**Table S2**. 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 fly communities associated to *Artibeus jamaicensis* and the level of parasitic infection.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Parameters** | **Group-level predictors** | **Coefficient (standard error)** | **Z-value; P-value** | | |
| ***Fly assemblage*** |  |  | **Pred. 1** | **Pred. 2** | **Pred. 3** |
| S | ARTJAM population | 0.03 (0.01) **ArtjamAb** | 2.07; 0.04 |  |  |
|  | Vegetation structure | – 0.29 (0.16) MDS2 | – 1.85; 0.06 |  |  |
| 1/D | Vegetation structure | – 0.05 (0.02) MDS1 | – 2.18; 0.06 |  |  |
| eH’ | Vegetation structure | – 0.06 (0.02) **MDS1** + 0.09 (0.04) **MDS2** | – 2.74; 0.03 | 2.52; 0.04 |  |
| ***Parasitic infection*** |  |  |  |  |  |
| Intensity | ARTJAM population | 0.02 (0.01) **ArtjamAb** | 2.51; 0.01 |  |  |
|  | Bat community composition | – 1.18 (0.35) **MDS2** | – 3.38; <0.001 |  |  |
|  | Bat community structure | – 0.58 (0.16) **BatS +** 0.21 (0.07) **Bat1/D +** 0.02 (0.01) **BatAb** | – 3.54; <0.001 | 2.92; <0.001 | 3.40; <0.001 |
|  | Vegetation structure | – 0.23 (0.07) **MDS2** | – 3.26; <0.001 |  |  |

Response variables: fly assemblage richness (S), and diversity, considering both the Simpson diversity index (1/D) and the Shannon diversity index (eH’); as well as the intensity of fly infestation on the populations of *A. jamaicensis*. The explanatory variables corresponding to the different groups of predictors (group-level predictors) are: 1) regarding the *A. jamaicensis* population attributes, the abundance (Ab) of *A. jamaicensis* (Artjam); 2) regarding the bat community composition, the scores of the first, second and third ordination axes (MDS1, MDS2, MDS3) reflecting bat assemblage’s dissimilarities in species composition; 3) regarding the bat community structure, bat assemblage richness (BatS), diversity (Bat1/D) and abundance (BatAb); and 4) regarding the vegetation structure, the scores of the first and second ordination axes (MDS1 and MDS2) reflecting plant assemblage’s dissimilarities in vegetation structural complexity. 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: fly assemblage abundance (Ab) and fly prevalence. 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.