**Supplementary materials**

**Location and timing of infection drives a sex-bias in *Haemoproteus* prevalence in a hole-nesting bird**

Table S1 Sample sizes across years of collared flycatchers in this study.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Year | 1 Females | 2+ Females | 1 Males | 2+ Males | Total |
| 2002 | 0 | 12 | 4 | 11 | 27 |
| 2003 | 16 | 17 | 18 | 12 | 63 |
| 2004 | 56 | 47 | 34 | 48 | 185 |
| 2005 | 32 | 39 | 31 | 36 | 138 |
| 2006 | 6 | 5 | 4 | 5 | 20 |
| 2007 | 13 | 21 | 12 | 20 | 66 |
| 2009 | 25 | 72 | 22 | 70 | 189 |
| 2010 | 20 | 30 | 19 | 32 | 101 |
| 2011 | 8 | 8 | 6 | 7 | 29 |
| 2012 | 19 | 41 | 3 | 39 | 102 |
| 2013 | 11 | 22 | 10 | 17 | 60 |
| 2014 | 5 | 12 | 2 | 17 | 36 |
| 2015 | 0 | 2 | 1 | 9 | 12 |
| 2016 | 16 | 73 | 11 | 106 | 206 |
| Total | 227 | 401 | 177 | 429 | 1234 |

Table S2. Determination of the transmission location for each of the 25 lineages detected in collared flycatchers. The number of migratory or resident hosts for each ecozone for each lineage are indicated. \*COLL2 was detected in a hatch year song thrush (*Turdus philomelos*) in Sweden 1, indicating transmission in Europe as well as in Africa, furthermore song thrushes rarely overwinter outside Europe. \*\*COLL3 was only detected in migratory species, however as the lineage was detected in fledglings before their first visit to Africa, this lineage is determined to be transmitted on the breeding grounds 2. \*\*\*GRW11 was detected in cape bulbuls (*Pycnonotus capensis*) in South Africa 3, however this is likely the result of a biological invasion, given that the lineage is widespread in several resident species in Europe that have been successfully introduced to southern South Africa. Given that the range of the cape bulbul does not overlap with the wintering range of collared flycatchers and given that the environmental conditions in southern South Africa resemble southern Europe, it is likely that transmission in tropical Africa is unlikely for this lineage. Additional details are available from the publicly accessible MalAvi Database (http://130.235.244.92/Malavi/).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Lineage** | **Hosts** | **Status** | **Ecozone** | **References** |
| ACCTAC01 | 17 | Resident | Afrotropical | 3–6 |
| ACCTAC01 | 4 | Migrant | Palearctic | 2,7–13 |
| AEMO01 | 1 | Migrant | Afrotropical | 14 |
| AEMO01 | 16 | Resident | Afrotropical | 5,6,15–17 |
| AEMO01 | 5 | Migrant | Palearctic | 2,7,9,13,18 |
| COLL10 | 1 | Migrant | Palearctic | 9–11 |
| COLL11 | 4 | Resident | Afrotropical | 6 |
| COLL11 | 1 | Migrant | Palearctic | 9–11 |
| COLL2 | 1 | Migrant | Afrotropical | 6 |
| COLL2 | 3 | Resident | Afrotropical | 4,6,16,19 |
| COLL2 | 1 | Resident | Australasia | 20 |
| COLL2 | 6 | Migrant | Nearctic | 21–23 |
| COLL2 | 7 | Resident | Oriental | 24–27 |
| COLL2 | 5 | Migrant | Palearctic\* | 1,2,9–13,16,18,28–31 |
| COLL3 | 5 | Migrant | Palearctic\*\* | 1,2,9–13,16,18,28–30,32 |
| COLL4 | 3 | Resident | Afrotropical | 15,33 |
| COLL4 | 2 | Migrant | Nearctic | 23,34 |
| COLL4 | 8 | Resident | Neotropical | 35–37 |
| COLL4 | 2 | Migrant | Palearctic | 9–11,18,28,38 |
| COLL6 | 3 | Migrant | Palearctic | 2,9,11,13,39,40 |
| COLL7 | 18 | Resident | Afrotropical | 3,5,6,15,17,33,41–43 |
| COLL7 | 2 | Migrant | Palearctic | 2,9–12,18,28 |
| GRW07 | 2 | Migrant | Palearctic | 9–11,44 |
| GRW09 | 72 | Resident | Afrotropical | 3–6,15–17,33,41,42,45–48 |
| GRW09 | 1 | Resident | Oriental | 41 |
| GRW09 | 13 | Migrant | Palearctic | 1,2,7,9–13,16,18,28–30,39,44,49–53 |
| GRW10 | 4 | Resident | Afrotropical | 6,15 |
| GRW10 | 4 | Migrant | Palearctic | 9,11,12,28,44,54,55 |
| GRW11 | 1 | Migrant | Afrotropical | 14,16 |
| GRW11 | 1 | Resident | Afrotropical\*\*\* | 3 |
| GRW11 | 20 | Migrant | Palearctic | 2,9,10,12,16,18,29,32,39,49,53,55–67 |
| GRW11 | 22 | Resident | Palearctic | 1,3,29,32,42,49,50,54,55,57,67–94 |
| LAMPUR03 | 19 | Resident | Afrotropical | 4,15 |
| LAMPUR03 | 4 | Migrant | Palearctic | 2,9–11,30,51,95 |
| PBPIP1 | 4 | Resident | Afrotropical | 6,16,43 |
| PBPIP1 | 1 | Resident | Oriental | 24 |
| PBPIP1 | 3 | Migrant | Palearctic | 1,2,10,96 |
| PBPIP1 | 1 | Resident | Palearctic | 89 |
| PFC1 | 2 | Migrant | Palearctic | 1,2,9–12,16,18,28,29,88,97–99 |
| PFC1 | 1 | Resident | Palearctic | 16 |
| PHSIB1 | 1 | Migrant | Afrotropical | 100 |
| PHSIB1 | 14 | Migrant | Palearctic | 1,2,9–12,16,29,44,98,101,102 |
| PHSIB1 | 12 | Resident | Palearctic | 1,16,29,71,79,88,91,92,98,101,103 |
| RTSR1 | 1 | Migrant | Afrotropical | 16 |
| RTSR1 | 3 | Resident | Afrotropical | 43,104 |
| RTSR1 | 13 | Migrant | Palearctic | 1,2,6,8–12,14,16,18,29,31,32,44,49,50,55,61,65,67,105–110 |
| SGS1 | 3 | Migrant | Afrotropical | 16,100 |
| SGS1 | 15 | Resident | Afrotropical | 3,15,16,81,100,111 |
| SGS1 | 2 | Resident | Australasia | 112,113 |
| SGS1 | 1 | Migrant | Nearctic | 114 |
| SGS1 | 2 | Resident | Nearctic | 115 |
| SGS1 | 9 | Resident | Neotropical | 116,117 |
| SGS1 | 1 | Resident | Oriental | 41 |
| SGS1 | 31 | Migrant | Palearctic | 1,2,9–11,13,14,16,29,31,32,44,49–51,53,54,57,59,61–67,82,94,95,98,110,118–124 |
| SGS1 | 55 | Resident | Palearctic | 1,7,16,29,32,41,49,50,54,55,57,64,67–71,73–94,110,119,125–140 |
| SYBOR05 | 1 | Resident | Afrotropical | 141 |
| SYBOR05 | 2 | Migrant | Palearctic | 11,14 |
| SYBOR10 | 1 | Migrant | Afrotropical | 14,16 |
| SYBOR10 | 1 | Resident | Afrotropical | 43 |
| SYBOR10 | 4 | Migrant | Palearctic | 8–11,55 |
| TERUF02 | 1 | Resident | Afrotropical | 4 |
| TERUF02 | 3 | Migrant | Palearctic | 9–11,18,28,60 |
| TURDUS1 | 1 | Migrant | Afrotropical | 14,16 |
| TURDUS1 | 23 | Migrant | Palearctic | 1,2,9–11,39,49,52,60,63,94,98,100,108,110,120,123,126,127,142–145 |
| TURDUS1 | 19 | Resident | Palearctic | 1,16,29,38,69,71,76,79,84–88,90,91,98,101,110,125,126,128,131,134,139,144,146,147 |
| WW2 | 23 | Migrant | Palearctic | 1,2,8,9,11,14,16,29,44,49,52,55,61,63,67,101,148–150 |
| WW2 | 9 | Resident | Palearctic | 1,16,29,71,79,85,91,94,101 |
| WW4 | 7 | Resident | Afrotropical | 6,15,33 |
| WW4 | 5 | Migrant | Palearctic | 1,9–11,13,18,61,67,149 |

Table S3. Investigation into the presence of indicator lineages in collared flycatchers, determining whether malaria communities are structured across flycatcher sex and age categories using the ‘indicspecies’ package in R. We found no significant indicator lineages in collared flycatcher communities.

|  |  |  |  |
| --- | --- | --- | --- |
| **Grouping** | **Lineage** | **Indicator value** | ***p*** |
| 2+ Females | hCOLL2 | 0.938 | 1.000 |
| 2+ Females & Males | hCOLL3 | 0.905 | 1.000 |
| 2+ Females | hPFC1 | 0.951 | 1.000 |
| 2+ Females | hPHSIB1 | 0.907 | 1.000 |
| 2+ Females | hWW2 | 1.000 | 1.000 |
| 2+ Females | pACCTAC01 | 1.000 | 1.000 |
| 1 Males | pAEMO01 | 1.000 | 1.000 |
| 2+ Females & Males | pCOLL10 | 0.905 | 1.000 |
| 2+ Females | pCOLL11 | 1.000 | 1.000 |
| 1 Females & 2+ Males | pCOLL4 | 0.905 | 1.000 |
| 1 Males | pCOLL6 | 1.000 | 1.000 |
| Females | pCOLL7 | 0.905 | 1.000 |
| 2+ Females | pGRW07 | 1.000 | 1.000 |
| 1 Males & 2+ Females & 2+ Males | pGRW09 | 1.000 | 1.000 |
| 2+ Males | pGRW10 | 1.000 | 1.000 |
| 2+ Females | pGRW11 | 1.000 | 1.000 |
| 2+ Females | pLAMPUR03 | 1.000 | 1.000 |
| 1 Females | pPBPIP1 | 1.000 | 1.000 |
| 2+ Males | pRTSR1 | 0.980 | 1.000 |
| 2+ Males | pSGS1 | 0.943 | 1.000 |
| 2+ Males | pSYBOR05 | 1.000 | 1.000 |
| 2+ Females & Males | pSYBOR10 | 0.905 | 1.000 |
| 1 Females & 2+ Males | pTERUF02 | 1.000 | 1.000 |
| 2+ Females | pTURDUS1 | 1.000 | 1.000 |
| Females | pWW4 | 0.905 | 1.000 |

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