

Old World and New World Phasmatodea: Phylogenomics Resolve the Evolutionary History of Stick and Leaf Insects

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This README and corresponding data refer to: Simon et al. (2019), Front. Ecol. Evol. - Phylogenetics, Phylogenomics, and Systematics

This README was written on August 27, 2019. If you have any questions regarding the nature of our data, please feel free to contact Sabrina Simon (sabrina.simon[AT]wur.nl)

Supplementary files and descriptions provided via the Digital Repository Dryad

NOTE: In several files and figures, some species names may be different in the Supplementary Online Material due to identification updates and corrections. Valid names are provided in Table S1.

Supplementary Archive 1.

This archive contains all files relevant to the phylogenetic analyses. [Supplementary_Archive_1.zip: 16,71 MB, md5sum:8507cced93f77d3bf987d8bb54e490b6]

This archive includes three supermatrices (PHYLIP format) and respective partition files (NEXUS format) including selected models (*partitions.nex, assigned models to each partition are listed at the bottom). The partitioning is based on protein domains annotation.

- decisive supermatrix (superalignment) on amino-acid level + corresponding partition file including selected models (“AA_{decisive}”, see Figure 2)
- decisive supermatrix on nucleotide level including only 2nd codon positions + corresponding partition file including selected models (“NT_{decisive}”, see Supplementary Figure S4)
- selected optimal subset (SOS) supermatrix (superalignment) on amino-acid level + corresponding partition file including selected models (“AA_{SOS}”, see Supplementary Figure S5)

Supplementary Archive 2.

This archive contains all files relevant to the divergence time estimations.

[Supplementary_Archive_2.zip: 221,32 MB, md5sum:6583426e7f0b65c080bf5128d901d5fa]

- BEAST_runs.1: tree and log files of BEAST run 1
- BEAST_runs.2: tree and log files of BEAST run 2
- BEAST_runs.3: tree and log files of BEAST run 3
- BEAST_runs.4: tree and log files of BEAST run 4

- Phas_beast.61.1.reduced.trees: tree files of run 1 with burnin excluded
- Phas_beast.61.2.reduced.trees: tree files of run 2 with burnin excluded
- Phas_beast.61.3.reduced.trees: tree files of run 3 with burnin excluded
- Phas_beast.61.4.reduced.trees: tree files of run 4 with burnin excluded
- Phas_beast.61.all.reduced.trees: trees without burnin, combined from all four runs
- Phas_beast.61.all.me.reduced.tre: BEAST maximum clade credibility (MCC) tree with mean node heights derived from all four runs
- Phas_beast.61.xml: BEAST input file
- AA_decisive_95_alignment.phy: decisive amino-acid dataset (AA_{decisive}) only containing sites with unambiguous data for at least 95% of the 61 taxa (AA_{decisive95})