**Can migratory** **birds spread avian haemosporidian parasites?**

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

Figure 2: Mean (±confidence intervals) geographical range in kilometers 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 four categories are shown on the graph.

Figure 3: Mean (±confidence intervals) geographical range in kilometers in which haemosporidian lineages are detected according to the type of birds in which they are found. Number of lineages in each of the two categories are shown on the graph.

Figure 4: Predicted model relationship (±95% confidence intervals) between local number of infections of *Plasmodium* parasites and proportion of migratory host individuals per locality. We observed negative effect of the proportion of migratory individuals on number of infected birds.

Figure 5: Predicted model relationship (±95% confidence intervals) between local number of infections of *Haemoproteus* parasites and proportion of migratory host individuals per locality. We observed positive effect of the proportion of migratory individuals on number of infected birds.

Figure 6: Parameter estimates relating to their influence on parasite richness. No correlation was found between the proportion of migratory individuals and haemosporidian richness.

Table 1: Parameter estimates, standard errors, and confidence intervals for the Bayesian model testing the differences in the geographical range of haemosporidian lineages among those that occur in migratory and/or resident avian host species. (Residents only = reference category)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Estimate** | **Std. error** | **Conf. Inter (95%)** | |
| Intercept | 7.20 | 0.12 | 6.87 | 7.33 |
| Resident and full migrant | 0.54 | 0.29 | 0.00 | 1.13 |
| Resident and partial migrant | 0.29 | 0.24 | -0.17 | 0.79 |
| Resident, partial and full migrant | 0.53 | 0.41 | -0.21 | 1.41 |
| Number of bird individuals | 0.00 | 0.01 | -0.02 | 0.03 |
| Number of host species per lineage | 0.05 | 0.03 | -0.01 | 0.11 |

Table 2: Parameter estimates, standard errors, and confidence intervals for the Bayesian model testing the differences in the geographical range of haemosporidian lineages among those that occur in migratory and/or resident avian host species. (Residents only = reference category)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Estimate** | **Std. error** | **Conf. Inter (95%)** | |
| Intercept | 7.10 | 0.11 | 6.88 | 7.32 |
| Resident and any migrant | 0.40 | 0.19 | 0.05 | 0.79 |
| Number of bird individuals | 0.00 | 0.01 | -0.02 | 0.03 |
| Number of host species per lineage | 0.05 | 0.03 | -0.01 | 0.11 |

Table 3: Parameter estimates, standard errors, and confidence intervals for the Bayesian model testing the variation of local number of birds infected by *Plasmodium* as a function of the proportion of migratory individuals out of all individual birds sampled per locality and parasite richness.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Estimate** | **Std. error** | **Conf. Inter (95%)** | |
| Intercept | -0.47 | 0.77 | -2.07 | 0.87 |
| Proportion of migrant individuals | -2.78 | 1.40 | -5.58 | 0.07 |
| Parasite Richness | 0.02 | 0.01 | -0.01 | 0.04 |

Table 4: Parameter estimates, standard errors, and confidence intervals for the Bayesian model testing the variation of local number of birds infected by *Haemoproteus* as a function of the proportion of migratory individuals out of all individual birds sampled per locality and parasite richness.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Estimate** | **Std. error** | **Conf. Inter (95%)** | |
| Intercept | -2.37 | 0.84 | -4.07 | -0.76 |
| Proportion of migrant individuals | 6.78 | 2.30 | 2.40 | 11.37 |
| Parasite Richness | 0.04 | 0.02 | 0.01 | 0.07 |

Table 5: Parameter estimates, standard errors, z and p values for the mixed model testing the variation of local haemosporidian richness as a function of the proportion of migratory individuals out of all individual birds sampled per locality, as well as other predictors.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Estimate** | **Std. error** | **Z** | **P** |
| Intercept | -6.16 | 1.71 | -3.60 | <0.001 |
| Proportion of migrant individuals | 0.57 | 1.07 | 0.53 | 0.59 |
| Host richness | 0.92 | 0.12 | 7.87 | <0.001 |
| Prevalence | 0.70 | 0.10 | 6.97 | <0.001 |
| Proportion of migrant species | -0.26 | 0.13 | -2.03 | 0.04 |
| Number of migrants | 0.11 | 0.10 | 1.04 | 0.30 |
| Temperature | 0.62 | 0.32 | 1.95 | 0.05 |