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. Positive correlation was found between percentage of migratory individuals and haemosporidian richness (p = 0.002).

Figure 6: Correlation between 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 positive effect between migratory behavior and 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 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 |