**The geography of evolutionary divergence in the highly endemic avifauna from the Sierra Madre del Sur, Mexico**

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**Supporting Information**

Table 2. Marginal likelihood estimates to a relaxed and strict clock for sequence evolution, estimated through the stepping-stone method (Xie et al., 2011), showing that the strict clock performed better than a relaxed clock for all species.

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| Dataset | Relaxed clock’s mean marginal likelihood (-Ln) | Strict clock’s mean marginal likelihood (-Ln) |
| *Aulacorhynchus* | 2859.22 | 2765.16 |
| *Chlorospingus* | 2727.45 | 2664.42 |
| *Cardellina* | 4766.77 | 4427.2 |
| *Eupherusa* | 2298.05 | 2228.31 |

Table 3. Marginal likelihood estimation (Log ml) calculated in BEAST using path sampling (PS) and stepping-stone (SS) methods under two evolutionary rate assumptions: calculated and body mass-corrected. Shown Bayes factors (BFs) are the result of comparisons made between Log mls obtained through SS. Asterisks (\*) after (log10) BF indicate the following according to Raftery (1996): \* low support of the hypothesis, \*\* positive support for the model, and \*\*\* very strong evidence favoring the hypothesis with higher log(ml).

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| --- | --- | --- | --- | --- |
| Dataset | Evolution Rate | Log ml (PS) | Log ml (SS) | BFs |
| *Aulacorhynchus* | Calculated | -4126.871875 | -4127.724235 | -392.41344 |
| Body mass-corrected | -3831.222778 | -3735.310795 | 392.41344\*\*\* |
| *Chlorospingus* | Calculated | -2730.394245 | -2731.516758 | -2.726148 |
| Body mass-corrected | -2728.641854 | -2728.79061 | 2.726148\* |
| *Cardellina* | Calculated | -2556.849255 | -2557.792954 | -2.095804 |
| Body mass-corrected | -2554.271126 | -2555.69715 | 2.095804\* |
| *Eupherusa* | Calculated | -2215.229914 | -2216.60914 | -3.12914 |
| Body mass-corrected | -2212.859479 | -2213.48 | 3.12914\*\* |