**Table S1.** Regression coefficient, standard error for regression coefficient, standardized regression coefficient as effect size index (Z-value), and the P-value, corresponding to each predictor included in the most plausible models explaining the variation on bat and bat fly assemblages, as well as on the interaction network.

|  |  |  |  |
| --- | --- | --- | --- |
| **Parameters** | **Group-level predictors** | **Coefficient (standard error)** | ***Z-value; P-value*** |
| ***Bat assemblage*** |  |  | **Pred. 1** | **Pred. 2** | **Pred. 3** | **Pred. 4** |
|  Ab | Vegetation structure  | 0.07 (0.02) **MDS1** – 0.18 (0.03) **MDS2**  | 4.20; <0.001 | – 5.90; <0.001 |  |  |
|  | Landscape500 | – 0.19 (0.04) **DFmeff** | – 4.54; <0.001 |  |  |  |
|  |  | – 0.18 (0.04) **DFLP** | – 4.61; <0.001 |  |  |  |
|  | Landscape1500 | – 0.69 (0.14) **DFLP** + 0.60 (0.14) **DFmeff**+ 0.24 (0.05) **RFmeff**  | – 5.03; <0.001 | 4.29; <0.001 | 4.59; <0.001 |  |
|  | Landscape2500 | – 0.17 (0.04) **DFmeff** – 0.48 (0.09) **RFLP** + 0.50 (0.08) **RFmeff**  | – 4.05; <0.001 | – 5.70; <0.001 | – 5.97; <0.001 |  |
|  |  | 0.30 (0.09) **DFLP** – 0.45 (0.10) **DFmeff** – 0.65 (0.10) **RFLP** + 0.57 (0.09) **RFmeff**  | 3.30; <0.001 | – 4.60; <0.001 | – 6.54; <0.001 | 6.51; <0.001 |
|  1/D | Vegetation structure | 0.03 (0.01) MDS1  | 2.13; 0.06 |  |  |  |
| ***Fly assemblage*** |  |  |  |  |  |  |
|  S | Bat community structure | 0.15 (0.08) BatS  | 1.89; 0.06 |  |  |  |
|  1/D | Bat community structure | – 0.04 (0.01) **Bat1/D** | – 2.95; 0.02 |  |  |  |
|  eH’ | Bat community structure | – 0.04 (0.01) **Bat1/D** | – 3.17; 0.01 |  |  |  |
| ***Host- bat fly network*** |  |  |  |  |  |  |
|  *H2’* | Landscape500 | 0.10 (0.04) **DFLP**  | 2.54; 0.04 |  |  |  |
|  | Landscape1500 | 0.09 (0.04) DFLP | 2.25; 0.06 |  |  |  |
|  |  | 0.09 (0.04) DFmeff  | 2.20; 0.06 |  |  |  |
|  | Landscape2500 | 0.11 (0.04) **DFmeff**  | 2.66; 0.03 |  |  |  |
| ***Parasitic infection*** |  |  |  |  |  |  |
|  Prevalence | Bat community structure | – 0.13 (0.05) **Bat1/D** | – 2.45; 0.01 |  |  |  |
|  | Vegetation structure | 0.10 (0.04) **MDS1**  | 2.82; <0.001 |  |  |  |
|  | Landscape500 | 0.18 (0.07) **RFmeff** | 2.68; 0.01 |  |  |  |
|  |  | 0.17 (0.07) **RFLP** | 2.32; 0.02 |  |  |  |
|  | Landscape1500 | 0.18 (0.07) **RFmeff** | 2.77; 0.01 |  |  |  |
|  |  | 0.20 (0.08) **RFLP** | 2.59; 0.01 |  |  |  |
|  | Landscape2500 | 0.20 (0.07) **RFmeff** | 2.75; 0.01 |  |  |  |
|  |  | 0.17 (0.07) **RFLP** | 2.33; 0.02 |  |  |  |
|  Intensity | Landscape1500 | 0.14 (0.07) **DFmeff** | 2.04; 0.04 |  |  |  |
|  |  | 0.14 (0.07) DFLP | 1.90; 0.06 |  |  |  |

Response variables: bat abundance (Ab) and diversity (1/D, Simpson diversity index); bat fly assemblage richness (S), and diversity (1/D and eH’, Shannon diversity index); the level of specialization of the host-bat fly network (*H2’*, specialization index); and the prevalence and intensity of fly infestation. The explanatory variables corresponding to the different groups of predictors (group-level predictors) are: 1) regarding the vegetation structure, the scores of the first and second ordination axes (MDS1 and MDS2), that reflect plant assemblage’s dissimilarities in vegetation structural complexity; 2) regarding the landscapes attributes, the landscape proportion (LP) and degree of fragmentation (meff) regarding the tropical dry forest (DF) and riparian forest (RF), at the 500, 1500, and 2500 m focal scales; and 3) regarding the bat community structure, bat assemblage richness (BatS) and diversity (Bat1/D). Predictors showing a significant (P < 0.05) relationship with the response variable are shown in bold. The null model was the most plausible model in all cases for the following parameters: bat assemblage’s richness (S) and diversity (eH’), and fly assemblage abundance (Ab). The standardized regression coefficient (Z-value) is calculated by dividing the regression coefficient by its standard error, and can be considered a measure of the association between the response and explanatory variables (predictors). This standardized coefficient indicates how many standard deviations the response variable will change per every standard deviation increase in the explanatory variable, and can be used as an effect size estimation (Nieminen et al. 2013). Z-values higher than 1.96 or lower than – 1.96 indicate a strong relationship among variables.

**Reference**

**Nieminen P., Lehtiniemi H., Vähäkangas K., Huusko A., Rautio A.** (2013). Standardised regression coefficient as an effect size in summarising findings in epidemiological studies. *Epidemiology Biostatistics and Public Health* **10** (4): e8854. doi: 10.2427/8854.