SUPPLEMENTARY MATERIAL

Supplementary Figure 1: Mean (±confidence intervals) proportions 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.

Supplementary Table 1: Parameter estimates, standard errors, and confidence intervals 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** | **Conf. Inter (95%)** | |
| Intercept | -4.76 | 0.00 | -4.83 | -4.70 |
| Full migrant | -0.22 | 0.17 | -0.56 | 0.09 |
| Partial migrant | -0.13 | 0.18 | -0.53 | 0.19 |
| Resident and full migrant | 0.64 | 0.12 | 0.38 | 0.87 |
| Resident and partial migrant | 0.29 | 0.12 | 0.06 | 0.51 |
| Resident, partial and full migrant | -1.01 | 0.48 | -1.98 | -0.12 |
| Number of bird individuals | -0.01 | 0.01 | -0.03 | 0.02 |
| Number of host species per lineage | 0.12 | 0.02 | 0.08 | 0.16 |

Supplementary Figure 2: Mean (±confidence intervals) proportions 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.

Supplementary Table 2: Parameter estimates, standard errors, and confidence intervals 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** | **Conf. Inter (95%)** | |
| Intercept | -4.73 | 0.04 | -4.81 | -4.65 |
| Full migrant | -0.03 | 0.15 | -0.34 | 0.25 |
| Partial migrant | -0.12 | 0.18 | -0.50 | 0.20 |
| Resident and full migrant | 0.79 | 0.12 | 0.54 | 1.02 |
| Resident and partial migrant | 0.22 | 0.13 | 0.02 | 0.52 |
| Resident, partial and full migrant | -1.26 | 0.42 | -2.22 | -0.56 |
| Number of bird individuals | 0.01 | 0.00 | 0.01 | 0.02 |
| Number of host species per lineage | 0.03 | 0.01 | 0.01 | 0.04 |

Supplementary Figure 3: Correlation between local number of bird individuals positive for *Plasmodium* and percentage of migratory host individuals per locality. We observed a negative effect of migratory individuals percentage on parasite prevalence.

Supplementary Table 3: Parameter estimates, standard errors, confidence intervals for the Bayesian model testing the variation of local *Plasmodium* prevalence per species as a function of the percentage of migratory all individual birds sampled per locality and parasite richness.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Estimate** | **Std. error** | **Conf. Inter (95%)** | |
| Intercept | -0.32 | 0.65 | -1.70 | 0.90 |
| Percentage of migrant individuals | -3.29 | 1.22 | -5.52 | -1.10 |
| Parasite richness | 0.01 | 0.01 | 0.00 | 0.03 |

Supplementary Figure 4: Correlation between local number of bird individuals positive for *Haemoproteus* and percentage of migratory host individuals per locality. We observed a positive effect of migratory individuals percentage in parasite prevalence.

Supplementary Table 4: Parameter estimates, standard errors, and confidence intervals for the Bayesian model testing the variation of local *Haemoproteus* prevalence per species as a function of the percentage of migratory all individual birds sampled per locality and parasite richness.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Estimate** | **Std. error** | **Conf. Inter (95%)** | |
| Intercept | -2.34 | 0.81 | -4.05 | -0.81 |
| Percentage of migrant individuals | 7.00 | 2.04 | 2.04 | 3.29 |
| Parasite richness | 0.03 | 0.01 | 0.01 | 0.06 |

Supplementary table 5: AIC values for mixed model. Below are represented all models tested with all fixed effects and AIC test value.

|  |  |  |  |
| --- | --- | --- | --- |
|  | **Variables** | **AIC value** | Δ**AIC** |
| **Model1** | No fixed variables | 714.97 | 307.79 |
| **Model2** | Host Richness | 521.08 | 113.9 |
| **Model3** | Prevalence | 602.62 | 195.44 |
| **Model4** | Host Richness + Prevalence | 422.14 | 14.96 |
| **Model5** | Percentage of Migrants | 698.13 | 290.95 |
| **Model6** | Host Richness + Prevalence + Percentage of Migrants | 416.40 | 9.22 |
| **Model7** | Number of Migrants | 620.46 | 213.28 |
| **Model8** | Host Richness + Prevalence + Percentage of Migrants + Number of Migrants | 417.34 | 10.16 |
| **Model9** | Temperature | 671.73 | 264.55 |
| **Model10** | Host Richness + Prevalence + Percentage of Migrants + Number of Migrants + Temperature | 407.18 | 0 |
| **Model11** | Precipitation | 666.99 | 259.81 |

Supplementary Figure 5: Standardized estimates as a function of *Plasmodium* richness. No correlation was found between the percentage of migratory individuals and *Plasmodium* richness.

Supplementary Table 6: Parameter estimates, standard errors, z and p values for the mixed model testing the variation of local *Plasmodium* richness as a function of the percentage of migratory individuals out of all individual birds sampled per locality, as well as other potential predictors.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Estimate** | **Std. error** | **Z** | **P** |
| Intercept | -6.46 | 1.42 | -4.55 | <0.001 |
| Percentage of migrant individuals | 1.30 | 0.92 | 1.45 | 0.15 |
| Host richness | 1.07 | 0.09 | 11.67 | <0.001 |
| Prevalence | 0.71 | 0.08 | 8.48 | <0.001 |
| Percentage of migrant species | -0.04 | 0.11 | -0.36 | 0.72 |
| Number of migrants | -0.20 | 0.09 | -2.29 | 0.02 |
| Temperature | 0.54 | 0.26 | 2.05 | 0.04 |

Supplementary Figure 6: Standardized estimates as a function of *Haemoproteus* richness. No correlation was found between the percentage of migratory individuals and *Haemoproteus* richness.

Supplementary Table 7: Parameter estimates, standard errors, z and p values for the mixed model testing the variation of local *Haemoproteus* richness as a function of the percentage of migratory individuals out of all individual birds sampled per locality, as well as other potential predictors.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Estimate** | **Std. error** | **Z** | **P** |
| Intercept | -6.12 | 3.44 | -1.78 | 0.08 |
| Percentage of migrant individuals | 0.73 | 1.39 | 0.53 | 0.6 |
| Host richness | 0.85 | 0.17 | 4.89 | <0.001 |
| Prevalence | 0.51 | 0.14 | 3.69 | <0.001 |
| Percentage of migrant species | -0.39 | 0.17 | -2.56 | 0.02 |
| Number of migrants | 0.25 | 0.13 | 1.88 | 0.06 |
| Temperature | 0.54 | 0.65 | 0.83 | 0.4 |