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 the percentage of migratory individuals 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, and 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 |