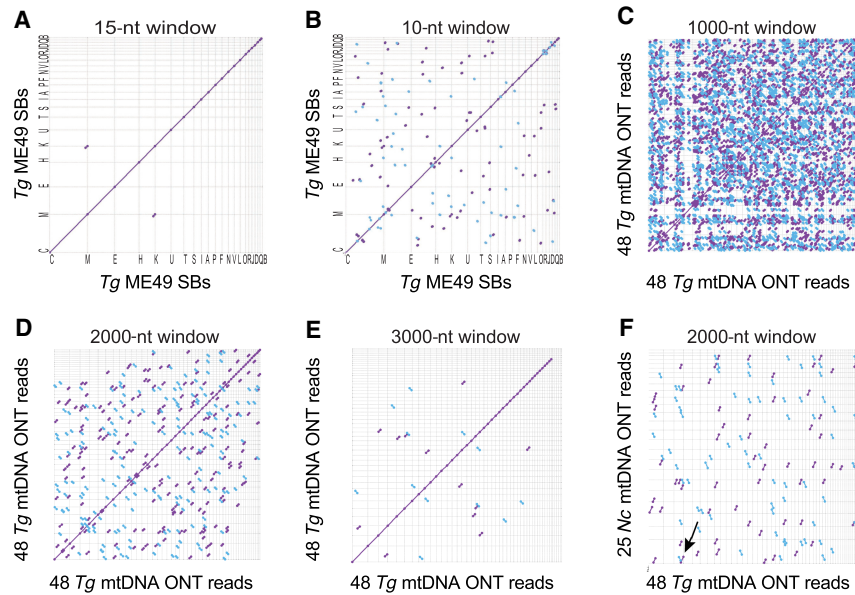


Figure 4. Dot plot comparisons of long *T. gondii* ME49 mtDNA SBs and ONT reads against themselves and *N. caninum* Nc-1. (A,B) *T. gondii* SBs (5909 nt) compared to themselves at differing window sizes; (C–E) 48 mtDNA-specific *T. gondii* ONT reads (313,102 nt) (Supplemental Methods; Supplemental Fig. S4; Supplemental Data S3) compared to themselves at differing window sizes; (F) 25 *N. caninum* ONT mtDNA reads (141,161 nt) (Supplemental Methods; Supplemental Fig. S10; Supplemental Data S8) compared to the same 48 mtDNA-specific *T. gondii* ONT reads and visualized as a dot plot (see also Supplemental Fig. S11). Matches in the forward and reverse orientation are indicated as purple and blue lines, respectively. Sequences were sorted, from longest to shortest. Window size is indicated above each panel. The arrow in F points to the only match observed to be longer than 3000 bp. The names of the sequences located on each axis are located in the Supplemental Methods.

2003) (~500 million years of divergence), for which a published mtDNA genome sequence exists (Hikosaka et al. 2011), did not reveal fragmented blocks as are observed in *T. gondii* (Supplemental Table S2). Examination of the *S. neurona* sequences using the assembled mtDNA and annotated genes of *E. tenella* does not strongly support an *E. tenella*-like mtDNA either. Together, the findings suggest that the unusual nature of the mtDNA is a derived state shared among the closest relatives of *T. gondii*.

The order, orientation, and number of the 2l sequence blocks are highly variable but not random

To detect regions of sequence identity within the SBs, dot plot analyses of the reads aligned against each other were performed. In a dot plot analysis, if identical sequence is observed between the sequences on each axis, a diagonal line is drawn with coordinates that span the alignment, using two different colors to indicate the orientation of the match. A dot plot of the SBs against themselves revealed that they are nonredundant except for the last 50 bp of SBs C and H,

Table 2. Lexicon of triplet block orders in *T. gondii* and *N. caninum* mtDNA

Sequence block	Detected orders	TgME49	Nc Nc-1	Sequence block	Detected orders	TgME49	Nc Nc-1	
A	E-A-T	Y	Y	Kp	D-Kp-U	Y	Y	
	E-A-P	Y	Y		I-Kp-U	Y	Y	
	N-A-P	Y	Y ^a		V-L-J	Y	Y	
	N-A-T	Y	Y		B-M-F	Y	Y	
B	J-B-M	Y	Y	M	B-M-Fp	Y	Y	
	J-B-Mp	Y	Y		B-Mp-U	Y	Y	
C	S-C-Q	Y	Y	Mp	Fp-N-A	Y	Y	
	V-D-K	Y	ND		O	J-O-F	Y	Y
D	V-D-Kp	Y	ND	P	J-O-K	Y	Y	
	Sp-D-K	ND	Y		A-P-H	Y	Y	
	Sp-D-Kp	ND	Y		A-P-I	Y	Y	
E	J-E-A	Y	Y	Q	C-Q-J	Y	Y	
	O-F-M	Y	Y		H-Q-J	Y	Y	
F	O-F-R	Y	Y	R	F-R-S	Y	Y ^b	
	N-Fp-M	Y	Y		Fp-R-S	Y	Y ^b	
Fp	N-Fp-R	Y	Y	S	V-S-C	Y	Y	
	P-H-Q	Y	Y		V-S-R	Y	Y	
H	P-I-K	Y	Y	Sp	V-Sp-D	ND	Y	
	P-I-Kp	Y	Y		T	A-T-V	Y	Y
I	L-J-B	Y	Y	U	Kp-U-Mp	Y	Y	
	O-J-B	Y	Y		V	L-V-D	Y	ND
	L-J-E	Y	Y		T-V-D	Y	ND	
	O-J-E	Y	Y		L-V-S	Y	Y	
	L-J-Q	Y	Y		L-V-Sp	ND	Y	
	O-J-Q	Y	Y		T-V-S	Y	Y	
K	D-K-O	Y	Y	V	T-V-Sp	ND	Y	
	I-K-O	Y	Y					

^aWhen block N and A occur together, the first 100 bp of A are missing, and instead this junction contains four new bp “CTAT” or “ATAG”.

^bWhen block R and F/Fp occur together, the last 4 bp of F/Fp are missing, and instead this junction contains the 2 nt “AC/GT” depending on orientation.

(SB) Sequence block, (Y) present, (ND) not detected.

which are identical (Fig. 4A). Small 10- to 14-bp regions of microhomology are detected between many SBs (Fig. 4B). Larger window sizes that can span multiple SBs were used to compare ONT reads against themselves. A 1000-nt window revealed numerous aligned regions between ONT reads (Fig. 4C). At a window size of 2000 nt, many aligned regions are still observed (Fig. 4D), but at a window size of 3000 nt, few shared sequence regions of at least this length are observed (Fig. 4E). Finally, *T. gondii* ONT reads were compared to *N. caninum* ONT reads and fewer alignments are observed than when *T. gondii* reads are compared to themselves with the same window size (Fig. 4D,F).

To further analyze sequence block order, a lexicon of all triplet block orders was constructed from all ONT mtDNA sequences for both *T. gondii* and *N. caninum* (Table 2). Certain SBs are always observed upstream of, or downstream from, specific SBs (e.g., block L), as if they are part of a larger conserved super block of sequence, whereas other blocks (e.g., block J) are observed to be flanked by several different blocks (Table 2), indicating that they occur in multiple distinct contexts. The lexicon also revealed that *T. gondii* and *N. caninum* share the majority of their triplets but not all (Table 2). To examine the frequency of each SB junction, we tallied the counts of the element observed directly at the 5' and 3' end of each sequence block in the *T. gondii* and *N. caninum* ONT mtDNA reads (Supplemental Fig. S12A,B) and *T. gondii* PRU ONT direct RNA strand sequencing and *N. caninum* Sanger EST reads to verify the occurrence of the same block relationships in transcripts (Supplemental Fig. S12C,D). The patterns observed in the RNA and DNA are shared for each species and molecule type except for the differences associated with the acquisition of Sp in *N. caninum*. Thus, the basic units of mtDNA secondary structure are evolutionarily conserved and transcripts are not edited or rearranged.

To examine sequence redundancy, we counted the number of full-length genes in the ONT reads, which yielded 22 and 57 *coxI*, 26 and 103 *coxIII*, and 23 and 52 *cob* in *T. gondii* ME49 and RH mtDNA reads and three, seven, and two in *N. caninum*. Of the 1165 ONT mtDNA sequences from two *T. gondii* and one *N. caninum* run (Supplemental Table S3), 77% do not encode full-length cytochromes (Supplemental Tables S7, S8). To estimate rel-

ative *T. gondii* ME49 mtDNA gene copy numbers based on read depth, we mapped genomic Illumina PE data from two different *T. gondii* strains to full-length cytochrome gene sequences and a single-copy nuclear gene, *GAPDH*, for normalization. *coxI*, *coxIII*, and *cob* were detected at 316, 423, and 297 \times for ME49 and 369, 523, and 313 \times for RH88 relative to *GAPDH* (Supplemental Table S9). For comparison, the *E. tenella* mtDNA was estimated to exist at \sim 50 copies per nuclear genome (Hikosaka et al. 2011).

The topology of the mitochondrial genome is dynamic

ONT single-molecule sequencing of *T. gondii* ME49 revealed molecules as long as 23 kb consisting fully of mtDNA SBs, although most ONT reads were shorter (Figs. 1F, 5). To assess whether the ONT reads were informative with respect to naturally occurring mtDNA size (a read cannot be longer than the naturally occurring molecule), we compared mtDNA and nuclear read lengths (Fig. 5A). *Toxoplasma* mtDNA ONT reads are shorter than nuclear reads, except for *N. caninum* where the nuclear reads are shorter due to apparent degradation. Yet, we note the *N. caninum* mtDNA distribution remains similar to *T. gondii*. The observed *T. gondii* mtDNA ONT read lengths are similar to the range of sizes observed in a Southern of a CHEF blot probed with a 1021-bp section of the *cob* gene, but the abundance of ONT reads in the 1–4 kb range (Fig. 5B) do not match the intense smear (\sim 5–16 kb) observed on the blot (Fig. 5C). A similar Southern smear was observed in *P. falciparum* (Preiser et al. 1996), where rolling circle replication creates tandem concatemers (Wilson and Williamson 1997). Physically, if the *Toxoplasma* mtDNA existed as a linear concatemer of tandemly repeating units, the dot plots of ONT reads (Fig. 4) should have revealed this topology. Restriction digest of a tandemly repeating sequence structure with an enzyme that has a single cut site within the unit should result in one major band and a trailing smear of smaller fragments, as is seen in *Plasmodium* (Preiser et al. 1996). However, when *T. gondii* genomic DNA was digested with XhoI, which uniquely cuts the *cob* gene, and probed with a *coxI* probe, two faint bands of \sim 1.35 and 1.65 kb in addition to a large smear

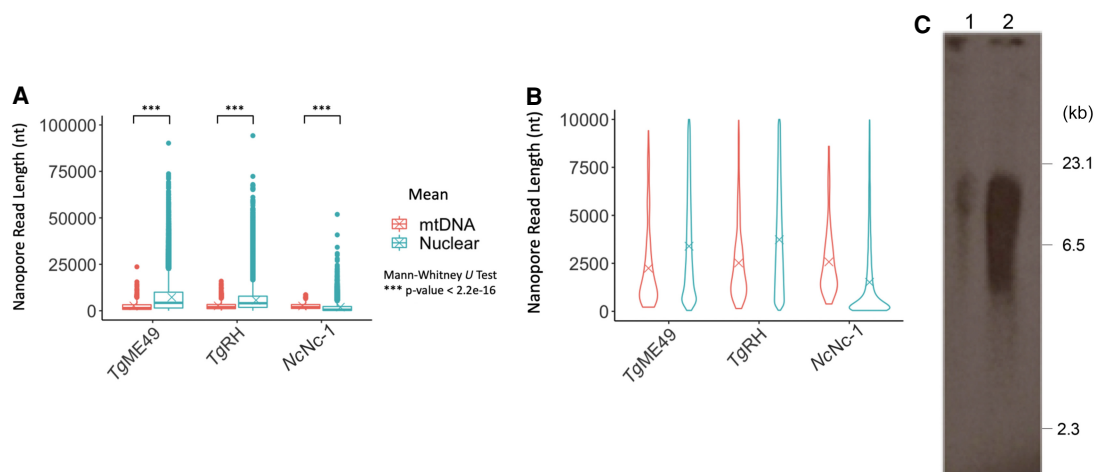


Figure 5. Size distribution of mtDNA versus nuclear ONT reads. (A) Three ONT runs are plotted and tested for statistical significance. Box plots cover the 25th–75th percentiles. See Supplemental Table S10 for mean and median values. (B) Violin plots of the same ONT reads $<$ 10 kb. (C) Southern of a CHEF gel electrophoresis of *T. gondii* total DNA (lane 1) and mitochondrial-enriched DNA (lane 2) probed with a 1012-bp section of the *cob* gene. DNA ladder is as indicated.

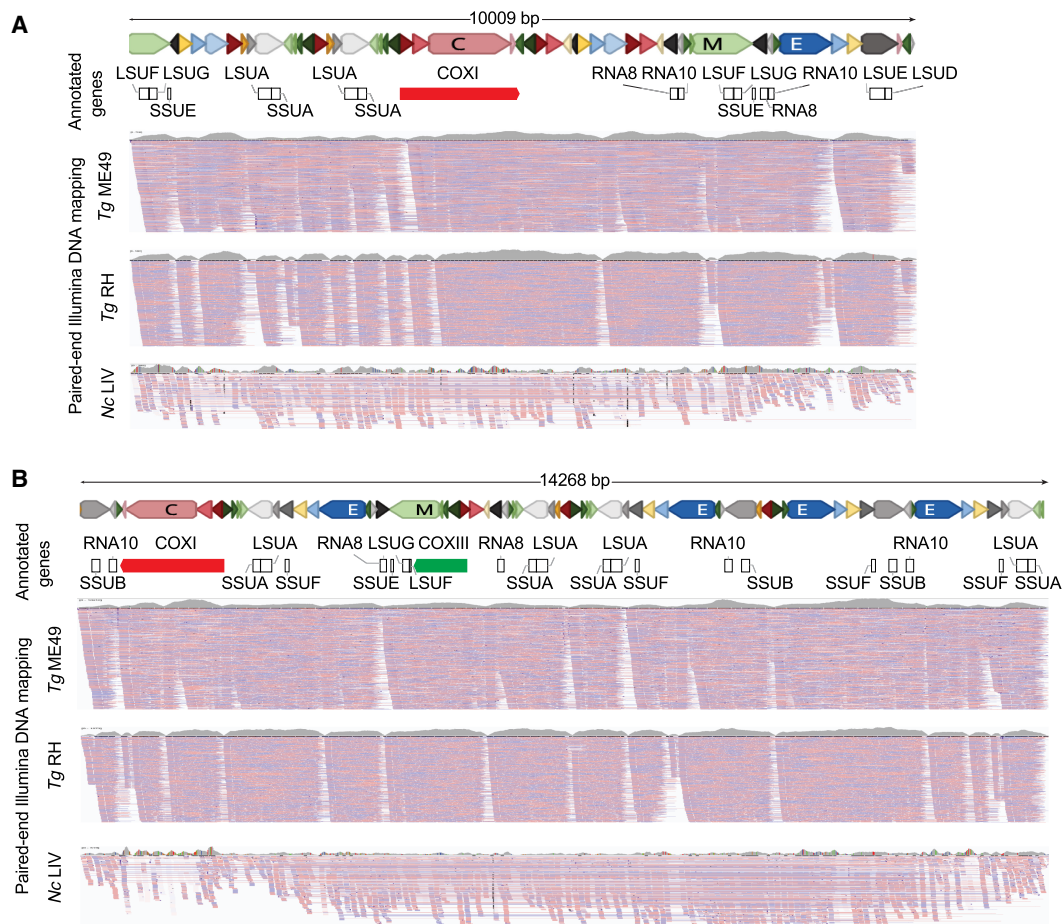


Figure 6. ONT and Illumina comparisons reveal sequence block order variability and decay with evolutionary time. (A,B) Two *T. gondii* ME49 ONT sequence reads were annotated with the gene sequences they contain. Reads and SBs are drawn to scale. The blocks are colored as shown in Table 1. “Annotated genes” track represents the annotation of the cytochrome genes and rRNA gene fragments on the ONT reads. The three “PE Illumina DNA mapping” tracks show PE read mapping of *T. gondii* ME49, *TgRH88*, and *N. caninum* (Nc) LIV mtDNA-specific reads. *TgME49* and *TgRH* reads mapping required 100% nucleotide identity whereas 1% mismatch was allowed for mapping NcLIV reads. Reads were independently mapped to each of the ONT mtDNA reads and visualized using IGV. Red and blue lines below each read indicate the mapped Illumina PE reads. Coverage plots of the mapped reads are shown above each mapping panel in gray to indicate the depth of all reads and not just those shown.

were detected (Supplemental Fig. S13). No pattern characteristic of a tandem repeat was observed.

The secondary structure of the mtDNA appears to be dynamic. Several years separated the isolation of *T. gondii* ME49 DNA for Illumina and ONT sequencing. During this time, the parasites were being passaged. We note that when our Illumina PE reads are mapped to our ONT reads, we observe gaps in the mapping (Fig. 6; Supplemental Fig. S6). The mapping further degenerates when PE Illumina reads from a different *T. gondii* strain, RH, are mapped, as evidenced by the increase in the number of white gaps in the mapping and dips in the overall coverage plots above the alignments (Fig. 6). The degeneration in mappability is even stronger when *N. caninum* PE Illumina sequence reads are mapped despite using a lower mapping stringency (Fig. 6). A similar trend was observed when *N. caninum* and *T. gondii* Illumina reads were mapped to *N. caninum* ONT reads (Supplemental Fig. S14). Given the fact that the SBs (Table 1) and lexicon (Table 2) are highly conserved, it seems likely that the long mtDNA molecules evolve rapidly. The mapping experiments also revealed the presence of different populations of PE reads, some that span particular ONT SB orders and others that do not, for example, right-hand edge of Figure 6A

or the beginning of the *TgRH* track in Figure 6B and Supplemental Figure S14.

The single-molecule ONT reads are riddled with inverted SBs throughout, but they do not appear to be located at the ends of the molecules where they could serve as telomeres (Smith and Keeling 2013). A few ONT reads have portions of the same sequence block on their ends, a feature characteristic of rolling-circle replication (Supplemental Fig. S15A), but most do not (Supplemental Fig. S15C). Attempts to circularize the ONT reads using the same program that was able to circularize the *P. falciparum* mtDNA revealed many potential circular chromosome candidates. The candidates range in size from 1.6 to 5.6 kb, some of which are shown in Supplemental Figures S15 and S16, but the putative circular chromosomes (Supplemental Figs. S15, S16) do not contain any measurable degree of support from other ONT reads. They do have support from PE-Illumina reads, but it is not always uniform (Supplemental Fig. S15A,C, top and bottom panels, respectively). Notably, full-length cytochrome genes are detected on the putative circular chromosomes. Finally, to address the possibility of a population of very small circular chromosomes, we identified all short ONT mtDNA reads 0.6–2.0 kb from the 779 mtDNA reads

identified in the *T. gondii* RH ELQ-316 mutant strain and asked if they could be clustered into significantly overlapping populations. They could not, suggesting the reads were not derived from one or more identical short templates.

Discussion

We show here how long-read single-molecule ONT sequences elucidated novel mtDNA sequence arrangements for *T. gondii* and its closest relatives that consist of redundant, highly rearranged strings of sequence blocks that do not appear to be the direct result of rolling-circle replication. The SBs are evolutionarily conserved with a few minor variations in *Hammondia hammondi* and the more divergent *N. caninum* but not *Sarcocystis*. We also show that this lineage has independently evolved fragmentation of the *coxI*, *coxIII*, and *cob* genes, a feature previously detected only in dinoflagellates (Flegontov et al. 2015; Obornik and Lukes 2015; Gagat et al. 2017), perhaps as a mechanism to generate novelty in these streamlined mtDNA genomes.

The evidence indicates that the mtDNA became shattered and redundantly rearranged by some unknown event during the evolution of the tissue coccidia. Single-molecule mtDNA ONT reads of 0.10–23.6 kb comprised exclusively of SBs, in nonrandom arrangements, are observed across libraries. The fragmented nature of the *T. gondii* mtDNA is supported by four different lines of evidence: (1) individual unassembled Sanger genomic and EST reads; (2) complex PCR patterns from mtDNA enriched cell fractions; (3) single-molecule ONT long-read sequences of DNA and RNA; and (4) evolutionary conservation of nearly identical sequence blocks in the related tissue coccidia, *Hammondia* and *Neospora*. Despite the novel genome sequence(s) which includes many redundant fragments and full-length copies of *coxI*, *coxIII*, and *cob* genes and rRNA genes, additional RNA and protein features were not detected. The CDSs of *coxI* and *cob* are well conserved with other apicomplexans, but *coxIII*, which is reported here for the first time, is divergent. Low conservation was also reported for the *coxIII* of a free-living ancestor of the Apicomplexa, *Chromera* (Obornik and Lukes 2015). *T. gondii*, like several species in the alveolata, has evolved overlapping CDSs in its mtDNA. Sequence block V is required to form the full open reading frame (using opposite DNA strands) for both *coxI* and *coxIII*, reminiscent of the fused *coxI* and *coxIII* in chromerids (Jackson et al. 2007), albeit a different fusion.

In addition to full-length transcripts, evidence for the expression of every single sequence block was seen in the ONT direct RNA strand sequences including SBs for which we have no annotation (blocks D, N, P, and R). As was observed in the dinoflagellates, partial cytochrome genes are expressed. There is no evidence of trans-splicing or RNA-editing. There is no evidence of self-splicing introns, a feature often observed in mtDNA (Lang et al. 2007). Limited ONT direct RNA transcripts revealed poly(A) tails on the subset of *coxI* transcripts flanked by block J which may encode a cryptic poly(A) signal. In the dinoflagellates, the cytochrome transcripts are polyadenylated, but this occurs upstream of the stop codon (Jackson et al. 2007). Dinoflagellates display strong stem-loop and multiple hairpin features (Jackson et al. 2007) in noncoding regions; however, we did not find strong evidence for long, nearly perfect hairpins other than a structure in sequence block J. Regulation of mtDNA gene expression in this highly polymorphic mtDNA context is unknown. All SBs are expressed.

Fragmented mtDNA sequences have been observed in other organisms, most notably the sister phylum to the Apicomplexa, the dinoflagellates, which also share fragmented rRNA genes and

a reduced mtDNA gene content of only *coxI*, *coxIII*, and *cob*. What is fascinating from an evolutionary perspective is the fact that many dinoflagellates, including a basal dinoflagellate, *Hematodinium*, have also redundantly fragmented their cytochrome genes and contain both full-length and fragmented copies (Ling and Shibata 2004; Bedoya et al. 2009). Examination of *Hematodinium* cytochrome gene fragments reveals that their sequences have been shattered in different locations relative to *T. gondii* and that there are a greater number of different, often overlapping fragments in the dinoflagellates. The capacity to both generate and survive structural rearrangements within such a small genome is a prominent feature of the Apicomplexa and dinoflagellates (Fig. 7).

The data do not reveal the exact topology of the mitochondrial genome or how it replicates. Our inability to assemble a single full-length mitochondrial genome sequence and the presence of redundant sequence block order and orientation variants suggests that the *T. gondii* mtDNA could exist as a number of distinct chromosomes as is seen in dinoflagellates and other organisms (Burger et al. 2003; Flegontov and Lukes 2012; Dong et al. 2014; Yahalomi et al. 2017). It is also likely that these chromosomes are recombining with each other to produce the larger molecules and variety of SB patterns that are observed in this study. Theoretically, the mtDNA of *Toxoplasma* and its relatives could be circular, linear, or some combination of both, or it could be contained on a single chromosome, as is observed in all Apicomplexa to date (Fig. 7). However, the data do not support a single circular topology containing all SBs that replicates via rolling-circle replication, as evidenced by sequencing, the dot plot comparisons, and Southern analysis of restricted DNA. Formally, each of the 21 SBs could exist on its own chromosome and replicates could become concatenated nonrandomly via some undiscovered process that guides particular ligations. We consider this unlikely because inverted repeats are not detected at the ends of individual SBs. We do, however, detect support from our copy number analysis for the hypothesis that, when the mtDNA shattered into smaller pieces, it shattered redundantly into many different units of sequence, each of which is capable of being annotated with more than one of the 21 SBs. Minimally, the mtDNA consists of these 21 nonredundant SBs, none of which individually encodes a full gene, for a total of 5909 bp of sequence in *T. gondii* and 5908 in *N. caninum*.

Most apicomplexan mtDNAs are ~6 kb. In *P. falciparum*, a Southern blot smear ranging from 6 to 23 kb was attributed to rolling-circle replication intermediates (Weissig and Rowe 1999) of the mtDNA. Smears of 6–10 kb or more were observed in dinoflagellates (Sandhu et al. 2007; Chen 2013; Gualberto and Newton 2017). *T. gondii* showed a smear ranging from 2 to 16 kb with greatest signal above 5 kb. mtDNA ONT reads are statistically shorter than ONT nuclear reads. Thus, the sizes are likely indicative of the biological reality that mtDNA molecules are mostly <10 kb. The fact that *N. caninum* mtDNA ONT reads do not appear to be degraded in contrast to nuclear reads could indicate circular molecules that were protected from exonucleases.

The observation that short stretches of mtDNA <3 kb are observed to occur multiple times within the ONT reads implies that regions of mtDNA longer than single SBs exist. The ONT reads and resulting lexicon prove that multiple distinct SB arrangements exist. More importantly, evolution of the lexicon in *N. caninum* to contain Sp, (and VSpD) indicates that these stretches of sequence are encoded together as a larger single unit. The data support a model in which parts of the mitochondrial genome, including at least one full-length copy of each cytochrome gene, are redundantly present on different chromosomes. We speculate that it is much

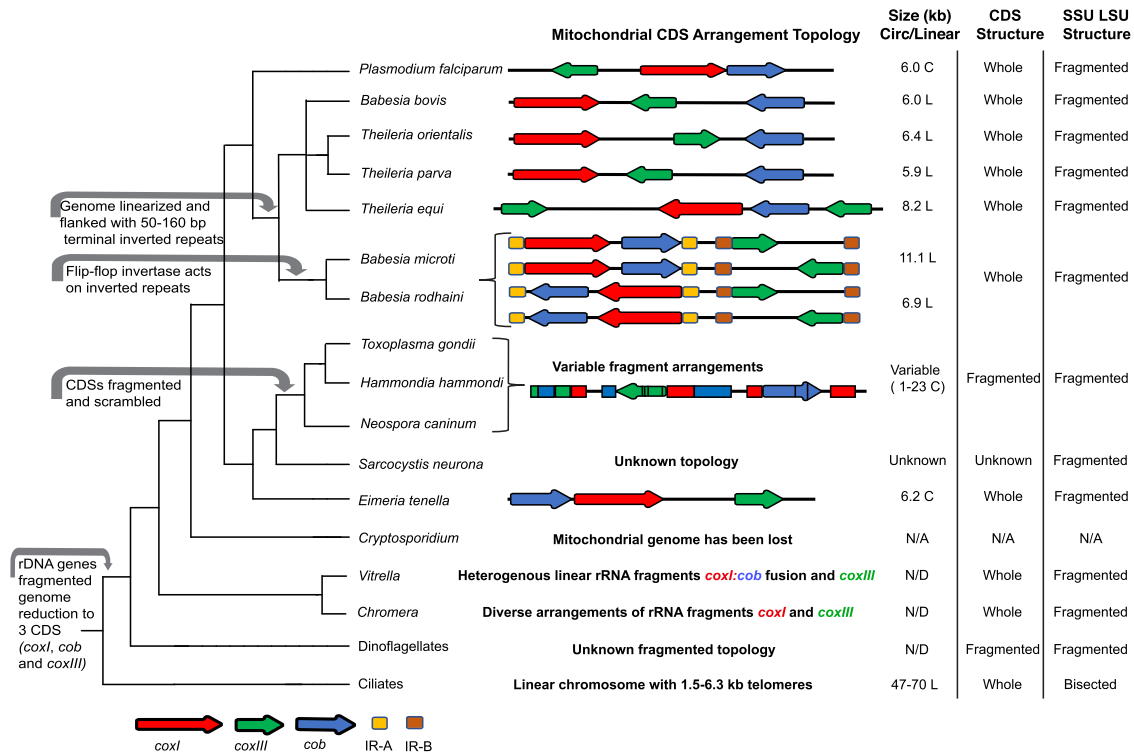


Figure 7. Alveolate mtDNA evolution and characteristics. (Left) Cladogram of alveolate relationships with major mitochondrial genome events indicated with gray arrows. (Center) Schematic of mtDNA CDS (red, green, and blue arrows) or inverted repeats (gold and brown) indicated. Spacing is approximate with CDS lengths exaggerated for ease of viewing. Ribosomal RNA and other RNA genes or fragments thereof are not represented. (Right) mtDNA size and topology. (L) Linear, (C) concatemer, presumably from circular progenitors. Status of CDS sequences and status of Short (SSU) and Long Subunit (LSU) rRNA are indicated.

less risky to the organism if it maintains at least one full-length copy of each gene or rRNA gene fragment. The situation is more complex when considering stretches of DNA >3 kb. It is probable and parsimonious to hypothesize that larger sequences are constructed, albeit uniquely, from smaller sequences. A possible mechanism is homologous recombination between circular chromosomes to create a larger single chromosome. If the mtDNA of *T. gondii* exists as a population of redundant circular chromosomes, each of which contains multiple portions of the ancestral mtDNA redundantly, then homologous recombination between two different circular chromosomes sharing a homologous region (or a stretch of microhomology) will create a novel larger molecule. Recombination among such a population is a plausible explanation for the variety of sequences that are detected by ONT. It would also explain some of the errors observed in the ONT reads where we see damaged SBs. Further, gaps in mapping of Illumina data to ONT reads generated from *T. gondii* ME49 DNA extracted several years apart is indicative of rapidly evolving mtDNA molecules, providing support for recombination events. Recombination has been observed in *P. falciparum* during mtDNA replication (Preiser et al. 1996), and it is a widely reported phenomenon within and between mitochondria across eukaryotes (Sandhu et al. 2007; Chen 2013; Gualberto and Newton 2017).

We do not yet know how much variation, if any, exists within a single parasite mitochondrion versus population level variation. The data presented here cannot address that question as DNA was extracted from millions of parasites and as of yet, individual mitochondrial organelle sequencing is not yet possible. However, the

ONT reads from the *T. gondii* RH ENU mutant strain are quite informative. DNA from the *T. gondii* ELQ-316 mutant was from a recently derived clone presumably originating from a single resistant parasite. The ONT reads from this mutant also yielded a myriad of long, unique sequence block concatemers, suggesting that they either already existed in the parent mitochondrion or are easily regenerated. We also observed that the point mutation was present in nearly all copies of sequence block E on the ONT reads. We do not know if this finding indicates that each mutant sequence block E (which is always flanked by J and A, i.e., JEA) originates from the same source molecule, or if *T. gondii* has the machinery needed to maintain homoplasmy, perhaps via MSH1, a MutS homolog that targets to the mitochondrion in *Toxoplasma* (Garbuz and Arrizabalaga 2017).

Although the lack of a single mtDNA sequence raises difficulties for those targeting the *T. gondii* mitochondrion, the presence of a possible mechanism for maintaining homoplasmy at the level of a sequence block was observed. This finding opens the door to further exploration of the *Toxoplasma* mitochondrion, as it is an important drug target. The need to be able to purify mitochondria in *Toxoplasma* remains strong. Elucidation of the *T. gondii* mtDNA might have happened years ago were it not for NUMTs. We now know that "REP" elements in *T. gondii* (Reid et al. 2012) are NUMTs that can be annotated with SBs (Supplemental Table S11). *Toxoplasma gondii* contains >9000 NUMTs in its nuclear genome (Namasivayam 2015), thwarting both molecular and sequence-based mtDNA identification. The NUMTs together with the unique architecture presented here generated a difficult puzzle

that required long single-molecule sequencing for a breakthrough. ONT offers the opportunity for re-analysis of dinoflagellate mtDNAs and further exploration of mitochondrial biology and evolution. Perhaps, the independent evolution of redundant fragmented mtDNA in the dinoflagellates and Apicomplexa provides a mechanism for the generation of evolutionary novelty in these tiny, streamlined organellar genome sequences.

Methods

Species and strains

T. gondii RH and ME49 tachyzoites were maintained in human fibroblast reverse transcriptase (hTERT) cells as described in Weiss and Kim (2007). Extracellular tachyzoites, washed twice in PBS, were used for mitochondrial enrichment or DNA extraction. *Neospora caninum* Nc-1 parasites were cultured on Vero cells using RPMI 1640 supplemented with 5% normal horse serum, purified by centrifugation through 30% isotonic Percoll and washed twice in PBS.

Enriched mitochondrial fractions

T. gondii tachyzoites ($\sim 2\text{--}4 \times 10^9$) were purified as in Miranda et al. (2010) and Supplemental Methods.

Nucleic acid extraction, PCR, RT-PCR, and sequencing

DNA for PCR was isolated through standard Proteinase K and RNase A digestion followed by phenol/chloroform extraction. Primer pairs are in Supplemental Table S1. PCR conditions are as in Namasivayam (2015) and Supplemental Methods.

T. gondii RH $\Delta ku80$ RNA extraction used the RNeasy Mini Kit (Qiagen) Quick-Start protocol with the DNase digestion step. RT-PCR used the SuperScript III first-strand synthesis kit (Invitrogen) and cytochrome gene-specific primers (*coxI* V2, *coxIII* M9, *cob* E5) (Supplemental Table S1) to amplify the three cytochrome transcripts which were sequenced with primers C9, M9, and T3 (Supplemental Table S1) to verify identity.

DNA for sequencing was extracted from *T. gondii* ME49 and *N. caninum* Nc-1 parasites using the DNeasy Blood and Tissue Kit (Qiagen) following the manufacturer's cultured cells protocol and sequenced with Illumina or an ONT flowcell 9.4.1 according to the manufacturer's instructions (see Supplemental Methods). MinKNOW version 18.03.1 was used to call bases. ONT Direct RNA sequence data generated from poly(A)⁺ purified RNA were provided by Stuart Ralph. Supplemental Table S3 summarizes all sequencing yields. Corrected mtDNA ONT reads are in Supplemental Data S3, S6, S8, and S10).

Sequence analysis

Sequenced PCR amplicons, public unassembled Sanger mtDNA-like EST, and genome sequence reads were compared to each other using BLASTN (E-value: e^{-10} , nucleotide identity $\geq 98\%$ in all instances unless noted). Mitochondrial SBs were determined based on their reproducible occurrence, sequence boundaries, and arrangements in the sequences. *T. gondii* reference sequences were obtained from ToxoDB (<https://toxodb.org/>) release 11 (Gajria et al. 2008). These contigs and all unassembled *T. gondii* Sanger genomic and EST reads from NCBI were screened via BLASTN for any additional mtDNA sequences using the determined mtDNA SBs as queries. A read was classified as mitochondrial if no adjoining nuclear sequence was found. All reads classified as mitochondrial were analyzed for length, sequence boundaries, and SB arrangements using BLASTN.

NUMT identification

RepeatMasker version 4.0.5 (Smit et al. 2015) with a repeat library composed of the 21 *T. gondii* mtDNA SBs and search engine "cross-match" was used to identify nuclear sequences of mitochondrial origin in the nuclear genome sequences of *T. gondii* and *N. caninum* (Namasivayam 2015).

Analysis of ONT reads

Two strategies were used to identify mtDNA reads. First, the ONT reads were screened for the 21 mtDNA SBs using BLASTN (nucleotide identity $\geq 60\%$ and $\leq 10\%$ alignment length mismatch). Second, the reads were aligned to the 21 mtDNA SBs using Exonerate v2.4.0 (Slater and Birney 2005). The best 2000 alignments with an alignment $\geq 60\%$ were classified as putative mtDNA. Reads containing NUMTs were removed and error correction was performed with Illumina reads (Supplemental Data S6; see Supplemental Materials for details).

Mapping of genomic Illumina reads

T. gondii ME49 DNA PE-Illumina reads were mapped requiring 100% identity to the 21 mtDNA SBs using BWA v0.7.17. mtDNA-containing reads were further examined for any new mtDNAs. To assess Illumina support for the ONT reads, *T. gondii* ME49 (SRR9200762), RH88 (SRR521957), and *N. caninum* LIV (ERR012900) mtDNA reads were independently mapped to corrected *T. gondii* ME49 ONT reads using BWA v0.7.17 (local alignment, requiring both pairs to match at 100% identity) and visualized using the Integrative Genomics Viewer (IGV) (Robinson et al. 2011). Any methodological deviation is indicated in figure legends. When estimating copy numbers for mtDNA relative to a single-copy nuclear gene, negative controls included mapping to manually created SB fusions not observed in our lexicon.

Gene prediction and annotation

Annotation was based on similarity to the cytochrome genes and rRNA fragments of *P. falciparum* and *E. tenella* (Feagin 1992; Feagin et al. 1997, 2012; Hikosaka et al. 2011). TBLASTN and ORF prediction (NCBI ORF finder, genetic code for protozoan mitochondria) was used to identify and annotate SB protein-coding regions. ORFs >50 aa from the SBs and the longest *T. gondii* ONT read were searched with InterProScan V5.31-70.0 to identify protein features. PE *T. gondii* RNA-seq reads obtained from NCBI (SRR6493545) were mapped to mtDNA SBs as described above to identify mtDNA-specific reads. These reads were then mapped to cytochrome CDSs using BWA v0.7.17 (local alignment, requiring both pairs to map at 100% identity). *Toxoplasma gondii* PRU $\Delta ku80$ ONT direct RNA strand reads (SRR9200760) (Supplemental Data S6) were processed like the genomic ONT reads and annotated. rRNA genes that did not align well with the rRNA gene fragments of *P. falciparum* were identified using conserved nucleotides, manually folded, and compared to *E. coli* rRNA secondary structures and their *Plasmodium* counterparts. All SBs and the longest ONT read were used to search Rfam v14.2 to identify any additional RNA genes or RNA features like catalytic RNAs or self-splicing introns.

Mitochondrial genome assembly

CAP3 with default parameters (Huang and Madan 1999) was used to assemble PCR amplicons and unassembled mtDNA Sanger reads. SPAdes 3.12.0 (Bankevich et al. 2012) was used to assemble mtDNA PE Illumina reads. Canu v1.9 (Koren et al. 2017), Flye v2.6

(Kolmogorov et al. 2019), CAP3, and Geneious Prime 2019.1.3 (Kearse et al. 2012) were used with corrected mtDNA ONT reads.

Identification of mtDNA sequences in *N. caninum*, *Hammondia*, and *S. neurona*

N. caninum genomic sequences were obtained from <ftp://ftp.sanger.ac.uk/pub/pathogens/Neospora/caninum/NEOS.contigs.072303>. A single contig containing mtDNA sequences was identified using the 21 *T. gondii* mtDNA SBs via BLASTN (E-value: e^{-10}). This contig was not present in later genome assemblies. *N. caninum* mtDNA SBs were annotated based on this contig, and the SBs were used to identify additional mtDNA sequence contigs. *N. caninum* ONT data were queried as above for *T. gondii*, and these reads were error-corrected using *N. caninum* PE Illumina genomic reads (ERR012900) and annotated using *N. caninum* SBs (Supplemental Data S8). Similarly, the genome sequence of *Hammondia hammondi* H.H.34 (Walzer et al. 2013) (ToxoDB version 2014-06-03) as well as sequences of other *Hammondia* species available in NCBI were mined for mtDNA sequences via BLASTN. *Sarcocystis neurona* SN3 and SN1 genome sequences (versions 2015-04-13 and 2015-07-23, respectively) obtained from ToxoDB and sequence data in NCBI were mined for mtDNA using *T. gondii* mtDNA SBs and the mitochondrial genome sequence of *E. tenella* (AB564272.1) using BLASTN and TBLASTX.

Other bioinformatic analyses and data visualization

The arrangements and permutations of SBs in the data sets were obtained via BLASTN and manually inspected. A GFF file containing the annotation of genes and SBs for each read and PCR amplicon was generated using BLASTN and a Perl script ([bp_search2gff.pl](#)) available from APPRIS (Rodriguez et al. 2018) and visualized using Geneious Prime v.2019 (Kearse et al. 2012). DotPlots were performed with NUCmer (MUMmer 4.0.0beta2-foss-2019b using the -maxmatch option) and plotted using mummerplot (Kurtz et al. 2004) and gnuplot 5.2.8. Alignments of Illumina reads to SBs, ONT, and cytochrome sequences were visualized using IGV and coverage was determined using BEDTools 2.21.0 genomeCoverageBed (Quinlan and Hall 2010).

Contour-clamped homogeneous electric field (CHEF) electrophoresis

T. gondii RH tachyzoite parasites were isolated and suspended in 1.0% low-melting agarose plugs and digested with 0.5 M EDTA, 1% lauroylsarcosine, 2 mg/mL Proteinase K, and 0.2 mg/mL RNase A at pH 8.0, 50°C for 48 h. Electrophoresis was performed using a CHEF Mapper (Bio-Rad Laboratories) in a 1% agarose gel (Sigma-Aldrich) with the following conditions: 6V/cm, linear 11s–22s, 15 h, and 4°C with a switching angle of 120°. A radioactive 1012-bp *cob* probe was synthesized through PCR, gel-extracted, and cleaned using mini Quick spin columns (Roche). Southern analysis was performed as described in Supplemental Methods.

Data access

The Illumina, ONT, and nucleotide data generated in this study have been submitted to the NCBI BioProject database (<https://www.ncbi.nlm.nih.gov/bioproject/>) under accession numbers PRJNA546244, PRJNA436351, and PRJNA560064.

Competing interest statement

The authors declare no competing interests.

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