# Supplementary material of ” Phylogenomic analysis of *Stylops* reveals the evolutionary history of a Holarctic Strepsiptera radiation parasitizing wild bees”

S1. Table of included material in the study.

S2. Saturation plots based on uncorrected-to-corrected distances (a) and uncorrected distances against tree-based distances (b) including ingroup and outgroup and ingroup only.

S3. Species tree of *Stylops* from 3,138 gene trees produced in ASTRAL-III. Scale bar indicates coalescent units. Node labels indicate support values. Terminal labels as in Fig. 2.

S4. Species tree of *Stylops* from 2,234 gene trees (short loci removed) produced in ASTRAL-III. Scale bar indicates coalescent units. Node labels indicate support values. Terminal labels as in Fig. 2.

S5. Species tree of Stylops from 2,234 gene trees without 3rd codon positions (nt12) produced in ASTRAL-III. Scale bar indicates coalescent units. Node labels indicate support values. Terminal labels as in Fig. 2.

S6. Species tree of Stylops from 2,234 gene trees without 3rd codon positions (nt12) produced with weighted ASTRAL—hybrid in ASTER to account for gene estimation error. Scale bar indicates coalescent units. Node labels indicate support values. Terminal labels as in Fig. 2.

S7. Phylogeny of *Stylops* based on Maximum likelihood analysis of 3,138 loci in IQ-TREE2. Node labels indicate support values (SH-aLRT/UFBoot). Terminal labels as in Fig. 2.

S8. Phylogeny of Stylops based on Maximum likelihood analysis of 2,234 loci without 3rd codon positions (nt12) in IQ-TREE2 with same substitution model as in Fig. 2 (GTR+F+R6). Node labels indicate support values (SH-aLRT/UFBoot). Terminal labels as in Fig. 2.

S9. Phylogeny of Stylops based on Maximum likelihood analysis of 2,234 loci without 3rd codon positions (nt12) in IQ-TREE2 with optimized substitution model (GTR+F+I+R6). Node labels indicate support values (SH-aLRT/UFBoot). Terminal labels as in Fig. 2.

S10. Maximum clade credibility tree of *Stylops* obtained from BEAST2 with the NF data set of 150 genes (no inclusion criteria of loci based on taxon occupancy). Node labels indicate posterior probability values. The scale axis is in substitutions per site. Terminal labels named as in Fig. 2.

S11. Maximum clade credibility tree of *Stylops* obtained from BEAST2 with the TO100 data set of 150 genes (inclusion criteria of loci required full taxon occupancy). Node labels indicate posterior probability values. The scale axis is in substitutions per site. Terminal labels named as in Fig. 2.

S12. Dated maximum clade credibility tree of *Stylops* obtained from BEAST2 with the TO50 data set of 150 genes (inclusion criteria of loci required at least 50% taxon occupancy). Node labels indicate nodes ages, and node bars are 95% HPD intervals of estimated node ages. Terminal labels named as in Fig. 2. The scale axis is in millions of years.

S13. Dated phylogeny and ancestral-range estimates for Stylops with model DIVALIKE. The phylogeny was inferred in BEAST2 with the TO50 data set of 150 genes (inclusion criteria of loci required at least 50% taxon occupancy). Biogeographical history inferred for the tree with BioGeoBEARS using the DIVALIKE model. The branch lengths are proportional to divergence times. Circles in nodes include inferred ancestral areas proportional to their likelihood, and colours for each area are given in the legend.

S14. Differences in individual host-parasite link residuals between clade I and clade II from PACo. The smaller the residual, the stronger is the link’s contribution to cophylogenetic signal.

S15. Table of Stylops species groups, their associated host subgenera, and the status of host subgenera (monophyletic/non-monophyletic) based on (Pisanty et al., 2022).