*Tables*

Table S1: Specimen locality data

Table S2: Specimens used in the combined analyses of genomic and transcriptomic data (DNAAA\_matrix).

Table S3: Character coding for web type ancestral state reconstruction

*Figures*

Supplemental Figure 1. Tree topology obtained in maximum likelihood (ML) analyses conducted in RAxML.

Supplemental Figure 2. Tree topology obtained in Bayesian inference (BI) analyses conducted in ExaBayes.

Supplemental Figure 3. Tree topology obtained in maximum likelihood (ML) analyses conducted in IQ-TREE.

Supplemental Figure 4. Phylogenetic tree inferred after removal of Paratropididae terminals (“No\_Paratropis” dataset).

Supplemental Figure 5. Tree topology obtained in species tree analysis conducted in ASTRAL.

Supplemental Figure 6. Comparison of resulting tree topologies obtained by concatenated analyses conducted in RAxML and ExaBayes and species tree approach conducted in ASTRAL.

Supplemental Figure 7. Divergence time estimates of mygalomorph spiders inferred by treePL with placement of the calibrations.

Supplemental Figure 8. Divergence time estimates of mygalomorph spiders inferred by treePL with the confidence intervals.

Supplemental Figure 9. Phylogenetic tree of Mygalomorphae with current classification scheme (World Spider Catalog 2019).

*Data Matrices and Input Files*

RASP\_ingroup.tre\_dis.csv

RAxML\_DNAAA.nex

RAxML\_DNAAA\_partitions.txt

RAxML\_ExaBayes\_all\_taxa.nex

RAxML\_ExaBayes\_all\_taxa\_partitions.txt

RAxML\_No\_Paratropis.nex

RAxML\_No\_Paratropis\_partitions.txt

*Tree Files*

ASTRAL\_all\_taxa.tre

ASTRAL\_all\_taxa.trees

ExaBayes\_all\_taxa.tre

RAxML\_DNAAA.tre

RAxML\_No\_Paratropis.tre

RAxML\_all\_taxa.tre

treePL\_boot\_dated.tre

*Sequence Files*

Sequences per locus: L1 - L556 (472 loci), sequences before MAFFT alignment and ALISCORE/ALICUT treatment