

Supplementary Archives

Combining molecular data sets with strongly heterogeneous taxon coverage enlightens the peculiar biogeographic history of Stoneflies (Insecta: Plecoptera)

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This README was written on May 17, 2021. If you have any questions regarding the nature of our data, please feel free to contact Harald Letsch (harald.letsch@univie.ac.at). Supplementary files and descriptions provided via the Digital Repository Dryad.

Supplementary Archive S1.

This archive contains all trees generated by supertree analyses of the combined data sets.

[Supplementary_information_S1.zip: 42 kb]

Supplementary Archive S2.

This archive contains the results of the BEAST Bayesian Inference analyses, showing the relationships and divergence times of stoneflies.

[Supplementary_information_S2.zip: 181 kb]

Supplementary Archive S3.

This archive contains the methods and results of the constrained IQ-TREE analyses of the concatenated Sanger sequence genes, with the best trees from the ML analyses of the four transcriptomic data sets.

[Supplementary_information_S3.zip: 644 kb]