

# Organelles that illuminate the origins of *Trichomonas* hydrogenosomes and *Giardia* mitosomes

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**Many anaerobic microbial parasites possess highly modified mitochondria known as mitochondrion-related organelles (MROs). The best-studied of these are the hydrogenosomes of *Trichomonas vaginalis* and *Spironucleus salmonicida*, which produce ATP anaerobically through substrate-level phosphorylation with concomitant hydrogen production; and the mitosomes of *Giardia intestinalis*, which are functionally reduced and lack any role in ATP production. However, to understand the metabolic specializations that these MROs underwent in adaptation to parasitism, data from their free-living relatives are needed. Here, we present a large-scale comparative transcriptomic study of MROs across a major eukaryotic group, Metamonada, examining lineage-specific gain and loss of metabolic functions in the MROs of *Trichomonas*, *Giardia*, *Spironucleus* and their free-living relatives. Our analyses uncover a complex history of ATP production machinery in diplomonads such as *Giardia*, and their closest relative, *Dysnectes*; and a correlation between the glycine cleavage machinery and lifestyles. Our data further suggest the existence of a previously undescribed biochemical class of MRO that generates hydrogen but is incapable of ATP synthesis.**

MROs are highly modified mitochondria found in diverse anaerobic and microaerophilic eukaryotes; they vary widely in the ancestral mitochondrial pathways that they have retained, and in their role in anaerobic ATP production (reviewed previously<sup>1</sup>). The greatest functional diversity of MROs is found in the excavate group Metamonada. This diversity encompasses the hydrogenosomes of *T. vaginalis* and *S. salmonicida*, which produce ATP anaerobically through substrate-level phosphorylation with concomitant hydrogen production<sup>1–4</sup>; the mitosomes of *G. intestinalis*, which are highly functionally reduced and lack any role in ATP production<sup>1,5</sup>; and *Monocercomonoides* sp., the first known eukaryote to have lost its MROs entirely<sup>6</sup>. However, little is known of the metabolic properties of MROs in free-living metamonads, nor of how the metabolically specialized MROs of parasitic metamonads evolved from those of their free-living ancestors. The free-living, bacterivorous *Carpediemonas*-like organisms (CLOs<sup>7,8</sup>) are the closest relatives of these parasitic metamonads, and are key to resolving this question. Here, we present the first large-scale comparative transcriptomic study of MROs across Metamonada. By sequencing the transcriptomes of eight free-living or commensal metamonads, and comparing

their predicted MRO proteomes with publicly available proteome and transcriptome data, we examine lineage-specific gain and loss of metabolic functions in MROs in 18 metamonads.

## Results

**A robust tree of the Metamonada.** To elucidate the relationships between *T. vaginalis*, *G. intestinalis* and their free-living close relatives, we mined 18 metamonad transcriptomes or genomes for orthologues of 159 conserved proteins to add to a phylogenomic super-matrix representing the full breadth of eukaryote diversity. Phylogenetic analyses of this dataset (Fig. 1a) show that Metamonada form a highly supported clade with three main subgroups, Preaxostyla, Parabasalia and Fornicata; Preaxostyla is the earliest diverging lineage. All CLOs branched within Fornicata, forming a long series of nested clades, with *Dysnectes brevis* being the closest relative of diplomonads<sup>7</sup>, and *Carpediemonas membranifera* forming the deepest branch. Branching order and position of all CLOs received maximum bootstrap and posterior probability support in most analyses, except in two cases where bootstrap support nevertheless remained strong (that is, >85%; see Supplementary Figs 1–3).

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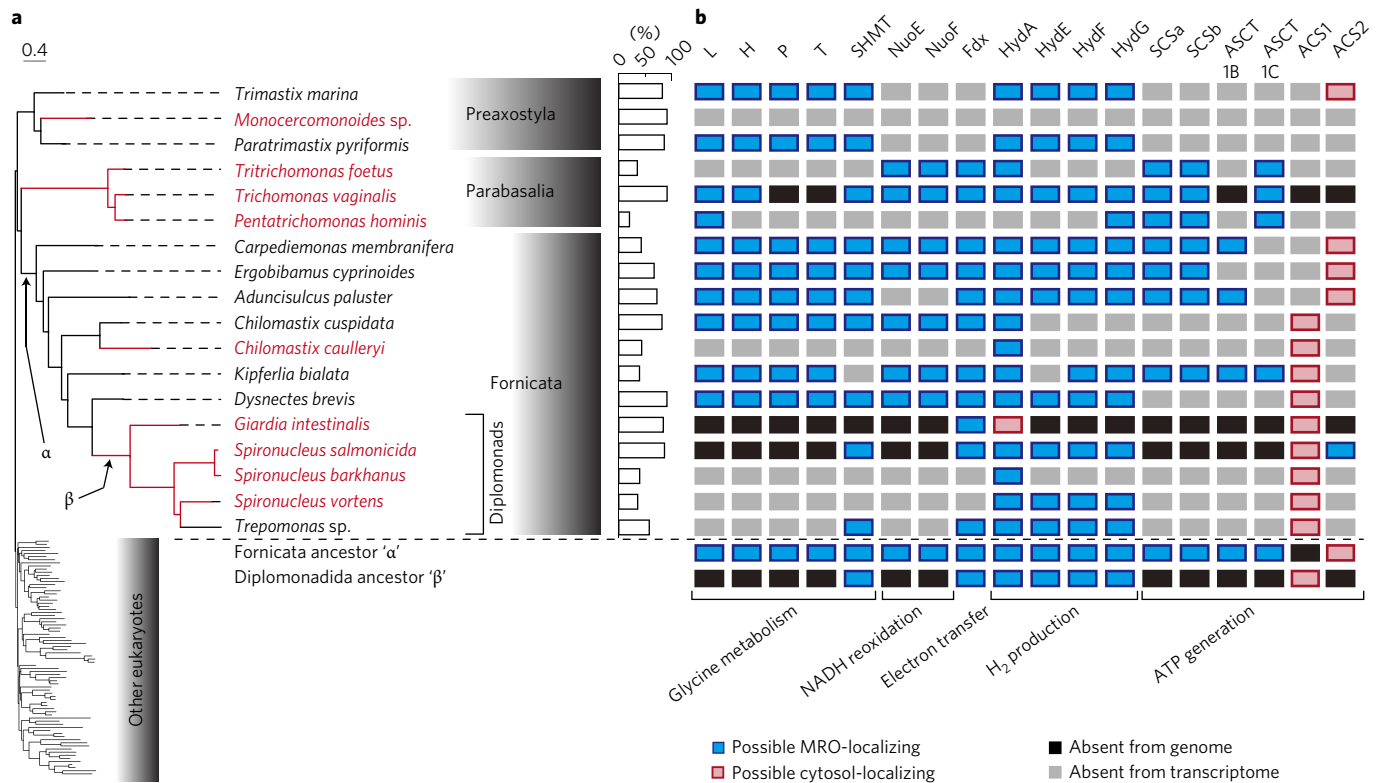
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**Figure 1 | Phylogeny of Metamonada and distribution of MRO-localizing proteins. a**, PhyloBayes tree of eukaryotes inferred from the phylogenomic dataset of 159 proteins (39,089 sites) and 94 taxa. The taxa other than Metamonada are not shown in detail. The topology shown was recovered by three out of four PhyloBayes chains tested, and in all maximum likelihood (ML) analyses. Parasitic species and lineages are highlighted in red. The bar graph indicates the percentage coverage of the amino acid sites used in the phylogenomic analysis present in each transcriptome (see Supplementary Figs 1–3 for more detail and support values). **b**, Distribution of MRO-targeted proteins in Metamonada. L, H, P and T represent L, H, P and T proteins of the glycine cleavage system; SHMT, serine hydroxymethyltransferase; NuoE, NADH:ubiquinone oxidoreductase, 24 kDa subunit; NuoF, NADH:ubiquinone oxidoreductase, NADH-binding 51 kDa subunit; Fdx, ferredoxin; HydA, [FeFe]-hydrogenase; HydE–G, [FeFe]-hydrogenase maturation proteins E–G; SCSa, succinyl-CoA synthase alpha subunit; SCSb, succinyl-CoA synthase beta subunit; ASCT, acetate:succinyl-CoA transferase (subtypes 1B and 1C); ACS1 and ACS2, acetyl-CoA synthase 1 and acetyl-CoA synthase 2. Note that *Monocercomonoides* sp. has undergone a complete secondary loss of MROs<sup>6</sup>.

**Mitochondrial targeting sequences and recognition proteins are reduced in CLOs.** Using hidden Markov model searches, we identified the core conserved mitochondrial protein transport components Tom40, Sam50, Tim44, Tim17/22/23, Pam16, Pam18, mtHsp70 and GrpE, as well as mitochondrial processing peptidase subunits, from one or more CLOs, although many accessory subunits were not detected (Fig. 2). This complement of mitochondrial protein import proteins is comparable to that of *T. vaginalis* hydrogenosomes<sup>9</sup>. A poorly conserved homologue of Tim44 had long remained unidentified, but was recently described in *G. intestinalis*<sup>10</sup>. It is therefore possible that additional protein import components are present in CLOs but could not be detected by our methods.

In most eukaryotes, the majority of mitochondrial proteins are targeted to the mitochondria by N-terminal mitochondrial targeting sequences (MTSs)<sup>11</sup>, which are cleaved by the heterodimeric mitochondrial processing peptidase (MPP) in the matrix<sup>12</sup>. However, some proteins that are known to localize to the *Giardia*, *S. salmonicida* and *Trichomonas* MROs have no predicted MTS, and lack any N-terminal extensions relative to prokaryotic homologues<sup>4,13,14</sup>. Likewise, we did not find MTS predictions for many proteins of clear mitochondrial origin identified in the transcriptome data from CLOs (for example mitochondrial chaperone Cpn60 and mitochondrial iron–sulfur cluster assembly proteins IscS and IscU; Supplementary Data 1). This reduction in the prevalence of MTS

was probably a feature of the last common ancestor of Metamonada, and suggests the existence of unknown MRO-targeting signals in addition to canonical MTSs (Supplementary Data 1).

In *Trichomonas* and *Giardia*, the decreased number of canonical MTSs is accompanied by reductive and/or divergent evolution of the MPP<sup>13</sup>, and hydrogenosome/mitosome protein import machineries are dependent on only a low membrane potential ( $\Delta\psi$ ) following the loss of electron transport<sup>14</sup>. *Giardia* possesses only the MPP-beta-subunit, which seems to function as a homodimer<sup>13</sup>. The *Trichomonas* genome encodes divergent homologues of the alpha- and beta-subunits, which seem to function as a canonical alpha/beta-subunit heterodimer but recognize only short mitochondrial targeting sequences<sup>13</sup>. We recovered both subunits of MPP in the transcriptome data from *Ca. membranifera*, *Ergobibamus cyprinoides*, and *D. brevis*, but identified only the beta-subunit in *Chilomastix cuspidata* and (Fig. 2).

**Loss of the glycine cleavage system correlates with a parasitic lifestyle.** The glycine cleavage system (GCS) consists of four proteins: GCSH, GCSSL, GCSP and GCST. The GCS catalyses the reversible conversion of glycine to ammonium and carbon dioxide, with the associated reduction of NAD<sup>+</sup> to ultimately produce 5,10-methylene-tetrahydrofolate (5,10-CH<sub>2</sub>-THF, which is essential for serine production in mitochondria and MROs<sup>15</sup>) and NADH. Previous studies showed a patchy distribution of these four enzymes

	Tom40	Tom22/Tom9	Tom20	Tom5	Tom6	Tom7	Sam50	Metaxin	Tim8/9/10/13	Mia40	Erv1	Tim44	Tim17/22/13	Tim21	Tim54	Tim18	Pam16	Pam18	mtHsp70	GpE	Oxa1	MPPa	MPPb
<i>Saccharomyces cerevisiae</i>	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
<i>Arabidopsis thaliana</i>	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	+	+	+	+	+	+	+
<i>Paratrimastix pyriformis</i>	+					+						+					+	+				+	
<i>Trimastix marina</i>												+							+				
<i>Trichomonas vaginalis</i>	+	-	-	-	-	-	+	-	+	-	-	+	+	-	-	-	+	+	+	+	-	+	+
<i>Pentatrichomonas hominis</i>																			+				
<i>Carpediemonas membranifera</i>	+							+				+	+				+	+	+	+		+	+
<i>Ergobibamus cyprinoides</i>	+											+	+					+	+			+	+
<i>Aduncisulcus paluster</i>	+							+					+					+	+				
<i>Kipferlia bialata</i>						+						+					+	+	+				
<i>Chilomastix caulleryi</i>								+										+	+				
<i>Chilomastix cuspidata</i>	+							+				+	+					+	+				+
<i>Dysnectes brevis</i>	+											+	+					+	+			+	+
<i>Giardia lamblia</i>	+	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	+	+	+	+	-	-	+
<i>Spiroucleus barkhanus</i>	+																						
<i>Spiroucleus salmonicida</i>	+	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	+	+	+		-	-	-
<i>Spiroucleus vortens</i>	+																						
<i>Trepomonas</i> sp.																		+	+				

**Figure 2 | Predicted mitochondrial protein import proteins in metamonads.** Blue +: present; white -: absent from genome; grey: absent from transcriptome. Data from *Saccharomyces cerevisiae*<sup>9</sup> and *Arabidopsis thaliana*<sup>31</sup> are provided for comparison.

across Metamonada (Fig. 1b; see also previous work<sup>1,16–18</sup>), and as a result the evolutionary history of the GCS remained unclear<sup>16</sup>. We identified all components of the GCS encoded in *D. brevis*, *Aduncisulcus paluster*, *Ca. membranifera*, *E. cyprinoides*, *Kipferlia bialata* and *Ch. cuspidata*. The 5,10-CH<sub>2</sub>-THF generated by the GCS is used by serine hydroxymethyl transferase (SHMT)<sup>15</sup>. We identified SHMT proteins encoded in the transcriptomes of some CLO species, usually with a clear predicted MTS (Supplementary Data 1).

The GCSP gene had an unexpectedly complex phylogenetic history. The eukaryotic-type GCSP contains two distinct N-terminal and C-terminal domains. These domains are consistently recovered as two separate contiguous sequences from the metamonad transcriptomes, an arrangement previously reported only in *Paratrimastix pyriformis*<sup>19</sup>. This split arrangement is also found in some alphaproteobacteria; Metamonada form a clade with these alphaproteobacteria, separate from other eukaryotes (Supplementary Figs 4 and 5, Supplementary Data 2). For all other components of the GCS, CLOs branched with other eukaryotes (Supplementary Figs 6–8). Whether metamonad GCSP proteins are truly present in the split form remains to be confirmed, and the possibility of *trans*-splicing to create a transcript encoding a single protein also cannot be excluded. However, the consistent recovery of two separate contigs for this protein, and the phylogenetic affinity to the split alphaproteobacterial GCSP proteins, suggest that GCSP is truly encoded as two single-domain proteins in metamonads.

An interesting evolutionary pattern emerges from the distribution of GCS across Metamonada: parasitic and secondarily free-living lineages always lack a complete GCS whereas ancestrally free-living lineages possess the complete system (Fig. 1a,b). A similar correlation between GCS distribution and lifestyle emerges when considering metabolically reduced MROs of other eukaryotic lineages (Supplementary Table 1)<sup>1</sup>. An apparent exception is the presence of only GCSH and GCSL in *Trichomonas*; however, the retention of these particular proteins by some parasites can be explained by the fact that they function in other pathways, such as peroxide detoxification<sup>20</sup>. GCS proteins are also absent from the transcriptome data in the free-living diplomonad *Trepomonas*. Phylogenies of diplomonads indicate that *Trepomonas* is secondarily

free-living (Fig. 1)<sup>21</sup>, suggesting that the GCS was lost in a parasitic ancestor. Although parasitic/commensal taxa may be able to rely on the host for some metabolites, it is not known whether *Trepomonas* has an alternative way to cleave glycine into carbon dioxide and ammonium. We examined the metabolic pathways of *Trepomonas* predicted by the KEGG Automatic Annotation pipeline, to identify candidate proteins that might allow this organism to metabolize glycine. However, we did not identify any such candidates. Further experimental studies will be required to understand how *Trepomonas* can function without a canonical GCS.

#### MROs in all CLO lineages are likely to be capable of H<sub>2</sub> production.

The GCS is localized exclusively in mitochondria and MROs, and its activity is sensitive to the redox balance of NAD<sup>+</sup>/NADH<sup>22</sup>, resulting in a need for NADH reoxidation in these compartments. From the transcriptomes of *Ca. membranifera*, *Ch. cuspidata*, *D. brevis*, *E. cyprinoides*, *K. bialata* and trichomonads, we identified two subunits of NADH dehydrogenase, NuoE and NuoF (Fig. 1; Supplementary Data 1), and no other electron transport chain components. These homologues of mitochondrial electron transport chain Complex I subunits are found exclusively in mitochondria and MROs, but have not previously been identified in preaxostylans or diplomonads (Fig. 1b; see also previous work<sup>4,5,19</sup>). In *Trichomonas* hydrogenosomes, [FeFe]-hydrogenase generates H<sub>2</sub> from protons by the oxidation of ferredoxin (Fdx<sup>-</sup>) coupled with the oxidation of NADH by NuoE and NuoF<sup>2,3</sup> (NADH is regenerated by the GCS; see above). We identified an MRO-type 2Fe–2S Fdx homologous to that of *Trichomonas* in all of the CLOs (Supplementary Data 1). The [FeFe]-hydrogenase HydA and its associated maturases, HydE, HydF and HydG, were identified in almost all metamonad lineages (Fig. 1b and Supplementary Data 1); each of the maturases showed phylogenetic affinity with homologues from other anaerobic eukaryotes (Supplementary Figs 9–11). Conversely, HydA in Metamonada may have multiple origins based on the phylogeny of this protein family (Supplementary Fig. 12). However, as with the maturases, we are unable to draw unambiguous conclusions as to the origins of these proteins because of the lack of bootstrap support across many parts of the tree. MTSs were identified for

some of these proteins, such as HydE and HydF from *D. brevis* and HydA and HydG from *Ca. membranifera* (Supplementary Data 1), further supporting their location within the MROs. Thus, it is likely that the MROs of all CLOs, like the hydrogenosomes of *T. vaginalis*, are capable of H<sub>2</sub> production, as well as NADH production (GCS), NADH reoxidation (NuoE/NuoF) and electron transfer (Fdx) (Fig. 3).

**MROs in *D. brevis* are incapable of ATP production.** In the hydrogenosomes in *Trichomonas* spp., ATP is generated through substrate-level phosphorylation by succinyl-CoA synthase (SCS), with the associated conversion of acetyl-CoA to succinyl-CoA by acetate:succinyl-CoA transferase (ASCT)<sup>3,23</sup>. These enzymes are found exclusively in mitochondria and MROs<sup>24,25</sup>. In contrast, acetyl-CoA synthase (ACS) generates ATP directly from the conversion of acetyl-CoA to acetate in both the MROs and cytosol of *S. salmonicida*<sup>4</sup>, and in the cytosol of *Giardia* spp.<sup>25,26</sup>. We identified the alpha- and beta-subunits of a eukaryotic-type SCS in *Ca. membranifera*, *E. cyprinoides*, *A. paluster* and *K. bialata* (as well as in parabasalid species). These subunits showed phylogenetic affinity to mitochondrion-targeted homologues of other eukaryotes (Supplementary Figs 13, 14). ASCT homologues were also found in three of the four CLOs that have SCS (*Ca. membranifera*, *A. paluster* and *K. bialata*; Fig. 1b). ASCT is divided into three classes, known as subtypes 1A, 1B and 1C; *T. vaginalis* is known to possess ASCT1C<sup>25</sup>. ASCT1B was identified in three CLOs; unlike in trichomonads, no CLO transcriptome encoded ASCT1C alone. Interestingly, *K. bialata* has both subtype 1B and subtype 1C. Thus, although the separate phylogenetic analyses of 1B and 1C do not show strong evidence for either vertical inheritance or lateral gene transfer (LGT) into Metamonada, it is possible that possession of both of these enzyme subtypes represents the ancestral state for metamonads (Supplementary Figs 15, 16). The presence of both SCS and ASCT strongly suggests that these deeper-branching CLOs can generate ATP in their MROs.

Two types of ACS were identified in metamonads, and at least one of these types of ACS was found in *Trimastix marina*, *Ca. membranifera*, *A. paluster*, *Chilomastix* spp., *E. cyprinoides*, *K. bialata*, *D. brevis* and diplomonad species. Although some ACSs function in MROs<sup>4,27</sup>, ACSs in *Chilomastix* spp., *K. bialata* and *D. brevis* were closely related to the cytosolically functioning ACSs of diplomonads (*Giardia* spp., *S. salmonicida* and *Trepomonas* sp.; henceforth, ACS1), and only distantly related to the MRO-localized homologue of *S. salmonicida* (Supplementary Figs 17, 18). This suggests that the cytosolic ACS1 was acquired through a single LGT event into the last common ancestor of *Chilomastix*, *Kipferlia*, *Dysnectes* and diplomonads. The other metamonad ACS homologues (ACS2) are of different origin(s), although because of the lack of resolution in this phylogeny it is unclear whether ACS2 was ancestrally present in metamonads (Supplementary Figs 17, 18). No predicted MRO-localizing homologues of ACS, SCS or ASCT were identified in the transcriptome of *D. brevis*, nor in any diplomonads, with the exception of *S. salmonicida*<sup>4</sup>.

As described above, GCS, NuoE and NuoF are metabolically linked enzyme systems that are only known to function within mitochondria and MROs. However, NuoE and NuoF require an electron sink in order to regenerate NAD<sup>+</sup> (required by the GCS), for example by reduction of protons to hydrogen. We recovered these proteins, and [FeFe]-hydrogenase maturases with predicted MTS, from the transcriptome of *D. brevis*, strongly suggesting that [FeFe]-hydrogenase is active in its MRO. Yet, despite the high transcriptome coverage in *D. brevis*, we have identified only the cytosolic-type ATP production machinery in *D. brevis* (ACS1; see above). We therefore hypothesize that *D. brevis* harbours a new type of mitochondrion-related organelle that evolves molecular hydrogen but does not produce ATP (Fig. 3).

**ATP synthesis was lost and regained in metamonad MROs.** The extremely patchy distribution of the ACS gene in the eukaryotic tree of life has been explained by multiple LGTs<sup>4,28,29</sup>. Our phylogenetic analyses placed the hydrogenosome-localizing ACS2 homologue of *S. salmonicida* separately from all other metamonad homologues (Supplementary Figs 17, 18). Meanwhile, since only cytosolic ACS1 was identified in other diplomonads and in their close relative *D. brevis*, a parsimonious explanation is that the common ancestor of diplomonads and *D. brevis* possessed an MRO incapable of ATP production. This would imply that the MROs of *S. salmonicida* acquired the capacity for ATP production secondarily, through LGT of the hydrogenosomal ACS2.

**Complex functions in the last common ancestor of metamonads.** The hydrogenosomes in *T. vaginalis* function in pyruvate metabolism and amino acid metabolism<sup>30</sup>, whereas in *Giardia* spp. these pathways occur in the cytosol<sup>5,17</sup>. We found homologues of enzymes of pyruvate metabolism and amino acid metabolism in CLOs (data not shown), *Trimastix* and *Paratrimastix*; but, in the absence of any predicted MTS, we could not conclude that they function in the MROs.

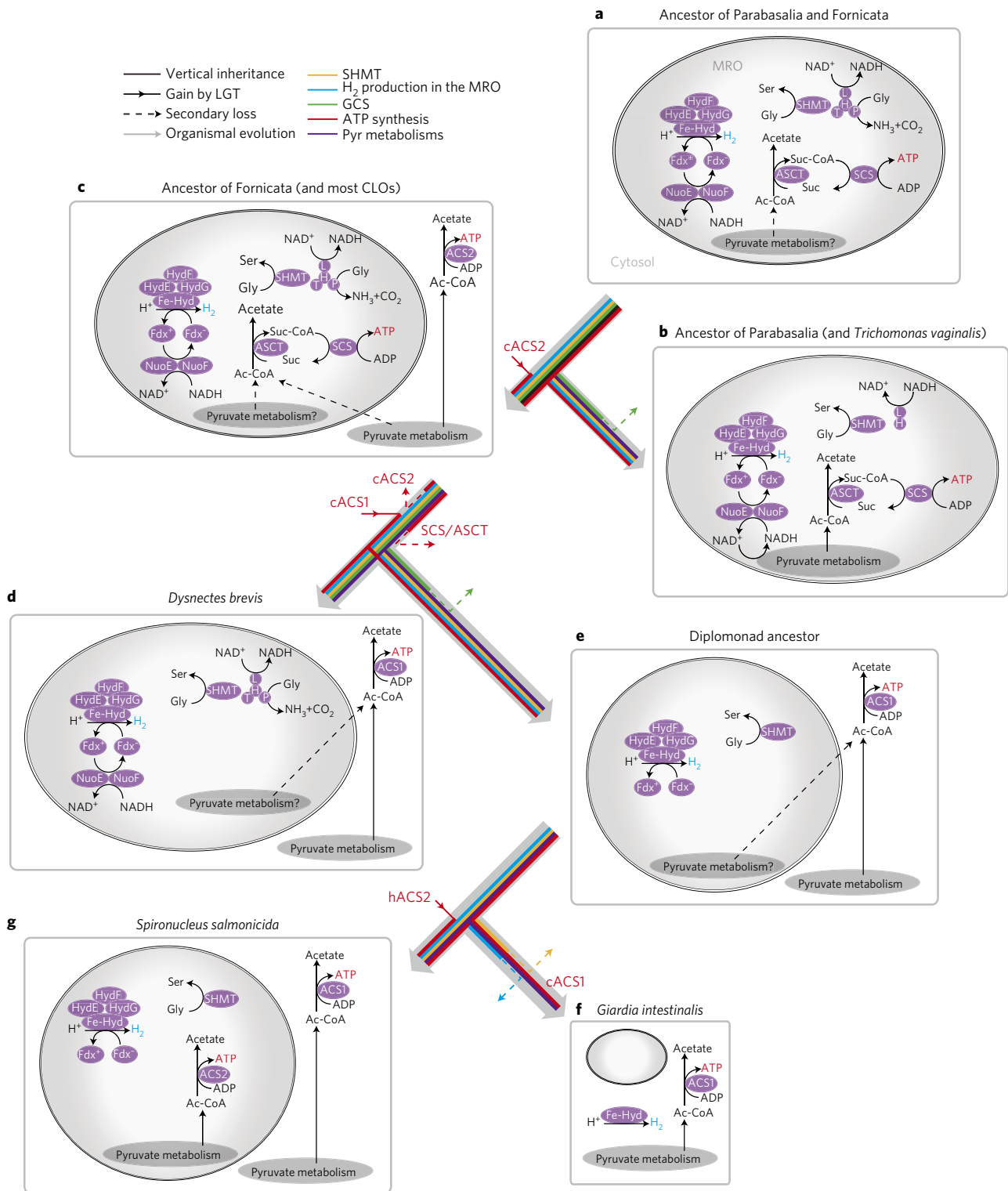
In addition to the proteins discussed above, we identified other possible MRO-localizing proteins that are not present in the hydrogenosomes of *Trichomonas* spp. or in the mitosomes of *Giardia* spp., but that are broadly conserved in canonical mitochondria. These include cardiolipin synthase in *Ca. membranifera* (Supplementary Fig. 19) and aminoadipate-semialdehyde dehydrogenase in *Trim. marina* (Supplementary Fig. 20). The metamonad homologues showed affinity to other eukaryotic homologues in phylogenetic analyses (Supplementary Figs 19, 20), indicating that they have probably been vertically inherited from the last eukaryotic common ancestor. These findings further support our inference that the metabolic pathways and functions in MROs of the last metamonad common ancestor were more complex than those of the hydrogenosomes of *Trichomonas* spp.

## Discussion

As a primarily transcriptomic analysis, our work is necessarily vulnerable to the possibility that the culture conditions under which the samples were generated affected the transcripts recovered. As a result, complete genome-based analyses will be helpful to cross-check our observations. Our transcriptome analyses indicate that the MROs of the last common ancestor of Fornicata resembled those of *T. vaginalis* in that they generated ATP with the associated production of hydrogen (Fig. 1b; Fig. 3). In contrast, the MROs of the last common ancestor of Diplomonadida had already secondarily lost the ATP synthesis machinery but had retained the capacity for hydrogen production (Fig. 1b; Fig. 3). Hydrogenosomes are generally characterized as functioning in anaerobic ATP production, with the concomitant production of hydrogen<sup>1,3</sup>. Our analyses suggest that in some CLOs, such as *Dysnectes*, these functions are spatially uncoupled within the cell. The MROs of these organisms resemble hydrogenosomes in their involvement in hydrogen production, but are more similar to mitosomes in their inability to synthesize ATP.

In organisms (such as *Dysnectes*) that possess this type of organelle, ATP is probably synthesized through the cytosolic ACS-based reaction, as in *Giardia*. Nevertheless, we hypothesize that there is a constraint against loss of hydrogen production from these MROs because hydrogen production functions as an electron acceptor, not for pyruvate metabolism but for amino acid metabolism. As parasites are able to rely on the host in terms of metabolites, the evolutionary transition to parasitism might lead to further functional reduction, allowing loss of amino acid metabolism pathways from MROs without affecting cell viability. As a result, MROs originally resembling those of *Dysnectes* might then lose both amino acid metabolism pathways and hydrogen production, resulting in





**Figure 3 | Evolutionary transitions of metabolic pathways of MROs from the common ancestor of Parabasalia and Fornicata to representative extant species. a**, Ancestor of Parabasalia and Fornicata. **b**, Ancestor of Parabasalia. **c**, Ancestor of Fornicata. **d**, *Dysnectes brevis*. **e**, Ancestor of diplomonads. **f**, *Giardia intestinalis*. **g**, *Spiroucleus salmonicida*. In this figure, only glycine cleavage (by the glycine cleavage system), hydrogen production and ATP production are shown. We cannot confidently assign cytosolic or MRO localization of proteins involved in pyruvate metabolism, other than in *Giardia*, *Trichomonas* and *Spiroucleus*. cACS1/cACS2, cytosolic acetyl-CoA synthase 1/cytosolic acetyl-CoA synthase 2; hACS2, hydrogenosomal acetyl-CoA synthase 2.

MROs like those found in *Giardia*, unable to produce either ATP or hydrogen. Thus, this type of MRO may represent an evolutionarily intermediate state between hydrogenosomes and mitosomes. In any

case, mitosomes in *G. intestinalis* were apparently shaped by step-wise losses from an organelle similar to the hydrogenosome of *T. vaginalis*, but possessing a richer set of metabolic pathways,

including a complete GCS. The MROs of *Dysnectes* are important snapshots of an intermediate step in this process.

## Methods

**Culturing, RNA isolation and sequencing.** Cultures were maintained as described by Zhang *et al.*<sup>32</sup> (in the case of *T. marina*, isolate PCT) and as described by Takishita *et al.*<sup>7</sup> (in the case of *Chilomastix caulleryi*), following the procedures set forth by the American Type Culture Collection (ATCC; <http://www.atcc.org/products/all/50927.aspx#culturemethod>) (in the case of *Ch. cuspidata*) or as described by Kolisko *et al.*<sup>33</sup> (all other *Carpodiemonas*-like organisms). RNA was isolated from ~1–31 of culture using TRIzol reagent (Invitrogen, USA; Life Technologies, USA) according to the manufacturer's instructions. Sanger and 454 sequencing libraries were prepared by Agencourt (Germany), and Illumina libraries by Genome Quebec (Canada). 454 (GS FLX Titanium, single-end) and Illumina (HiSeq2000, paired-end) sequencing were carried out by Genome Quebec. For *A. paluster* and *D. brevis*, cDNA synthesis and sequencing by Illumina (HiSeq2000, paired-end) were instead carried out by Eurofins Genetic Services (Eurofins, Germany). In the case of *E. cyprinoides*, an initial Sanger transcriptome was sequenced: mRNA was double purified from total RNA using magnetic beads (Ambion, USA), a Sanger sequencing cDNA library was prepared, and Expressed Sequence Tag (EST) reads were sequenced. This cDNA library was subsequently modified for 454 sequencing by Agencourt, and subjected to 454 sequencing by Genome Quebec. The number of reads per species is as follows: *Ca. membranifera*, 57.6 thousand 454 reads and 16.4 million Illumina reads; *E. cyprinoides*, 15.9 thousand 454 reads and 5,220 Sanger reads; *A. paluster*, 147 million Illumina reads; *K. bialata* (isolate NY0173), 28.1 thousand 454 reads; *D. brevis*, 148.6 million Illumina reads; *Ch. cuspidata*, 183.4 million Illumina reads; *Ch. caulleryi*, 28.3 thousand reads; and *T. marina* PCT, 35.2 million Illumina reads. Raw sequencing data were deposited into the NCBI Short Reads Archive (SRA) database under accession number SRP077666.

**Assembly.** Sanger and 454 sequence data were assembled using the MIRA3 assembler with miraEST<sup>34</sup>, using default assembly parameters. Where both types of data were available, a hybrid assembly was performed. Adapter (SSAHA scan output) and quality clipping were performed by MIRA3. RNA-Seq data were quality-trimmed using an in-house script (25 minimum quality score over a 20-nucleotide sliding window; minimal length of read after trimming 50 nucleotides) and assembled using the program inchworm from the Trinity software package with default parameters<sup>35</sup>.

**Phylogenomic dataset assembly.** Data were added to our previously published phylogenomic dataset<sup>36</sup>, and the new taxa were added to the dataset using procedures described previously<sup>36</sup>. Briefly, each reference protein was used as a query in tblastn searches of each metamonad species, and the five top hits (with an expected value (e-value)  $<1 \times 10^{-10}$ ) were retained. These were then added to the alignments, and preliminary single-gene trees were constructed using MAFFT<sup>37</sup> for alignment, BMGE<sup>38</sup> for trimming of ambiguously aligned positions, and FastTree<sup>39</sup> for tree construction. The single gene trees were inspected by eye, and paralogues were removed (in the case of multiple in-paralogues, the best coverage or shortest branching sequence was selected). Final single-gene datasets were constructed using MAFFT L-INS-I, and trimmed with BMGE. Final concatenation was carried out using the program alvert from Barrel-O-Monkeys (<http://rogerlab.biochemistryandmolecularbiology.dal.ca/monkeybarrel.php>). The final alignment used for the phylogenomic analysis consisted of 94 taxa and 39,089 sites. The phylogenomic tree was constructed using RAXML<sup>40</sup> under the PROTGAMMALGF model, with 25 independent searches and 500 regular non-parametric bootstraps; and using IQ-TREE<sup>41</sup> under the LG+C60+F+Gamma model, with 1,000 ultrafast bootstrap replicates<sup>42</sup>. A Bayesian phylogeny was constructed using the CAT-GTR model incorporating among-site rate variation approximated by a discrete gamma distribution with four categories (CAT-GTR +  $\Gamma$  model), implemented in PhyloBayes-MPI 1.5a<sup>43</sup>, after the exclusion of constant sites. Four independent Markov-chain Monte Carlo chains were run for over 10,000 cycles, sampling every two cycles. After this time, three of the four chains converged on the topology for metamonads shown in Fig. 1 with a 20% burn-in, but failed to converge on a single topology for several other parts of the tree.

**Mitochondrial gene tree construction.** A custom metamonad protein database was assembled from our newly sequenced datasets, as well as from publicly available genomes and transcriptomes of other metamonads (*Pa. pyriformis*, *T. vaginalis*, *Pentatrichomonas hominis*, *Tritrichomonas foetus*, *S. vortens*, *S. barkhanus*, *S. salmonicida*, *G. intestinalis* and *Trepomonas* sp.). For each gene, an initial tree was assembled as follows:

- (1) A seed sequence was used as a blast query against the NCBI non-redundant (nr) database with an e-value  $<1 \times 10^{-10}$ , and the top 250 hits were retrieved.
- (2) The same seed sequence was used as a blast query against the custom metamonad protein database, recovering all sequence hits with an e-value threshold of  $1 \times 10^{-5}$ , creating the raw Metamonada dataset.

- (3) The raw Metamonada dataset sequences were clustered using CD-HIT<sup>44</sup> at 99% identity, creating the clustered Metamonada dataset.
- (4) For each sequence in the clustered Metamonada dataset, the top three hits were recovered by blast searches against each major group of bacteria and eukaryotes in the nr taxonomy database. Duplicate sequences were removed.
- (5) The sequences from steps 1, 3 and 4 were grouped to make a final dataset. Sequences were aligned using MAFFT, ambiguously aligned positions were removed using trimAl<sup>45</sup> and initial trees were constructed using FastTree.

Each initial tree was then visually inspected to select orthologues of interest. After removal of paralogues, each alignment was refined using MAFFT L-INS-I<sup>46</sup>, ambiguously aligned positions were removed using BMGE, and the final phylogenies were constructed in RAXML with 100 rapid bootstrap replicates under the PROTGAMMALGF model. In the cases of MPP and ACS, removal of paralogues or manual addition of sequences was performed several times to ensure that the correct orthologue was present in the final tree.

The cardioplin synthase phylogeny was constructed by adding the *Ca. membranifera* sequence to a dataset previously assembled and published by Noguchi *et al.*<sup>47</sup>.

**Mitochondrial targeting prediction.** For each protein sequence of interest, the presence of a MTS was predicted using MitoPro<sup>48</sup>, TargetP<sup>49</sup> (with default parameters for non-plant sequences) and MitoFates<sup>50</sup> (with default parameters for fungal sequences).

**Data availability.** Sequence data that support the findings of this study have been deposited in the NCBI Short Reads Archive (SRA) database under accession number SRP077666. The alignment data that support the findings of this study have been made available through the Dryad Digital Repository (<http://doi.org/10.5061/dryad.34qd7>).

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## Author contributions

M.K., R.K., J.O.A., Y.I., A.G.B.S., T.H. and A.J.R. conceived and designed the experiments; M.K., K.K., I.Č., J.D.S., F.X., A.Y. and Q.Z. performed the experiments; M.M.L., M.K., R.K., C.W.S., K.K., L.E. and Y.I. analysed the data; R.K., C.W.S., J.D.S., K.T., Y.I., A.G.B.S., T.H. and A.J.R. contributed materials and/or analysis tools; and M.M.L., M.K., R.K., A.G.B.S. and A.J.R. wrote the paper.

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## Competing interests

The authors declare no competing financial interests.