

Summary of the phylogenetic and sequencing coverage analyses

| EC number | Enzyme name | Pathway | Alignment length | # distinct alignment patterns | Presence | Cluster / sister group of trypanosomatids | Cluster / sister group of TPEs | Figure / Additional file | Genome's average coverage* | Contig's average coverage* | Gene's average coverage* | Genome* |
|-----------|---|---------------------------------|------------------|-------------------------------|---|--|---|--------------------------|----------------------------|----------------------------|--------------------------|--------------------------|
| 5.1.1.7 | diaminopimelate epimerase | Lysine | 1661 | 1409 | <i>Herpetomonas</i> and TPEs | Group within Bacteroidetes (BSV=99). | Alcaligenaceae family (BS=98). | Additional file 2 | 18x | 17x | 21x | <i>H. muscarum</i> |
| 4.1.1.20 | diaminopimelate decarboxylase | Lysine | 2171 | 1869 | SHTs (<i>A. desouzai</i> not in the tree, incomplete sequence similar to <i>A. deanei</i>), <i>Herpetomonas</i> and TPEs. | Group with a few other Eukaryota (Dictyostelium, Polysphondylium, and Capsaspora, BSV=65), all as the sister group of a large group of Actinobacteria (BSV=79). | Alcaligenaceae family (BS=95). | Additional file 3 | 28x | 19x | 21x | <i>S. galati</i> |
| 2.3.1.30 | serine O-acetyltransferase | Cysteine | 1500 | 1248 | SHTs and RTs | Group inside a group of diverse bacterial taxa (BS=80), including Bacteroidetes, Betaproteobacteria, Gammaproteobacteria and Firmicutes. | - | Additional file 4 | 23x | 19x | 31x | <i>A. deanei</i> |
| 2.5.1.47 | cysteine synthase | Cysteine | 2809 | 2577 | SHTs and RTs | SHTs, RTs (one copy of <i>T. cruzi</i> CL Brener) and one <i>Entamoeba</i> sp. clade has Actinobacteria as sister group (low BS), and far from the other eukaryotic groups. | - | Additional file 5 | 28x | 23x | 28x | <i>S. galati</i> |
| 2.3.1.46 | homoserine O-succinyltransferase | Cysteine – Methionine | 975 | 808 | SHTs and <i>Herpetomonas</i> | Trypanosomatid clade (BS=91). Group within the Bacteroidetes (BS=89). | - | Additional file 6 | 28x | 19x | 16x | <i>S. galati</i> |
| 2.1.1.37 | DNA (cytosine-5-)methyltransferase | Cysteine – Methionine | 2123 | 2095 | SHTs and RTs | The few Eukaryota in the tree form a clade (low BS) among the several different phyla of Bacteria (low BS). | - | Additional file 7 | 28x | 23x | 22x | <i>S. galati</i> |
| 2.5.1.48 | cystathionine gamma-synthase | Cysteine – Methionine | 2848 | 2522 | SHTs and RTs | Group with <i>Trypanosoma</i> sp. and a few other Eukaryota, mostly Apicomplexa and Stramenopiles, within Acidobacteria (BS=94). | - | Additional file 8 | ND | ND | ND | |
| 2.5.1.49 | O-acetylhomoserine aminocarboxypropyltransferase | Cysteine – Methionine | 2848 | 2522 | SHTs and <i>Herpetomonas</i> | Cluster with diverse groups of Bacteria (low BS). | - | Additional file 8 | 24x | 27x | 53x | <i>A. desouzai</i> |
| 4.4.1.8 | cystathionine beta-lyase | Cysteine – Methionine | 2848 | 2522 | SHTs and RTs | Two copies: one clusters with eukaryotes (BS=95) and the other seems to be of bacterial descent, grouping mostly with Alphaproteobacteria of the Rhizobiales order (BS=99). | - | Additional file 8 | 18x | 20x | 21x | <i>H. muscarum</i> |
| 2.1.1.10 | homocysteine S-methyltransferase | Methionine | 2771 | 2445 | SHTs and RTs | Clade SHTs and RTs (BS=96) grouped next to mostly Gammaproteobacteria (low BS). | - | Additional file 9 | 18x | 14x | 11x | <i>C. acanthocephali</i> |
| 2.1.1.14 | 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase | Methionine | 1811 | 1662 | SHTs and RTs (except <i>Herpetomonas</i>) | The <i>Angomonas</i> species group with <i>C. acanthocephali</i> (BS=98) while the <i>Strigomonas</i> group with <i>Leishmania</i> (BS=100). The trypanosomatids group deep within the Gammaproteobacteria (BS=74). | - | Additional file 10 | 23x | 15x | 15x | <i>S. culicis</i> |
| 2.7.1.100 | S-methyl-5-thioribose kinase | Methionine salvage | 1358 | 1080 | <i>C. acanthocephali</i> and <i>Herpetomonas</i> | Group deep within the Gammaproteobacteria (BS=97). | - | Additional file 11 | 18x | 15x | 24x | <i>H. muscarum</i> |
| 1.1.1.3 | homoserine dehydrogenase | Cysteine – Methionine Threonine | 2189 | 1921 | SHTs, RTs and TPEs | Cluster within the Firmicutes, with <i>Solibacillus silverstris</i> and <i>Lysinibacillus fusiformis</i> and <i>L. sphaericus</i> as sister group (BS=100). | Placed in the Alcaligenaceae family (BS=91). | Figure 8 | 24x | 26x | 34x | <i>A. desouzai</i> |
| 4.1.2.5 | L-threonine aldolase | Glycine <=> Threonine | 2083 | 1700 | SHTs and RTs (except <i>Herpetomonas</i>) | SHTs and RTs group in very distant clades: <i>Leishmania</i> and <i>C. acanthocephali</i> group within Firmicutes, specially <i>Clostridium</i> (BS=63), while the SHT group basally with Eukaryota, interrupted by an assorted group of Bacteria (low BS). SHTs and RTs are in opposite sides of the tree, separated by a relatively long branch. | - | Additional file 12 | 23x | 16x | 12x | <i>S. culicis</i> |
| 4.2.1.20 | tryptophan synthase | Tryptophan | 1392 | 1339 | SHTs, <i>Herpetomonas</i> and TPEs | SHTs and <i>Herpetomonas</i> group together (BS=50) and group robustly with the Bacteroidetes phylum (BS=97). | Group with the Alcaligenaceae family (BS=90). | Additional file 13 | 23x | 15x | 21x | <i>S. culicis</i> |
| 3.5.1.14 | aminoacylase | Ornithine | 2397 | 1920 | SHTs and RTs | <i>Angomonas</i> has two different copies (in different clades), while <i>Strigomonas</i> have one (grouped with <i>Angomonas</i> , BS=96). RTs also have multiple different copies. All gene copies group as one clade and have as nearest sister group a Gammaproteobacterium (BS=98). Group with Bacteria of different phyla (low BS). | - | Additional file 14 | 23x | 36x | 36x | <i>A. deanei</i> |
| 3.5.1.16 | acetylornithine deacetylase | Ornithine | 920 | 831 | SHTs and RTs | The gene copies of SHTs and RTs group together (BS=84). Group within mainly Betaproteobacteria (BS= 80), and no other Eukaryota seem to have these orthologs. | - | Additional file 15 | 24x | 17x | 13x | <i>A. desouzai</i> |
| 6.3.4.5 | argininosuccinate synthase | Arginine | 2322 | 1311 | SHTs and RTs | Clade trypanosomatid (BS=100) group within mainly Firmicutes (BS=69). | - | Additional file 16 | 23x | 28x | 35x | <i>A. deanei</i> |
| 4.3.2.1 | argininosuccinate lyase | Arginine | 1960 | 1520 | SHTs and RTs | Trypanosomatid clade groups within Firmicutes (BS=82). | - | Additional file 17 | 23x | 28x | 31x | <i>A. deanei</i> |
| 3.5.3.1 | arginase | Ornithine | 2403 | 1548 | SHTs and RTs | All but the <i>Herpetomonas</i> ortholog are of eukaryotic origin (BS=61). <i>Herpetomonas</i> gene groups in a distant bacterial clade (BS=79) containing several different assorted phyla. | - | Additional file 18 | 18x | 21x | 15x | <i>H. muscarum</i> |
| 4.3.1.12 | ornithine cyclodeaminase | Ornithine <=> Proline | 1108 | 990 | Only in SHTs | Group close to several Alcaligenaceae (BS=63). | - | Additional file 19 | 23x | 15x | 19x | <i>A. deanei</i> |

Cells in red and pale yellow indicate HGT cases with strong and moderate support (bootstrap and tree patterns), respectively, while gray cells indicate cases that are currently indeterminate and can not be assigned to an HGT event.

* Genome, contig, and gene average sequencing coverages were calculated for the organism indicated in the "Genome" column. ND: not determined.

Abbreviations: TPE = trypanosomatid proteobacterial endosymbiont; SHT = symbiont-harboring trypanosomatid; RT = regular trypanosomatid.