Figure 1: Bird collection localities. Collection localities comprise a total of 156 localities (including offshore islands) combining our dataset and the MalAvi database.

Figure 2. Mean (±confidence intervals) proportions of localities in which haemosporidian lineages are detected according to the type of birds in which they are found. M = full migratory, PM = partial migratory, R = resident, R\_M = resident and full migratory, R\_PM = resident and partial migratory and R\_PM\_M = resident, partial migratory and full migratory. Number of lineages in each of the six categories are shown on the graph.

Figure 3: Correlation between local number of infections of haemosporidian parasites and percentage of migratory host individuals per locality. We observed no effect of migratory individuals percentage on parasite prevalence.

Figure 4: Parameters estimates as a function of parasite richness. No correlation was found between the percentage of migratory individuals and haemosporidian richness.

Table 1: Parameter estimates, standard errors, and confidence intervals for the Bayesian model testing the differences in the distribution of haemosporidian lineages among those that occur in migratory and/or resident avian host species.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Estimate** | **Std. error** | **Conf. Inter (95%)** | |
| Intercept | -4.71 | 0.03 | -4.76 | -4.65 |
| Full migrant | -0.08 | 0.10 | -0.38 | 0.10 |
| Partial migrant | 0.12 | 0.13 | -0.46 | 0.12 |
| Resident and full migrant | 0.31 | 0.11 | 0.03 | 0.52 |
| Resident and partial migrant | 0.34 | 0.08 | 0.12 | 0.51 |
| Resident, partial and full migrant | -0.55 | 0.20 | -0.92 | -0.04 |
| Number of bird individuals | 0.01 | 0.0 | 0.01 | 0.02 |
| Number of host species per lineage | 0.06 | 0.01 | 0.05 | 0.07 |

Table 2: Parameter estimates, standard errors, confidence intervals for the Bayesian model testing the variation of local haemosporidian prevalence per species as a function of the percentage of migratory individuals out of all individual birds sampled per locality and parasite richness.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Estimate** | **Std. error** | **Conf. Inter (95%)** | |
| Intercept | 0.49 | 0.36 | -0.22 | 1.25 |
| Percentage of migrant individuals | 0.70 | 0.79 | -0.91 | 2.23 |
| Parasite Richness | 0.02 | 0.01 | 0.01 | 0.03 |

Table 3: Parameter estimates, standard errors, z and p values for the mixed model testing the variation of local haemosporidian richness as a function of the percentage of migratory individuals out of all individual birds sampled per locality, as well as other predictors.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Estimate** | **Std. error** | **Z** | **P** |
| Intercept | -6.18 | 1.15 | -5.36 | <0.001 |
| Percentage of migrant individuals | 0.83 | 0.74 | 1.11 | 0.27 |
| Host richness | 0.94 | 0.08 | 12.10 | <0.001 |
| Prevalence | 0.69 | 0.07 | 9.80 | <0.001 |
| Percentage of migrant species | -0.28 | 0.09 | -3.06 | 0.002 |
| Number of migrants | 0.10 | 0.06 | 1.52 | 0.13 |
| Temperature | 0.63 | 0.21 | 2.93 | 0.003 |