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

Figure 2. Mean (±SE) percentage 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: Mean (±SE) percentage of localities in which *Plasmodium* 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 4: Mean (±SE) percentage of localities in which *Haemoproteus* 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 5: Local richness of haemosporidian parasites as a function of the percentage of migratory individuals out of all bird individuals sampled per locality. Each point represents a different locality. A positive correlation was found between the percentage of migratory individuals and haemosporidian richness (p = 0.002).

Figure 6: Correlation between local prevalence of haemosporidian parasites and percentage of migratory host individuals per locality. Each point represents the prevalence value per host species per site. We observed a positive effect of migratory behavior on parasite prevalence (p = 0.03).

Table 1: Parameter estimates, standard errors, and p values 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** | **p** |
| Resident | -4.54 | 0.03 | <0.001 |
| Full migrant | -0.04 | 0.11 | 0.42 |
| Partial migrant | -0.13 | 0.15 | 0.36 |
| Resident and full migrant | 0.79 | 0.11 | <0.001 |
| Resident and partial migrant | 0.67 | 0.09 | <0.001 |
| Resident, partial and full migrant | 1.47 | 0.13 | <0.001 |

Table 2: Parameter estimates, standard errors, and p values for the Bayesian model testing the differences in the distribution of *Plasmodium* lineages among those that occur in migratory and/or resident avian host species.

|  |  |  |  |
| --- | --- | --- | --- |
|  | **Estimate** | **Std. error** | **P** |
| Resident | -3.86 | 0.08 | <0.001 |
| Full migrant | 0.06 | 0.08 | 0.21 |
| Partial migrant | -0.04 | 0.13 | 0.42 |
| Resident and full migrant | 0.65 | 0.12 | <0.001 |
| Resident and partial migrant | 0.46 | 0.12 | <0.001 |
| Resident, partial and full migrant | 0.81 | 0.39 | <0.001 |

Table 3: Parameter estimates, standard errors, and p values for the Bayesian model testing the differences in the distribution of *Haemoproteus* lineages among those that occur in migratory and/or resident avian host species.

|  |  |  |  |
| --- | --- | --- | --- |
|  | **Estimate** | **Std. error** | **P** |
| Resident | -4.64 | 0.05 | <0.001 |
| Full migrant | -0.04 | 0.16 | 0.47 |
| Partial migrant | -0.14 | 0.20 | 0.83 |
| Resident and full migrant | 1.03 | 0.12 | <0.001 |
| Resident and partial migrant | 0.57 | 0.11 | <0.001 |
| Resident, partial and full migrant | 0.05 | 0.35 | 0.79 |

Table 4: Parameter estimates, standard errors, 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** | **p** |
| Intercept | 1.55 | 0.14 | <0.001 |
| Percentage of migrant individuals | -5.38 | 0.17 | 0.002 |
| Host richness | 0.01 | 0.0 | <0.001 |
| Prevalence | 0.02 | 0.0 | <0.001 |
| Percentage of migrant species | 0.05 | 0.02 | 0.005 |
| Number of migrants | 0.0 | 0.0 | 0.002 |

Table 5: Parameter estimates, standard errors, and p values for the mixed 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 temperature.

|  |  |  |  |
| --- | --- | --- | --- |
|  | **Estimate** | **Std. error** | **P** |
| Intercept | -0.86 | 1.41 | 0.54 |
| Percentage of migrant individuals | 3.61 | 1.64 | 0.03 |
| Temperature | -0.005 | 0.005 | 0.32 |