**Effects of colonization, geography and environment on genetic divergence in the intermediate leaf-nosed bat, *Hipposideros larvatus***

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**Table S1.** The codes of 19 bioclimatic variables used in this study. This scheme follows those of WorldClim and ANUCLIM.

| Abbreviation | Bioclimatic Variable |
|---|---|
| Bio1 | Annual Mean Temperature [°C] |
| Bio2 | Mean Diurnal Range [°C] |
| Bio3 | Isothermality (Bio2/Bio7) (* 100) |
| Bio4 | Temperature Seasonality (standard deviation *100) |
| Bio5 | Max Temperature of Warmest Month [°C*10] |
| Bio6 | Min Temperature of Coldest Month [°C*10] |
| Bio7 | Temperature Annual Range (Bio5–Bio6) |
| Bio8 | Mean Temperature of Wettest Quarter [°C*10] |
| Bio9 | Mean Temperature of Driest Quarter [°C*10] |
| Bio10 | Mean Temperature of Warmest Quarter [°C*10] |
| Bio11 | Mean Temperature of Coldest Quarter [°C*10] |
| Bio12 | Annual Precipitation [mm/year] |
| Bio13 | Precipitation of Wettest Month [mm/month] |
| Bio14 | Precipitation of Driest Month [mm/month] |
| Bio15 | Precipitation Seasonality [coefficient of variation] |
| Bio16 | Precipitation of Wettest Quarter [mm/quarter] |
| Bio17 | Precipitation of Driest Quarter [mm/quarter] |
| Bio18 | Precipitation of Warmest Quarter [mm/quarter] |
| Bio19 | Precipitation of Coldest Quarter [mm/quarter] |

Table S2. Sampled populations with geographical coordinates and the GenBank accession numbers of cytb gene and control region sequences of *Hipposideros larvatus*.

| **Population** | **Longitude** | **Latitude** | **cytb** | **CR** |
|---|---|---|---|---|
| **GD1** | 111.944 | 22.434 | MW670581-MW670586 | MW670746-MW670751 |
| **GD2** | 113.561 | 24.772 | MW670587-MW670595 | MW670752-MW670760 |
| **GX1** | 107.824 | 22.862 | MW670596-MW670605 | MW670761-MW670770 |
| **GX2** | 106.919 | 22.563 | MW670606-MW670615 | MW670771-MW670780 |
| **GX3** | 110.683 | 25.413 | MW670616-MW670625 | MW670781-MW670790 |
| **GX4** | 109.674 | 23.477 | MW670626-MW670635 | MW670791-MW670800 |
| **GX5** | 110.380 | 24.510 | MW670636-MW670641 | MW670801-MW670806 |
| **GZ** | 105.533 | 25.283 | MW670642-MW670649 | MW670807-MW670814 |
| **JX** | 114.091 | 25.462 | MW670708-MW670721 | MW670873-MW670886 |
| **YN1** | 103.847 | 22.603 | MW670722-MW670726 | MW670887-MW670891 |
| **YN2** | 100.709 | 22.605 | MW670727-MW670730 | MW670892-MW670895 |
| **YN3** | 103.906 | 22.743 | MW670731-MW670738 | MW670896-MW670903 |
| **YN4** | 99.550 | 22.320 | MW670739-MW670745 | MW670904-MW670910 |
| **HN1** | 109.467 | 18.623 | MW670650-MW670654 | MW670815-MW670819 |
| **HN2** | 109.428 | 18.598 | MW670655-MW670664 | MW670820-MW670829 |
| **HN3** | 109.448 | 18.585 | MW670665-MW670674<br>MW670688-MW670674 | MW670830-MW670839<br>MW670853-MW670862 |
| **HN4** | 110.212 | 19.945 | MW670675-MW670687 | MW670840-MW670852 |
| **HN5** | 110.127 | 19.231 | MW670698-MW670707 | MW670863-MW670872 |

**Table S3.** Results of Tajima's D test for *Hipposideros larvatus* based on the sequences of cytb and CR. None of these appear to be significant.

| | **Tajima's D** |
|---|---|
| **Cytb** | |
| **Clade A** | -1.281 |
| **Clade B** | -0.890 |
| **Subclade B1** | -1.298 |
| **Subclade B2** | -0.878 |
| **CR** | |
| **Clade A** | -1.727 |
| **Clade B** | -1.490 |
| **Subclade B1** | -1.450 |
| **Subclade B2** | -0.362 |

**Table S4.** Results of mismatch distribution analysis and estimation of the time of population expansion ($T_{MD}$, Ma) for *Hipposideros larvatus* based on the cytb gene. Statistically significant results are indicated by asterisks: *P < 0.05, **P < 0.01.

| | **SSD** | **r** | **Tao (95% CI)** | **$T_{MD}$ (95% CI)** |
|---|---|---|---|---|
| **Clade A** | 0.031 | 0.029 | 8.641(0.479–14.344) | 0.146 (0.008–0.237) |
| **Clade B** | | | | |
| **Subclade B1** | 0.005 | 0.041 | 2.438(0.893–4.047) | 0.041(0.015–0.068) |
| **Subclade B2** | 0.123* | 0.269** | - | - |

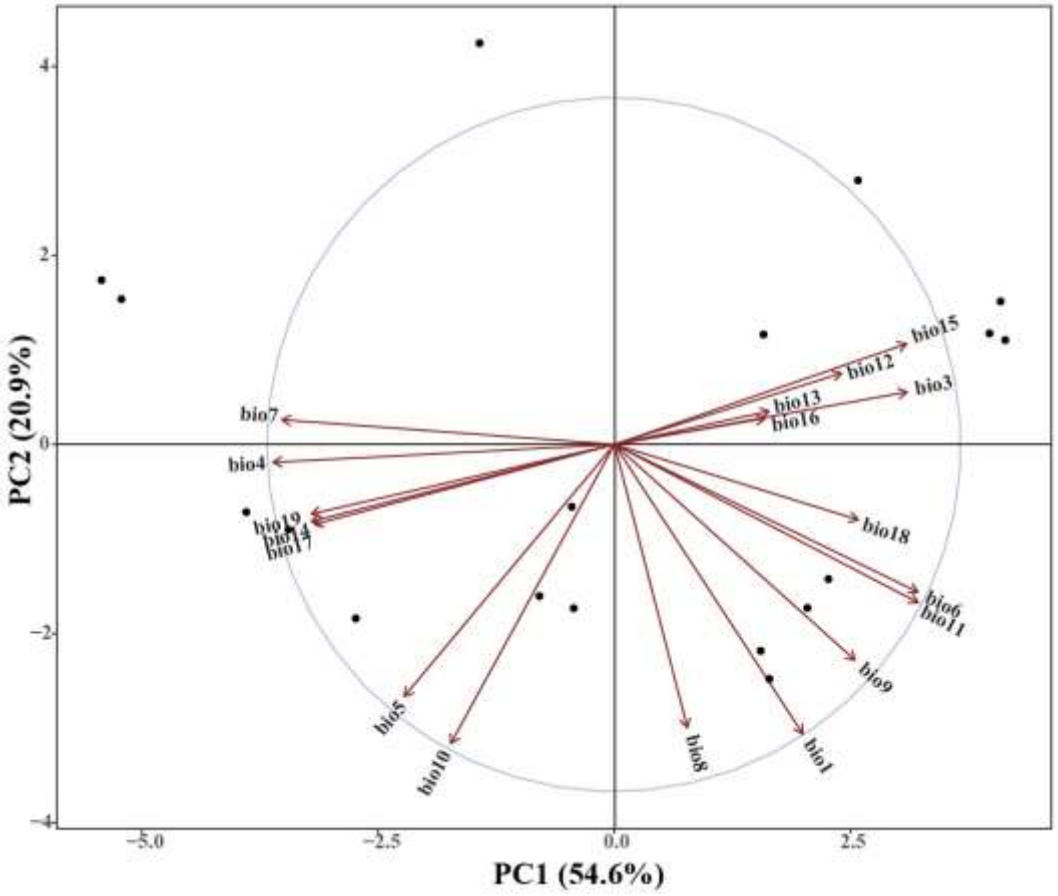


**Figure S1.** Principle component analysis (PCA) of *Hipposideros larvatus*, based on 19 bioclimatic variables across 18 localities. The first two principle components accounted for 54.6% and 20.9% of the variation, respectively. Black dots represent the sampling localities. The code of each bioclimatic variable follows those of WorldClim and ANUCLIM, and is shown in Table S1.

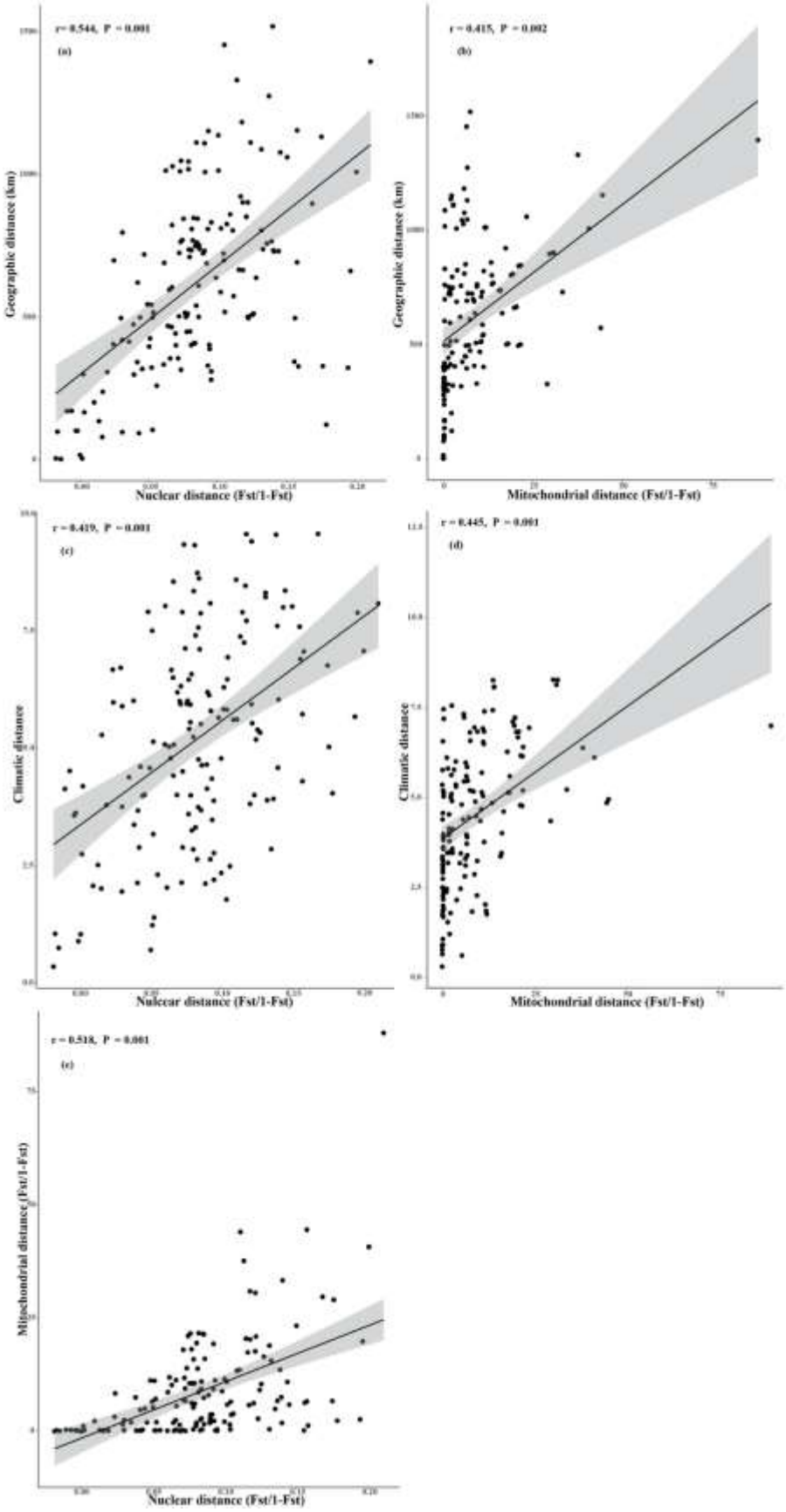
r= 0.544, P = 0.001
(a)
Geographic distance (km)
Nuclear distance (Fst/1-Fst)
r = 0.415, P = 0.002
(b)
Geographic distance (km)
Mitochondrial distance (Fst/1-Fst)
r = 0.419, P = 0.001
(c)
Climatic distance
Nuclear distance (Fst/1-Fst)
r = 0.445, P = 0.001
(d)
Climatic distance
Mitochondrial distance (Fst/1-Fst)
r = 0.518, P = 0.001
(e)
Mitochondrial distance (Fst/1-Fst)
Nuclear distance (Fst/1-Fst)

**Figure S2.** Scatter plots of the relationships between genetic distance ($F_{st}$ /1- $F_{st}$) and geographic distance (a, b), and climatic distance (c, d), and between nuclear distance and mitochondrial distance (e). $F_{st}$ values were calculated based on nuclear microsatellites (a, c) and concatenated mitochondrial cytb and control region (b, d). Correlation coefficient *r* and significance were estimated by Mantel tests.