**Supplementary material**

**Table S1.** Taxa included in the median-joining network (Figure S1) and phylogenetic tree reconstruction (Figure S2) of mitochondrial cytochrome b gene lineages of *Plasmodium* spp.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Lineage**  **(MalAvi)** | **Host** | **Locality** | **GenBank**  **accession no.** | **Reference** |
| BT7 | *Parkesia noveboracensis* (Passeriformes: Parulidae) | USA | MF817784 | Smith *et al*., 2018 |
| COLPAL03 | *Columba palumbus* (Columbiformes: Columbidae) | Germany | MT888851 | Schumm *et al*., 2021 |
| CXPIP09 | *Larus argentatus* (Charadriiformes: Laridae) | Japan\* | - | Inumaru *et al*., 2017 |
| DENPET03 | *Rynchops niger* (Charadriiformes: Laridae) | Brazil | KJ469132 | Roos *et al*., 2015 |
| FALTIN14 | *Falco tinnunculus* (Falconiformes: Falconidae) | China | MT281523 | Huang *et al*., 2020 |
| PARUS67 | *Parus major* (Passeriformes: Paridae) | Sweden | KU695264 | Dubiec *et al*., 2016 |
| PHPAT01 | *Rynchops niger* (Charadriiformes: Laridae) | Brazil | - | Roos *et al*., 2015 |
| SFC6 | *Muscicapa striata* (Passeriformes: Muscicapidae) | Europe | DQ368389 | Pérez-Tris *et al*., 2007 |
| SGS1 | *Larus* spp. (Charadriiformes: Laridae) | Poland | - | Zagalska-Neubauer and Bensch, 2016 |
| STEHIR01 | *Sterna hirundo* (Charadriiformes: Laridae) | Argentina | ON872158 | Present study |
| STEHIR02 | *Sterna hirundo* (Charadriiformes: Laridae) | Argentina | ON872159 | Present study |
| TURDUS1 | *Cyanistes caeruleus* (Passeriformes: Paridae) | Europe | HQ537478 | Szöllősi *et al*., 2011 |

\*captivity

For phylogenetic tree reconstruction, DNA sequences were aligned by CLUSTALW using MEGA version 10 (Kumar *et al*., 2018). The best-fit model of DNA sequence evolution was selected using jModeltest 2.1.7 (Darriba *et al*., 2012). According to the Akaike information criterion, we used the General Time Reversible model including invariable sites and variation among sites (GTR+I+G; Gu *et al*., 1995). Phylogenetic reconstruction was performed with BEAST 1.8.4. (Drummond *et al*., 2012). Tree priors were selected using the interface BEAUTi 1.8.4. with strict clock and a Yule speciation process (Yule, 1925; Gernhard, 2008). Markov chain Monte Carlo (MCMC) simulations were run with 25,000,000 generations and one tree was recorded every 1000 generations. In all, 10% of the trees were discarded as burn-in in TreeAnnotator (BEAST package). We validated the results of the Bayesian analyses in Tracer 1.6. (Drummond and Rambaut, 2007). The phylogenetic tree was constructed with FigTree 1.4.3 (Rambaut, 2007). Values < 0.70 are indicated by a dash.

**Diagram

Description automatically generated**

**Fig. S1.** Median-joining network of mitochondrial cytochrome b gene lineages of *Plasmodium* spp. (the two lineages found in the present study and reference lineages from Laridae family from wildlife present in MalAvi database, all of 479 bp, are presented). Circles represent distinct genetic lineages, and the circle sizes are proportional to the lineage frequencies. One hatch mark represents one mutation. Lineage names are noted at the associated circles

**Diagram

Description automatically generated with low confidence**

**Fig. S2** Phylogeny of mitochondrial cytochrome b gene lineages of *Plasmodium* spp. from Laridae family present in MalAvi database (only from wildlife) and the first five reference lineages from MalAvi blastn inferred using Bayesian analysis. Branch support values indicate Bayesian posterior probabilities. Lineages found in the present study are shown in bold. *Leucocytozoon* sp. (MT888851) was included as outgroup.

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