

Supplements

The structure of the Cardiophorinae-Dendrometrinae clade (Coleoptera: Elateridae) is the weakest point of the current click-beetle phylogenetics and classification

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Contents

Supplementary Text.

Overview of topologies proposed by Douglas et al. (2021)

Taxonomy – formal classification and detailed justification

Table S1. An overview of the classification of hypnoidines.

Table S2. Morphological characters supporting the monophyly and relationships of focal taxa.

Table S3. Overview of topologies published by Motyka et al. (2026).

Table S4. Summary of Gene Concordance Factor (gCF) and Gene Discordance Factor (gDF) statistics across three alternative phylogenetic hypotheses (topo1, topo2, topo3). Results are shown for amino acid (AA) and nucleotide (NT) datasets

Table S5. Summary of Site Concordance Factor (sCF) and Site Discordance Factor (sDF) statistics for three alternative phylogenetic hypotheses (topo1, topo2, topo3). Analysis was performed using amino acid (AA) and nucleotide (NT) datasets,

ICZN Case – Plastoceridae Crowson, 1972 (Insecta, Coleoptera): proposed conservation of the family-group name by suppression of Plastocerini Leconte, 1861 (Insecta, Coleoptera)

Figure S1. Overview of topologies published by Motyka et al. (2026)

Figure S2. Maximum-likelihood phylogeny of click beetles inferred from nucleotide (NT) sequences. Node support is shown as SH-aLRT / UFBoot values.

Figure S3. Maximum-likelihood phylogeny of click beetles inferred from amino acid (AA) sequences. Node support is shown as SH-aLRT / UFBoot values.

Figure S4. Species tree inferred by wASTRAL from nucleotide (NT) gene trees (full set; no branch collapsing). Branch annotations include local posterior probabilities and quartet support values (q1/q2/q3).

Figure S5. Species tree inferred by wASTRAL from amino acid (AA) gene trees (full set; no branch collapsing). Branch annotations include local posterior probabilities and quartet support values (q1/q2/q3).

Figure S6. Species tree inferred by wASTRAL from nucleotide (NT) gene trees with branches below 50% UFBoot support collapsed to polytomies (b50up). Branch annotations include local posterior probabilities and quartet support values (q1/q2/q3).

Figure S7. Species tree inferred by wASTRAL from amino acid (AA) gene trees with branches below 50% UFBoot support collapsed to polytomies (b50up). Branch annotations include local posterior probabilities and quartet support values (q1/q2/q3).

- Figure S8. Cross-dataset topology evaluation in ASTRAL: maximum-likelihood topology evaluated using nucleotide (NT) gene trees. Branch annotations include local posterior probabilities and quartet support values (q1/q2/q3).
- Figure S9. Cross-dataset topology evaluation in ASTRAL: maximum-likelihood topology evaluated using amino acid (AA) gene trees. Branch annotations include local posterior probabilities and quartet support values (q1/q2/q3).
- Figure S10. Cross-dataset topology evaluation in ASTRAL: topology inferred from nucleotide (NT) gene trees evaluated using amino acid (AA) gene trees. Branch annotations include local posterior probabilities and quartet support values (q1/q2/q3).
- Figure S11. Cross-dataset topology evaluation in ASTRAL: topology inferred from amino acid (AA) gene trees evaluated using nucleotide (NT) gene trees. Branch annotations include local posterior probabilities and quartet support values (q1/q2/q3).
- Figure S12. Species network inferred from nucleotide (NT) gene trees using the NANUQ algorithm, visualized with the NeighborNet algorithm in SplitsTree. (A) Network inferred under relaxed parameter settings ($\alpha = 0.05$, $\beta = 0.95$); (B) network inferred under stringent parameter settings ($\alpha = 5 \times 10^{-29}$, $\beta = 0.95$).
- Figure S13. Species network inferred from amino acid (AA) gene trees using the NANUQ algorithm, visualized with the NeighborNet algorithm in SplitsTree. (A) Network inferred under relaxed parameter settings ($\alpha = 0.05$, $\beta = 0.95$); (B) network inferred under stringent parameter settings ($\alpha = 5 \times 10^{-29}$, $\beta = 0.95$).
- Figure S14. Four-cluster likelihood mapping (FcLM) results based on amino acid (AA) and nucleotide (NT) datasets. Percentages indicate support for each of the three possible quartet topologies.
- Figure S15. Gene concordance factors (gCF) and site concordance factors (sCF) for the three alternative topologies (Topologies 1–3; see Figure 2A–C). gCF values were computed using both the full gene tree set and collapsed gene trees (b50up). sCF was estimated using parsimony- and likelihood-based quartet sampling. Analyses were performed at both the NT and AA levels.
- Figure S16. Morphology of *Hypnoidus jeffrey*, *Prosternon tessellatum*, *Dima yunnana*, and *Cardiophorus* sp. Heads and antennae.
- Figure S17. Morphology of *Hypnoidus jeffrey*, *Prosternon tessellatum*, *Dima yunnana*, and *Cardiophorus* sp. Pronota.
- Figure S18. Morphology of *Hypnoidus jeffrey*, *Prosternon tessellatum*, *Dima yunnana*, and *Cardiophorus* sp. Mesoscutella and elytra.
- Figure S19. Morphology of *Hypnoidus jeffrey*, *Prosternon tessellatum*, *Dima yunnana*, and *Cardiophorus* sp. Meso- and metasterna, metanota.
- Figure S20. Morphology of *Hypnoidus jeffrey*, *Prosternon tessellatum*, *Dima yunnana*, and *Cardiophorus* sp. Abdomens and hind tarsi.

Supplementary Text. Overview of topologies proposed by Douglas et al. (2021)

1. The DEN + HYP + CAR + NEG clade is present; DEN is monophyletic; HYP is a sister to CAR + NEG. Supplements, Figs. 1, 2 in Douglas et al. (2021): maximum likelihood, ML; amino acid, AA, data; partitioned/unpartitioned, 50% data completeness. This topology, shown in the main text as Fig. 3, was preferred and is consistent with the HYP and DEN subfamily ranks.
2. The DEN + HYP + CAR + NEG clade is absent, monophyletic Dendrometrinae, incl. hypnoidines, the latter sister to Dendrometrini; the CAR + NEG clade is unrelated, a sister to Agrypninae: Tetralobini Fig. 3; ML, nucleotide, NT, level; unpartitioned, 50% completeness. The topology is consistent with the HYP and DEN subfamily ranks.
3. The DEN + HYP + CAR + NEG clade is absent, Tetralobinae + CAR + NEG; paraphyletic Dendrometrinae; hypnoidines are a sister to Dendrometrini (Figs. 4, 5; ML, NT; partitioned without/with flanking regions added, 50% completeness). The topology is inconsistent with the Hypnoidinae being a subfamily. DEN cannot be accepted as a valid taxon.
4. The DEN + HYP + CAR + NEG clade is present; paraphyletic DEN; HYP is a sister to CAR + NEG. Figs. 6, 7, 8; ML, NT, partitioned/unpartitioned/partitioned, with/without/without flanking regions, 3rd position removed, 50% completeness. The topology is inconsistent with the Hypnoidinae being a subfamily. DEN cannot be accepted as a valid taxon.
5. The DEN + HYP + CAR + NEG clade is absent; HYP + DEN is a sister to Agrypninae; CAR + NEG is a sister to Tetralobinae + (Eucnemidae + Throscidae + Cerophytidae). Fig. 9; ML, NT, partitioned, with flanking regions added, 75% completeness. The topology is inconsistent with the Elateridae being monophyletic. Seven elateroid families are recovered within Elateridae. DEN, HYP, CAR, and NEG can be accepted as valid taxa.
6. The DEN + HYP + CAR + NEG clade is present, monophyletic DEN; HYP is a sister to CAR + NEG. Elateridae paraphyletic; Lycidae a sister to Lissominae, Cantharidae a terminal within the Hapatesinae + Pityobiinae clade. Fig. 10; ML, AA, unpartitioned, 75% completeness; Six elateroid families recovered within Elateridae, DEN, HYP, CAR, and NEG, can be accepted as valid taxa.
7. the DEN + HYP + CAR + NEG clade is present, monophyletic DEN + HYP is a sister to CAR + NEG ($lpp = 0.49$). Fig. 11: coalescent analysis, AA, 50% completeness. DEN, HYP, CAR, and NEG can be accepted as valid taxa.
8. the DEN + HYP + CAR + NEG clade is absent. HYP + DEN is a sister to Hapatesinae + Pityobiinae; CAR + NEG is a sister to Tetralobinae; Cantharidae is a sister to Agrypninae. Fig. 12: coalescent analysis, NT, 50% completeness. DEN, HYP, CAR, and NEG can be accepted as valid taxa. Four elateroid families are recovered within Elateridae.

Supplementary Text. Taxonomy – formal classification and detailed justification

The five clades, CAR, NEG, HYP, OXY[s.l.], and DEN[s.str.] were consistently recovered across data filtering methods, analytical approaches, partitions, and NT/AA levels (Figs. 2A–C). Two of them are widely accepted as subfamilies, Cardiophorinae and Negastrinae, and we retain their current rank, following Costa et al. (2010). No analysis based on 4,000 loci recovered a topology consistent with the current Linnean classification proposed by Douglas et al. (2021). Hypnoidinae *sensu* Douglas et al. (2021), recently raised to the subfamily rank (Table S1). These authors recovered HYP as either a sister to the CAT + NEG clade (ML analyses, subfamily rank possible) or to the DEN[s.str.] clade within Dendrometrinae *sensu lato* (coalescent analyses, subfamily rank rejected). However, the DEN[s.str.] + OXY[s.l.] clade, an equivalent of the Dendrometrinae *sensu* Douglas et al. (2021), (DEN[s.l.]), was absent in all recovered topologies (Figs. 2A–C) in this study and in all 32 topologies presented by Motyka et al. (2026). Douglas et al.'s concept of Dendrometrinae was compromised either by the inclusion of *Hypnoidus* (HYP) as an internal branch (the coalescent analysis at the AA level; Fig. 2B) or by the serial splits of DEN[s.str.] and OXY[s.l.] (all ML analyses and the coalescent analysis at the NT level, Fig. 2B, C).

Based on the recovered topologies, the results presented by Motyka et al. (Motyka et al., 2026), the ranks assigned to family-group taxa recently (Costa et al., 2010; Douglas et al., 2021), and an attempt to avoid unnecessary rank changes, we propose the revised classification:

Oxynopterinae Candèze, 1857, new status, new sense

Oxynoptérides Candèze, 1857: 355. Type genus: *Oxynopterus* Hope, 1842.

= Oxynoptérides Lacordaire, 1857: 158, current usage maintained (Bouchard et al., 2011).

= Mélanactides Candèze, 1857: 182. Type genus: *Melanactes* LeConte, 1853, see (Bouchard et al., 2011).

Dimini Candèze, 1863

Dimites Candèze, 1863: 237. Type genus: *Dima* Charpentier, 1825.

Plastocerini Crowson, 1972

Plastoceridae Crowson, 1972: 37, in key. Type genus: *Plastocerus* Schaum, 1852.

Note: In 2023, an application was submitted to the Commission to suppress Plastoceri J. L. LeConte, 1861 for the Principles of Priority and Homonymy (Art. 65.2.1) to conserve this name as valid. See Supplements for the application submitted in 2023. The application waits to be handled.

Oxynopterini Candèze, 1857: 355. Type genus: *Oxynopterus* Hope, 1842.

=Pectocerini Gurjeva, 1974: 107, in key. Type genus: *Pectocera* Hope, 1842.

Notes. The Dimini position is less supported than the subsequent splits Plastocerini + Oxynopterini. However, all topologies place them as their sister. Douglas et al. (2021) found monophyletic OXY[s.l.] in ten and paraphyletic in two trees. Pectocerini was listed as a synonym by Bouchard et al. (2011), but we found no study formally proposing synonymy. Kundera et al. (2016) and Motyka et al. (2026) used Pectocerini as a valid name. Given the low species diversity and the split between *Pectocera* and *Oxynopterus* in the mid Paleogene (Kusy et al., in press), we follow Bouchard et al. (2011).

Dendrometrinae Gistel, 1848, new sense

Dendrometrinae Gistel, 1848: [5]. Type genus: *Dendrometrus* Gistel, 1848.

= Denticollinae Stein & Weise, 1877 (1848), see Sánchez-Ruiz (1996).

Dendrometrini Gistel 1848: [5]. Type genus: *Dendrometrus* Gistel, 1848.

Selatosomini Schimmel et al., 2015: 30. Type genus: *Selatosomus* Stephens, 1830.

=Diacanthidae Gistel, 1848: [5]. Type genus: *Diacanthus* Latreille, 1834 [= *Selatosomus* Stephens, 1830], *nomen oblitum*.

Pleonomini Semenov-Tian-Shanskij & Pjatakova, 1936: 103. Type genus: *Pleonomus* Ménétriés, 1848.

Note. Bouchard et al. (2011) protected Prosternini as a younger synonym of Diacanthidae. However, *Diacanthus* is a synonym of *Selatosomus*, and Diacanthidae is a younger synonym of Selatosomini. We follow the opinion that Diacanthidae is a *nomen oblitum*.

Prosterninae Gistel, 1856, new status

Prosterninae Gistel, 1856: 367, Type genus: *Prosternon* Latreille, 1834, *nomen protectum* (Bouchard et al., 2011).

Prosternini Gistel, 1856: 367, Type genus: *Prosternon* Latreille, 1834.

Note. High-quality phylogenomic data for Prosterninae were unavailable, and we base our decision on the topologies presented by Motyka et al. (2026) (Fig. S1) and consistency with all topologies presented by Douglas et al. (2021). Motyka et al. (2026) recovered prosternines either as a second branch in the (Oxy[s.l.](Prosterninae (HYP + DEN[s.str.]))) clade (Prosternini can be kept, but Hypnoidinae must be lowered to a tribe) or as a sister to OXY[s.l.], when Dendrometrinae *sensu latissimo* (=including Hypnoidinae) was recovered (the subfamily rank is needed if Hypnoidinae *sensu* Douglas et al. (2021) is accepted). Alternatively, Prosterninae was either a second branch in OXY[s.l.], Prosterninae, and DEN[s.str.], or OXY[s.l.] + Prosterninae, DEN[s.str.] grade if Hypnoidinae was a sister to the CAT + NEG clade (Fig. S1). Twelve of 32 topologies permitted Prosternini; 20 analyses requested that the subfamily rank be assigned. All analyses are compatible with the subfamily rank, whereas none are compatible with their current placement. Therefore, we propose the subfamily rank, Prosterninae, with a single tribe, Prosternini.

Hypnoidinae Schwarz, 1906 (1860)

Hypnoidini Schwarz, 1906: 150. Type genus: *Hypnoidus* Dillwyn, 1829; conserved name.

Note. The rank of hypnoidines fluctuated (Table S1), and we follow the latest change (Douglas et al., 2021).

Incertae sedis

Crepidomenini Candèze, 1863

Crépidoménites Candèze, 1863: 190. Type genus: *Crepidomenus* Erichson, 1842.

Note. No WGS/TSA data were available for the current study. Therefore, we can base the relationships solely on Sanger data (Kundera et al., 2016), which proposed the Hypnoidinae + Crepidomenini clade. Morphology-based studies have never proposed such relationships nor strong evidence for alternative positions (Calder, 1986, 1996;

Calder et al., 1993). If Sanger-based topology is accepted, Crepidomeninae should be either a senior synonym of Hypnoidinae, Hypnoidinae could be a tribe of Crepidomeninae, or Crepidomeninae and Hypnoidinae could be accepted as subfamilies. Provisionally, we propose Crepidomenini *incertae sedis*.

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Table S1. An overview of the classification of hypnoidines. Markings designate the proposed placement of hypnoidines: ❖ no information, ● a tribe within Dendrometrinae, including a sister relationship with Dendrometrinae, ◆ a subfamily in sister relationships to Negastrinae + Cardiophorinae; □ an invalid taxon, the monophyly rejected.

Year	Rank	Additional information
Schwarz, 1906	❖Hypnoidini	Hypnoidini established the as one of 28 tribes within the Elateridae. The subfamily rank was not used
Dolin, 1975, 1978	●Hypnoidini	A tribe within Dendrometrinae
Stibick (1979)	●Hypnoidinae	A subfamily rank; hypothesized their relationships with Melanactinae (=Oxynopterini within Dendrometrinae, now). Hypnoidines + oxynopterines as a sister to Dendrometrinae <i>sensu</i> Stibick 1979: 146; Fig. 1).
Ohira, 1999	●Hypnoidini	A tribe within Dendrometrinae
Sagegami-Oba et al., 2007	●Hypnoidinae	Three hypnoidine genera as sisters of Prosternini within Dendrometrinae (28S rRNA tree; p. 416; Fig.3)
Kundrata & Bocak, 2011	●Hypnoidini	<i>Hypolithus</i> sp. as a sister to Prosternini within monophyletic Dendrometrinae. Cardiophorinae and Negastrinae a distantly related clade.
Bouchard et al., 2011	❖Hypnoidini	Placed in Dendrometrinae in the family-group taxa overview.
Douglas, 2011	□Hypnoidini	Hypnoidini formally retained in Dendrometrinae. Still, the morphology-based analysis rejected the hypnoidine's monophyly.
Bocak et al., 2014	●Hypnoidini	A tribe within Dendrometrinae; <i>Hypolithus</i> sp. recovered within Dendrometrinae in the 8,000-taxa whole-order analysis of Coleoptera.
Schimmel et al., 2015	●Hypnoidinae	Hypnoidines as a sister to Dendrometrinae based on an earlier unpublished analysis of 12 DNA fragments. Negastrinae and Cardiophorinae a sister clade of Hypnoidinae + Dendrometrinae.
Han et al., 2016	●Hypnoidini	Hypnoidines within Dendrometrinae (= Denticollinae <i>sensu</i> Han et al. 2016) based on the analysis of barcodes.
Kundrata, et al., 2016	●Hypnoidini	Sanger data analysis recovered <i>Hypolithus</i> sp. as a sister to Crepidomenini. Dendrometrinae were recovered as a paraphylum preceding Negastrinae and Cardiophorinae (p. 296, Fig. 2).
Douglas et al., 2021	◆Hypnoidinae	
Motyka et al., 2026	◆Hypnoidinae	Formal rank retained as in Douglas et al., 2021; evidence presented for alternative relationships.

Table S2. Morphological characters supporting the monophyly and relationships of focal taxa.

Relationships and diagnostic characters	Character	Reference	Comments	
			Morphology-based relationships	Molecular relationships
diagnostic	ridged frons	Stibick, 1975	Shared with Dendrometrinae (sometimes incomplete or absent), some Elaterinae, Negastrinae, and Cardiophorinae, separates from <i>Melanactes</i>	Designated as 'nonunique synapomorphy' (Douglas et al., 2011); possible multiple origins or losses; homoplastic character state
hypnoidines + <i>Melanactes</i>	open mesocoxal cavities in which the mesepimeron reaches the cavity while cutting off the mesepisternum	Stibick, 1975	shared with <i>Melanactes</i>	Separate origins in hypnoidines and <i>Melanactes</i>
Hypnoidines + Negastrinae + Cardiophorinae	Partially or completely closed mesocoxal cavities	Douglas et al., 2011	Mesepimeron reaching cavity in hypnoidines; closed cavities in Cardiophorinae + Negastrinae	Designated as 'nonunique synapomorphy' (Douglas et al., 2011)
Paraphyly	head & prosternum of <i>Tropihypnus</i> + Negastrinae or Neg. + Card.	Douglas et al., 2011		Paraphyly rejected by molecular studies
diagnostic	tarsi without pads	Stibick, 1975	shared with DEN: Prosternini	
diagnostic	anteriorly lobed prosternum			
Hypnoidines + Dendrometrinae + Elaterinae + Pityobiinae	the absence of setae on the claws near the base	Stibick, 1975, 1979	shared with Dendrometrinae including Oxynopterini, Elaterinae, Oestodinae and Pityobiinae	Low consistency with mol. phylogeny, independently in Pityobiinae, reversal or independent origins in the elaterine clade and Dendrometrinae + hypnoidines
Hypnoidines + Dendrometrines	Flat head	Stibick, 1975, 1975	Shared with Dendrometrinae except for Oxynopterus	
Hypnoidines + Dendrometrines	mouthparts prognathous	Stibick, 1975, 1979, but not Douglas et al., 2011		Shared with Dendrometrinae; Douglas et al. (2011: 21) considers Dendrometrinae head hypognathous
Hypnoidines + Dendrometrines	Bisected nasal area	Nakane & Kishii, 1956	Justification of the transfer to Dendrometrinae	
	Flat body	ditto	ditto	
	Male genitalia	ditto	ditto	
Hypnoidines + Negastrinae + Cardiophorinae	Male genitalia with fused parameres	Douglas et al., 2011	Justification of hypnoidines + Negastrinae + Cardiophorinae	Commonly encountered in Elateridae and Elateroidea

Table S3. Overview of topologies published by Motyka et al. (2026).

Motyka et al. (2026)			
Fig #	The analysis: dataset	Dendrom. Monoph. Hypnoidini included	Dendrom. paraph. Hypnoidinae
All genes			
S5	IQ-TREE analysis all genes at nucleotide level		yes
S6	ASTRAL analysis: all genes at nucleotide level	yes	
S7	IQ-TREE analysis: all genes at amino acid level		yes
S8	ASTRAL analysis: all genes at amino acid level	yes (one AHE out)	
Sym Test valid and invalid genes			
S9	IQ-TREE analysis: SymTest valid genes at the NT level		yes
S10	ASTRAL analysis: SymTest valid genes at the NT level	yes	
S11	IQ-TREE analysis: SymTest valid genes at the AA level		yes
S12	ASTRAL analysis: SymTest valid genes at the AA level	yes	
S13	IQTREE analysis: SymTest refused genes at the NT level	yes	
S14	ASTRAL analysis: SymTest refused genes at the NT level	yes	
S15	IQTREE analysis: SymTest refused genes at the AA level		yes
S16	ASTRAL analysis: SymTest refused genes at the AA level	yes (one AHE out)	
CG-content based subsets			
S17	IQTREE analysis: SymTest valid genes, extra high GC at the NT level	yes	
S18	ASTRAL analysis: SymTest valid genes, extra high GC at the NT level	yes	
S19	IQTREE analysis: SymTest valid genes, extra high GC at the AA level		yes
S20	ASTRAL analysis: SymTest valid genes, extra high GC at the AA level	yes (one AHE out)	
S21	IQTREE analysis: SymTest valid genes, high GC at the NT level		yes
S22	ASTRAL analysis: SymTest valid genes, high GC at the NT level	yes	
S23	IQTREE analysis: SymTest valid genes, high GC at the AA level		yes
S24	ASTRAL analysis: SymTest valid genes, high GC at the AA level	yes	
S25	IQTREE analysis: SymTest valid genes, medium GC at the NT level		yes
S26	ASTRAL analysis: SymTest valid genes, medium GC at the NT level	yes	
S27	IQTREE analysis: SymTest valid genes, medium GC at the AA level		yes
S28	ASTRAL analysis: SymTest valid genes, medium GC at the AA level	yes	
S29	IQTREE analysis: SymTest valid genes, low GC at the NT level		yes
S30	ASTRAL analysis: SymTest valid genes, low GC at the NT level	yes	
S31	IQTREE analysis: SymTest valid genes, low GC at the AA level		yes
S32	ASTRAL analysis: SymTest valid genes, low GC at the AA level	yes	
S33	IQTREE analysis: SymTest valid genes, extra low GC at the NT level		yes
S34	ASTRAL analysis: SymTest valid genes, extra low GC at the NT level	yes	
S35	IQTREE analysis: SymTest valid genes, extra low GC at the AA level		yes
S36	ASTRAL analysis: SymTest valid genes, extra low GC at AA level		yes

Table S4. Summary of Gene Concordance Factor (gCF) and Gene Discordance Factor (gDF) statistics across three alternative phylogenetic hypotheses (topo1, topo2, topo3). Results are shown for amino acid (AA) and nucleotide (NT) datasets

topology	datatype	method	node letter	node id	cf value	gCF_N	gDF1	gDF1_N	gDF2	gDF2_N	gDFP	gDFP_N	gN	Length
topo1	AA	b50up	A	28	23.66	839	0.14	5	0.51	18	75.69	2684	3546	1.12273
topo1	AA	b50up	B	29	3.26	109	0.57	19	0.72	24	95.46	3195	3347	0.250262
topo1	AA	b50up	C	33	0.65	23	4.89	173	4.47	158	89.99	3183	3537	0.05808
topo1	AA	full	A	28	30.57	1084	0.9	32	1.66	59	66.86	2371	3546	1.12273
topo1	AA	full	B	29	8.49	284	2.03	68	1.79	60	87.69	2935	3347	0.250262
topo1	AA	full	C	33	2.52	89	9.61	340	9.22	326	78.65	2782	3537	0.05808
topo1	NT	b50up	A	28	35.96	1406	1.18	46	0.31	12	62.56	2446	3910	1.12273
topo1	NT	b50up	B	29	5.97	220	1.03	38	1.6	59	91.4	3369	3686	0.250262
topo1	NT	b50up	C	33	5.07	198	4.38	171	6.02	235	84.53	3300	3904	0.05808
topo1	NT	full	A	28	43.12	1686	3.02	118	1.36	53	52.51	2053	3910	1.12273
topo1	NT	full	B	29	12.45	459	3.23	119	5.43	200	78.89	2908	3686	0.250262
topo1	NT	full	C	33	9.73	380	9.96	389	13.17	514	67.14	2621	3904	0.05808
topo2	AA	b50up	A	28	23.7	836	5.98	211	2.21	78	68.1	2402	3527	0.534242
topo2	AA	b50up	B	32	4.89	173	0.65	23	4.47	158	89.99	3183	3537	0.194993
topo2	AA	b50up	C	36	3.24	108	0.93	31	1.89	63	93.94	3131	3333	0.218461
topo2	AA	full	A	28	30.62	1080	9.58	338	5.13	181	54.66	1928	3527	0.534242
topo2	AA	full	B	32	9.61	340	2.52	89	9.22	326	78.65	2782	3537	0.194993
topo2	AA	full	C	36	8.34	278	2.64	88	5.01	167	84.01	2800	3333	0.218461
topo2	NT	b50up	A	28	35.98	1398	5.64	219	3.58	139	54.81	2130	3886	0.534242
topo2	NT	b50up	B	32	4.38	171	5.07	198	6.02	235	84.53	3300	3904	0.194993
topo2	NT	b50up	C	36	5.94	218	0.46	17	2.15	79	91.45	3358	3672	0.218461
topo2	NT	full	A	28	43.18	1678	9.93	386	6.33	246	40.56	1576	3886	0.534242
topo2	NT	full	B	32	9.96	389	9.73	380	13.17	514	67.14	2621	3904	0.194993
topo2	NT	full	C	36	12.42	456	1.44	53	6.94	255	79.19	2908	3672	0.218461
topo3	AA	b50up	A	28	23.65	835	1.19	42	1.39	49	73.77	2604	3530	0.038831
topo3	AA	b50up	B	32	4.46	158	2.23	79	0.59	21	92.71	3281	3539	0.013848
topo3	AA	b50up	C	36	9.09	304	3.26	109	0.48	16	87.17	2916	3345	0.032544
topo3	AA	full	A	28	30.51	1077	2.8	99	3.54	125	63.14	2229	3530	0.038831
topo3	AA	full	B	32	9.21	326	5.65	200	2.2	78	82.93	2935	3539	0.013848
topo3	AA	full	C	36	14.35	480	8.49	284	2.03	68	75.13	2513	3345	0.032544
topo3	NT	b50up	A	28	35.98	1401	0.87	34	1.31	51	61.84	2408	3894	0.038831

topo3	NT	b50up	B	32	6.01	235	2.51	98	1.41	55	90.08	3522	3910	0.013848
topo3	NT	b50up	C	36	11.28	415	5.98	220	1.01	37	81.74	3008	3680	0.032544
topo3	NT	full	A	28	43.12	1679	2.39	93	3.9	152	50.59	1970	3894	0.038831
topo3	NT	full	B	32	13.17	515	7.39	289	3.71	145	75.73	2961	3910	0.013848
topo3	NT	full	C	36	19.21	707	12.45	458	3.07	113	65.27	2402	3680	0.032544

COLUMN EXPLANATIONS

- **topology:** The tested phylogenetic hypothesis (**topo1** / **topo2** / **topo3**), corresponding to the hypotheses defined in the manuscript.
- **datatype:** Type of sequence data used for the analysis — **AA** (amino acid) or **NT** (nucleotide).
- **method:** Analysis strategy used; **b50up** (only gene trees with bootstrap $\geq 50\%$ used) or **full** (all gene trees used).
- **node_letter:** Node identifier within the hypothesis (**A**, **B**, or **C**), referencing the specific split shown in the hypothesis diagram.
- **node_id:** Internal IQ-TREE node ID, provided for traceability to the source files.
- **cf_value:** Gene Concordance Factor (%). The percentage of gene trees that contain the focal bipartition.
- **gCF_N:** Absolute number of gene trees supporting the focal bipartition.
- **gDF1:** Gene Discordance Factor 1 (%). Percentage of gene trees supporting the most common alternative bipartition.
- **gDF1_N:** Absolute number of gene trees supporting the first alternative bipartition.
- **gDF2:** Gene Discordance Factor 2 (%). Percentage of gene trees supporting the second alternative bipartition.
- **gDF2_N:** Absolute number of gene trees supporting the second alternative bipartition.
- **gDFP:** Gene Discordance Factor — Polyphyletic (%). Percentage of gene trees where the focal taxa are not monophyletic. High values (e.g., $> 70\%$) are typical of rapid radiations and suggest strong incomplete lineage sorting (ILS).
- **gDFP_N:** Absolute number of gene trees showing a polyphyletic pattern.
- **gN:** Total number of gene trees used for the calculation ($\text{gCF} + \text{gDF1} + \text{gDF2} + \text{gDFP} \approx 100\%$).
- **Length:** Branch length of the focal node in the reference tree used for the analysis.

Table S5. Summary of Site Concordance Factor (sCF) and Site Discordance Factor (sDF) statistics for three alternative phylogenetic hypotheses (topo1, topo2, topo3). Analysis was performed using amino acid (AA) and nucleotide (NT) datasets,

topology	datatype	method	node letter	node id	cf value	sCF N	sDF1	sDF1 N	sDF2	sDF2 N	sN	Length
topo1	AA	likelihood	A	25	42.47	1949.82	26.37	1210.71	31.16	1430.34	4590.87	0.03952
topo1	AA	likelihood	B	26	38.31	4445.69	30.41	3528.98	31.27	3628.66	11603.33	0.015788
topo1	AA	likelihood	C	30	30.31	2117.47	38.06	2658.9	31.63	2209.47	6985.84	0.004287
topo1	AA	parsimony	A	28	40.55	8667.07	28.21	6093.21	31.25	6776.36	21536.64	1.12273
topo1	AA	parsimony	B	29	40.2	8113.14	30.7	6224.34	29.1	5824.61	20162.09	0.250262
topo1	AA	parsimony	C	33	27.79	5840.04	40.73	8515.17	31.48	6634.51	20989.72	0.05808
topo1	NT	likelihood	A	32	37.42	23941.62	32.18	20587.1	30.4	19449.94	63978.66	0.039924
topo1	NT	likelihood	B	24	33.3	54931.1	34.55	56991.15	32.15	53039.85	164962.1	0.013826
topo1	NT	likelihood	C	25	34.35	36983.25	34.87	37546.27	30.79	33149.33	107678.9	0.012492
topo1	NT	parsimony	A	28	35.35	68579.12	33.01	64245.35	31.64	61711.75	194536.2	1.12273
topo1	NT	parsimony	B	29	35.71	71577.08	31.28	62607.92	33.01	65449.06	199634.1	0.250262
topo1	NT	parsimony	C	33	33.05	66790.71	36.22	72868.66	30.73	61996.58	201656	0.05808
topo2	AA	likelihood	A	25	33.25	1456.97	37.06	1623.98	29.7	1301.35	4382.3	0.02662
topo2	AA	likelihood	B	26	38.01	2656.9	31.66	2213.07	30.32	2119.5	6989.47	0.01433
topo2	AA	likelihood	C	27	36.57	3256.15	34.67	3086.73	28.76	2560.56	8903.44	0.012374
topo2	AA	parsimony	A	28	36.35	8301.15	33.66	7656.9	29.98	6837.57	22795.62	0.534242
topo2	AA	parsimony	B	32	39.69	8389.12	28.27	5984.31	32.04	6806.84	21180.27	0.194993
topo2	AA	parsimony	C	36	37.14	7081.96	29.42	5634.67	33.44	6398.11	19114.74	0.218461
topo2	NT	likelihood	A	32	31.33	20158.46	38.1	24516.7	30.56	19664.56	64339.72	0.030962
topo2	NT	likelihood	B	28	34.85	37491.72	30.75	33083.79	34.4	37015.99	107591.5	0.014496
topo2	NT	likelihood	C	24	33.59	40716.2	36.22	43901.95	30.18	36582.71	121200.9	0.014259
topo2	NT	parsimony	A	28	34.67	74866.43	32.7	70180.28	32.63	70242.03	215288.7	0.534242
topo2	NT	parsimony	B	32	36.03	73115.53	33.16	67717.97	30.81	62737.7	203571.2	0.194993
topo2	NT	parsimony	C	36	35.15	66718.27	31.17	59380.55	33.68	63509.63	189608.5	0.218461
topo3	AA	likelihood	A	25	41.49	1618.94	30.25	1180.42	28.25	1102.48	3901.84	0.014714
topo3	AA	likelihood	B	26	35.28	2485.68	35.15	2476.81	29.58	2084.09	7046.58	0.006041
topo3	AA	likelihood	C	30	35.43	3627.81	33.12	3391.03	31.45	3220.62	10239.46	0.008903
topo3	AA	parsimony	A	28	40	8524.59	29.78	6408.36	30.22	6534.19	21467.14	0.038831
topo3	AA	parsimony	B	32	33.79	6717.65	37.63	7529.74	28.57	5712.64	19960.03	0.013848
topo3	AA	parsimony	C	36	33.02	7263.41	39.45	8770.36	27.53	6083.51	22117.28	0.032544
topo3	NT	likelihood	A	32	35.86	19140.12	34.35	18333.02	29.79	15900	53373.14	0.038771

topo3	NT	likelihood	B	28	32.86	33874.47	34.65	35721.32	32.48	33481.88	103077.7	0.01383
topo3	NT	likelihood	C	24	31.59	49016.78	36.47	56591.68	31.94	49557.85	155166.3	0.032496
topo3	NT	parsimony	A	28	36.44	68571.53	30.96	58504.31	32.6	61752.66	188828.5	0.038831
topo3	NT	parsimony	B	32	31.11	60677.3	36.39	71206.76	32.5	63987.26	195871.3	0.013848
topo3	NT	parsimony	C	36	31.86	66947.51	37.14	78052.81	31.01	65204.73	210205.1	0.032544

COLUMN EXPLANATIONS

- **topology:** The tested phylogenetic hypothesis (**topo1** / **topo2** / **topo3**), corresponding to the hypotheses defined in the manuscript.
- **datatype:** Type of sequence data used for the analysis — **AA** (amino acid) or **NT** (nucleotide).
- **method:** The method used to calculate site support: **likelihood** (site quartet sampling based on ML optimization) or **parsimony** (site quartet sampling based on parsimony).
- **node_letter:** Node identifier within the hypothesis (**A**, **B**, or **C**), referencing the specific split shown in the hypothesis diagram.
- **node_id:** Internal IQ-TREE node ID, provided for traceability to the source files.
- **cf_value:** Site Concordance Factor (%). The percentage of informative sites (averaged over 100 random quartets) that support the focal bipartition. Values near 33.3% indicate that all three possible resolutions of the quartet are equally supported.
- **sCF_N:** Average number of informative sites supporting the focal bipartition across the sampled quartets.
- **sDF1:** Site Discordance Factor 1 (%). Percentage of informative sites supporting the first alternative quartet resolution.
- **sDF1_N:** Average number of informative sites supporting alternative resolution 1.
- **sDF2:** Site Discordance Factor 2 (%). Percentage of informative sites supporting the second alternative quartet resolution.
- **sDF2_N:** Average number of informative sites supporting alternative resolution 2.
- **sN:** Average number of informative sites per quartet over 100 replicates ($sCF + sDF1 + sDF2 \approx 100\%$).
- **Length:** Branch length of the focal node in the reference tree used for the analysis.

Case – Plastoceridae Crowson, 1972 (Insecta, Coleoptera): proposed conservation of the family-group name by suppression of Plastocerini Leconte, 1861 (Insecta, Coleoptera)

Case – Plastoceridae Crowson, 1972 (Insecta, Coleoptera): proposed conservation of the family-group name by suppression of Plastocerini Leconte, 1861 (Insecta, Coleoptera)

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Abstract. The purpose of this application, under Articles 55.1 and 81.2.1 of the Code, is to resolve the homonymy of the family group name PLASTOCERIDAE Crowson, 1972 (Insecta, Coleoptera) by suppressing its senior homonym PLASTOCERINI Leconte, 1861 (Coleoptera, Elateridae) for the purposes of both the Principle of Priority and the Principle of Homonymy. The family group name PLASTOCERINI LeConte, 1861 threatens the widely used names PLASTOCERINI Crowson, 1972 in ELATERIDAE: DENDROMETRINAE and APLASTINA Stibick, 1979 in ELATERIDAE: ELATERINAE: CEBRIONINI.

Keywords. Family-group name; Arthropoda; Insecta; Coleoptera; ELATEROIDEA; ELATERIDAE; PLASTOCERIDAE; PLASTOCERINAE; PLASTOCERINI; click beetles.

1. Schaum (1852: 52) validly established the genus *Plastocerus* for *Callirhipis angulosa* Germar (Germar, 1844) (Coleoptera, ELATERIDAE). *Callirhipis angulosa* Germar, 1844 is the type species by monotypy. The genus now includes two valid species (Bocak, 2007; Bocak et al., 2018; Hájek, Ivie, & Lawrence, 2020; Lin & Yang, 2012) from the Palearctic region (*P. angulosus* Germar and *P. thoracicus* Fleutiaux (Fleutiaux, 1918)).

2. LeConte (1853: 502) established *P. schaumii* Leconte, 1853: 502 [nota: should be '*schaumi*,' ICZN 1999, Art. 31.1.2] in *Plastocerus* Schaum, 1852 based on information from H. R. Schaum, that *P. schaumii* from California and *P. angulosus* from Turkey are congeneric. Simultaneously, Leconte (1853: 502) declares that *Callirhipis angulosus* Germar, 1844 [= *angulosa*] is the type [species] of the genus *Plastocerus* [*Callirhipis angulosus* Germ. ... forms in the Catalogus Coleopterorum Europa the type of the unpublished genus *Plastocerus*]. As *Plastocerus* was considered unpublished, Candèze (1863: 484–487) (Candèze, 1863) designated LeConte (1853) as the author of the name *Plastocerus* [the title in Candèze 1863: 484: "*Plastocerus* (Schaum) LeC."]. *Plastocerus* LeConte, 1853 was designated 'monobasic' (=monotypic) by Hyslop (1921: 665). Therefore, Hyslop (1921: 665) considered *P. schaumii* LeConte, 1853 as the type species of *Plastocerus* LeConte, 1853 [*nec* Schaum, 1852].

3. *Plastocerus* LeConte, 1853 is a junior homonym of *Plastocerus* Schaum, 1852.

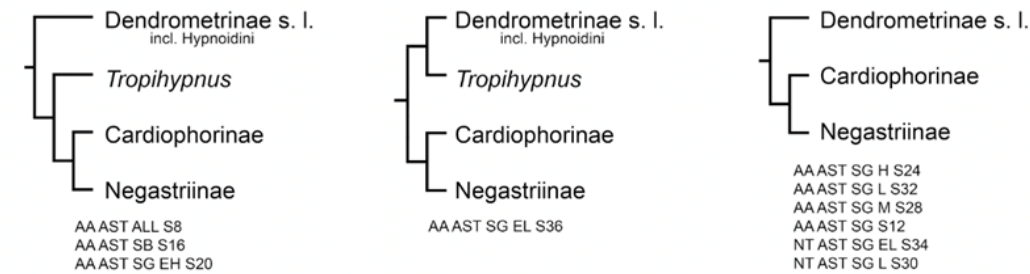
4. Candèze (1863: 487) established the monotypic genus *Octinodes* (Coleoptera, Elateridae) for *Octinodes capillatus* Candèze, 1863 from Venezuela.
5. Leng (1918: 205) synonymized *Plastocerus* LeConte, 1853 (monotypic, type species *P. schaumii* LeConte, 1853, see Hyslop, 1921) with *Octinodes* Candèze, 1853 (type species *Octinodes capillatus* Candèze, 1863). Hyslop (1921: 665) and others followed the proposed synonymization. *Octinodes* Candèze, 1863 is a junior subjective synonym of *Plastocerus* LeConte, 1853 *sensu* Candèze (1863) and Hyslop (1921).
6. LeConte (1859: 73) established *Aplastus* for *Aplastus speratus* LeConte, 1859, which became the type species by monotypy.
7. LeConte (1861: 172) established the tribe PLASTOCERINI with the type-genus *Plastocerus sensu* LeConte, 1853 [not *Plastocerus* Schaum, 1852]. PLASTOCERINI LeConte, 1861 is a senior homonym of PLASTOCERIDAE Crowson, 1972. It is based on a misidentified type-genus. PLASTOCERINI LeConte, 1861 is not used in modern literature on ELATERIDAE (Bocak et al., 2018; Costa, Lawrence, & Rosa, 2010; Douglas et al., 2021; Johnson, 2002; Stibick, 1979).
8. Crowson (1972: 44) established the family-group name PLASTOCERIDAE in Coleoptera, Cantharoidea (=Elateroidea now). *Plastocerus* Schaum, 1852 *nec* LeConte, 1853 is the nominotypical genus of the family. PLASTOCERINAE Crowson, 1972 is a junior homonym of PLASTOCERINI LeConte, 1861, but it is in prevailing use. The family group name PLASTOCERIDAE Crowson, 1972 (=PLASTOCERINAE, and PLASTOCERINI) has been used in recent catalogs, taxonomic and faunistic studies (Bocak, 2007; Bocak et al., 2018; Branham, 2010; Hajek, Ivie, & Lawrence, 2020; Lin & Yang, 2012; Nemeth et al., 2023) PLASTOCERIDAE Crowson, 1972 was downranked and included in ELATERIDAE (Bocak et al. 2018) as a subfamily, and it is now a tribe in DENDROMETRINAE (ELATERIDAE) (Douglas et al. 2021).
9. Stibick (1979: 175) established APLASTINAE in ELATERIDAE for *Aplastus* LeConte, 1859, *Euthysanius* LeConte, 1853; and *Octinodes* Candèze, 1863 [= *Plastocerus* LeConte, 1853 *nec* Schaum, 1852], and several other genera now excluded from the group. *Plastocerus* LeConte, 1853 is listed as a synonym of *Octinodes* Candèze, 1863 and placed in APLASTINAE Stibick, 1979, now as APLASTINA (ELATERIDAE: ELATERINAE: CEBRIONINI). The family group name APLASTINA is in prevalent use (Bouchard et al., 2011; Johnson, 2002), and it is a junior subjective synonym of PLASTOCERINI LeConte, 1861.
10. The International Commission on Zoological Nomenclature is accordingly asked
 - (1) to use its plenary power to give the family-group name PLASTOCERIDAE Crowson, 1972, type genus *Plastocerus* Schaum, 1852, precedence over the family-group name PLASTOCERINI LeConte, 1861, type genus *Plastocerus* LeConte, 1853 *nec* Schaum, 1852 for the Principles of Priority and Homonymy (Art. 65.2.1).
 - (2) to place on the Official List of Family-Group Names in Zoology the family group name PLASTOCERIDAE Crowson, 1972.

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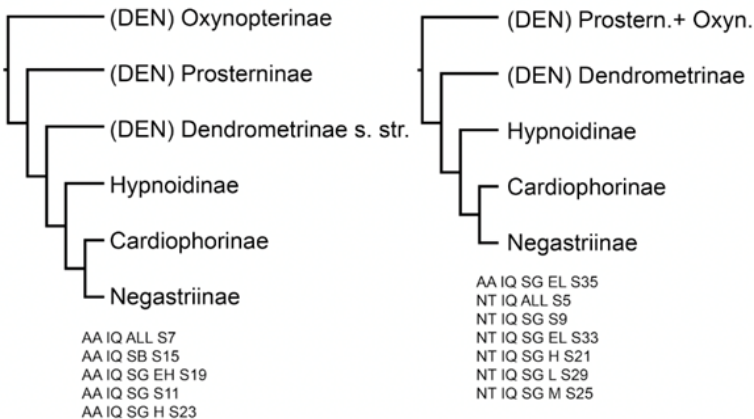
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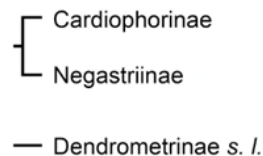
The Dendrometrinae, hypnoidines, Cardiophorinae and Negastrinae clade is recovered
The Dendrometrinae s. l. clade is recovered



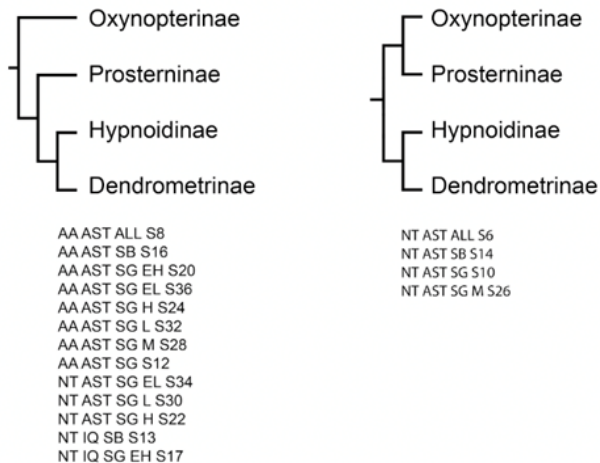
The Dendrometrinae s. l. paraphyletic



The Dendrometrinae, hypnoidines, Cardiophorinae and Negastrinae clade is absent



Internal structure of Dendrometrinae s. l. when the clade is recovered



Legend:

NT / AA
AST / IQ
ALL / SG / SB
EL / L / M / H / EH
nucleotide / amino acid level
ASTRAL / IQtree analysis
all genes / symtest good / symtest bad
GC content: extra low / low / medium / high / extra high
S6-S36 the number of supplementary Figure in Motyka et al.

Figure S1. Overview of topologies published by Motyka et al. (2026)

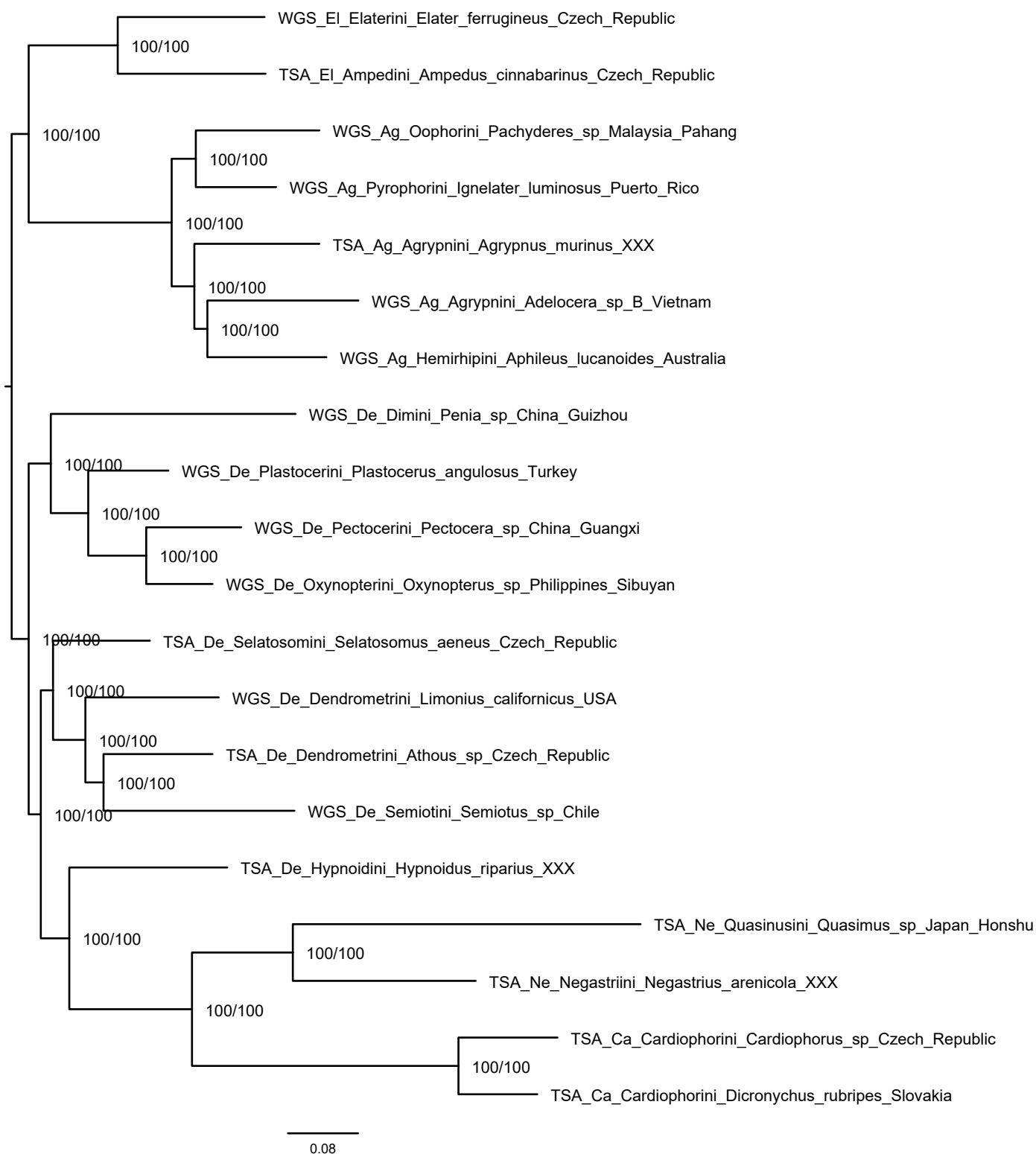


Figure S2. Maximum-likelihood phylogeny of click beetles inferred from nucleotide (NT) sequences. Node support is shown as SH-aLRT / UFBoot values.

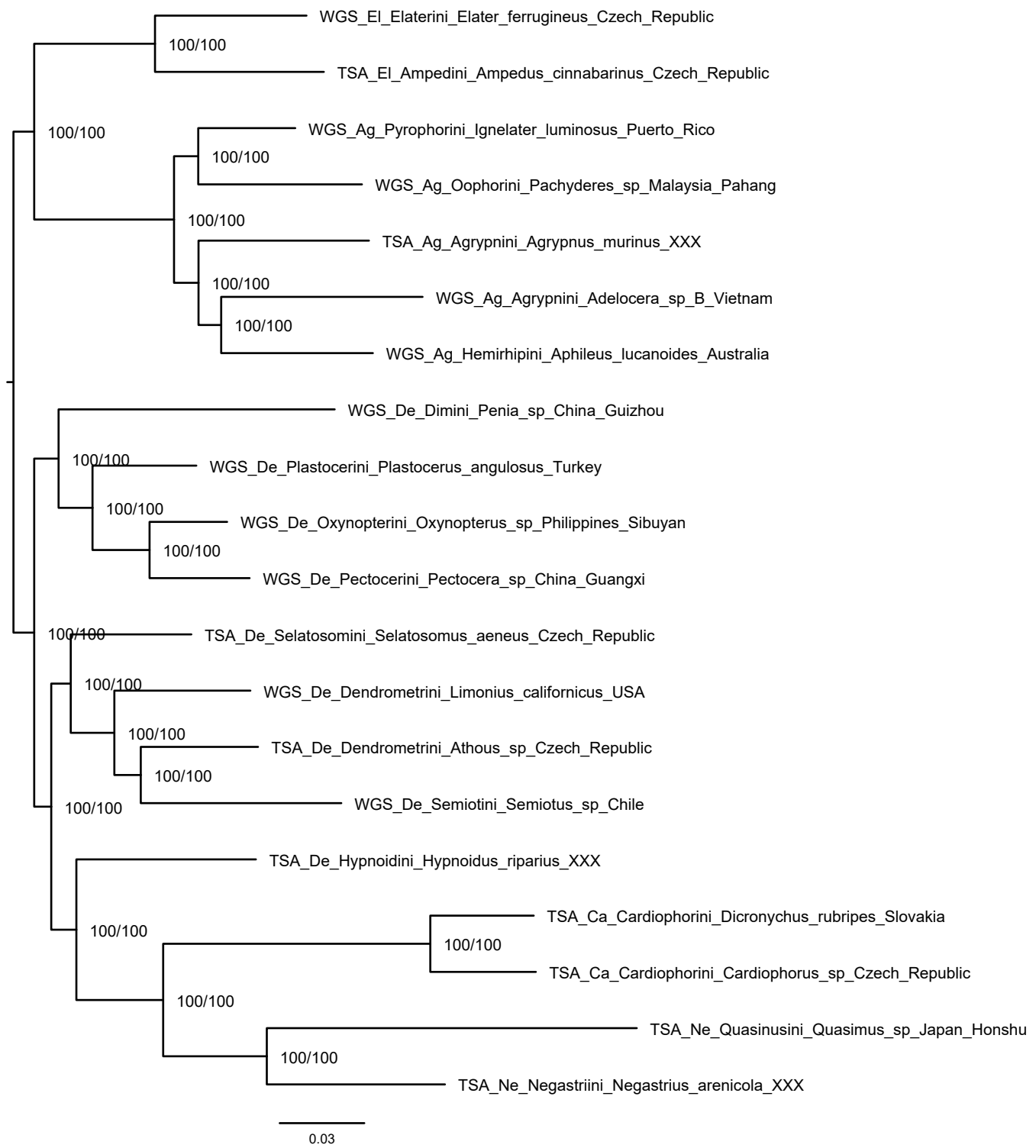


Figure S3. Maximum-likelihood phylogeny of click beetles inferred from amino acid (AA) sequences. Node support is shown as SH-aLRT / UFBoot values.

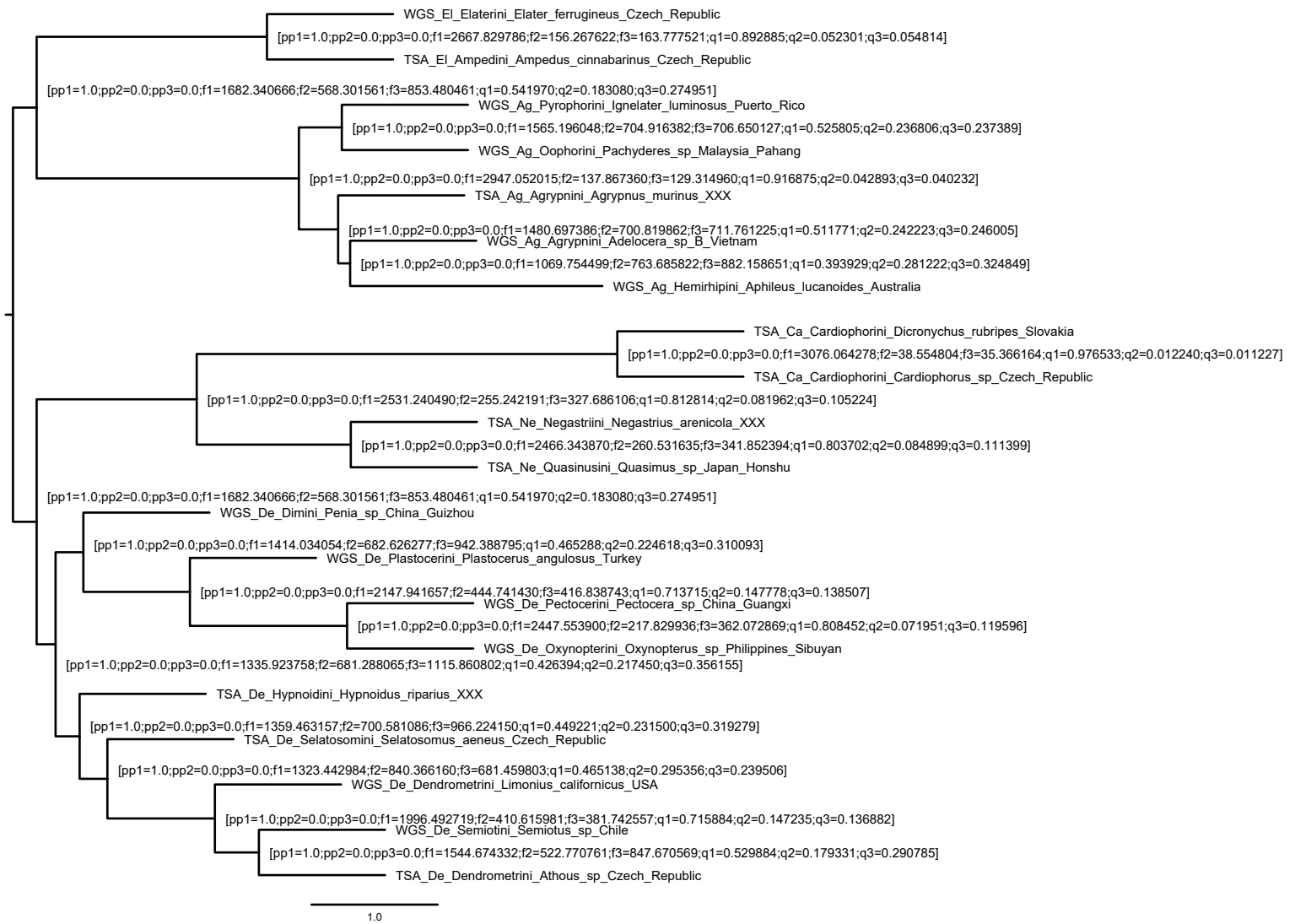


Figure S4. Species tree inferred by wASTRAL from nucleotide (NT) gene trees (full set; no branch collapsing). Branch annotations include local posterior probabilities and quartet support values (q1/q2/q3).

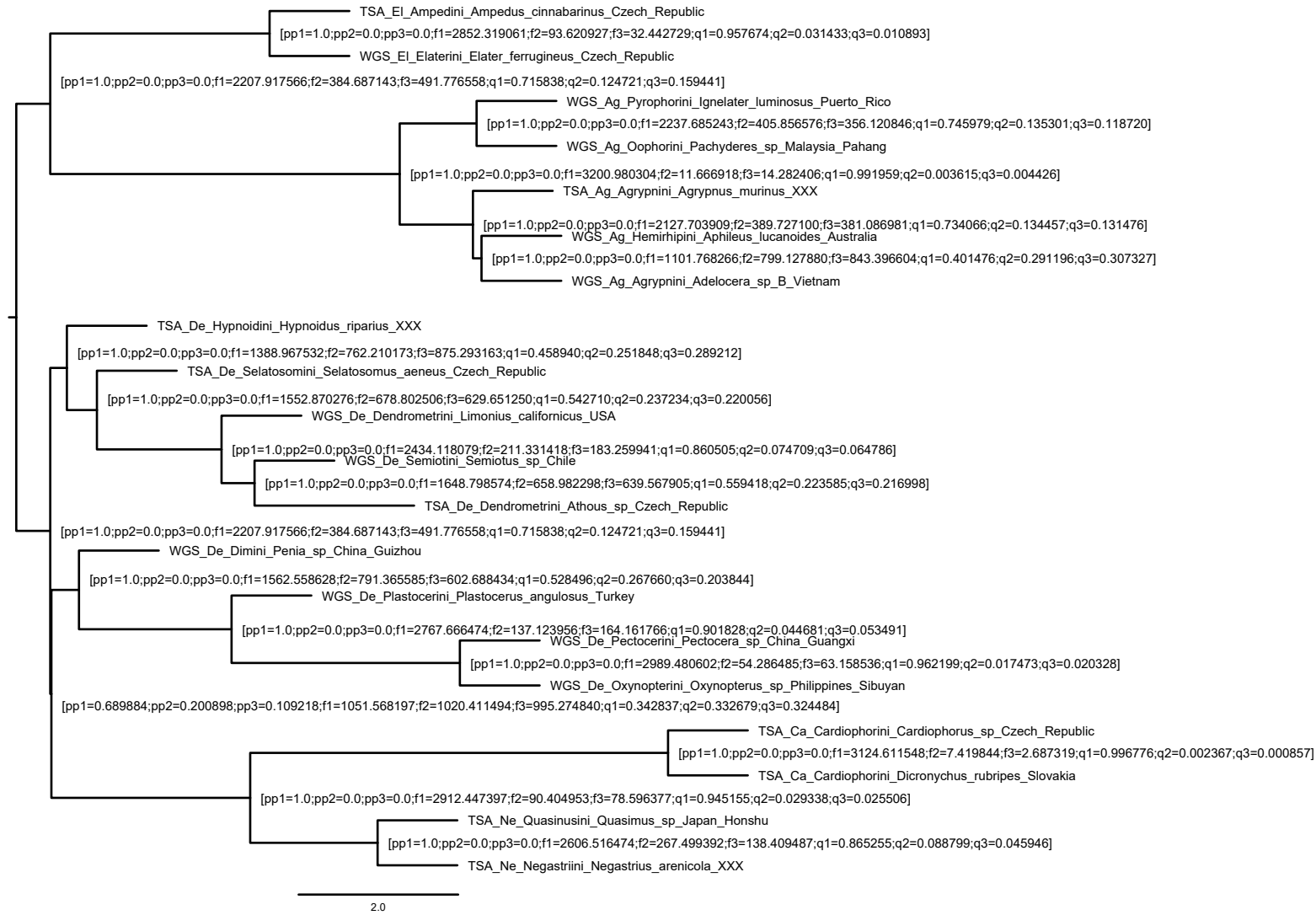


Figure S5. Species tree inferred by wASTRAL from amino acid (AA) gene trees (full set; no branch collapsing). Branch annotations include local posterior probabilities and quartet support values (q1/q2/q3).

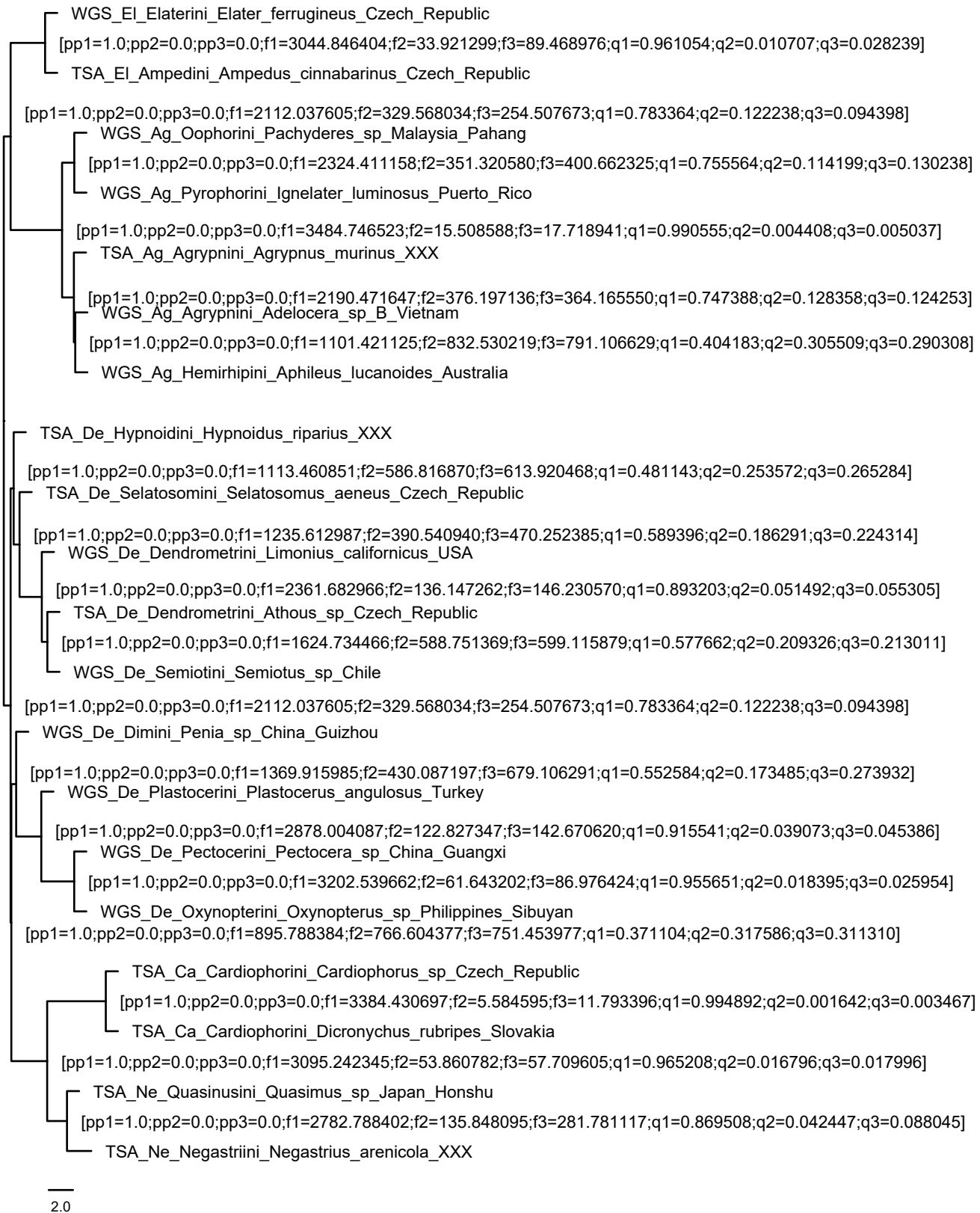


Figure S6. Species tree inferred by wASTRAL from nucleotide (NT) gene trees with branches below 50% UFBoot support collapsed to polytomies (b50up). Branch annotations include local posterior probabilities and quartet support values (q1/q2/q3).



Figure S7. Species tree inferred by wASTRAL from amino acid (AA) gene trees with branches below 50% UFBoot support collapsed to polytomies (b50up). Branch annotations include local posterior probabilities and quartet support values (q1/q2/q3).



Figure S8. Cross-dataset topology evaluation in ASTRAL: maximum-likelihood topology evaluated using nucleotide (NT) gene trees. Branch annotations include local posterior probabilities and quartet support values (q1/q2/q3).

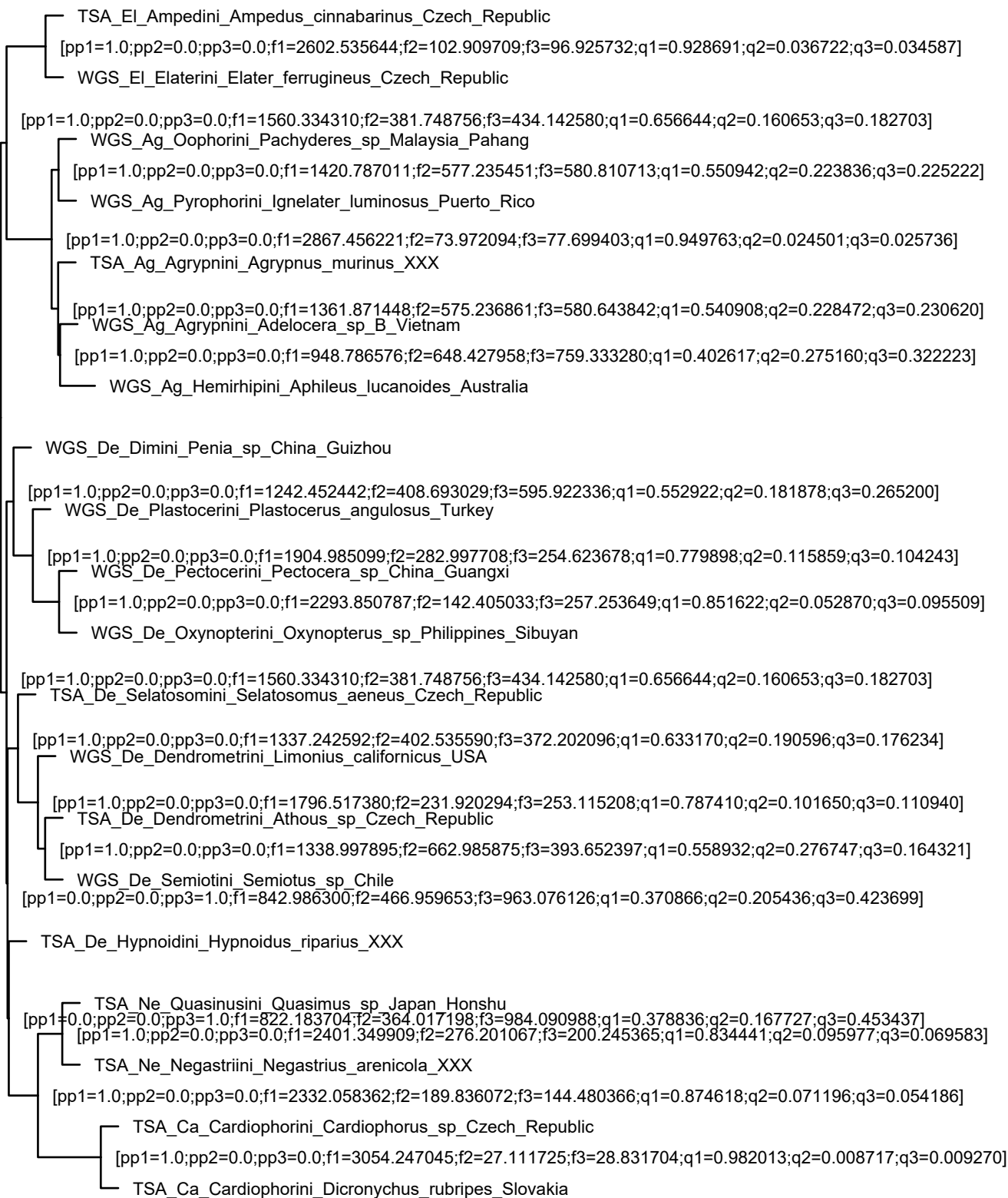
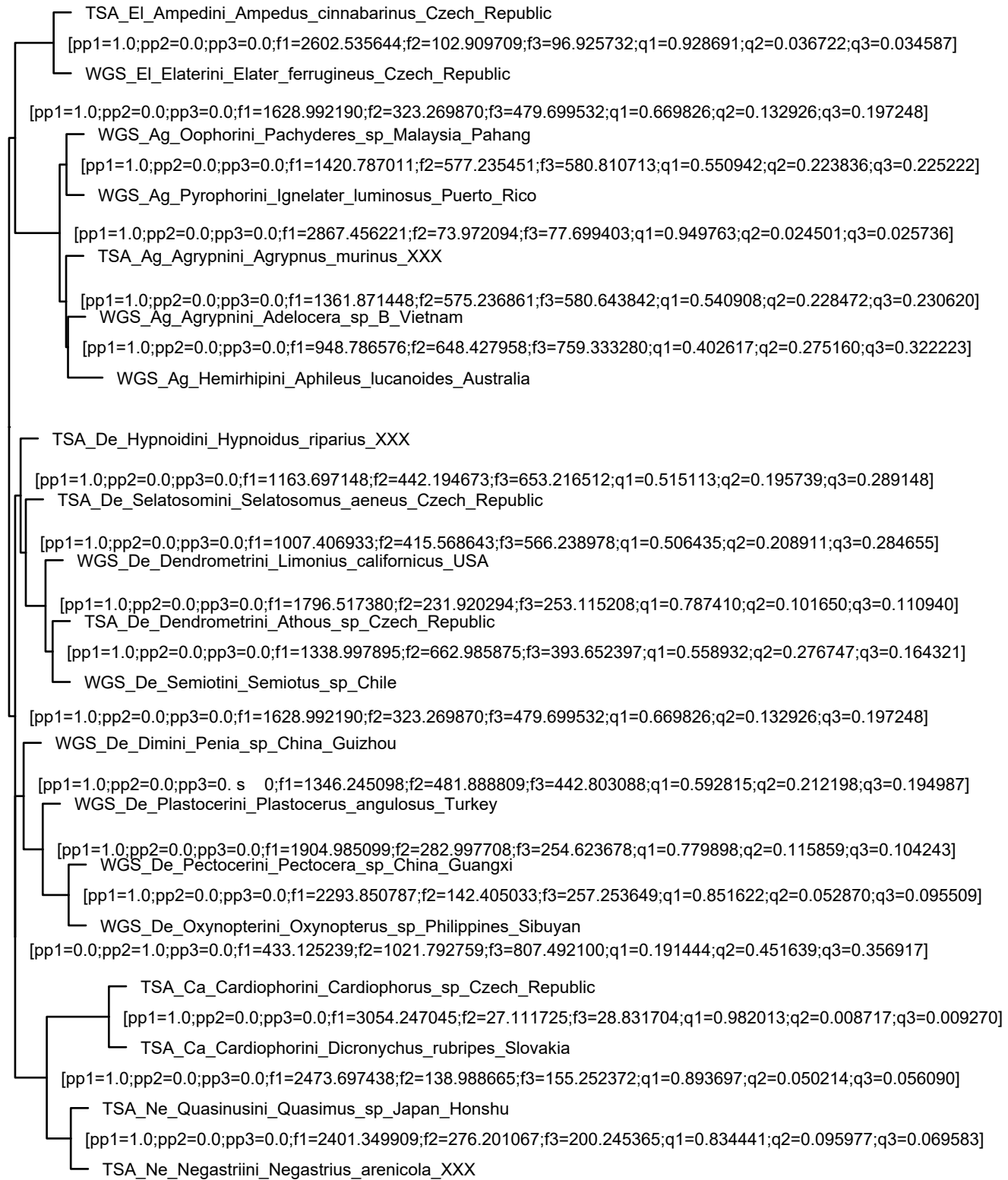


Figure S9. Cross-dataset topology evaluation in ASTRAL: maximum-likelihood topology evaluated using amino acid (AA) gene trees. Branch annotations include local posterior probabilities and quartet support values (q1/q2/q3).



2.0

Figure S10. Cross-dataset topology evaluation in ASTRAL: topology inferred from nucleotide (NT) gene trees evaluated using amino acid (AA) gene trees. Branch annotations include local posterior probabilities and quartet support values (q1/q2/q3).

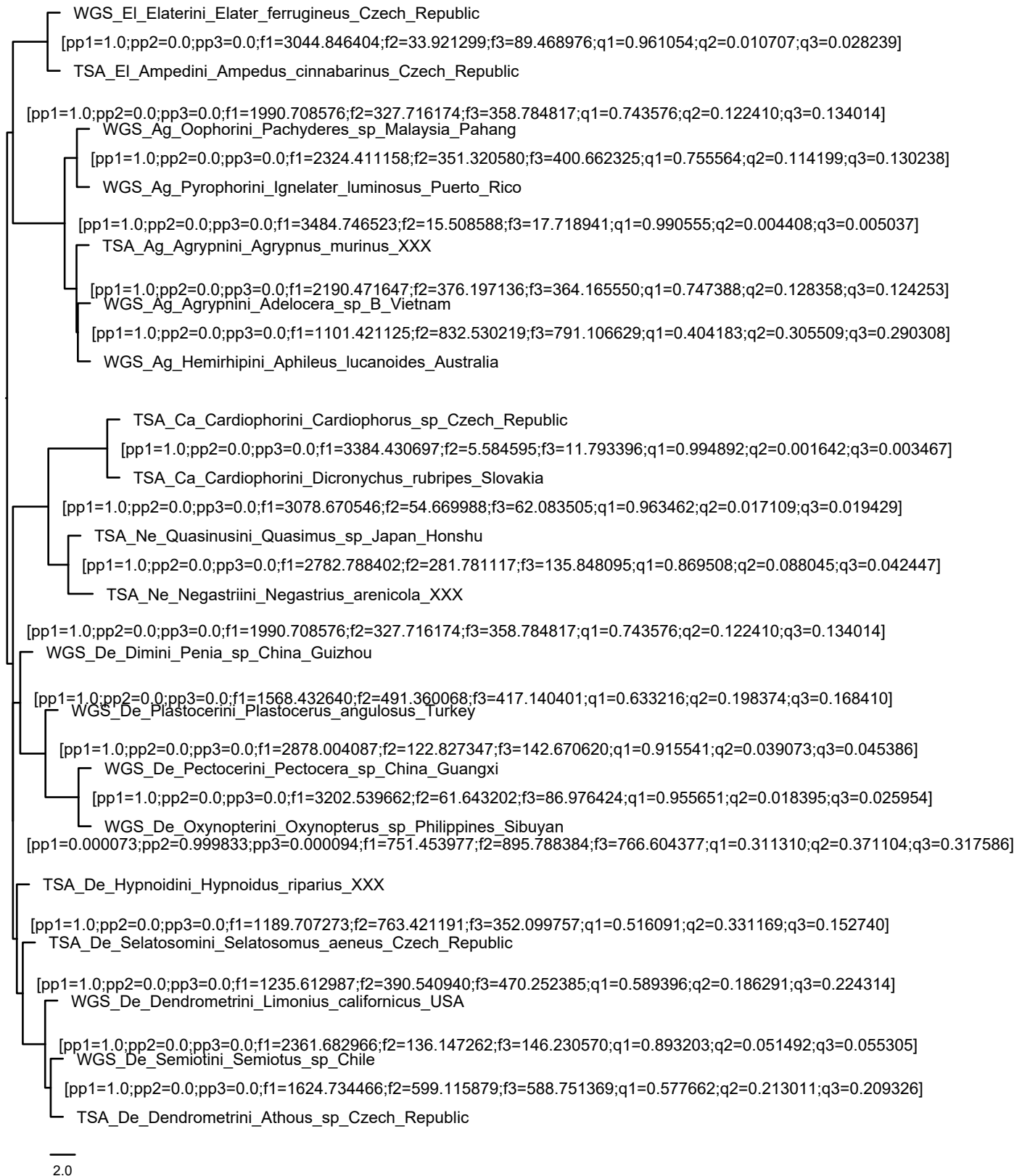
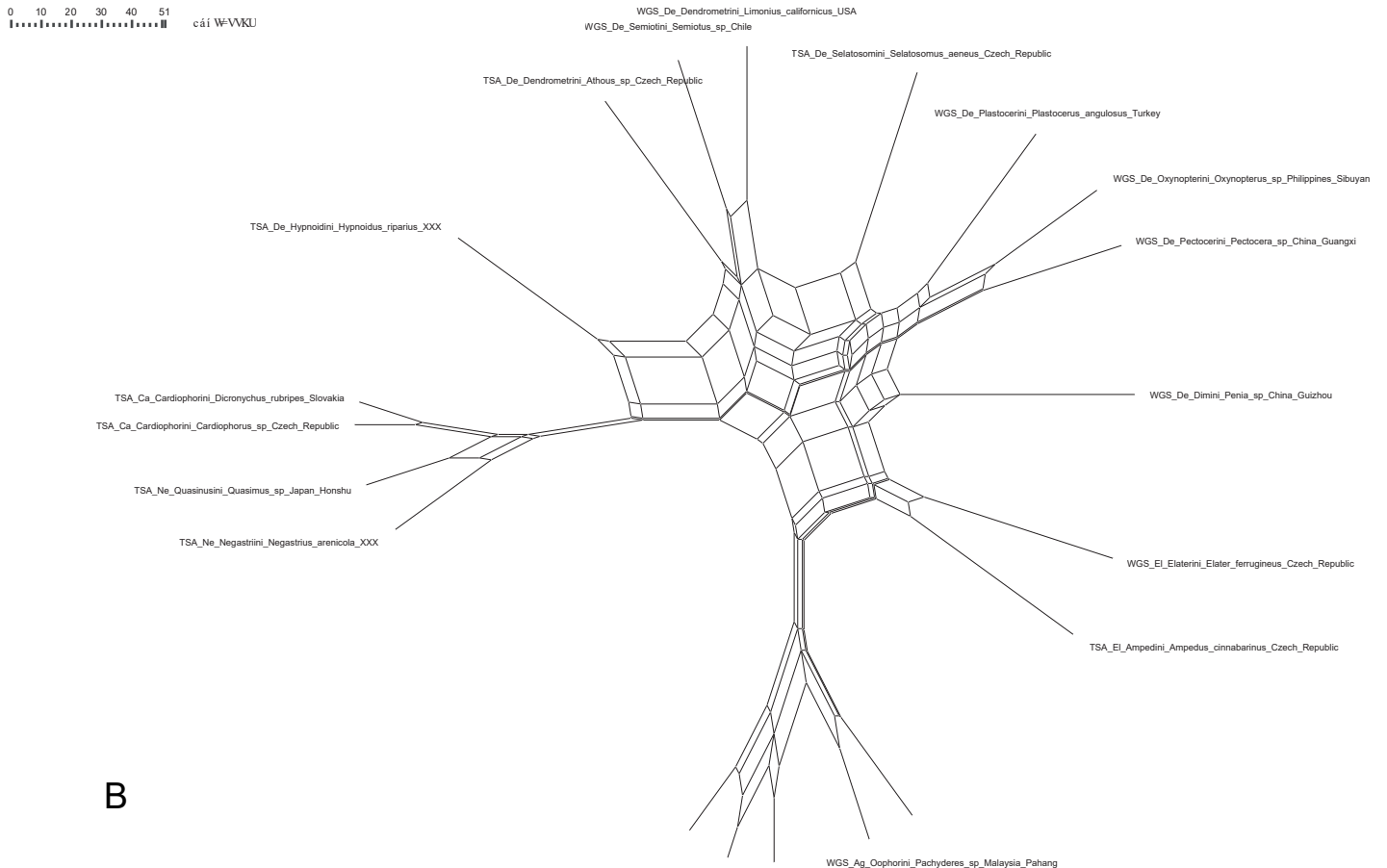


Figure S11. Cross-dataset topology evaluation in ASTRAL: topology inferred from amino acid (AA) gene trees evaluated using nucleotide (NT) gene trees. Branch annotations include local posterior probabilities and quartet support values (q1/q2/q3).

A



B

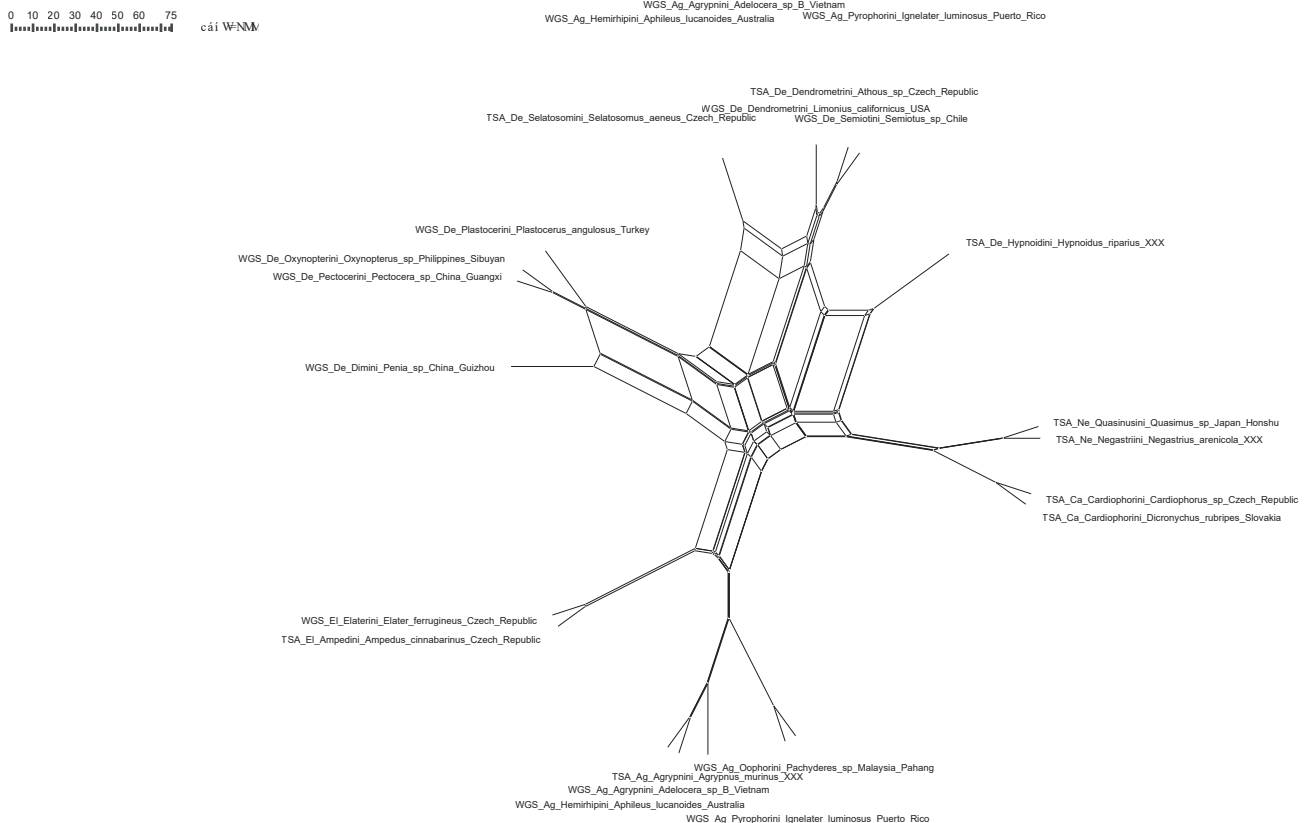
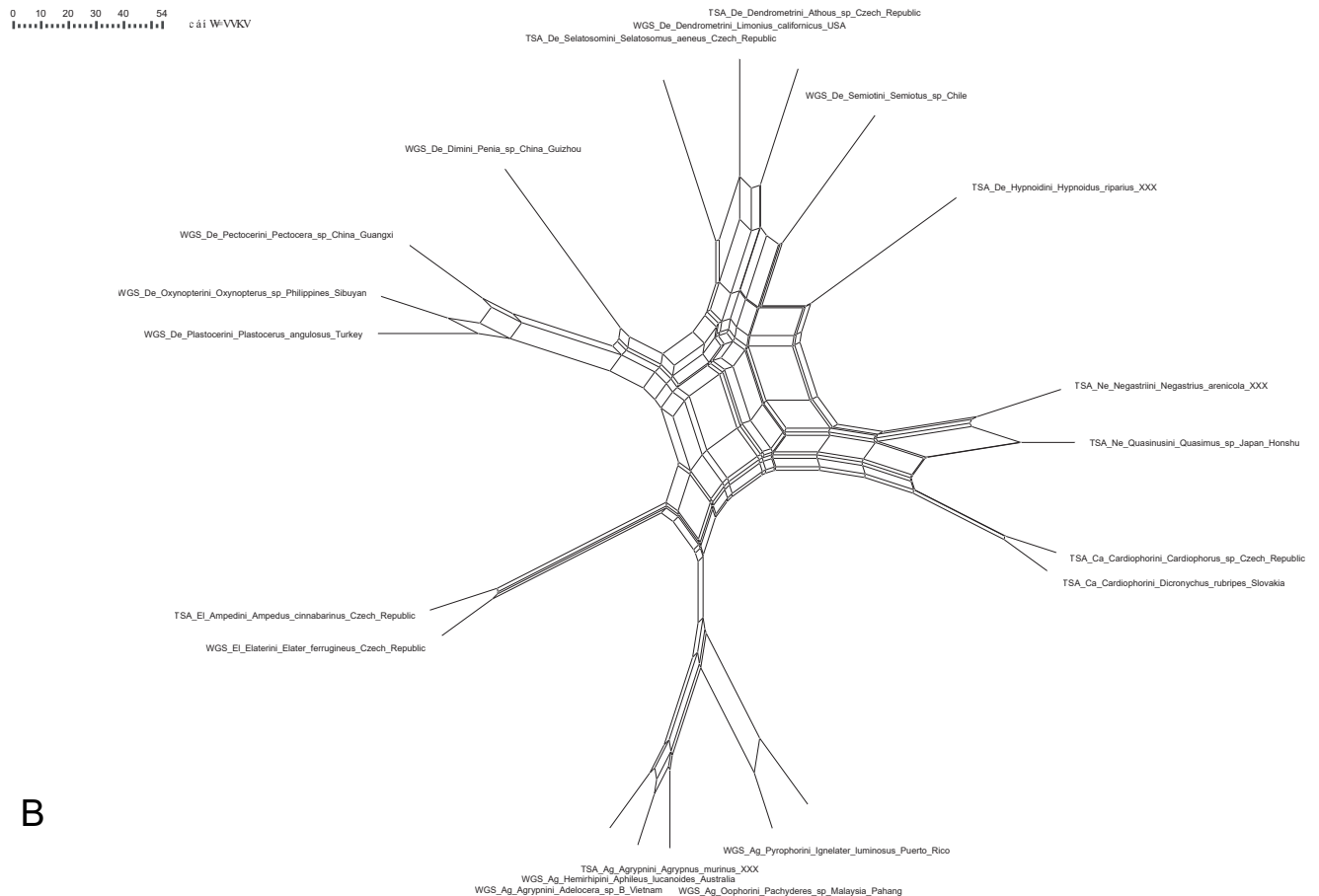


Figure S12. Species network inferred from nucleotide (NT) gene trees using the NANUQ algorithm, visualized with the NeighborNet algorithm in SplitsTree. (A) Network inferred under relaxed parameter settings ($\alpha = 0.05$, $\beta = 0.95$); (B) network inferred under stringent parameter settings ($\alpha = 5 \times 10^{-29}$, $\beta = 0.95$). Fit values indicate the percentage of variation in the pairwise distance matrix represented by the displayed network. Reticulation edges reflect gene tree discordance; parallel edges indicate competing phylogenetic signals.

A



B

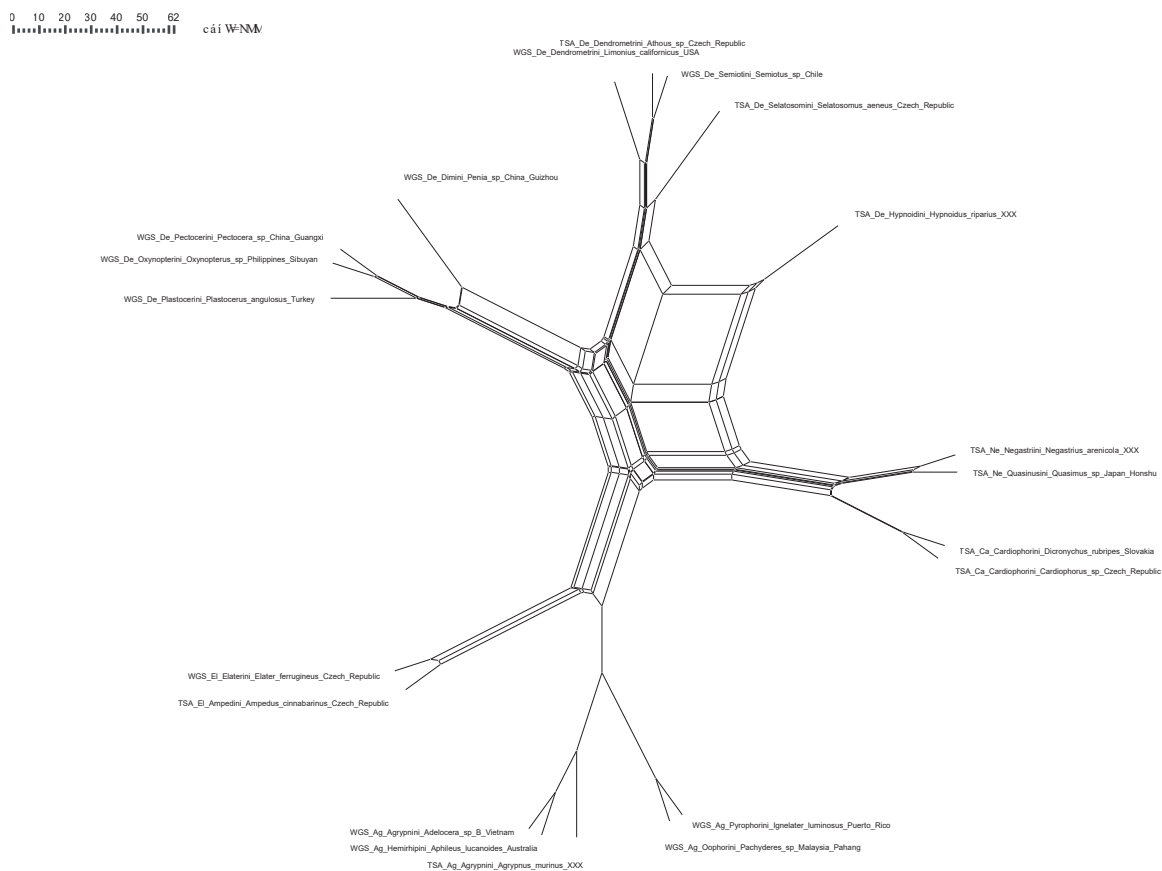
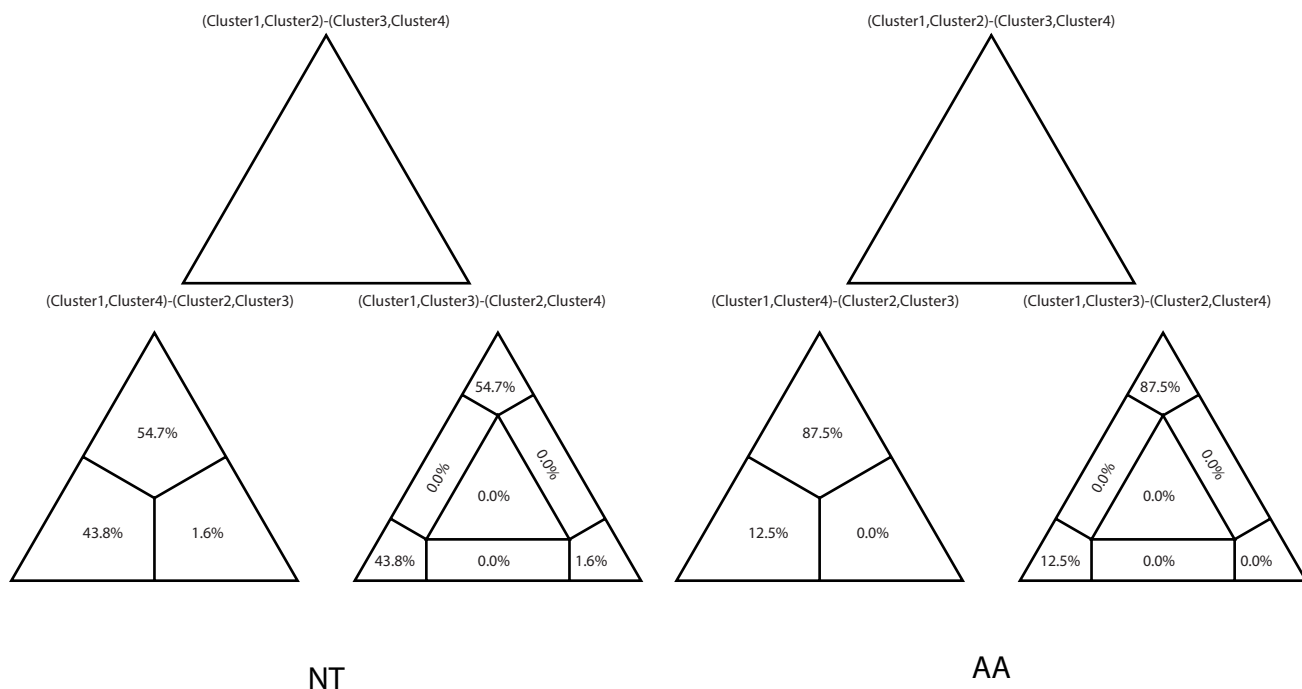


Figure S13. Species network inferred from amino acid (AA) gene trees using the NANUQ algorithm, visualized with the NeighborNet algorithm in SplitsTree. (A) Network inferred under relaxed parameter settings ($\alpha = 0.05$, $\beta = 0.95$); (B) network inferred under stringent parameter settings ($\alpha = 5 \times 10^{-29}$, $\beta = 0.95$). Fit values indicate the percentage of variation in the pairwise distance matrix represented by the displayed network. Reticulation edges reflect gene tree discordance; parallel edges indicate competing phylogenetic signals.



taxset Cluster1
WGS_De_Dimini_Penia_sp_China_Guizhou WGS_De_Plastocerini_Plastocerus_angulosus_Turkey WGS_De_Pectocerini_Pectocera_sp_China_Guangxi
WGS_De_Oxynopterini_Oxynopterus_sp_Philippines_Sibuyan;

taxset Cluster2
TSA_De_Selatosomini_Selatosomus_aeneus_Czech_Republic WGS_De_Dendrometrini_Limonius_californicus_USA WGS_De_Semiotini_Semiotus_sp_Chile
TSA_De_Dendrometrini_Athous_sp_Czech_Republic;

taxset Cluster3
TSA_De_Hypnoidini_Hypnoidus_riparius_XXX;

taxset Cluster4
TSA_Ca_Cardiophorini_Cardiophorus_sp_Czech_Republic TSA_Ca_Cardiophorini_Dicronychus_rubripes_Slovakia TSA_Ne_Quasiusini_Quasimus_sp_-
Japan_Honshu TSA_Ne_Negastriini_Negastrius_arenicola_XXX;

Figure S14. Four-cluster likelihood mapping (FcLM) results based on amino acid (AA) and nucleotide (NT) datasets. Percentages indicate support for each of the three possible quartet topologies.

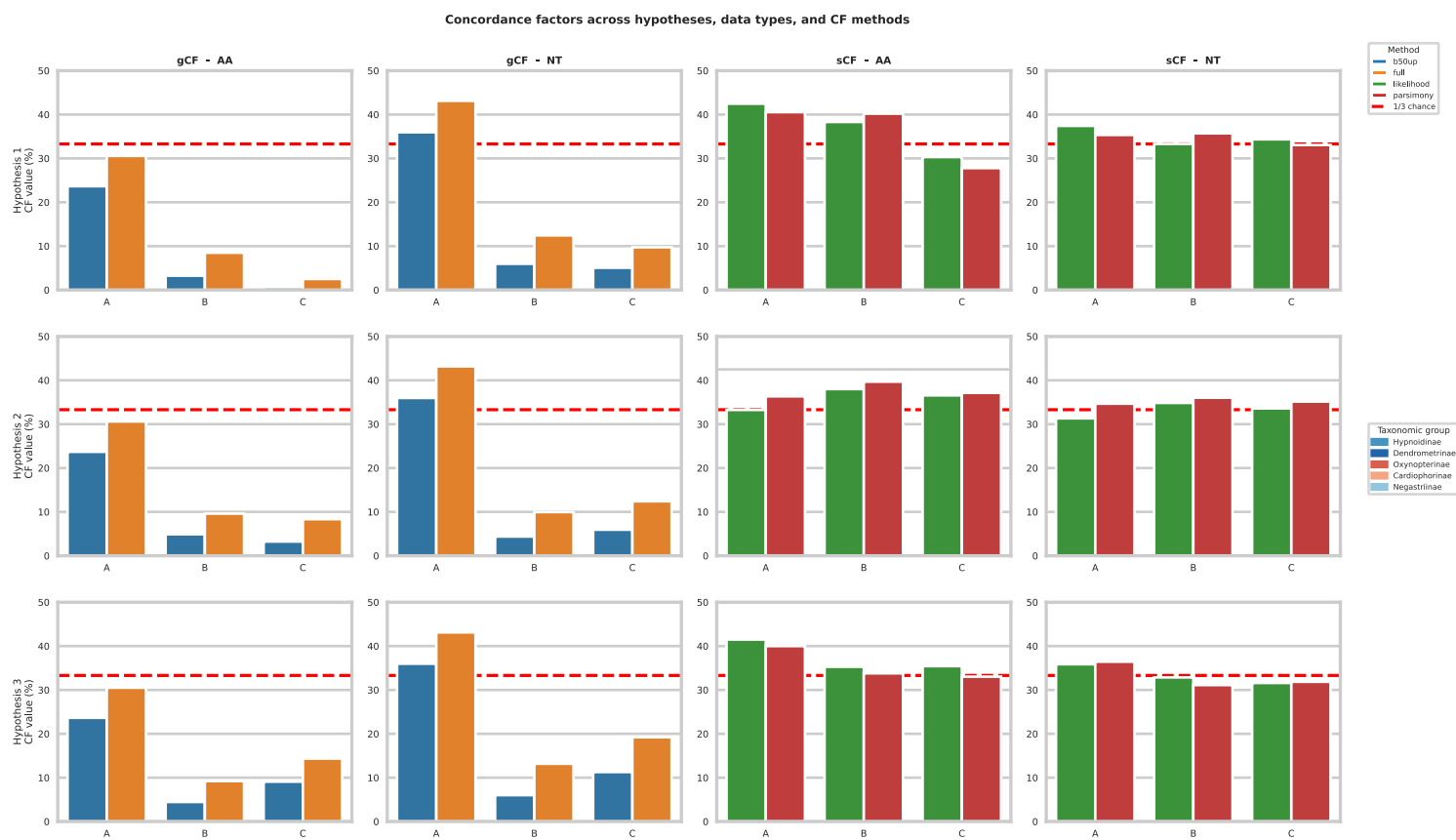


Figure S15. Gene concordance factors (gCF) and site concordance factors (sCF) for the three alternative topologies (Topologies 1–3; see Figure 2A–C). gCF values were computed using both the full gene tree set and collapsed gene trees (b50up). sCF was estimated using parsimony- and likelihood-based quartet sampling. Analyses were performed at both the NT and AA levels.

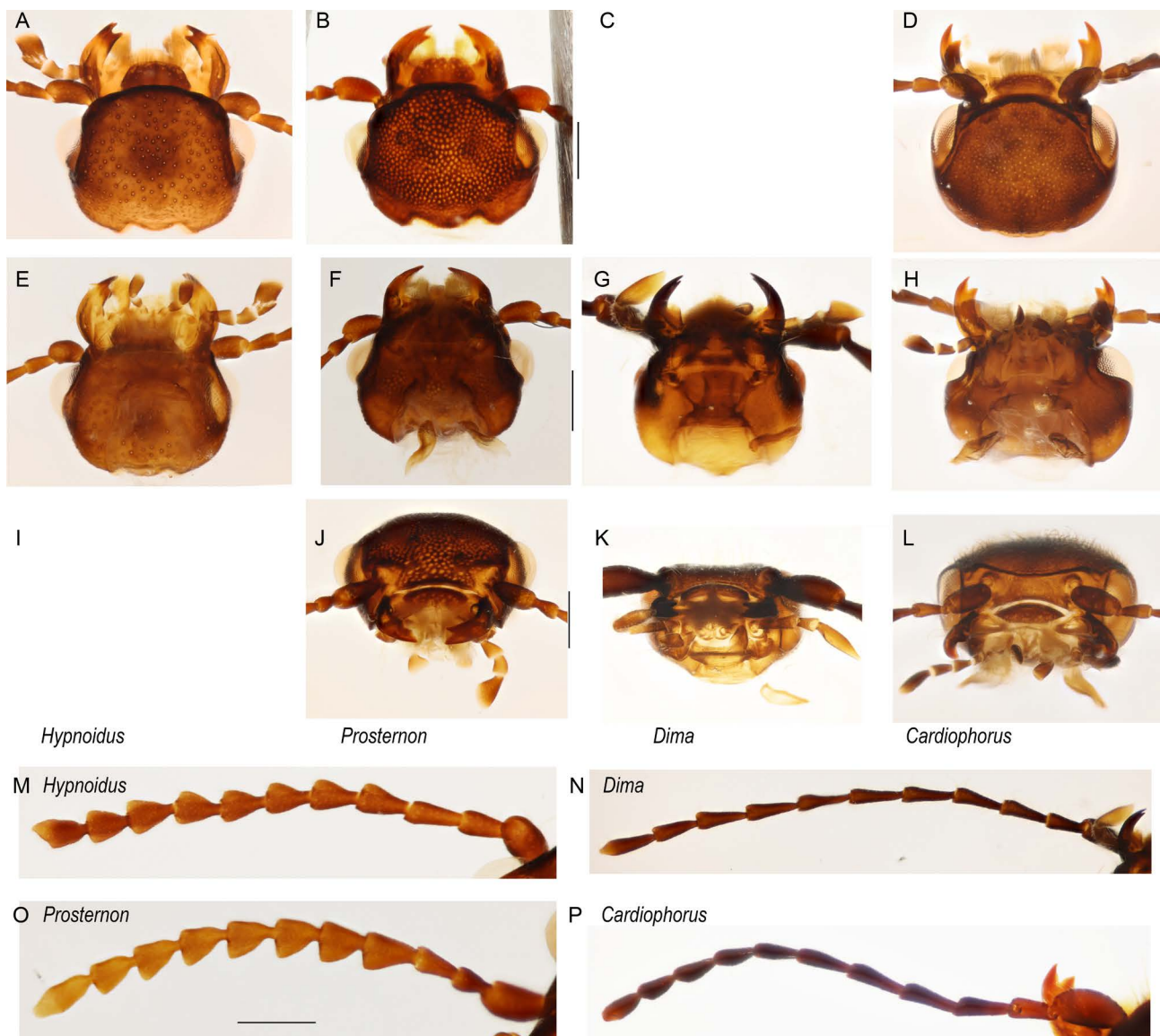


Figure S16. Morphology of *Hypnoidus jeffrey*, *Prosternon tesselatum*, *Dima yunnana*, and *Cardiophorus* sp. Heads and antennae.

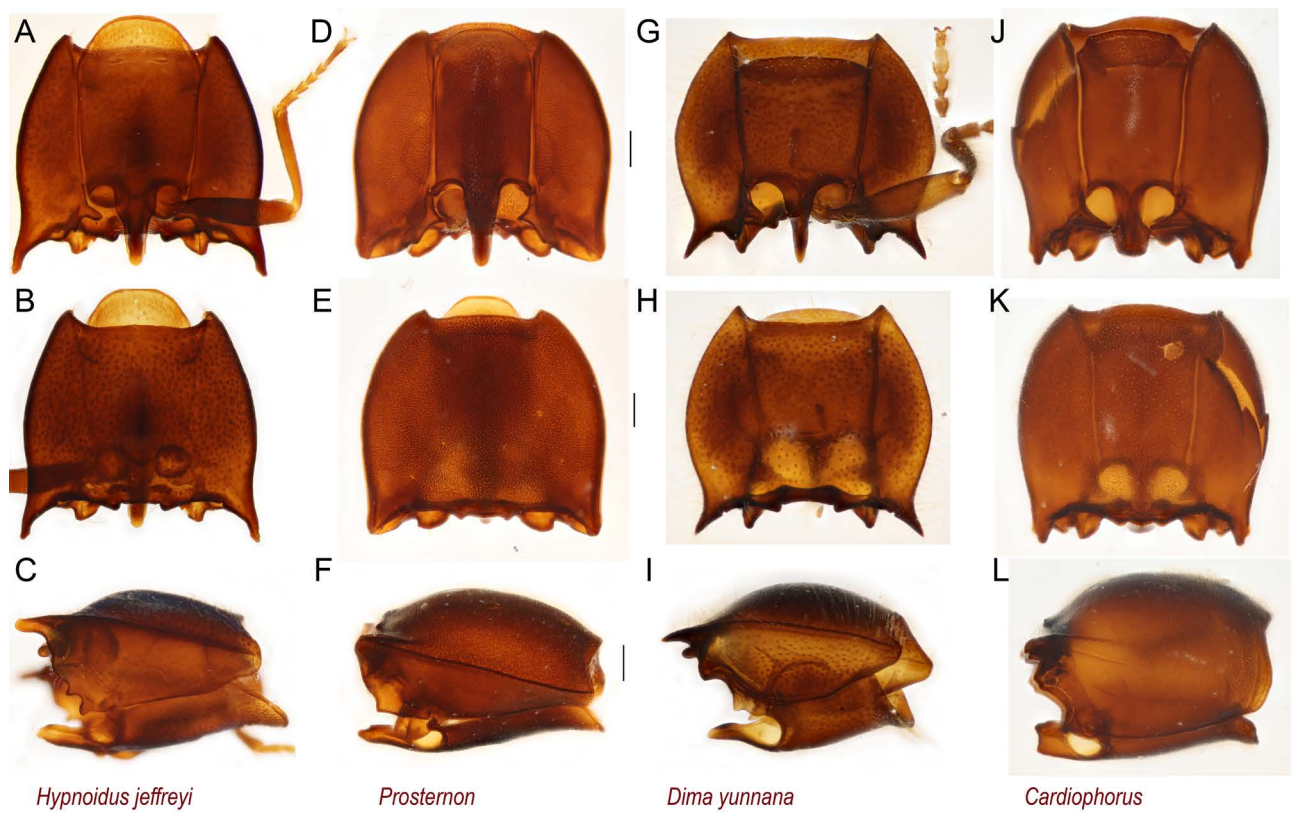


Figure S17. Morphology of *Hypnoidus jeffreyi*, *Prosternon tessellatum*, *Dima yunnana*, and *Cardiophorus* sp. Pronota.

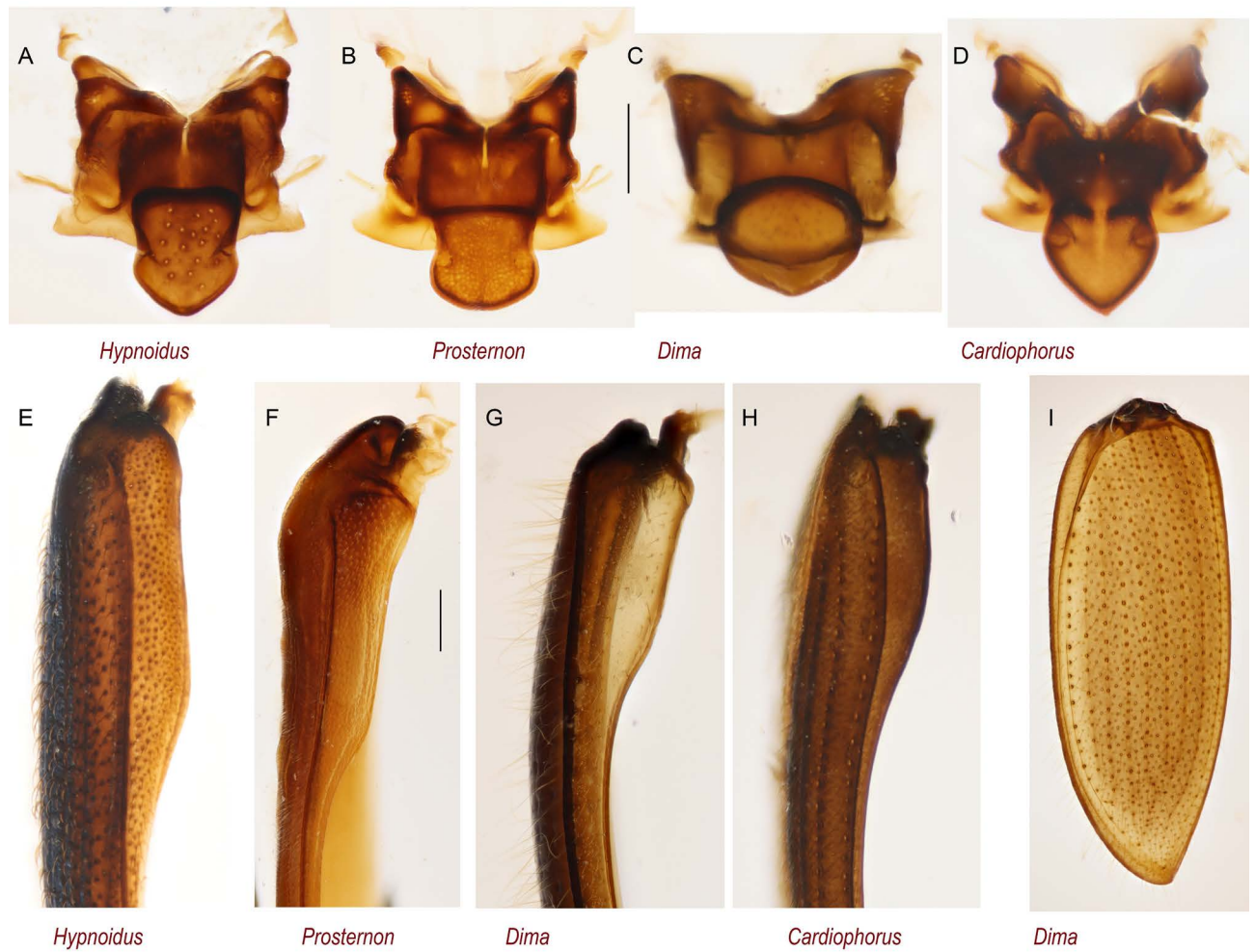


Figure S18. Morphology of *Hypnoidus jeffrey*, *Prosternon tessellatum*, *Dima yunnana*, and *Cardiophorus* sp. Mesoscutella and elytra.



Figure S19. Morphology of *Hypnoidus jeffreyi*, *Prosternon tessellatum*, *Dima yunnana*, and *Cardiophorus* sp. Meso- and metasterna, metanota.

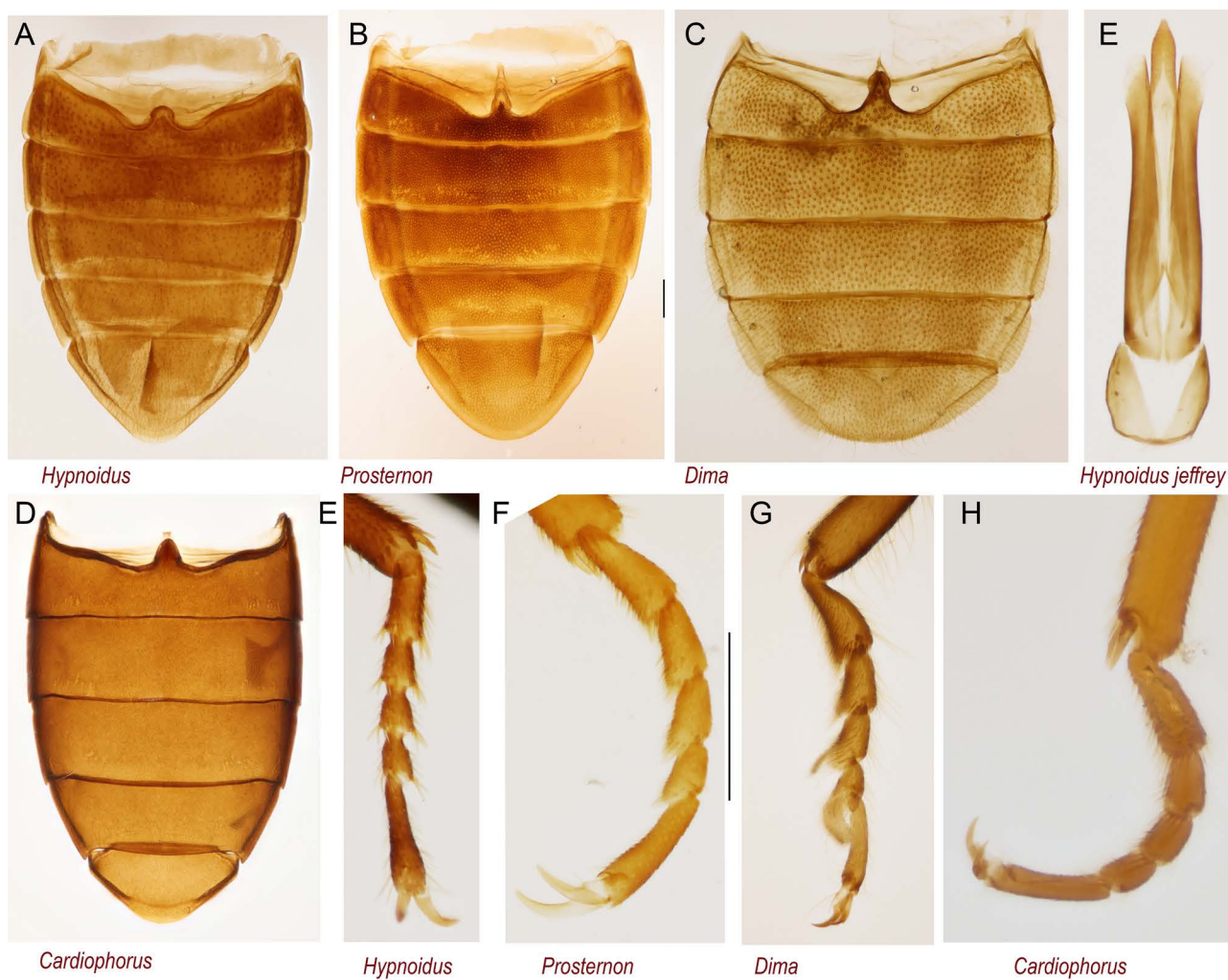


Figure S20. Morphology of *Hypnoidus jeffrey*, *Prosternon tessellatum*, *Dima yunnana*, and *Cardiophorus* sp. Abdomens and hind tarsi.