Supplementary Material 1

Direct whole-plastome alignment systematically inflates long-branch artifacts in chloroplast phylogenomics: a 468-paper audit and three-method reanalysis

Zhi-Jie Xu

College of Biological Science and Medical Engineering, Donghua University, Shanghai, China

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Supplementary reanalysis of 38 archived cases: 36 strict positives and 2 negatives. This PDF contains the per-case paper-versus-C/A/B sheets, strict-clock branch-length diagnostics, and the unrooted RF summary table. Supplementary Material 2 contains structural-variant dot plots for the manually verified cases.

Contents and methods

This PDF contains 38 completed, manually confirmed datasets. Four papers (2290339, 2294894, 2294898, 2357681) are excluded because their original M&M; used CDS/PCG data, so their topology differences are not comparable to whole-genome MSA artifacts. Each dataset has a paper-vs-reanalysis sheet (paper, C, A, B) and a strict-clock branch-length diagnostic. Red branches/labels mark curated long-branch taxa/clades; for uncurated datasets they mark terminal outliers for C/B and RTT outliers for A.

C = whole-genome MAFFT + trimAl + IQ-TREE; A = SibeliaZ LCB + RAxML-NG T92+F+FreeRate; B = single-copy orthologs + IQ-TREE TESTMERGE.

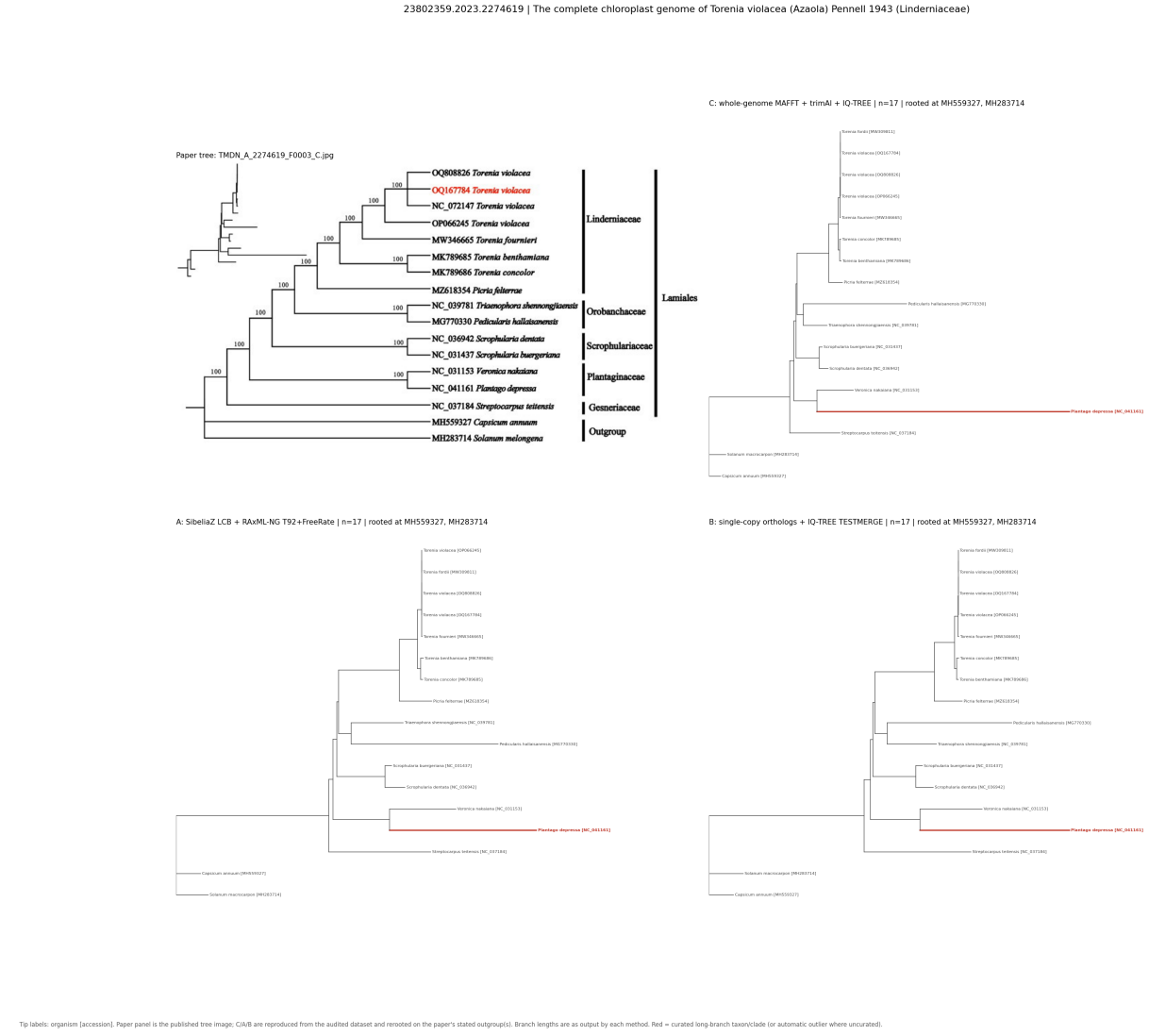
Dataset status

dataset	status	dataset	status
23802359.2023.2274619	Verified	23802359.2023.2275827	Verified
23802359.2023.2281029	Verified	23802359.2023.2282225	Verified (tree)
23802359.2023.2288889	Verified (root fixed)	23802359.2023.2290844	Verified (root fixed)
23802359.2023.2294896	Verified (root fixed)	23802359.2023.2301012	Verified
23802359.2024.2306203	Verified	23802359.2024.2306207	Verified
23802359.2024.2309262	Verified	23802359.2024.2324928	Verified
23802359.2024.2347508	Verified	23802359.2024.2378966	Verified
23802359.2024.2383680	Verified	23802359.2024.2412239	Verified (shortened)
23802359.2024.2420842	Verified (root fixed)	23802359.2024.2420847	Verified (root/highlight fixed)
23802359.2024.2432370	Verified (shortened/highlight fixed)	23802359.2024.2437099	Verified (highlight clarified)
23802359.2025.2466604	Verified (highlight clarified; Clade III not discussed)	23802359.2025.2505249	Verified (highlight narrowed)
23802359.2024.2438290	Verified (B name-based fallback; self-contradictory M&M)	23802359.2025.2559713	Verified (B name-based fallback)
23802359.2025.2528566	Verified	23802359.2025.2530712	Verified (root fixed)
23802359.2025.2544681	Verified (root fixed)	23802359.2025.2548850	Verified
23802359.2026.2635835	Verified (root fixed)	23802359.2026.2694148	Verified (root/accession note)
23802359.2026.2694188	Verified	23802359.2026.2742618	Verified (paper figure restored)
23802359.2025.2567461	Verified (highlight corrected)	23802359.2026.2621456	Verified
23802359.2026.2621463	Verified	23802359.2026.2622811	Verified (local-clock)
23802359.2026.2629683	Verified (local-clock)	23802359.2026.2704257	Verified

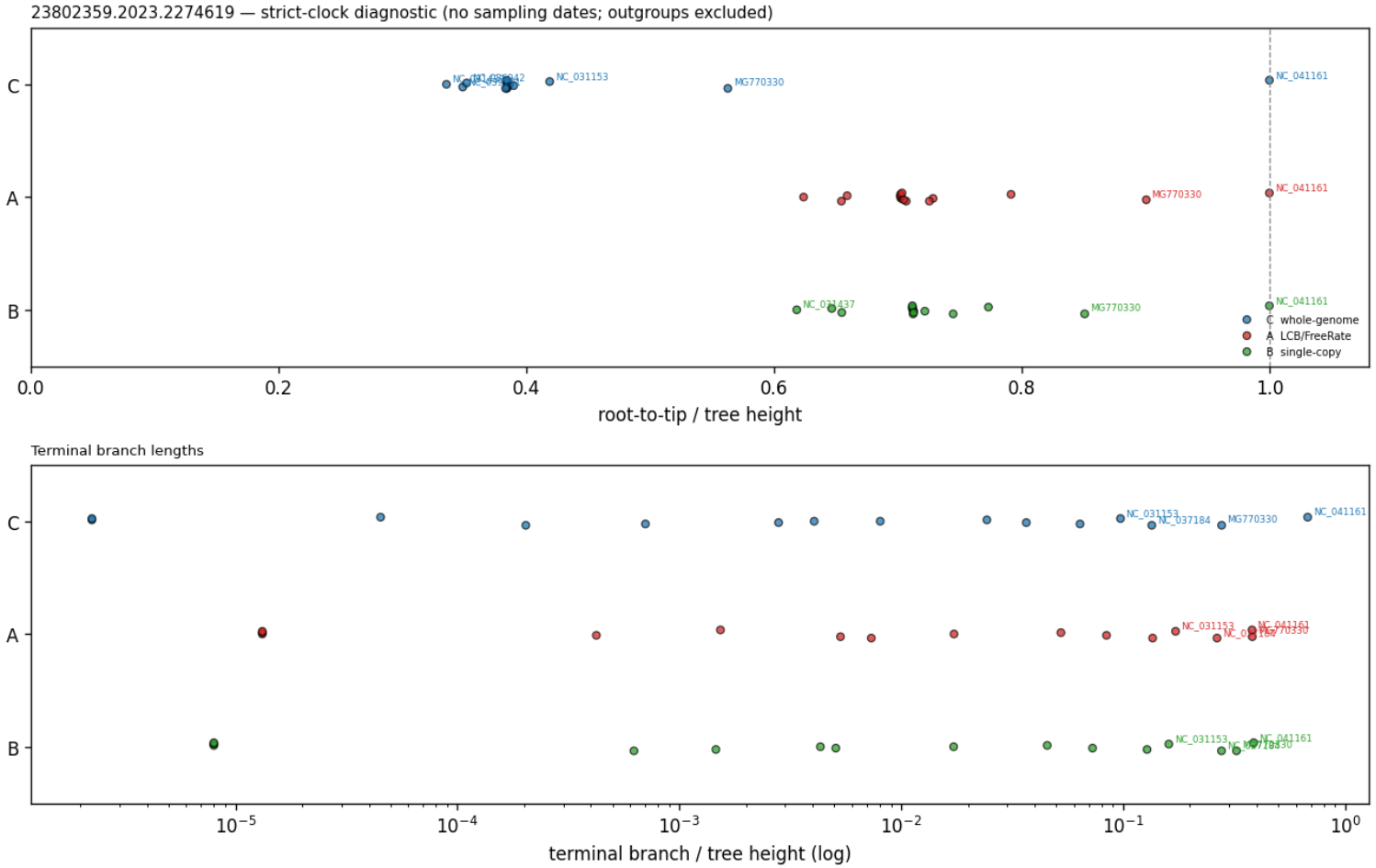
23802359.2023.2274619

The complete chloroplast genome of Torenia violacea (Azaola) Pennell 1943 (Linderniaceae)

Status: Verified. 17-taxon rerun; NC_031153 added; long branch disappeared.



23802359.2023.2274619 - strict-clock branch-length diagnostic



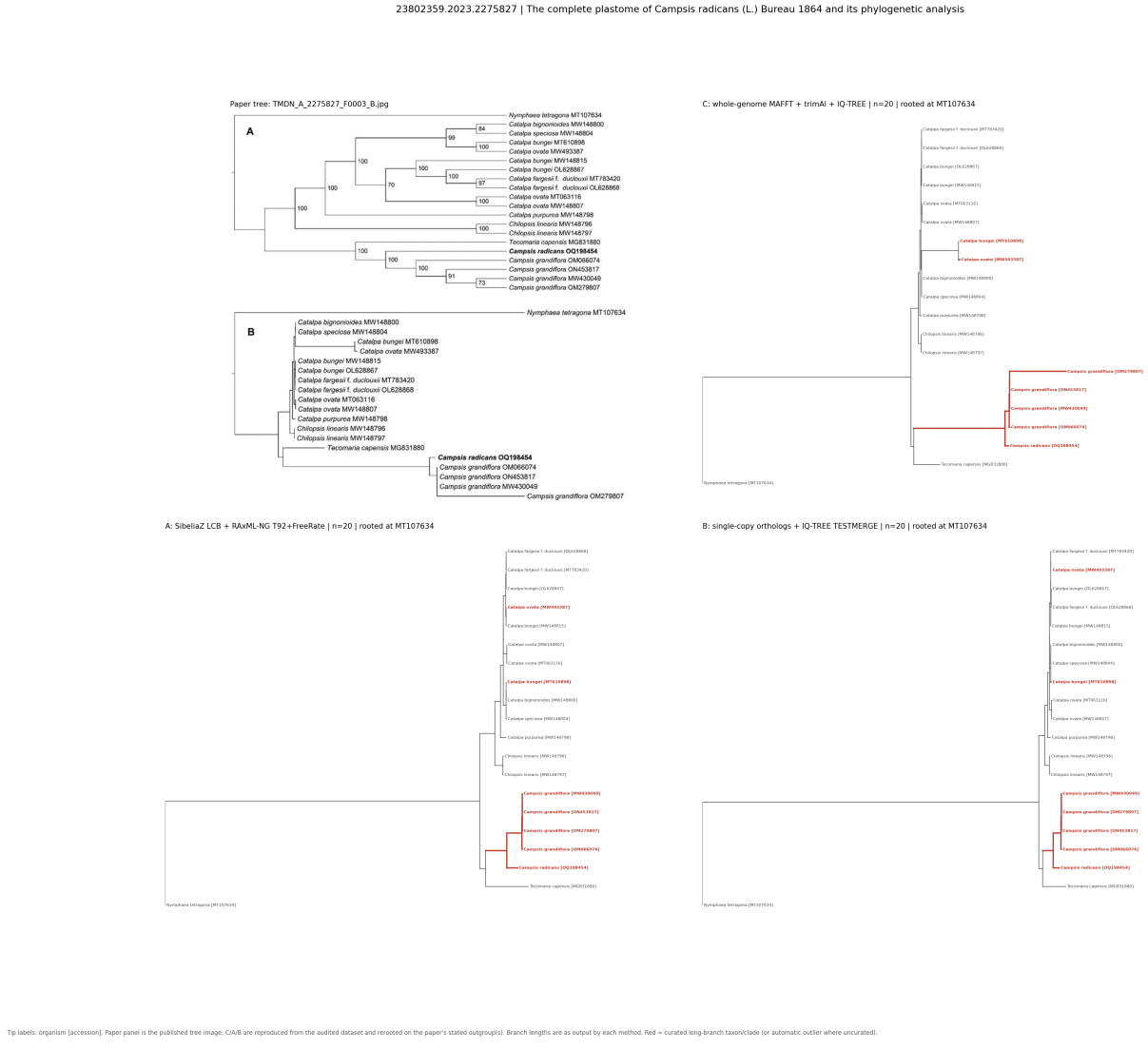
method	RTT outliers	terminal outliers	flagged clades
C naive	7	4	4
A FreeRate	3	4	1
B ortho	4	4	1

A terminal branches are estimated under RAxML-NG T92+F+FreeRate. RTT z-scores are sensitive to small MAD; ranks/clade flags should be read together.

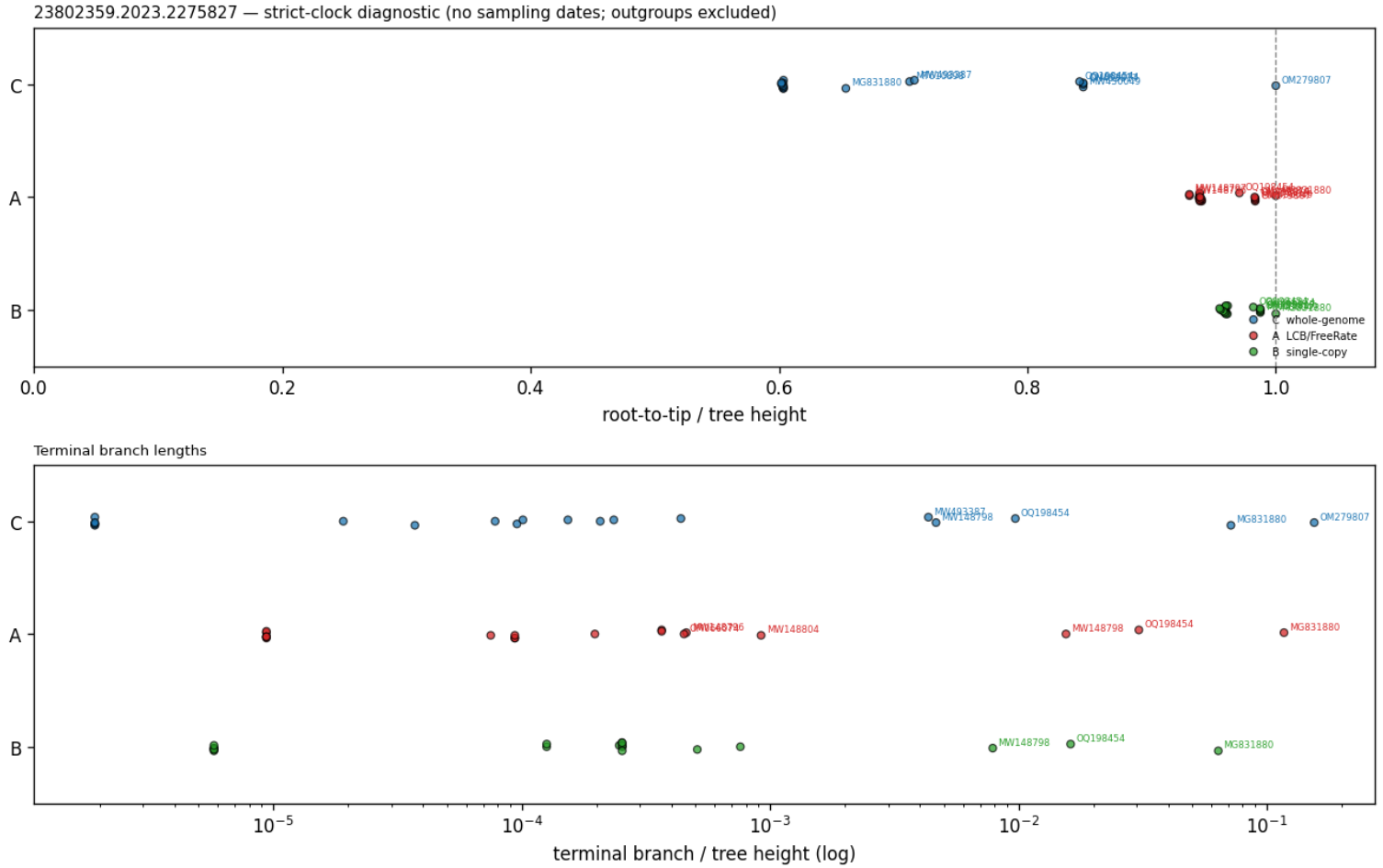
23802359.2023.2275827

The complete plastome of Campsis radicans (L.) Bureau 1864 and its phylogenetic analysis

Status: Verified. Three long branches disappeared.



23802359.2023.2275827 - strict-clock branch-length diagnostic



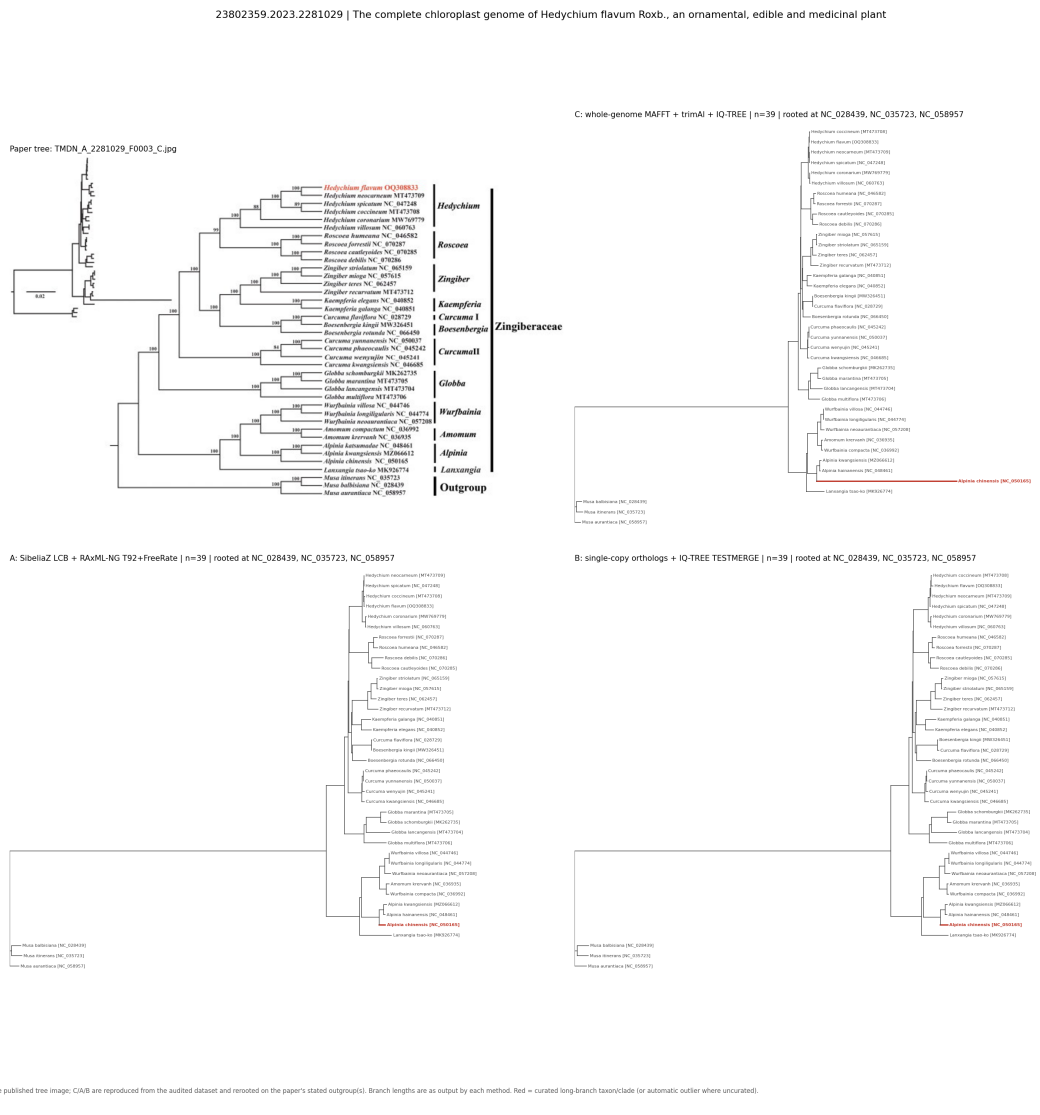
method	RTT outliers	terminal outliers	flagged clades
C naive	8	5	7
A FreeRate	8	6	7
B ortho	6	3	5

A terminal branches are estimated under RAxML-NG T92+F+FreeRate. RTT z-scores are sensitive to small MAD; ranks/clade flags should be read together.

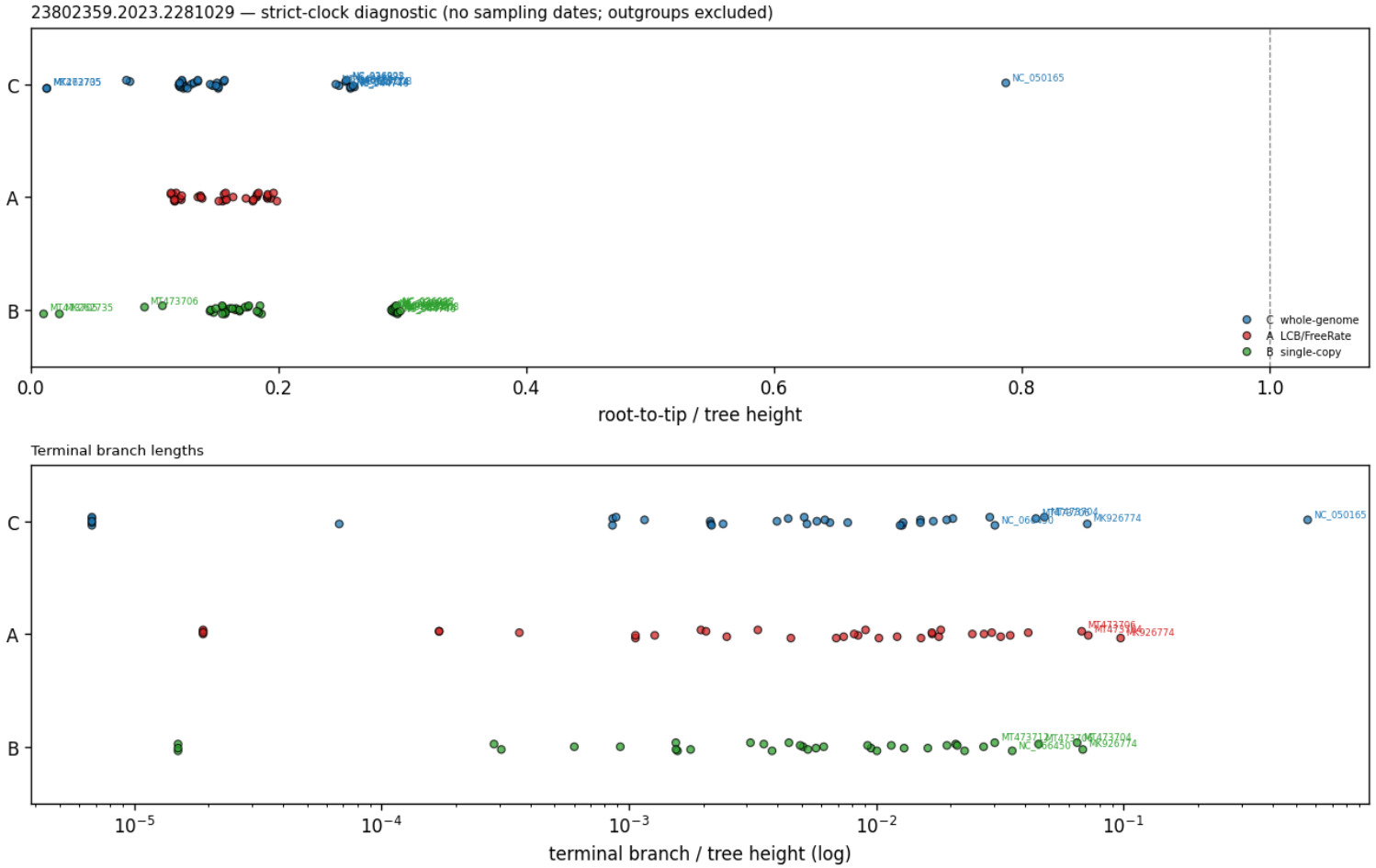
23802359.2023.2281029

The complete chloroplast genome of Hedychium flavum Roxb., an ornamental, edible and medicinal plant

Status: Verified. One long branch disappeared.



23802359.2023.2281029 - strict-clock branch-length diagnostic



method	RTT outliers	terminal outliers	flagged clades
C naive	14	5	11
A FreeRate	3	3	3
B ortho	15	8	11

A terminal branches are estimated under RAxML-NG T92+F+FreeRate. RTT z-scores are sensitive to small MAD; ranks/clade flags should be read together.

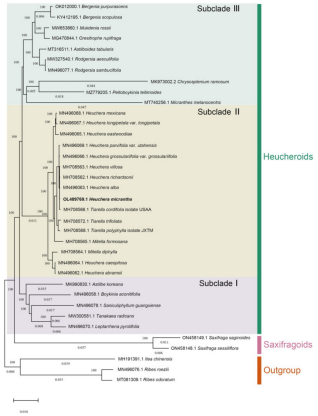
23802359.2023.2282225

The complete plastome sequence of Heuchera micrantha Douglas ex Lindl. (Saxifragaceae), an ornamental plant

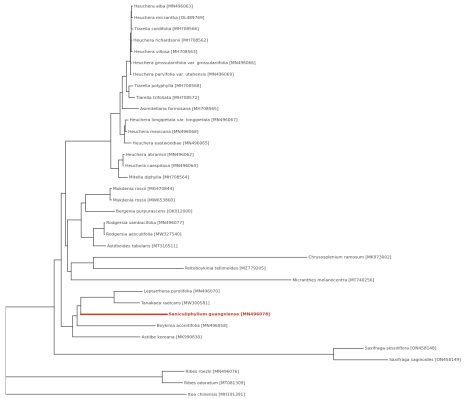
Status: Verified (tree). Tree reproduced; local-clock issue, not a long-branch case.

23802359.2023.2282225 | The complete plastome sequence of Heuchera micrantha Douglas ex Lindl. (Saxifragaceae), an ornamental plant

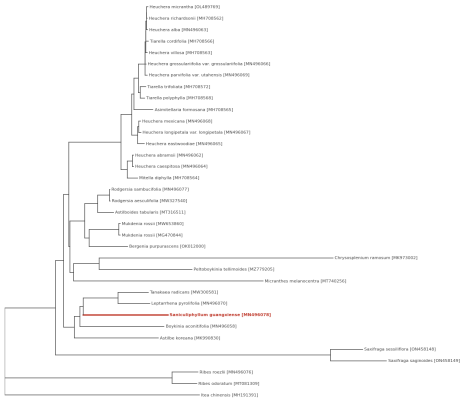
Paper tree: TMDN_A_2282225_F0003_C.jpg



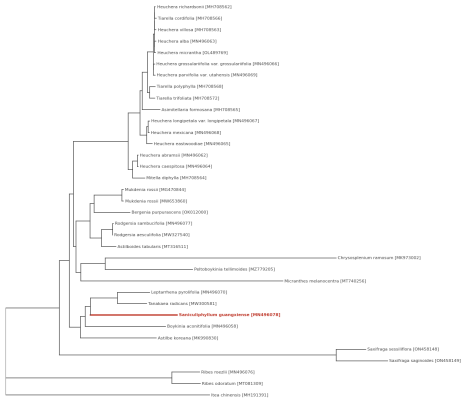
C: whole-genome MAFFT + trimAl + IQ-TREE | n=35 | rooted at MH191391, MN496076, MT081309



A: SibeliaZ LCB + RAxML-NG T92+FreeRate | n=35 | rooted at MH191391, MN496076, MT081309

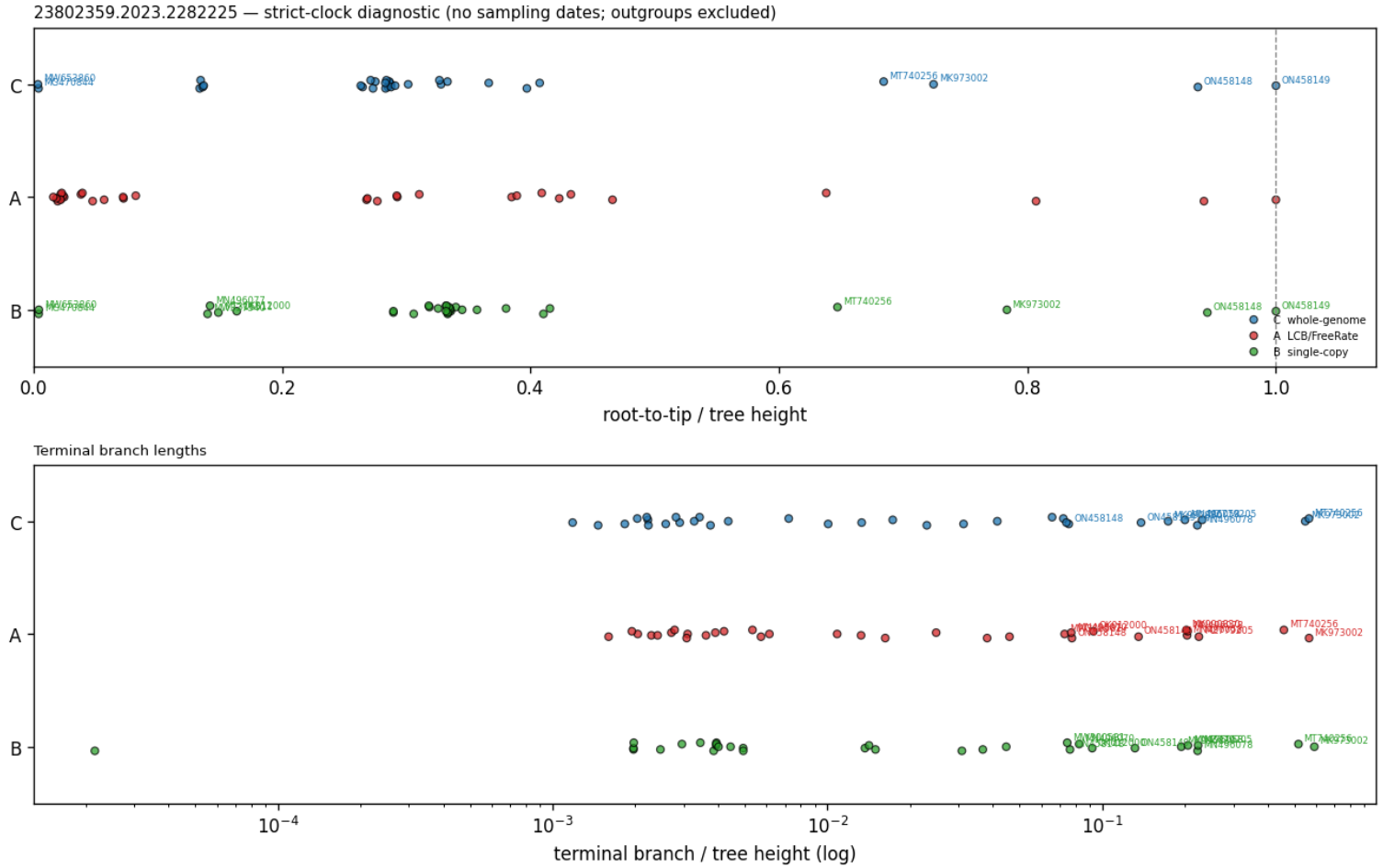


B: single-copy orthologs + IQ-TREE TESTMERGE | n=35 | rooted at MH191391, MN496076, MT081309



Tip labels: organism [accession]. Paper panel is the published tree image; C/A/B are reproduced from the audited dataset and rerooted on the paper's stated outgroup(s). Branch lengths are as output by each method. Red = curated long-branch taxon/clade (or automatic outlier where uncurated).

23802359.2023.2282225 - strict-clock branch-length diagnostic



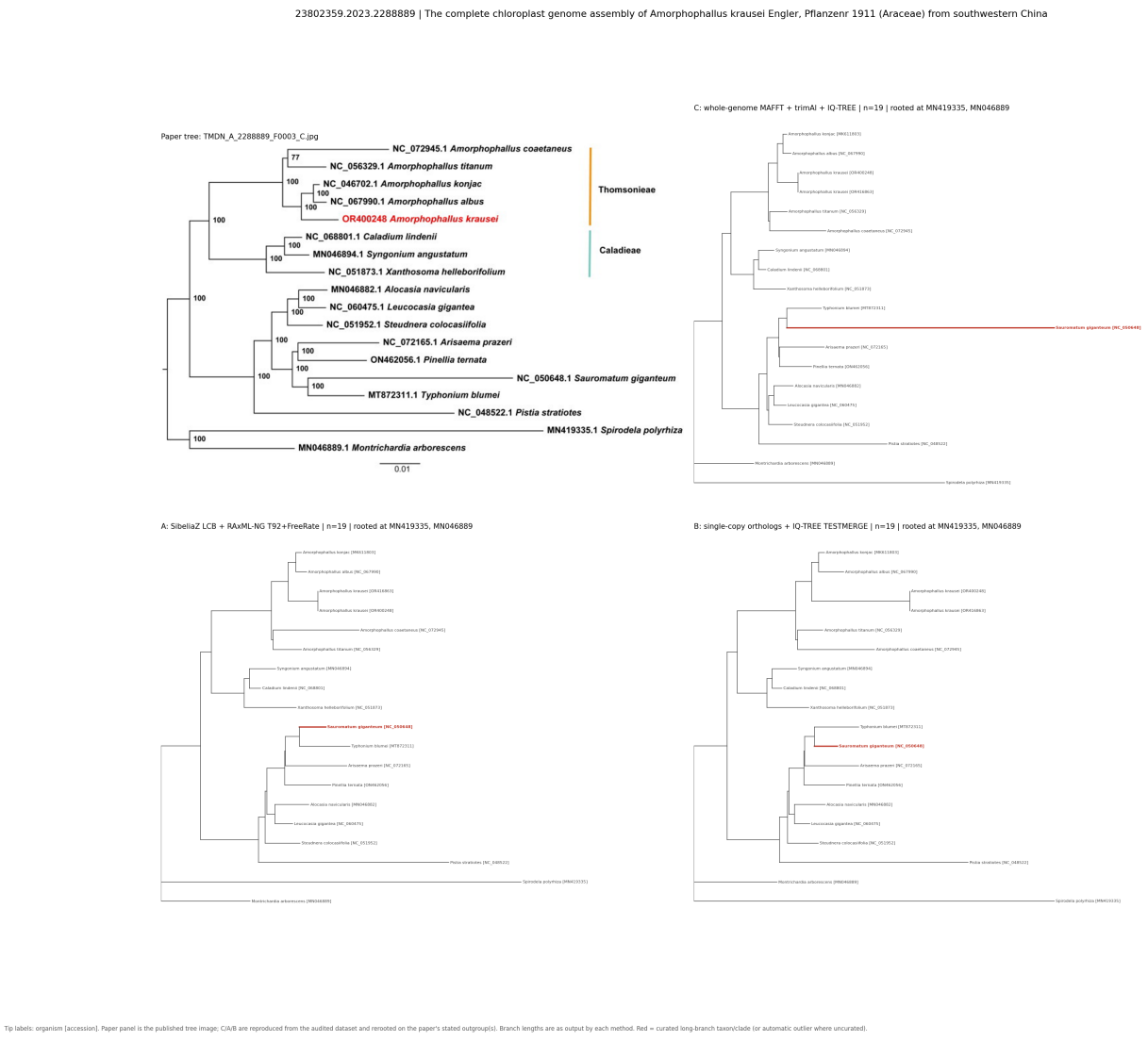
method	RTT outliers	terminal outliers	flagged clades
C naive	9	9	9
A FreeRate	0	12	11
B ortho	13	14	15

A terminal branches are estimated under RAxML-NG T92+F+FreeRate. RTT z-scores are sensitive to small MAD; ranks/clade flags should be read together.

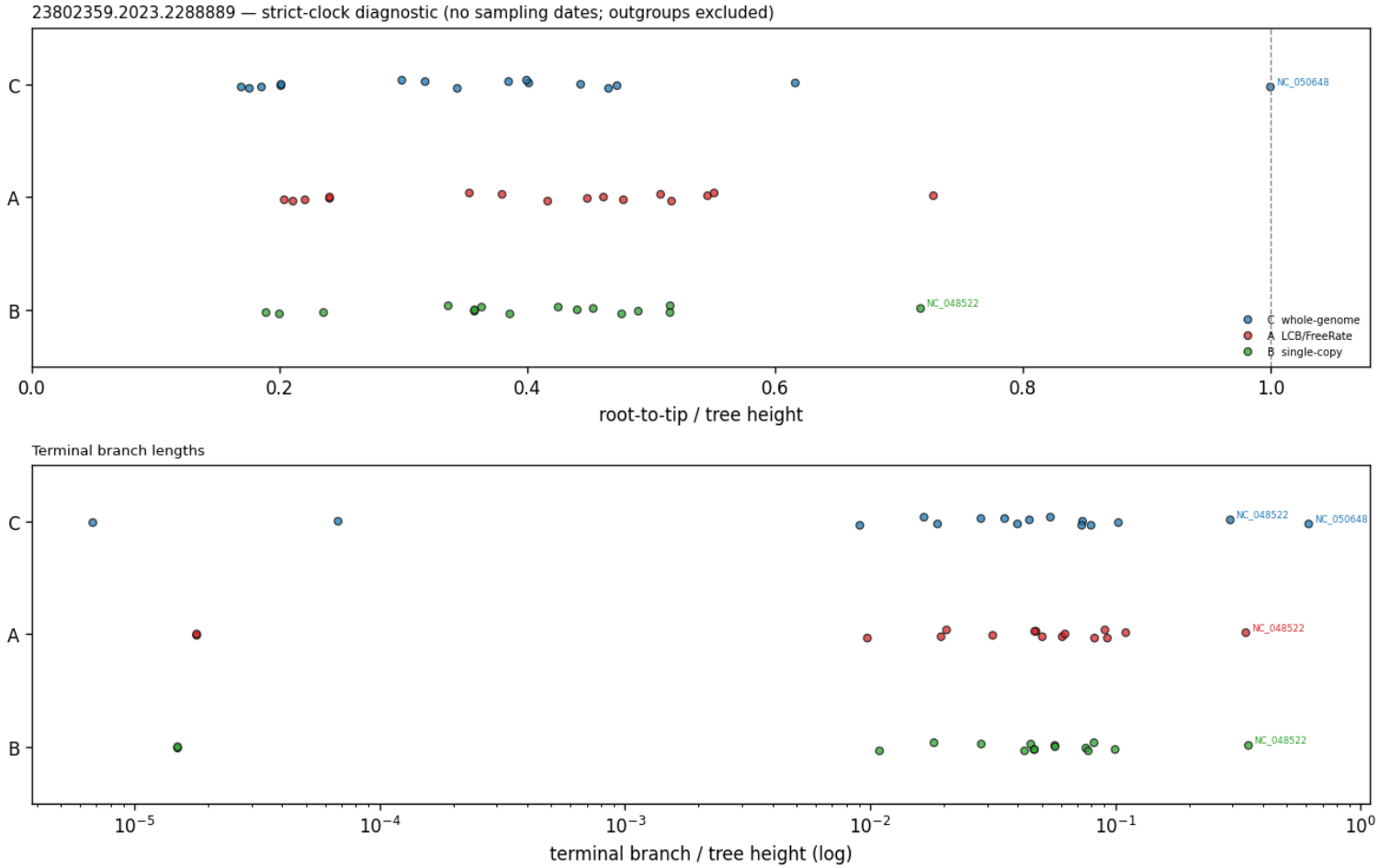
23802359.2023.2288889

The complete chloroplast genome assembly of Amorphophallus krausei Engler, Pflanzenr 1911 (Araceae) from southwestern China

Status: Verified (root fixed). Rooted at MN419335 + MN046889; NC_050648 highlighted; long branch reproduced and disappeared.



23802359.2023.2288889 - strict-clock branch-length diagnostic



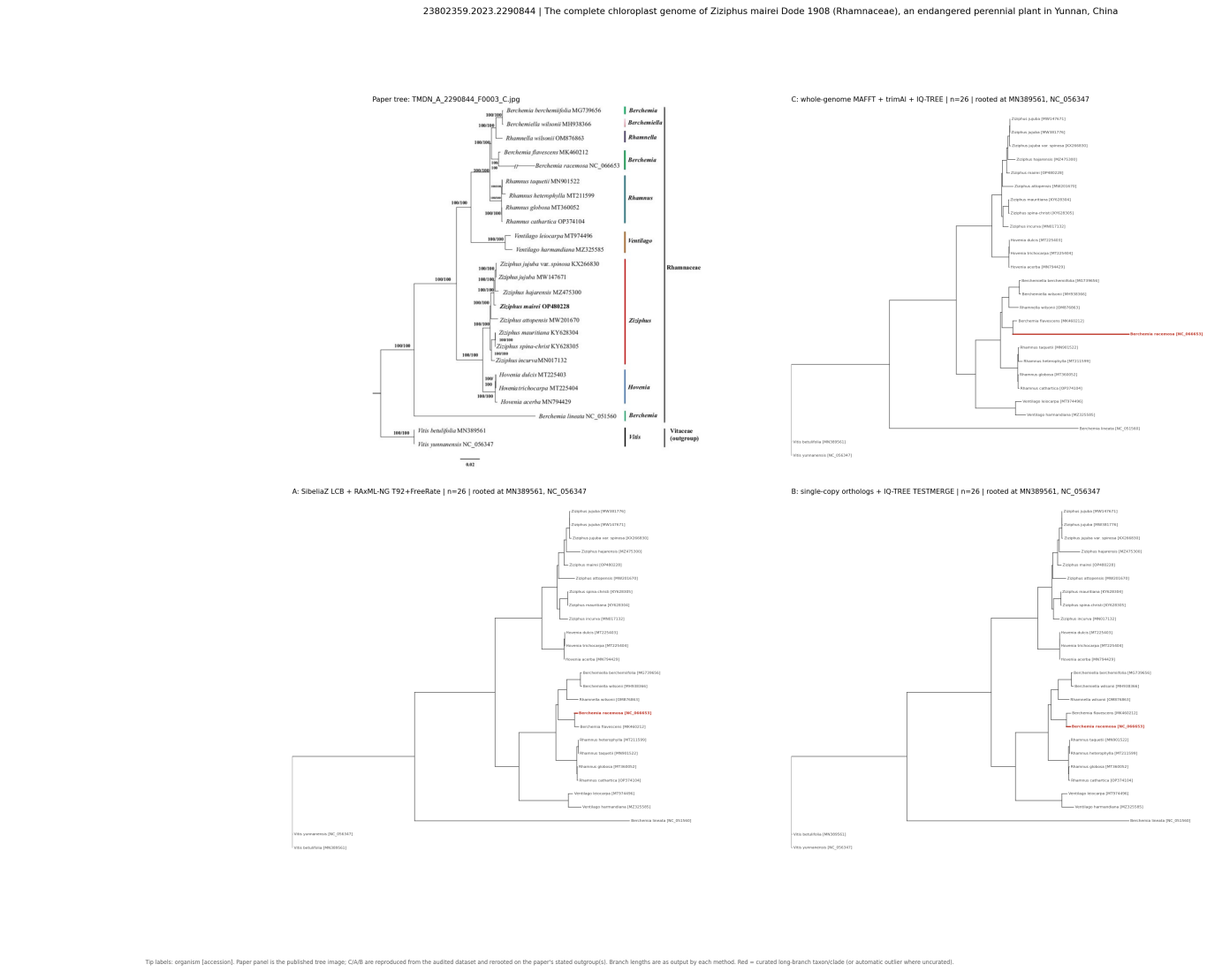
method	RTT outliers	terminal outliers	flagged clades
C naive	2	3	0
A FreeRate	1	2	0
B ortho	2	2	0

A terminal branches are estimated under RAxML-NG T92+F+FreeRate. RTT z-scores are sensitive to small MAD; ranks/clade flags should be read together.

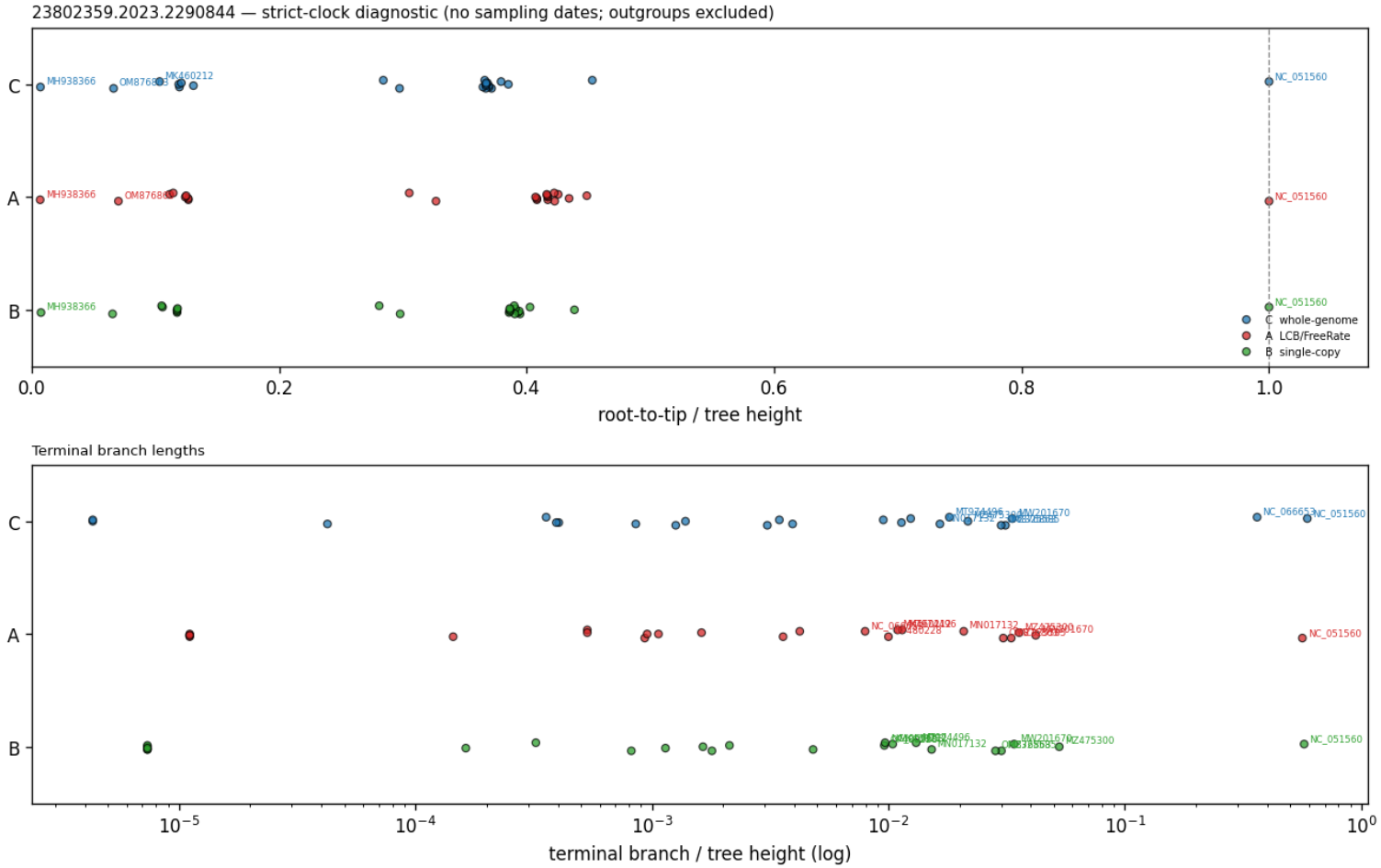
23802359.2023.2290844

The complete chloroplast genome of Ziziphus mairei Dode 1908 (Rhamnaceae), an endangered perennial plant in Yunnan, China

Status: Verified (root fixed). Rooted at MN389561 + NC_056347; NC_066653 highlighted; long branch reproduced and disappeared.



23802359.2023.2290844 - strict-clock branch-length diagnostic



method	RTT outliers	terminal outliers	flagged clades
C naive	6	8	4
A FreeRate	5	10	8
B ortho	4	10	8

A terminal branches are estimated under RAxML-NG T92+F+FreeRate. RTT z-scores are sensitive to small MAD; ranks/clade flags should be read together.

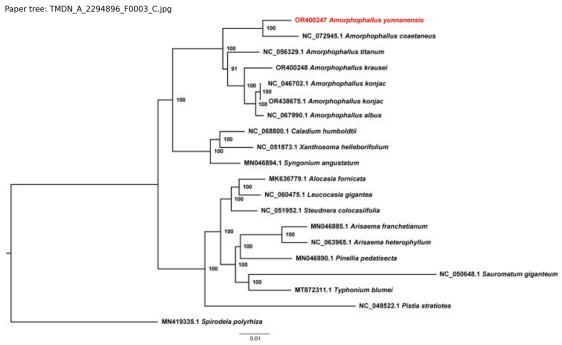
23802359.2023.2294896

Characterization of the complete chloroplast genome assembly of Amorphophallus yunnanensis Engler, Pflanzenr (Araceae) from southwestern China

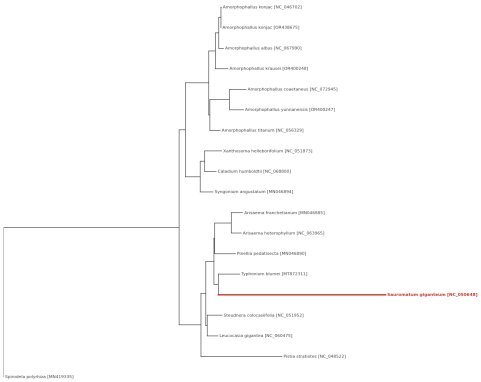
Status: Verified (root fixed). Rooted at MN419335; NC_050648 highlighted; long branch reproduced and disappeared.

23802359.2023.2294896 | Characterization of the complete chloroplast genome assembly of Amorphophallus yunnanensis Engler, Pflanzenr (Araceae) from southwestern China

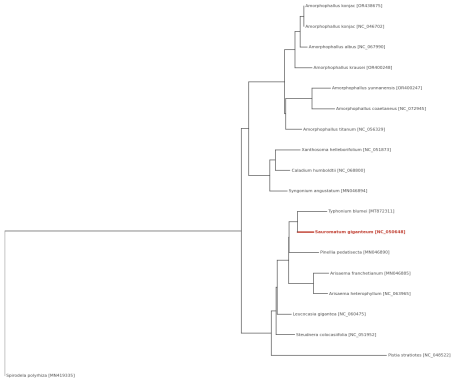
Paper tree: TMDN_A_2294896_F0003_C.jpg



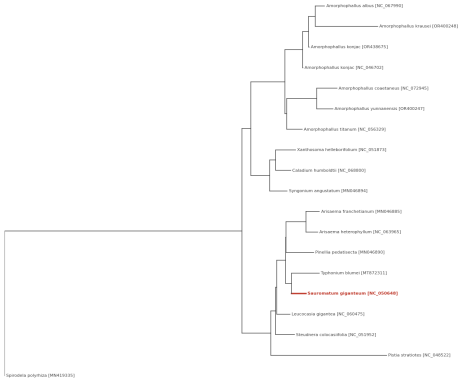
C: whole-genome MAFFT + trimAl + IQ-TREE | n=19 | rooted at MN419335



A: SibeliaZ LCB + RAxML-NG T92+FreeRate | n=19 | rooted at MN419335

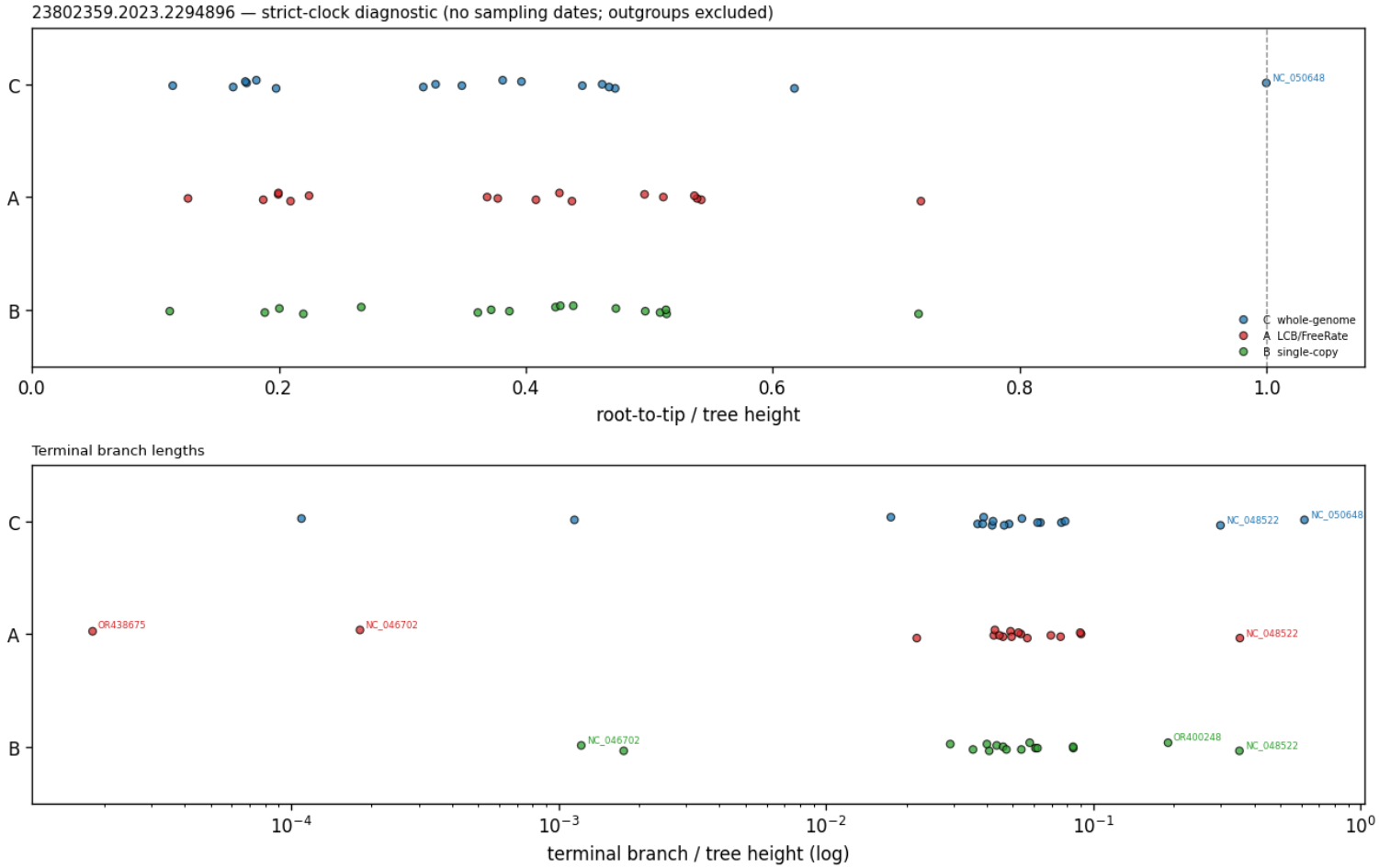


B: single-copy orthologs + IQ-TREE TESTMERGE | n=19 | rooted at MN419335



Tip labels: organism [accession]. Paper panel is the published tree image; C/A/B are reproduced from the audited dataset and rerooted on the paper's stated outgroup(s). Branch lengths are as output by each method. Red = curated long-branch taxon/clade (or automatic outlier where uncurated).

23802359.2023.2294896 - strict-clock branch-length diagnostic



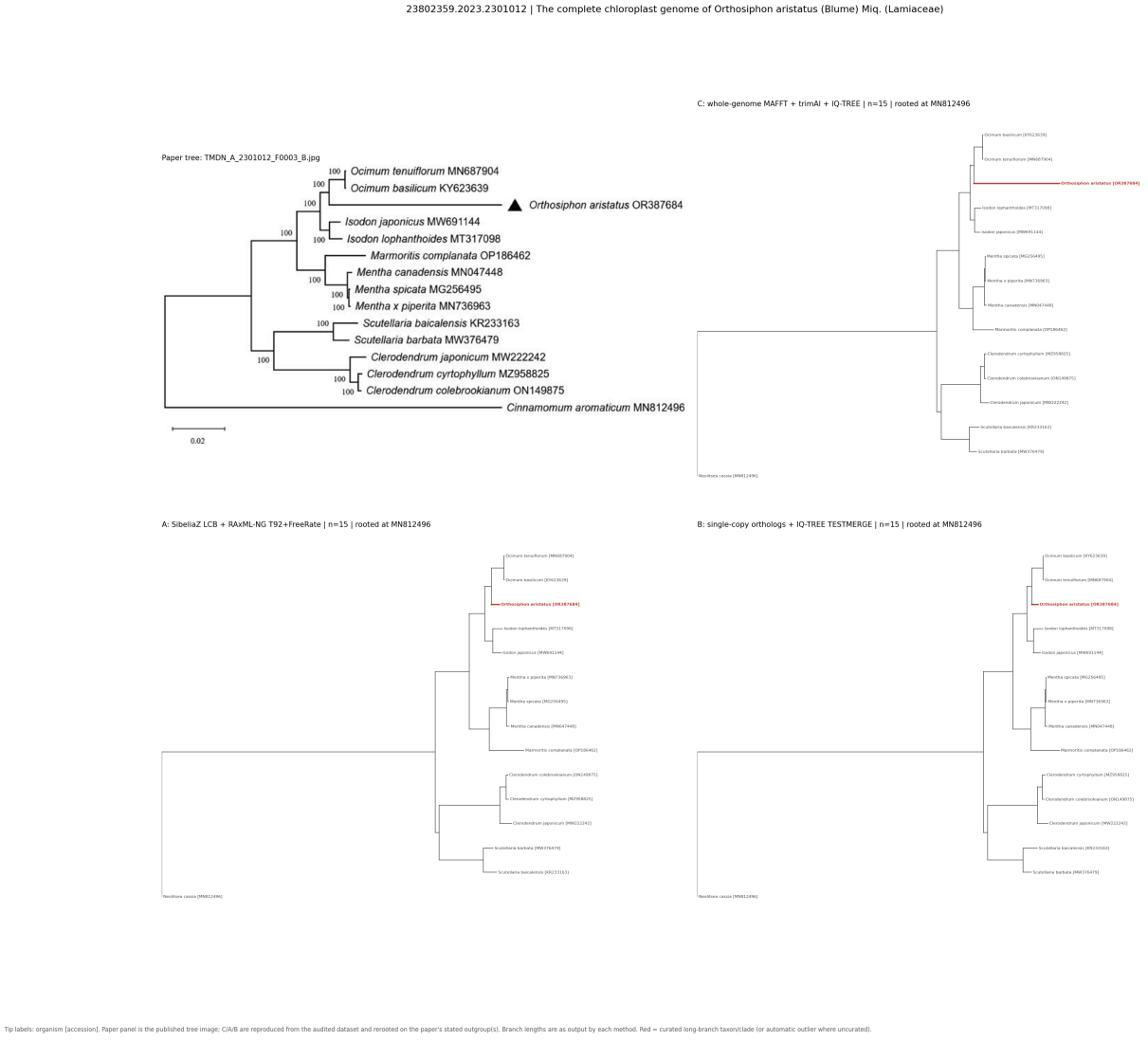
method	RTT outliers	terminal outliers	flagged clades
C naive	2	3	0
A FreeRate	1	4	3
B ortho	1	4	1

A terminal branches are estimated under RAxML-NG T92+F+FreeRate. RTT z-scores are sensitive to small MAD; ranks/clade flags should be read together.

23802359.2023.2301012

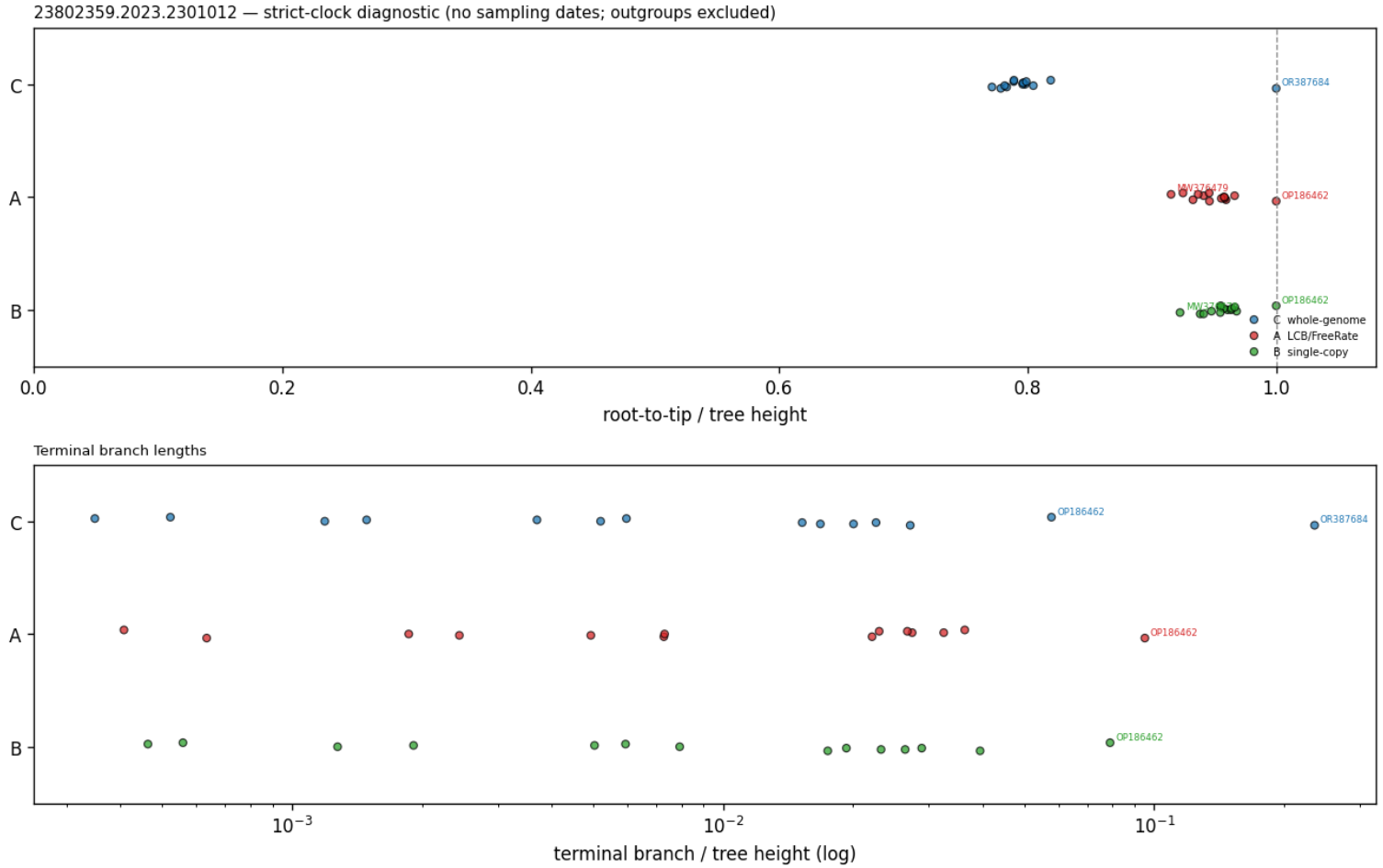
The complete chloroplast genome of Orthosiphon aristatus (Blume) Miq. (Lamiaceae)

Status: Verified. OR387684 SSC reversal confirmed by SSC-flip control; long branch reproduced and disappeared.



Tip labels: organism [accession]. Paper panel is the published tree image; C/A/B are reproduced from the audited dataset and rerooted on the paper's stated outgroup(s). Branch lengths are as output by each method. Red = curated long-branch taxon/clade (or automatic outlier where uncurated).

23802359.2023.2301012 - strict-clock branch-length diagnostic



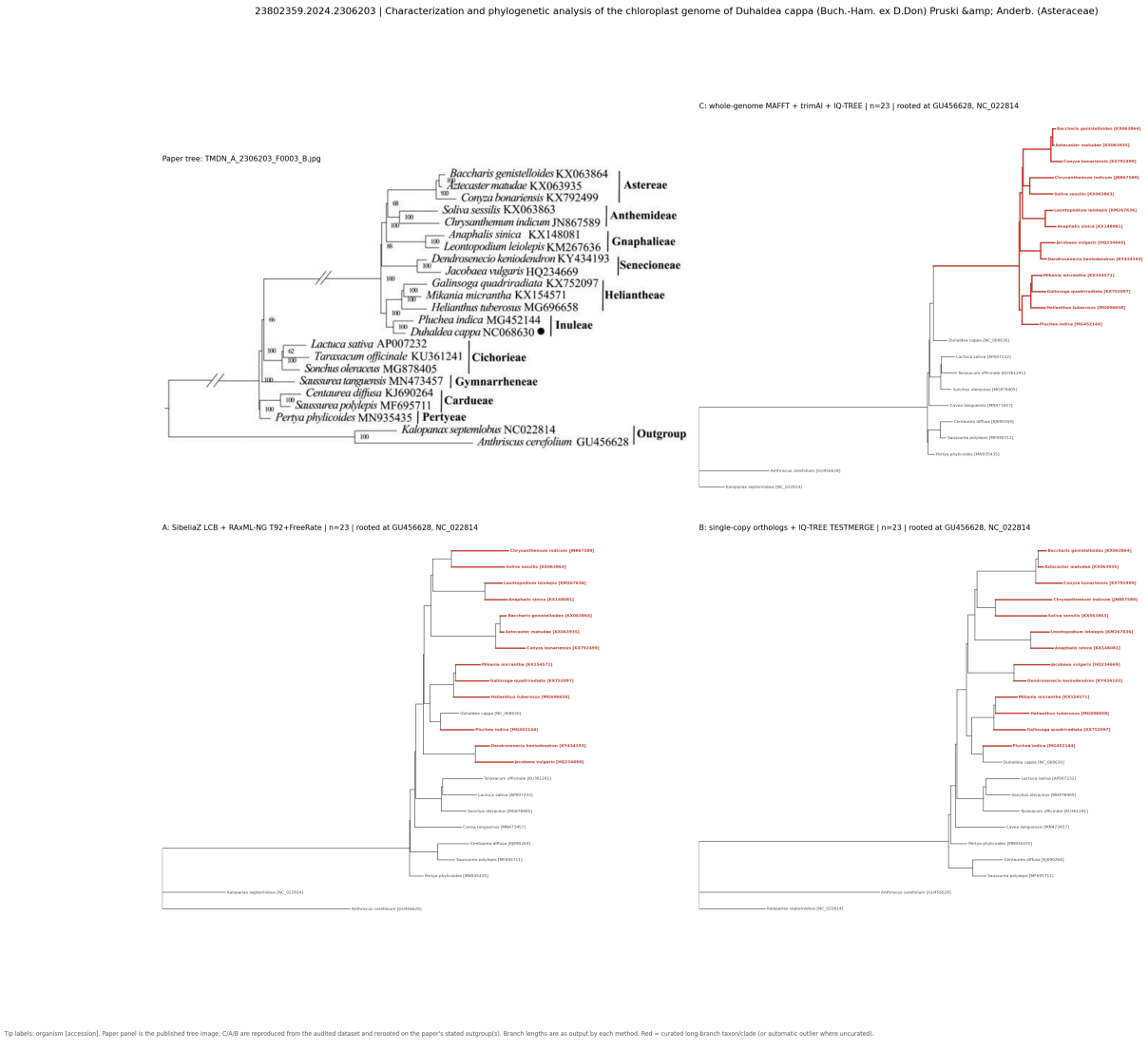
method	RTT outliers	terminal outliers	flagged clades
C naive	1	2	0
A FreeRate	2	1	0
B ortho	2	1	0

A terminal branches are estimated under RAxML-NG T92+F+FreeRate. RTT z-scores are sensitive to small MAD; ranks/clade flags should be read together.

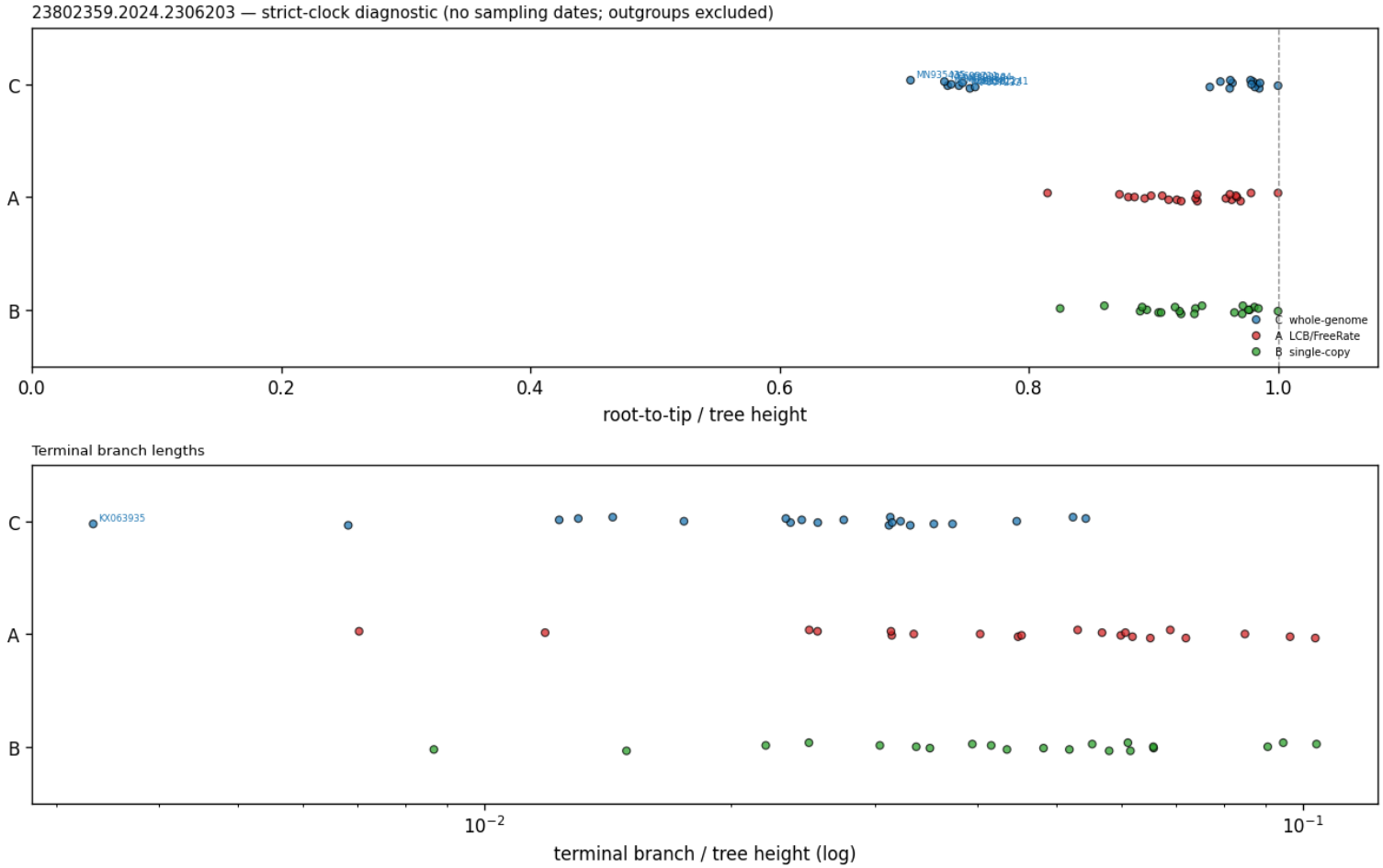
23802359.2024.2306203

Characterization and phylogenetic analysis of the chloroplast genome of Duhaldea cappa (Buch.-Ham. ex D.Don) Pruski & Anderb. (Asteraceae)

Status: Verified. Corrected 23-taxon set; C-specific 13-tip clade highlighted; long branch absent from A/B.



23802359.2024.2306203 - strict-clock branch-length diagnostic



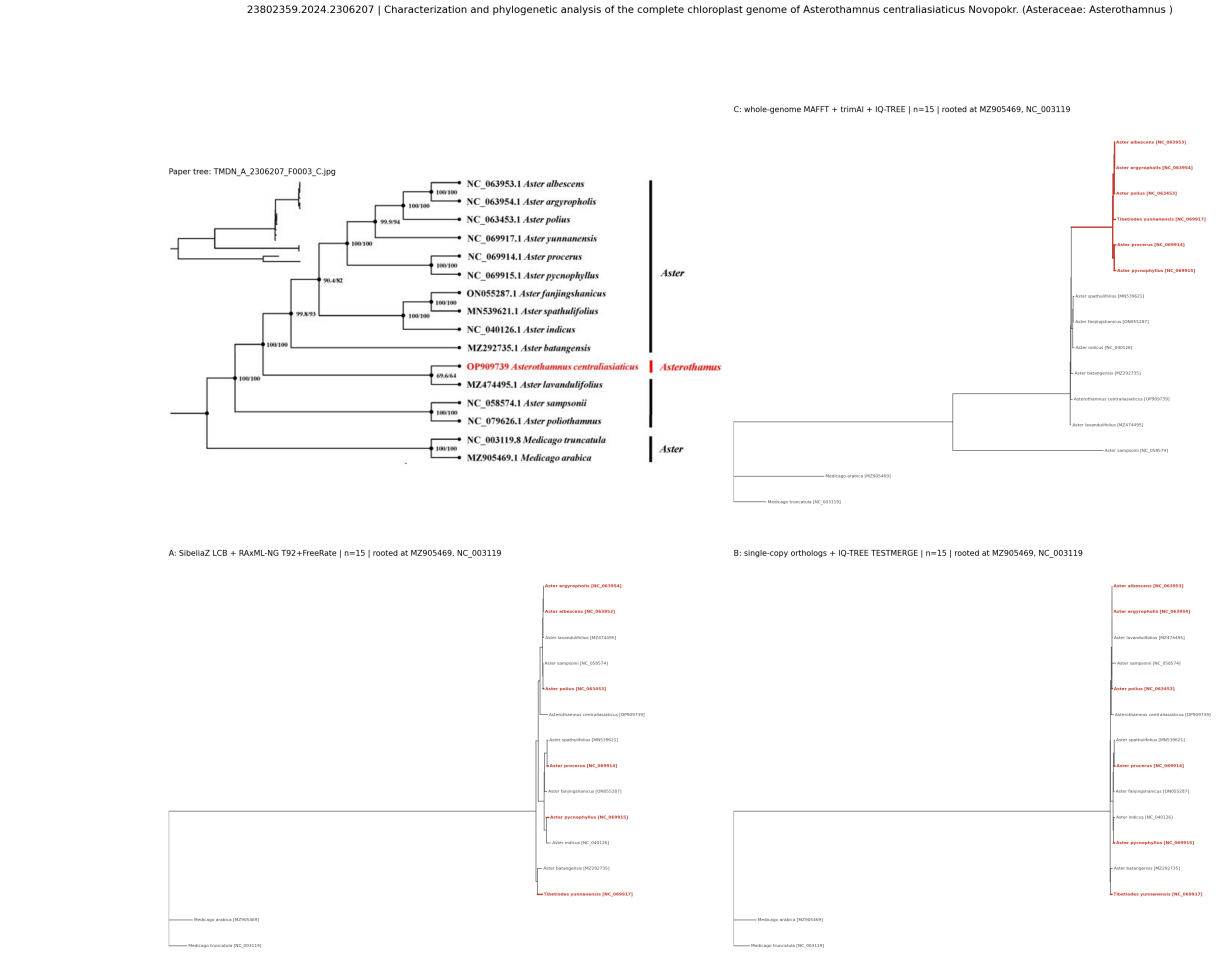
method	RTT outliers	terminal outliers	flagged clades
C naive	9	2	4
A FreeRate	1	0	0
B ortho	1	1	0

A terminal branches are estimated under RAxML-NG T92+F+FreeRate. RTT z-scores are sensitive to small MAD; ranks/clade flags should be read together.

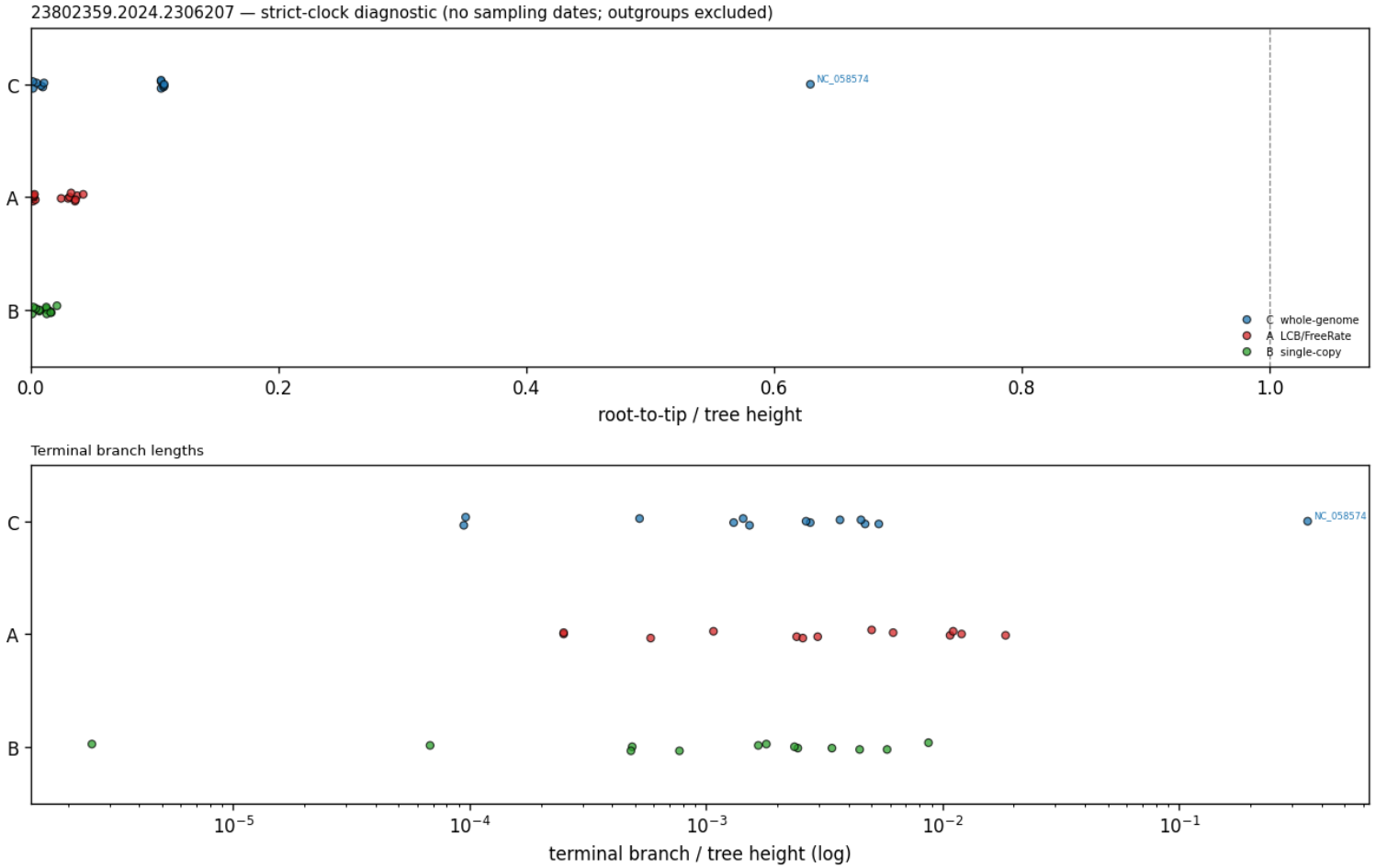
23802359.2024.2306207

Characterization and phylogenetic analysis of the complete chloroplast genome of Asterothamnus centraliasiaticus Novopokr. (Asteraceae: Asterothamnus)

Status: Verified. C-specific 6-tip clade highlighted; MZ474495 is present outside that clade.



23802359.2024.2306207 - strict-clock branch-length diagnostic



method	RTT outliers	terminal outliers	flagged clades
C naive	3	3	5
A FreeRate	2	2	2
B ortho	2	2	2

A terminal branches are estimated under RAxML-NG T92+F+FreeRate. RTT z-scores are sensitive to small MAD; ranks/clade flags should be read together.

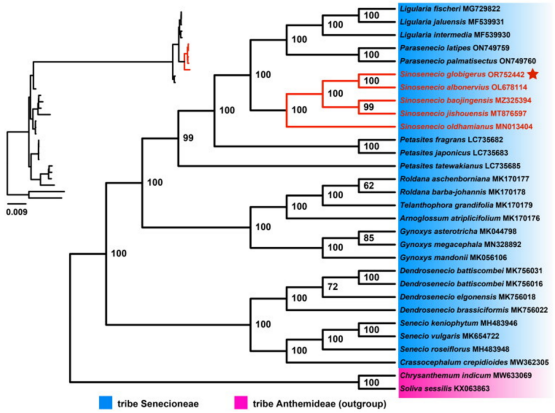
23802359.2024.2309262

The complete chloroplast genome of Sinosenecio globigerus (C. C. Chang) B. Nordenstam (Asteraceae)

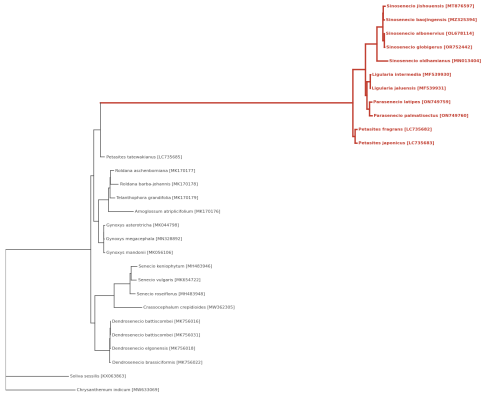
Status: Verified. 29 taxa; 11-taxon clade MT876597-LC735683 highlighted; long branch recovered.

23802359.2024.2309262 | The complete chloroplast genome of Sinosenecio globigerus (C. C. Chang) B. Nordenstam (Asteraceae)

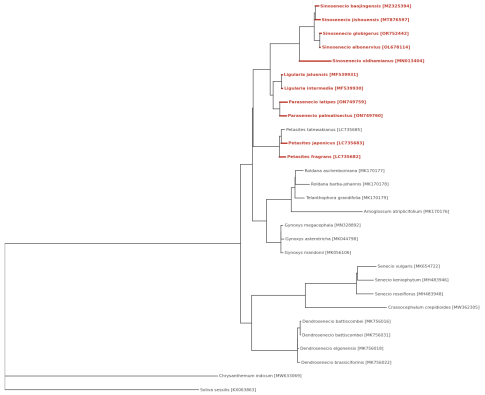
Paper tree: TMDN_A_2309262_F0004_C.jpg



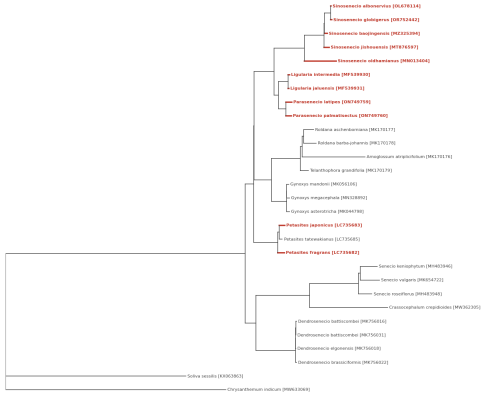
C: whole-genome MAFFT + trimAl + IQ-TREE | n=29 | rooted at MW633069, KX063863



A: SibeliaZ LCB + RAxML-NG T92+FreeRate | n=29 | rooted at MW633069, KX063863

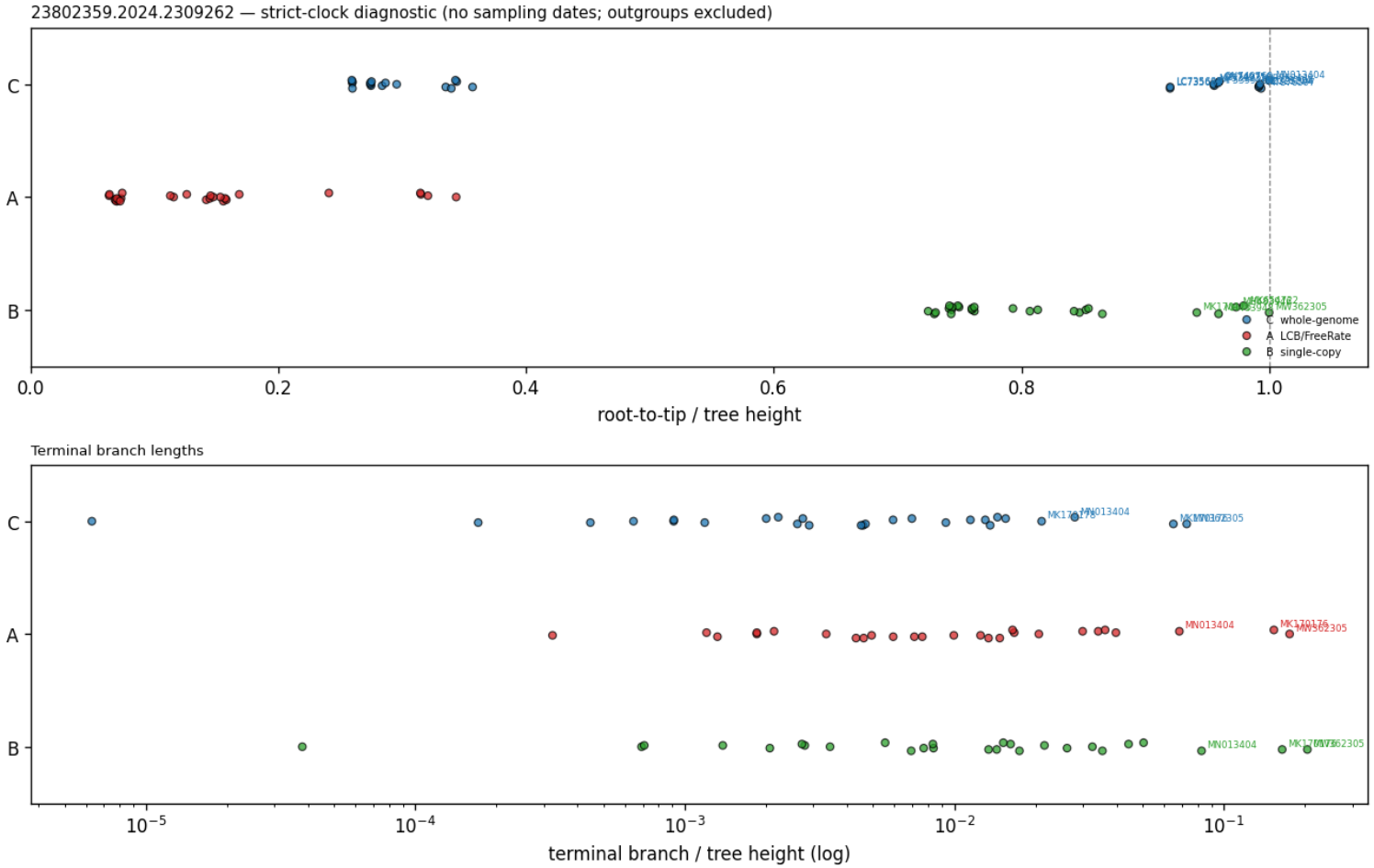


B: single-copy orthologs + IQ-TREE TESTMERGE | n=29 | rooted at MW633069, KX063863



Tip labels: organism [accession]. Paper panel is the published tree image; C/A/B are reproduced from the audited dataset and rerooted on the paper's stated outgroup(s). Branch lengths are as output by each method. Red = curated long-branch taxon/clade (or automatic outlier where uncurated).

23802359.2024.2309262 - strict-clock branch-length diagnostic



method	RTT outliers	terminal outliers	flagged clades
C naive	11	6	14
A FreeRate	2	5	1
B ortho	7	5	4

A terminal branches are estimated under RAxML-NG T92+F+FreeRate. RTT z-scores are sensitive to small MAD; ranks/clade flags should be read together.

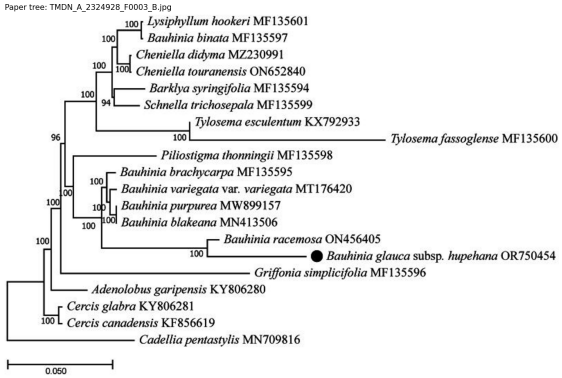
23802359.2024.2324928

The complete chloroplast genome and phylogenetic analysis of Bauhinia glauca subsp . hupehana (Craib) T. C. Chen 1988

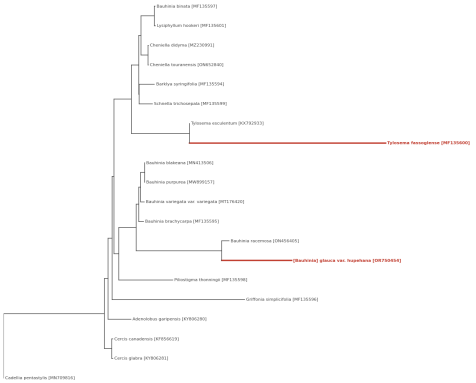
Status: Verified. Only MF135600 and OR750454 highlighted; long branch recovered; A-B nearly identical.

23802359.2024.2324928 | The complete chloroplast genome and phylogenetic analysis of Bauhinia glauca subsp . hupehana (Craib) T. C. Chen 1988

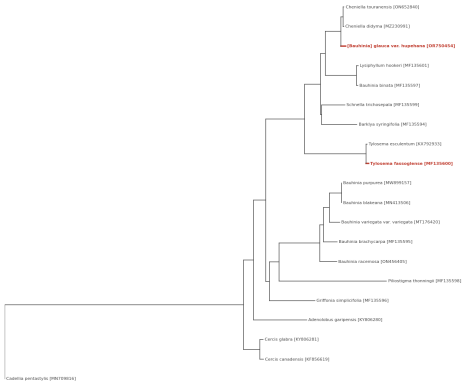
Paper tree: TMDN_A_2324928_F0003_B.jpg



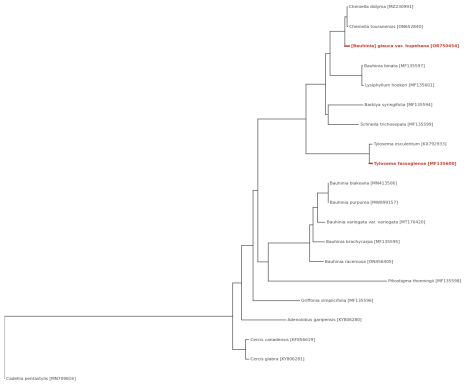
C: whole-genome MAFFT + trimAl + IQ-TREE | n=20 | rooted at MN709816



A: SibeliaZ LCB + RAxML-NG T92+FreeRate | n=20 | rooted at MN709816

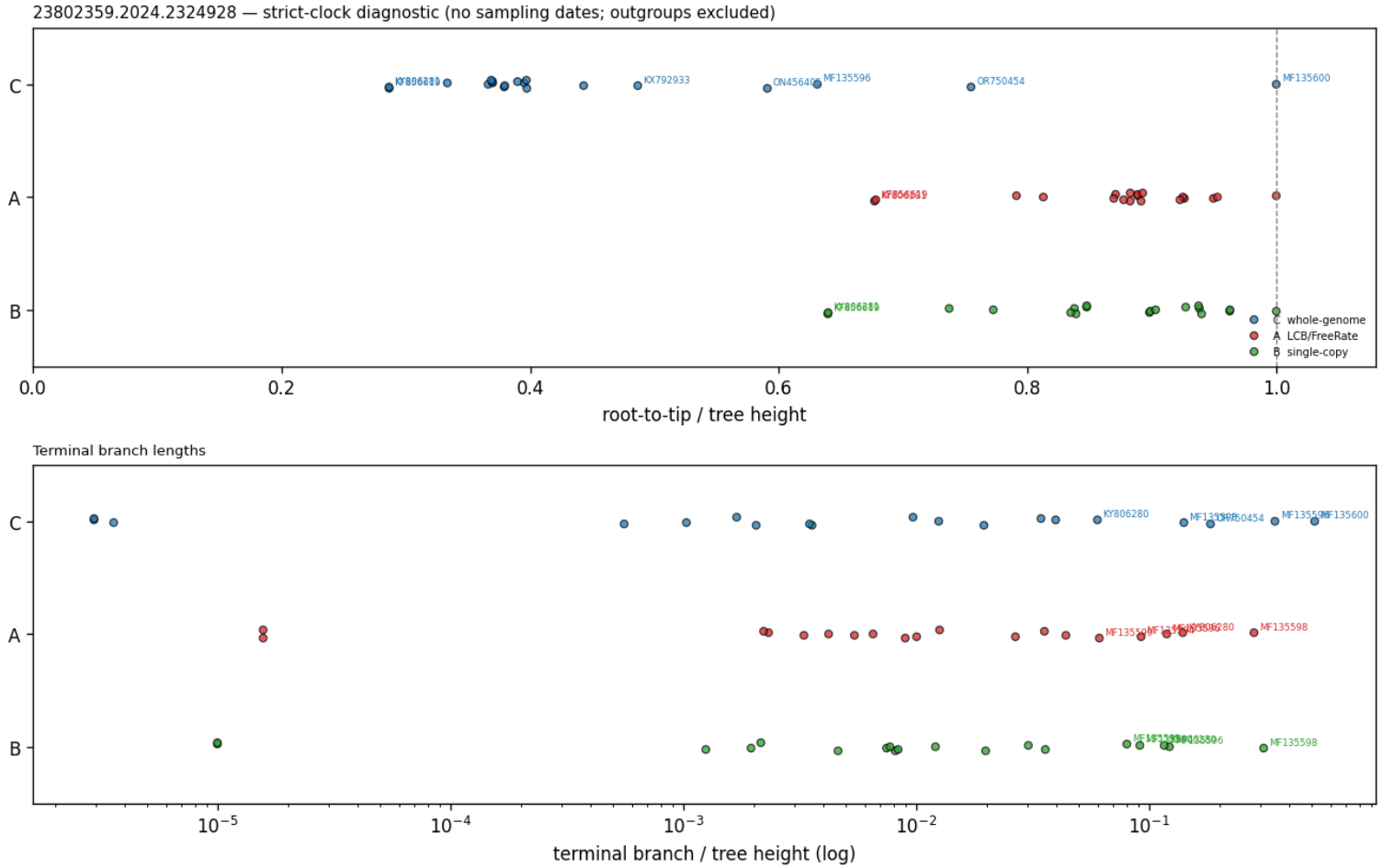


B: single-copy orthologs + IQ-TREE TESTMERGE | n=20 | rooted at MN709816



Tip labels: organism [accession]. Paper panel is the published tree image; C/A/B are reproduced from the audited dataset and rerooted on the paper's stated outgroup(s). Branch lengths are as output by each method. Red = curated long-branch taxon/clade (or automatic outlier where uncurated).

23802359.2024.2324928 - strict-clock branch-length diagnostic



method	RTT outliers	terminal outliers	flagged clades
C naive	7	5	3
A FreeRate	2	5	2
B ortho	2	5	2

A terminal branches are estimated under RAxML-NG T92+F+FreeRate. RTT z-scores are sensitive to small MAD; ranks/clade flags should be read together.

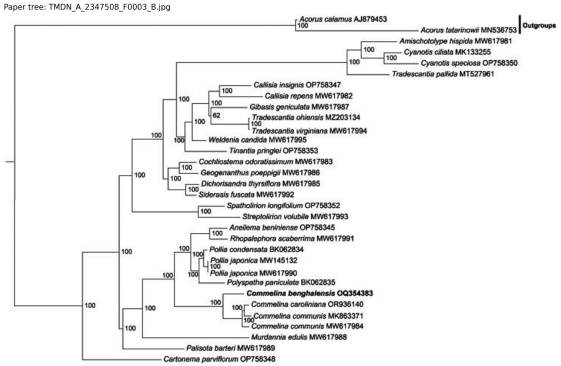
23802359.2024.2347508

The complete plastome and phylogenetic analysis of Commelina benghalensis L.1753 (Commelinaceae)

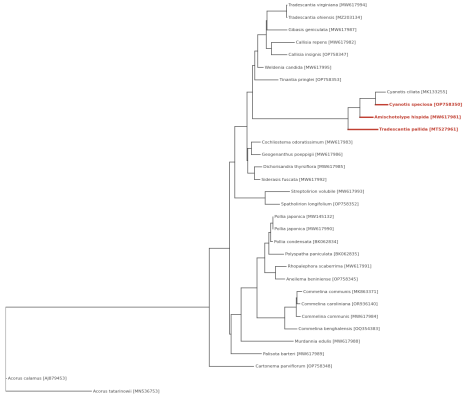
Status: Verified. 4-taxon clade MK133225/OP758350/MW617981/MT527961 highlighted; long branch recovered.

23802359.2024.2347508 | The complete plastome and phylogenetic analysis of Commelina benghalensis L.1753 (Commelinaceae)

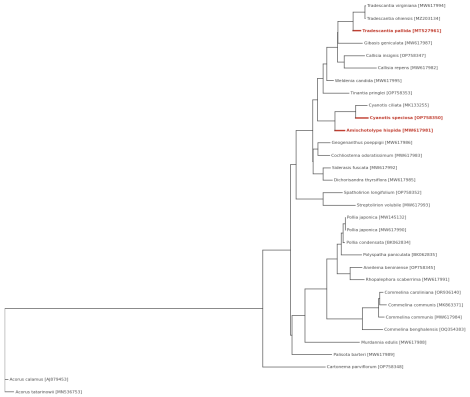
Paper tree: TMDN_A_2347508_F0003_B.jpg



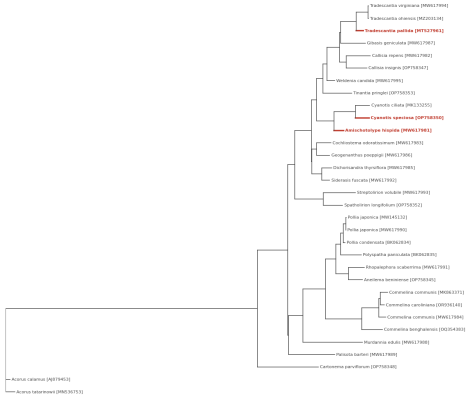
C: whole-genome MAFFT + trimAl + IQ-TREE | n=32 | rooted at AJ879453, MN536753



A: SibeliaZ LCB + RAxML-NG T92+FreeRate | n=32 | rooted at AJ879453, MN536753

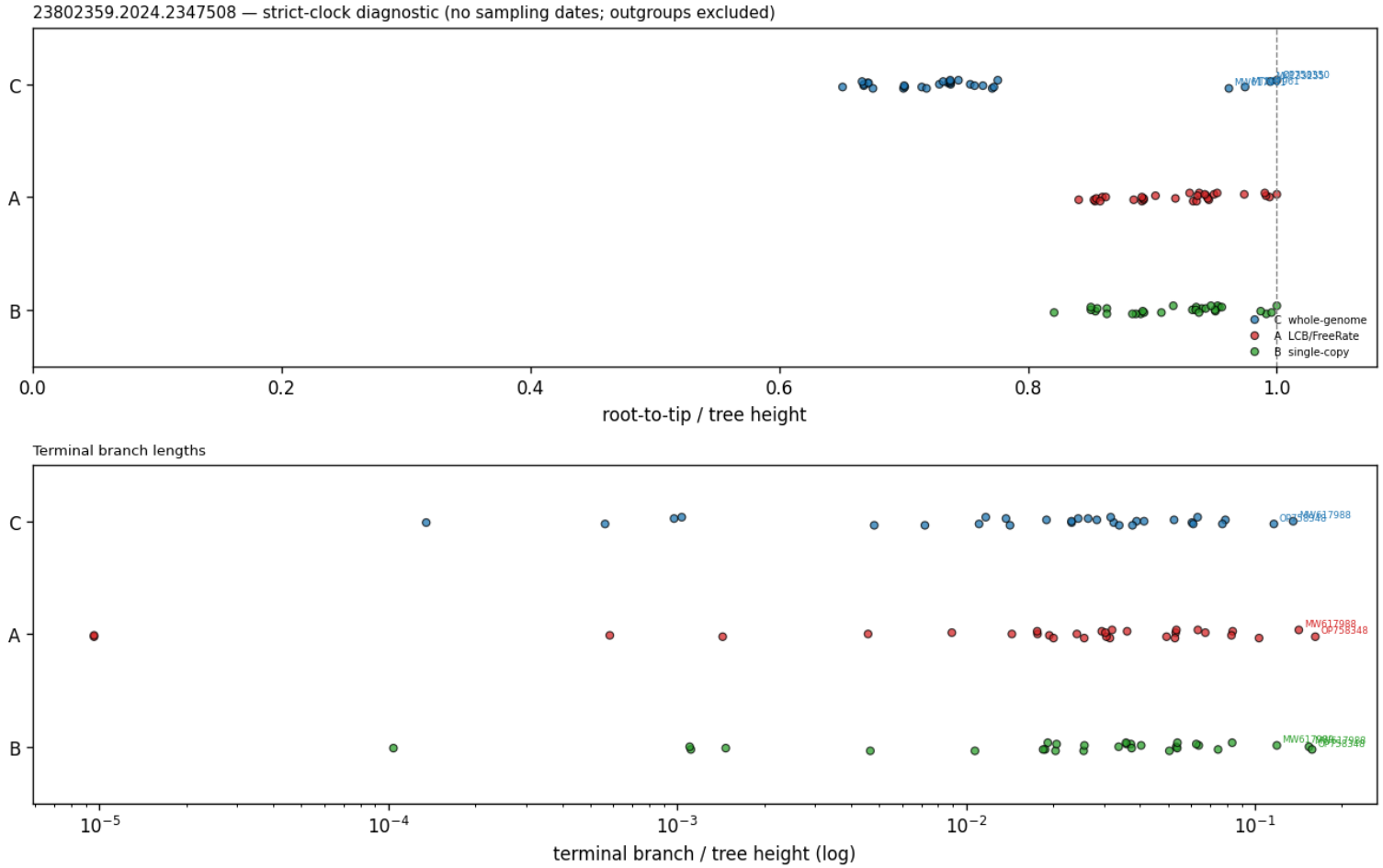


B: single-copy orthologs + IQ-TREE TESTMERGE | n=32 | rooted at AJ879453, MN536753



Tip labels: organism [accession]. Paper panel is the published tree image; C/A/B are reproduced from the audited dataset and rerooted on the paper's stated outgroup(s). Branch lengths are as output by each method. Red = curated long-branch taxon/clade (or automatic outlier where uncurated).

23802359.2024.2347508 - strict-clock branch-length diagnostic



method	RTT outliers	terminal outliers	flagged clades
C naive	5	3	3
A FreeRate	1	2	0
B ortho	1	3	0

A terminal branches are estimated under RAxML-NG T92+F+FreeRate. RTT z-scores are sensitive to small MAD; ranks/clade flags should be read together.

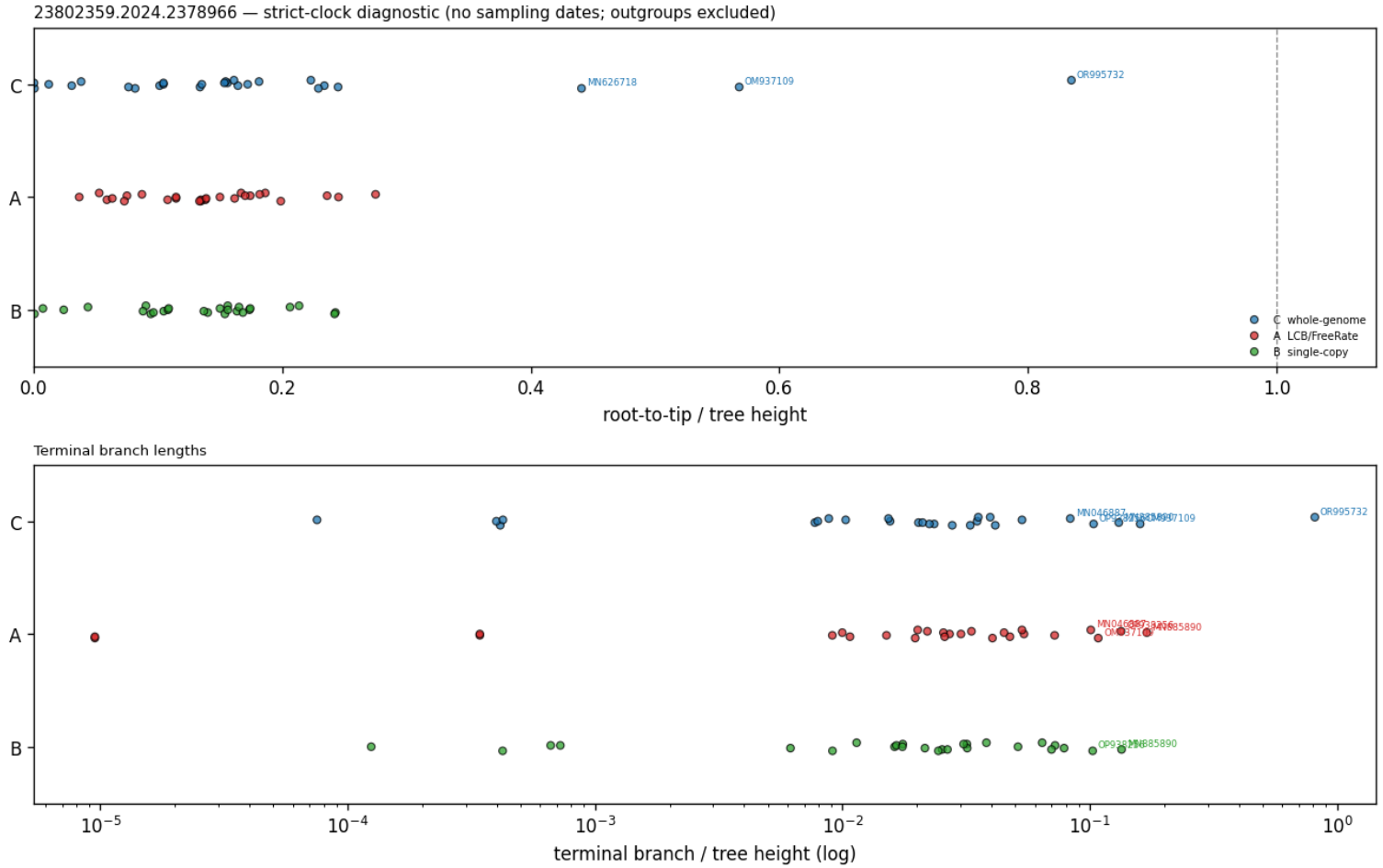
23802359.2024.2378966

Complete chloroplast genome and phylogenetic analysis of Amorphophallus paeoniifolius (Araceae)

Status: Verified. OR995732 plus OM937109-MN626718 clade highlighted; long branch recovered.



23802359.2024.2378966 - strict-clock branch-length diagnostic



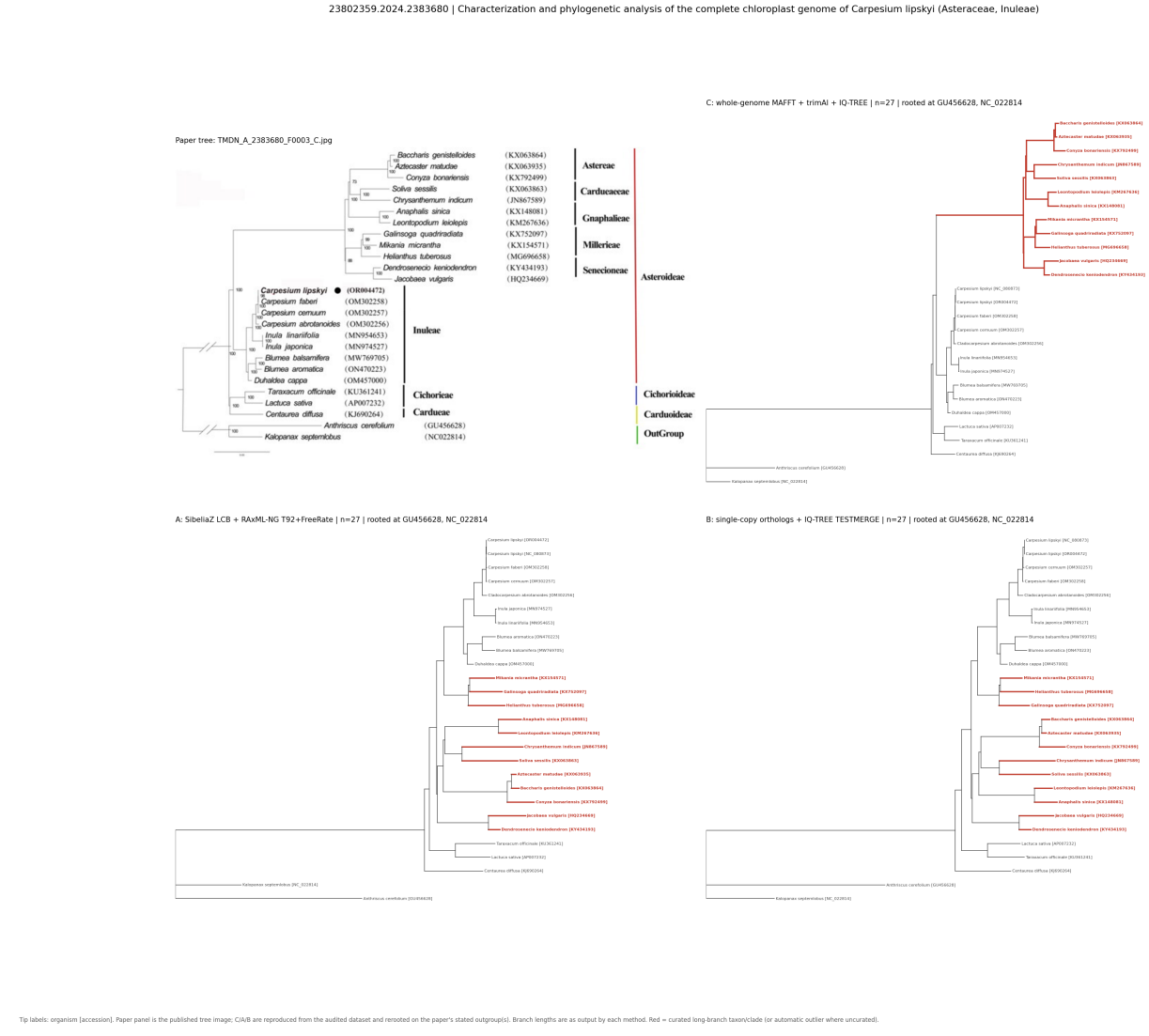
method	RTT outliers	terminal outliers	flagged clades
C naive	4	6	2
A FreeRate	1	5	2
B ortho	1	3	1

A terminal branches are estimated under RAxML-NG T92+F+FreeRate. RTT z-scores are sensitive to small MAD; ranks/clade flags should be read together.

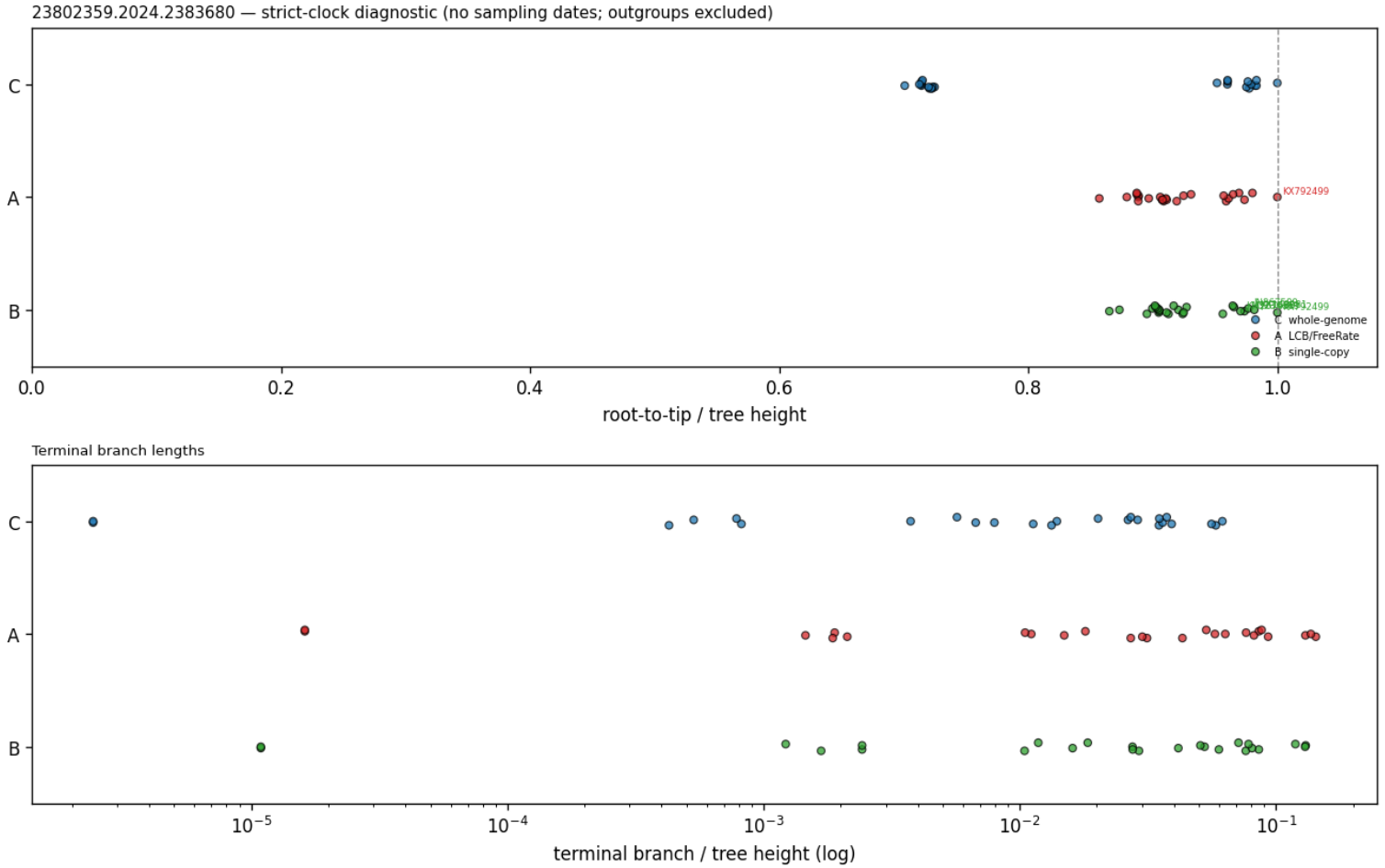
23802359.2024.2383680

Characterization and phylogenetic analysis of the complete chloroplast genome of Carpesium lipskyi (Asteraceae, Inuleae)

Status: Verified. 12-taxon clade KX063864-HQ234669 highlighted; long branch recovered.



23802359.2024.2383680 - strict-clock branch-length diagnostic



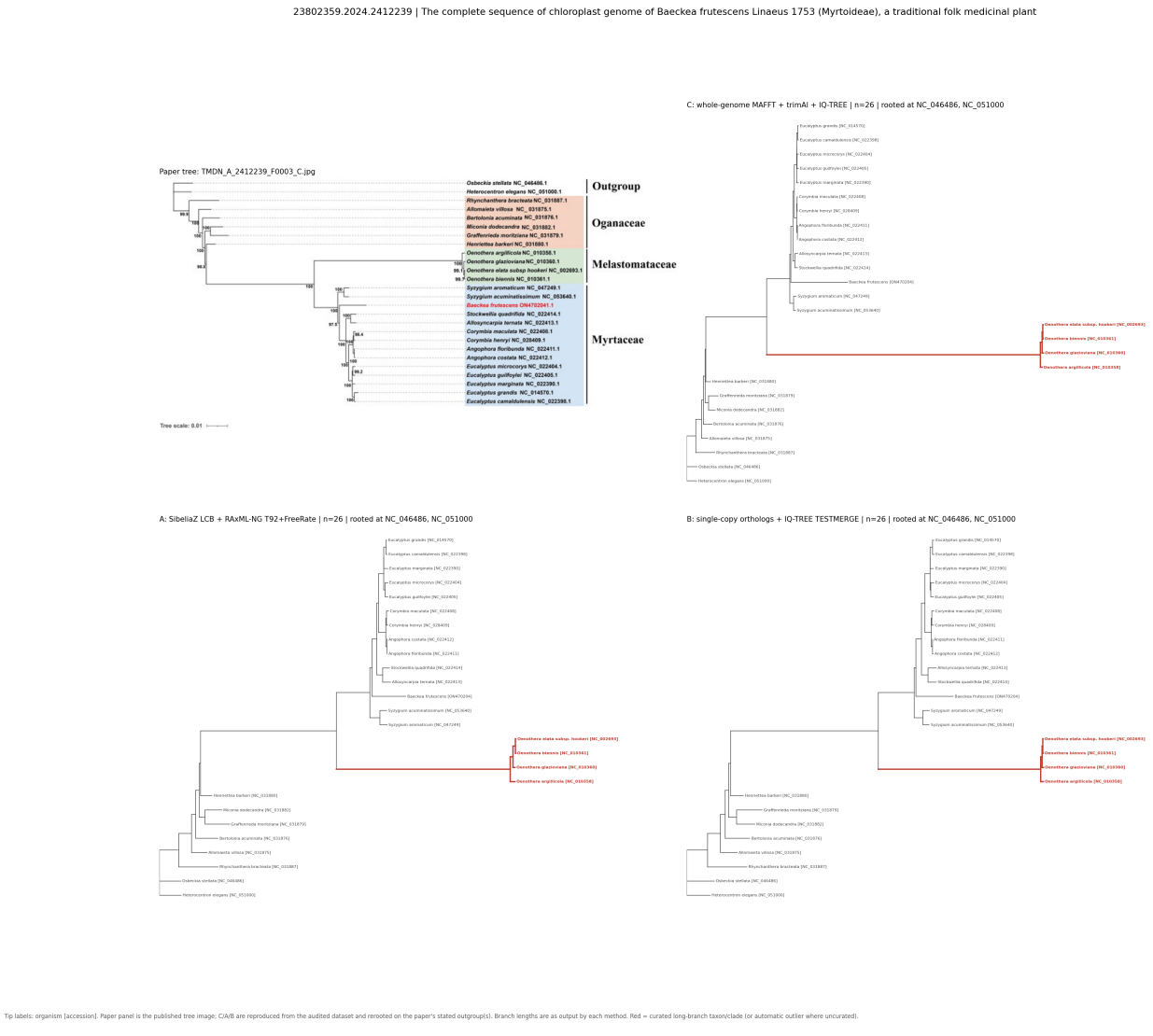
method	RTT outliers	terminal outliers	flagged clades
C naive	1	1	0
A FreeRate	2	1	0
B ortho	6	1	3

A terminal branches are estimated under RAxML-NG T92+F+FreeRate. RTT z-scores are sensitive to small MAD; ranks/clade flags should be read together.

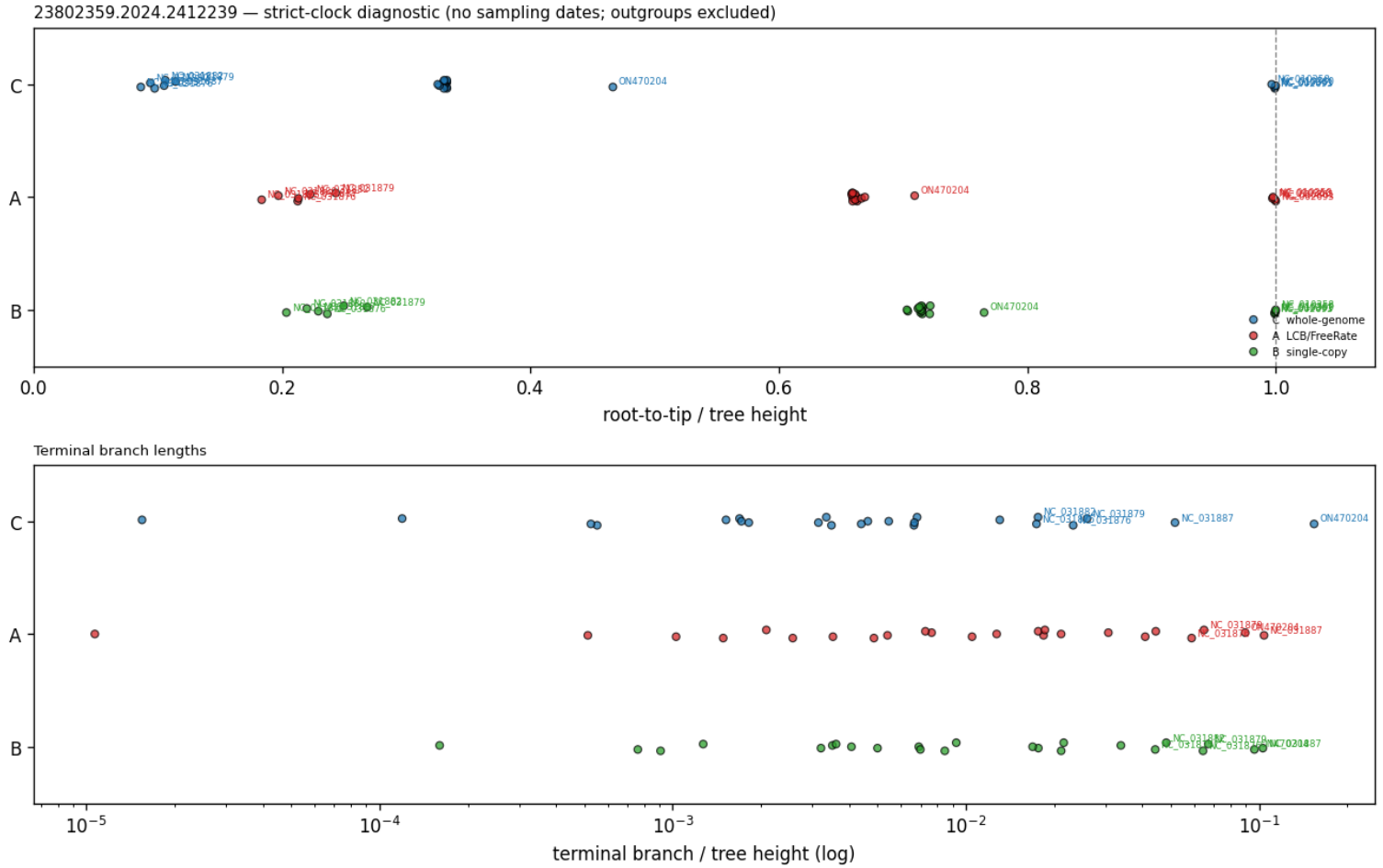
23802359.2024.2412239

The complete sequence of chloroplast genome of Baeckea frutescens Linaeus 1753 (Myrtoideae), a traditional folk medicinal plant

Status: Verified (shortened). 25 Myrtales cp genomes + 2 outgroups; Oenothera 4-tip clade highlighted; long branch reproduced and shortened.



23802359.2024.2412239 - strict-clock branch-length diagnostic



method	RTT outliers	terminal outliers	flagged clades
C naive	12	7	4
A FreeRate	12	5	4
B ortho	12	7	4

A terminal branches are estimated under RAxML-NG T92+F+FreeRate. RTT z-scores are sensitive to small MAD; ranks/clade flags should be read together.

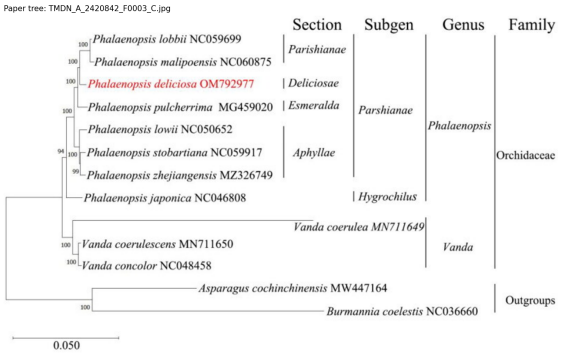
23802359.2024.2420842

Characterization and phylogenetic analysis of the complete chloroplast genome sequence of Phalaenopsis deliciosa (Rchb. f. 1854)

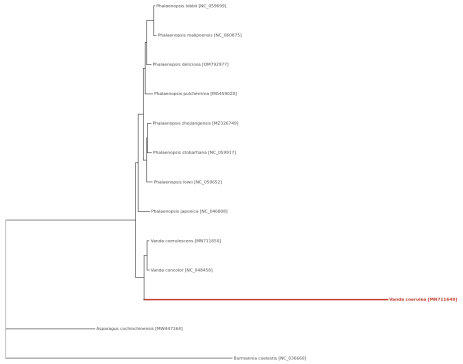
Status: Verified (root fixed). Rooted at MW447164 + NC_036660; MN711649 highlighted; long branch reproduced and disappeared.

23802359.2024.2420842 | Characterization and phylogenetic analysis of the complete chloroplast genome sequence of Phalaenopsis deliciosa (Rchb. f. 1854)

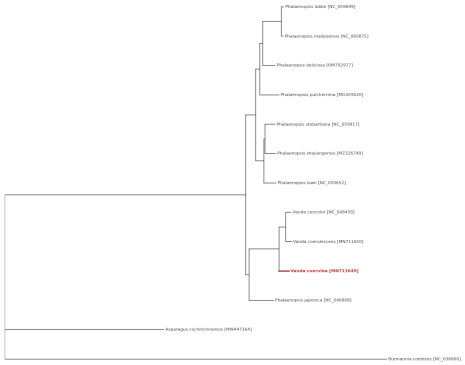
Paper tree: TMDN_A_2420842_F0003_C.jpg



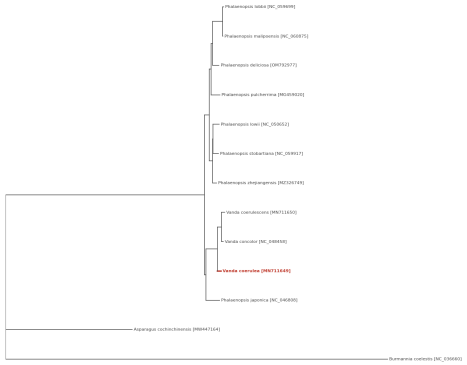
C: whole-genome MAFFT + trimAl + IQ-TREE | n=13 | rooted at MW447164, NC_036660



A: SibeliaZ LCB + RAxML-NG T92+FreeRate | n=13 | rooted at MW447164, NC_036660

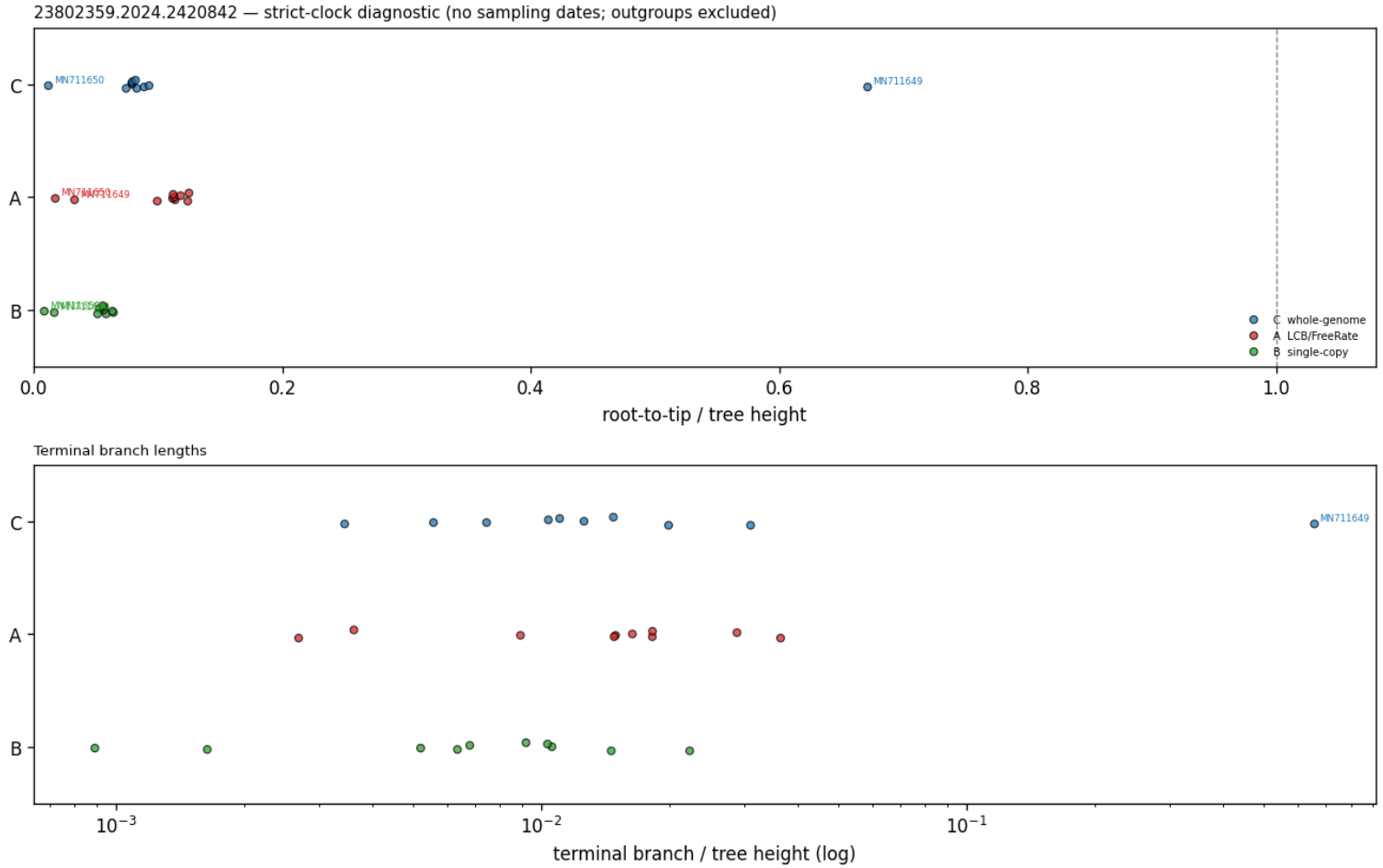


B: single-copy orthologs + IQ-TREE TESTMERGE | n=13 | rooted at MW447164, NC_036660



Tip labels: organism [accession]. Paper panel is the published tree image; C/A/B are reproduced from the audited dataset and rerooted on the paper's stated outgroup(s). Branch lengths are as output by each method. Red = curated long-branch taxon/clade (or automatic outlier where uncurated).

23802359.2024.2420842 - strict-clock branch-length diagnostic



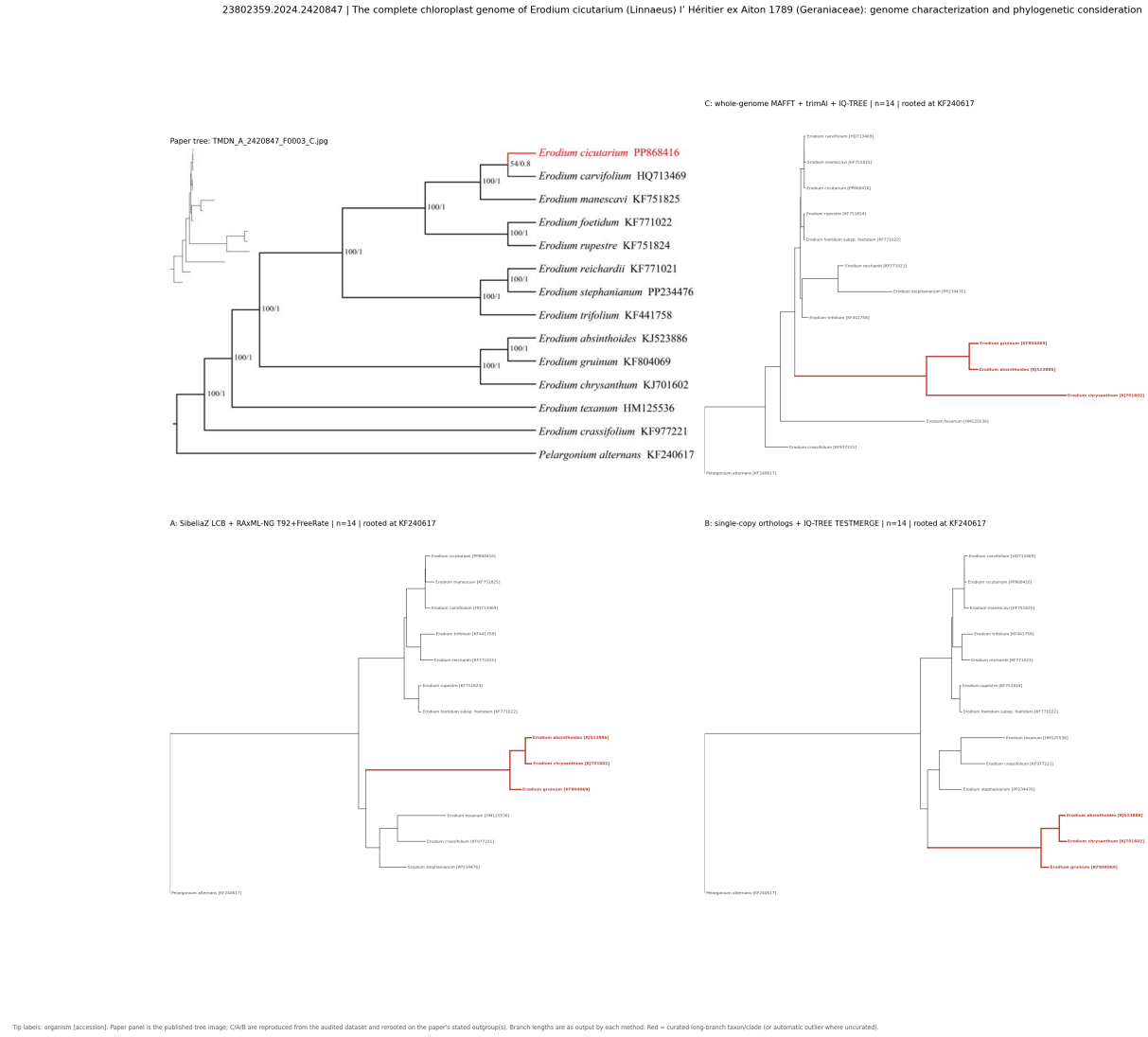
method	RTT outliers	terminal outliers	flagged clades
C naive	4	3	1
A FreeRate	4	2	1
B ortho	4	2	1

A terminal branches are estimated under RAxML-NG T92+F+FreeRate. RTT z-scores are sensitive to small MAD; ranks/clade flags should be read together.

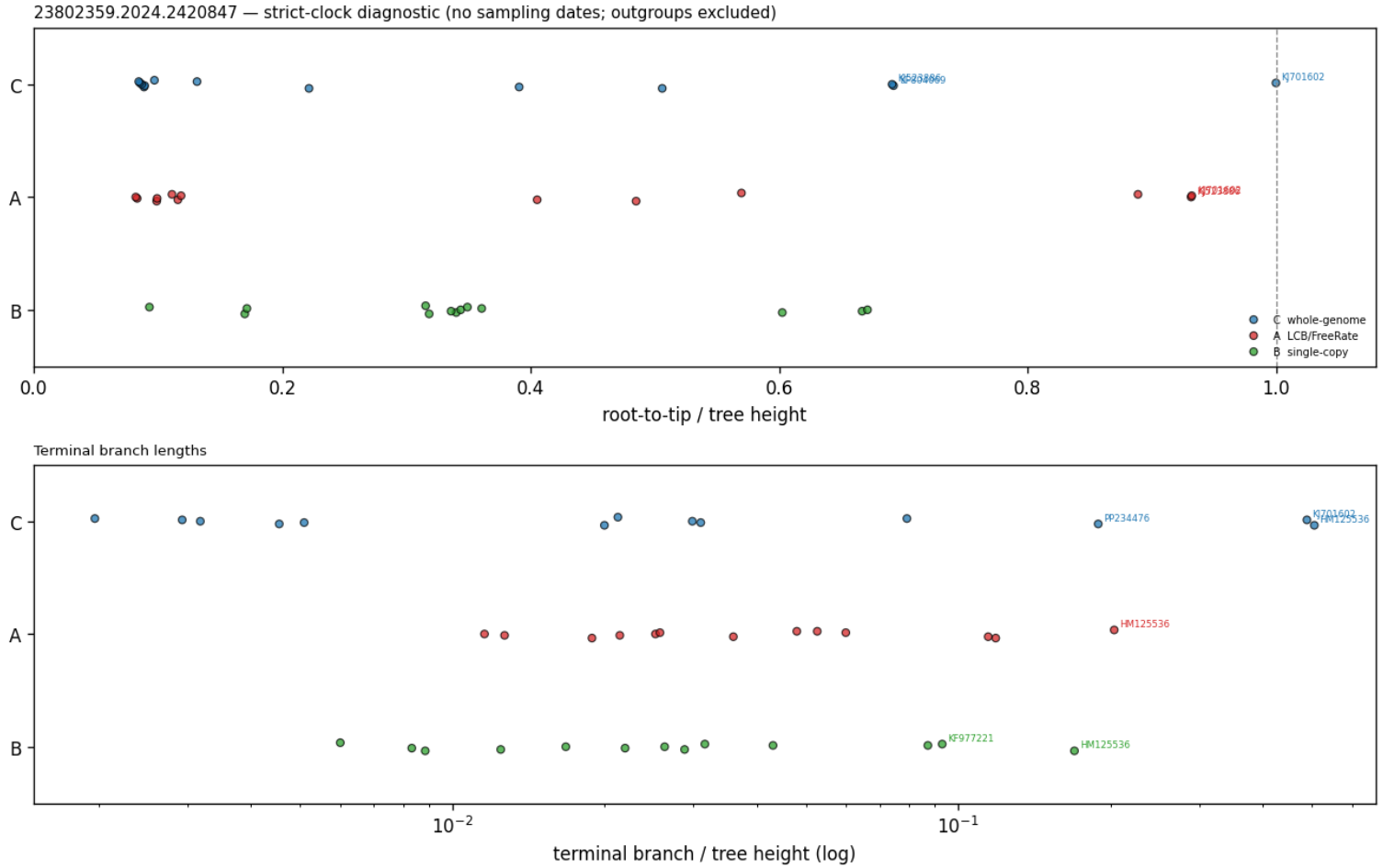
23802359.2024.2420847

The complete chloroplast genome of Erodium cicutarium (Linnaeus) l' Héritier ex Aiton 1789 (Geraniaceae): genome characterization and phylogenetic consideration

Status: Verified (root/highlight fixed). Rooted at KF240617; KF804069-KJ523886-KJ701602 clade highlighted; long branch reproduced and disappeared.



23802359.2024.2420847 - strict-clock branch-length diagnostic



method	RTT outliers	terminal outliers	flagged clades
C naive	3	4	2
A FreeRate	3	2	4
B ortho	1	3	0

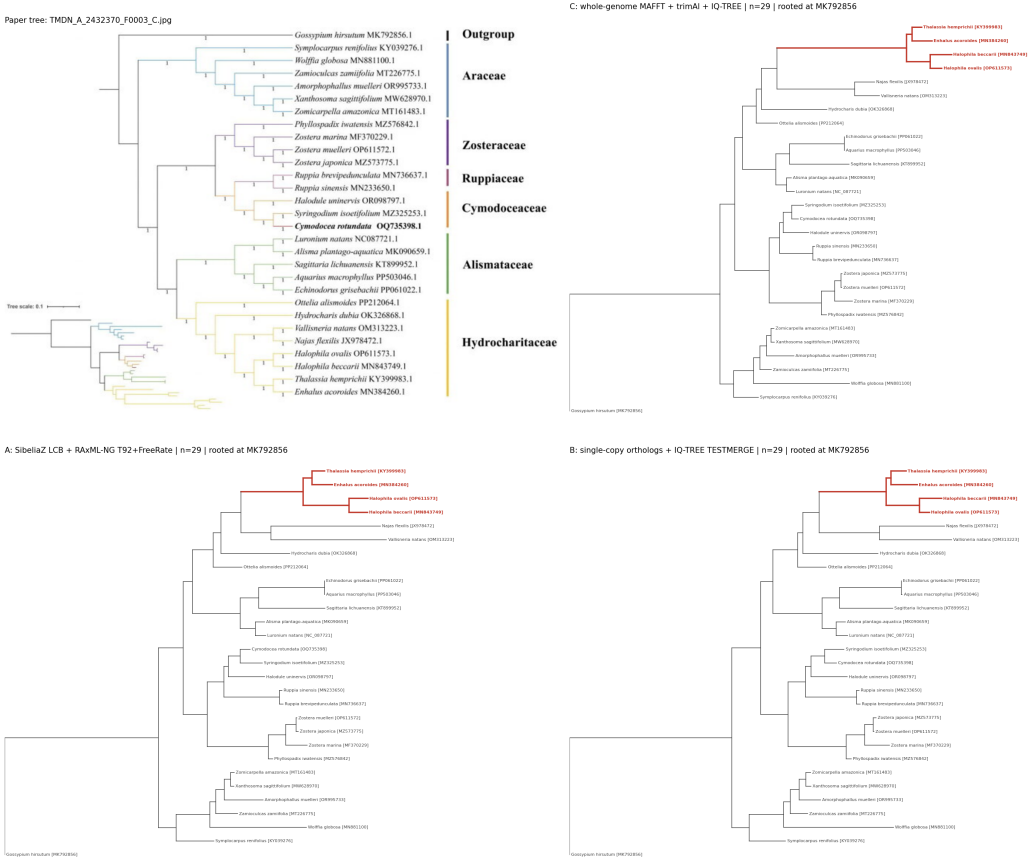
A terminal branches are estimated under RAxML-NG T92+F+FreeRate. RTT z-scores are sensitive to small MAD; ranks/clade flags should be read together.

23802359.2024.2432370

The first complete chloroplast genome of Cymodocea rotundata Asch. & Schweinf. 1870 (Cymodoceaceae), an Indo-Pacific seagrass

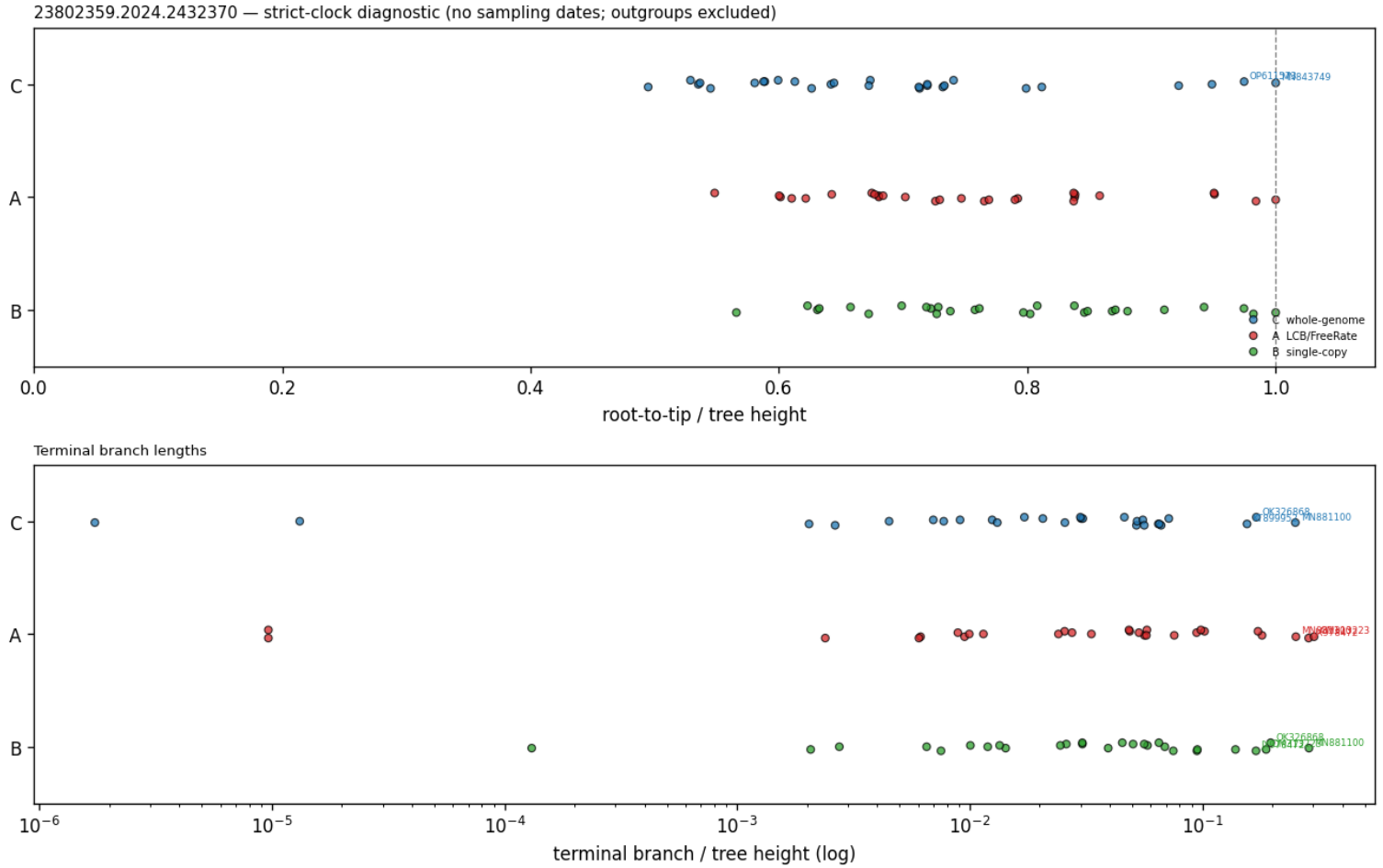
Status: Verified (shortened/highlight fixed). Rooted at MK792856; KY399983-MN384260-MN843749-OP611573 clade highlighted; long branch reproduced and shortened.

23802359.2024.2432370 | The first complete chloroplast genome of Cymodocea rotundata Asch. & Schweinf. 1870 (Cymodoceaceae), an Indo-Pacific seagrass



Tip labels: organism [accession]. Paper panel is the published tree image; C/A/B are reproduced from the audited dataset and rerooted on the paper's stated outgroup(s). Branch lengths are as output by each method. Red = curated long-branch taxon/clade (or automatic outlier where uncurated).

23802359.2024.2432370 - strict-clock branch-length diagnostic



method	RTT outliers	terminal outliers	flagged clades
C naive	2	3	2
A FreeRate	0	3	1
B ortho	0	4	1

A terminal branches are estimated under RAxML-NG T92+F+FreeRate. RTT z-scores are sensitive to small MAD; ranks/clade flags should be read together.

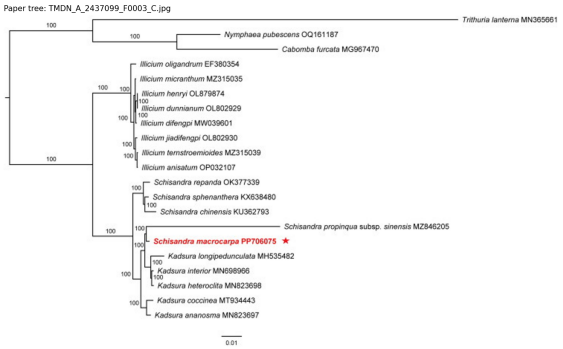
23802359.2024.2437099

The complete chloroplast genome and phylogenetic analysis of a rare species Schisandra macrocarpa (Schisandraceae)

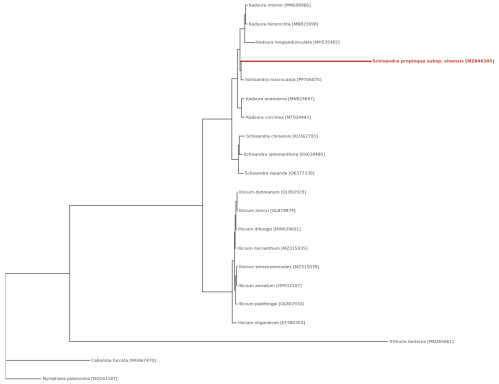
Status: Verified (highlight clarified). Rooted at MG967470 + OQ161187 + MN365661; MZ846205 long branch reproduced and eliminated, highlighted in C/A/B.

23802359.2024.2437099 | The complete chloroplast genome and phylogenetic analysis of a rare species Schisandra macrocarpa (Schisandraceae)

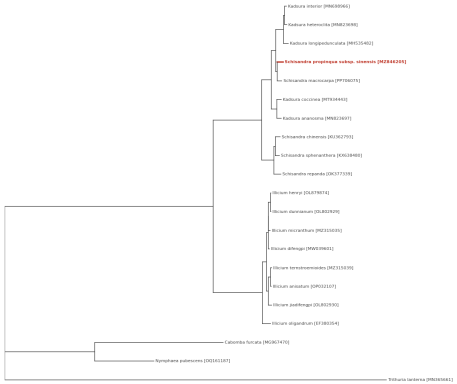
Paper tree: TMDN_A_2437099_F0003_C.jpg



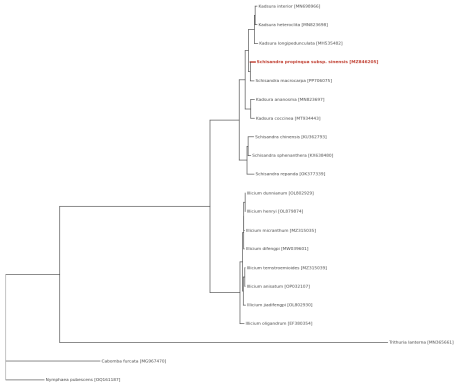
C: whole-genome MAFFT + trimAl + IQ-TREE | n=21 | rooted at MG967470, OQ161187, MN365661



A: SibeliaZ LCB + RAxML-NG T92+FreeRate | n=21 | rooted at MG967470, OQ161187, MN365661

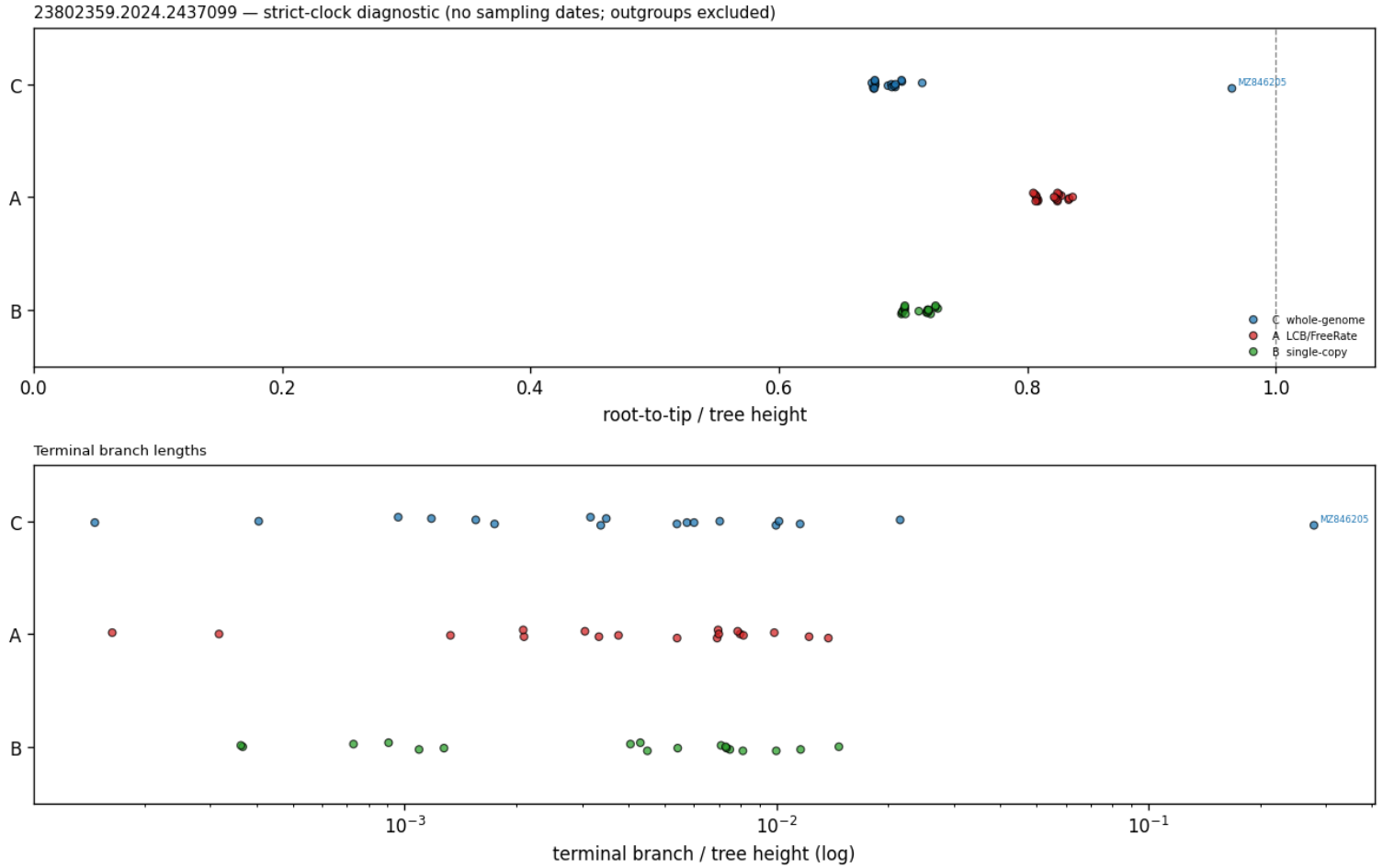


B: single-copy orthologs + IQ-TREE TESTMERGE | n=21 | rooted at MG967470, OQ161187, MN365661



Tip labels: organism [accession]. Paper panel is the published tree image; C/A/B are reproduced from the audited dataset and rerooted on the paper's stated outgroup(s). Branch lengths are as output by each method. Red = curated long-branch taxon/clade (or automatic outlier where uncurated).

23802359.2024.2437099 - strict-clock branch-length diagnostic



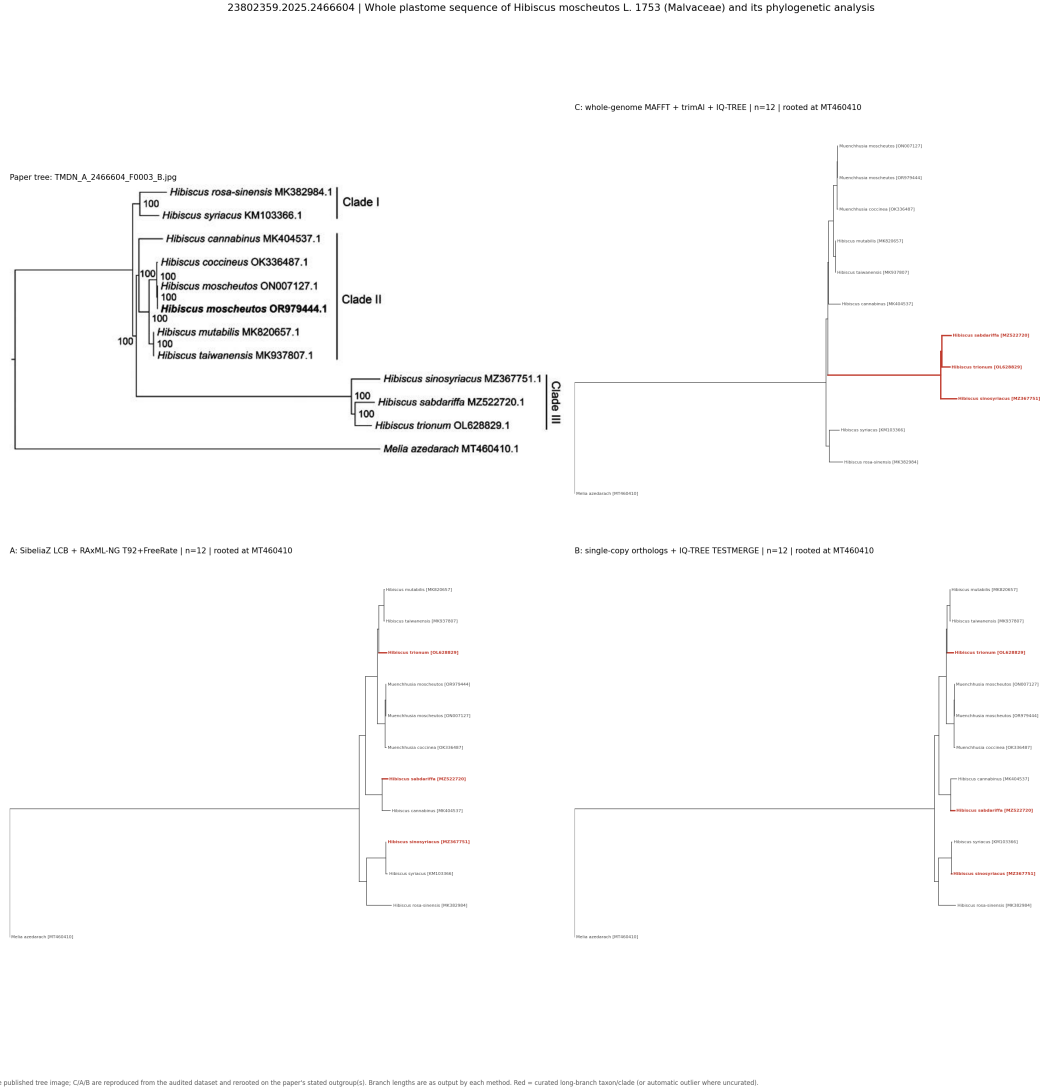
method	RTT outliers	terminal outliers	flagged clades
C naive	3	3	0
A FreeRate	2	2	0
B ortho	2	2	0

A terminal branches are estimated under RAxML-NG T92+F+FreeRate. RTT z-scores are sensitive to small MAD; ranks/clade flags should be read together.

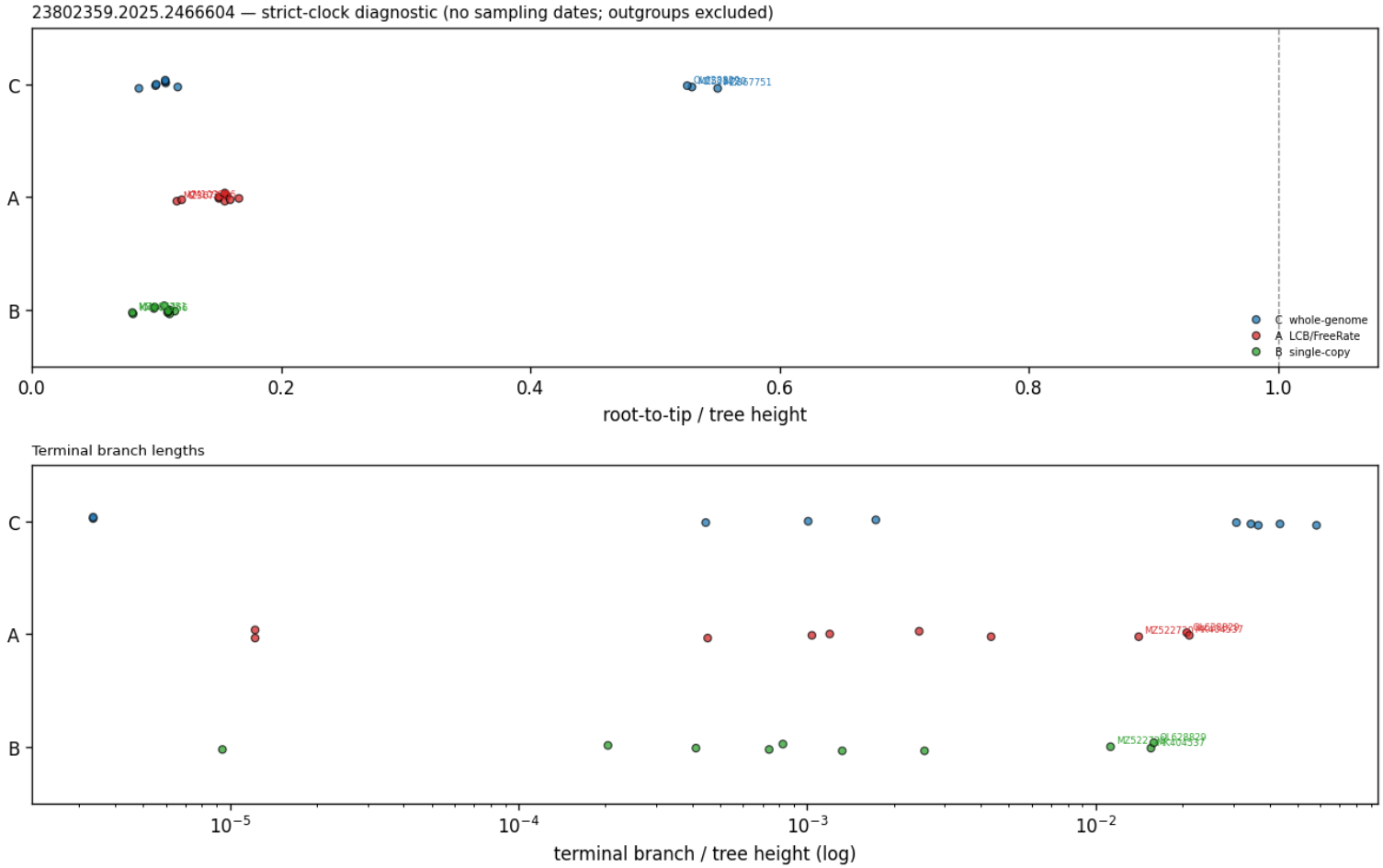
23802359.2025.2466604

Whole plastome sequence of Hibiscus moscheutos L. 1753 (Malvaceae) and its phylogenetic analysis

Status: Verified (highlight clarified; Clade III not discussed). Rooted at MT460410; MZ367751-MZ522720-OL628829 clade highlighted; long branch reproduced and disappeared. Results defines Clade III as these three taxa, but Discussion/Conclusions do not discuss Clade III or the effect on Clade I/II composition.



23802359.2025.2466604 - strict-clock branch-length diagnostic



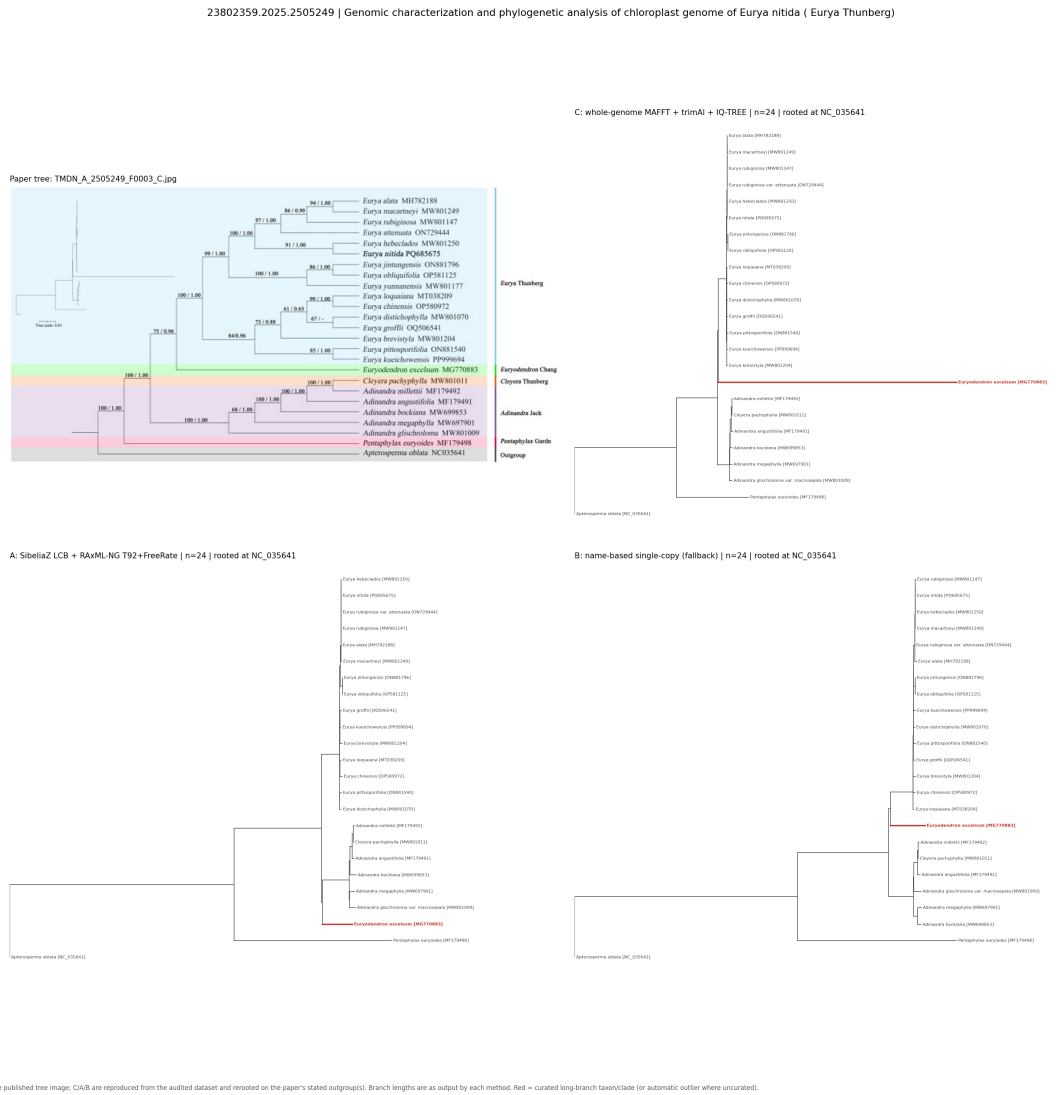
method	RTT outliers	terminal outliers	flagged clades
C naive	4	1	2
A FreeRate	3	4	3
B ortho	3	4	3

A terminal branches are estimated under RAxML-NG T92+F+FreeRate. RTT z-scores are sensitive to small MAD; ranks/clade flags should be read together.

23802359.2025.2505249

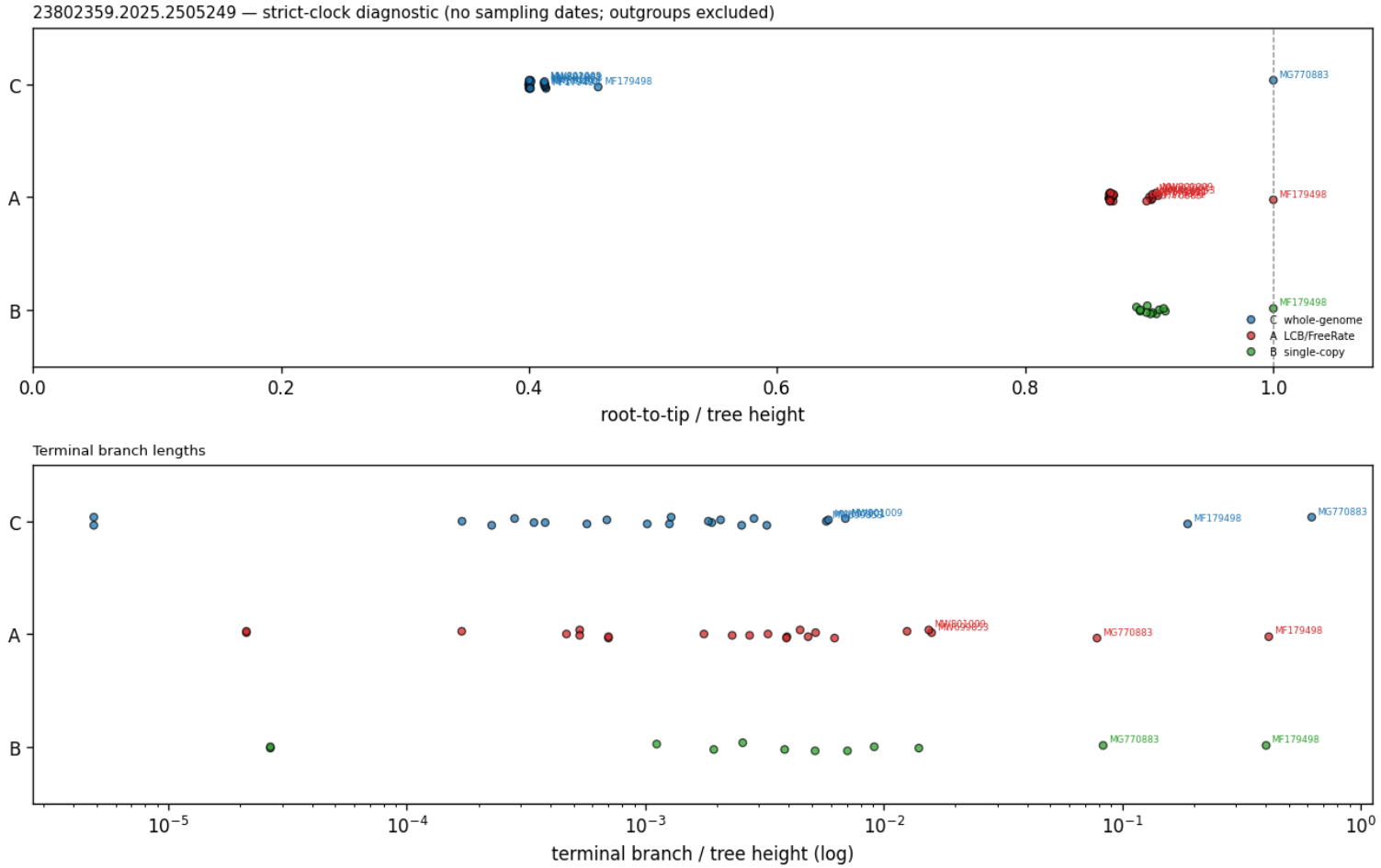
Genomic characterization and phylogenetic analysis of chloroplast genome of Eurya nitida (Eurya Thunberg)

Status: Verified (highlight narrowed). Rooted at NC_035641; only MG770883 highlighted; long branch reproduced and recovered. C/A/B all have 24 taxa; B is a name-based fallback (24 taxa, 81 genes).



Tip labels: organism [accession]. Paper panel is the published tree image; C/A/B are reproduced from the audited dataset and rerooted on the paper's stated outgroup(s). Branch lengths are as output by each method. Red = curated long-branch taxon/clade (or automatic outlier where uncurated).

23802359.2025.2505249 - strict-clock branch-length diagnostic



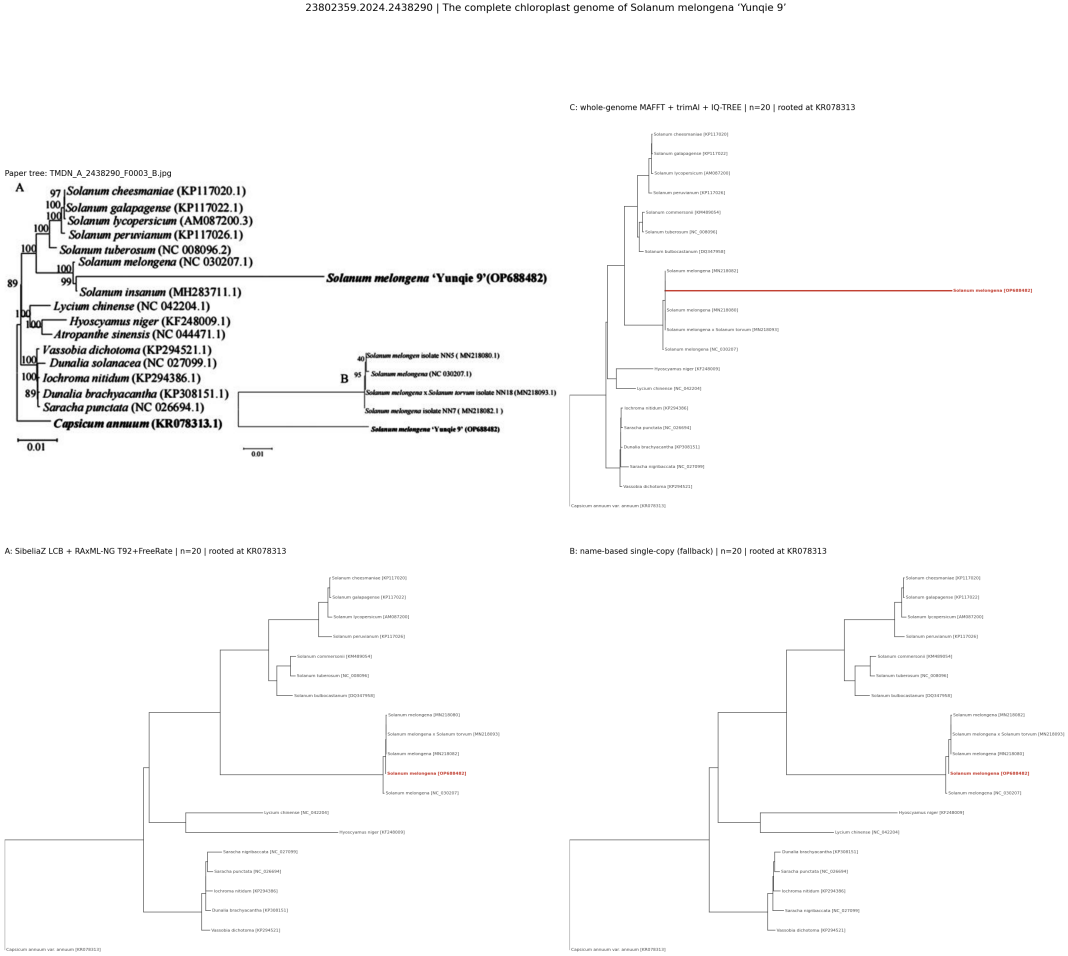
method	RTT outliers	terminal outliers	flagged clades
C naive	8	5	5
A FreeRate	8	4	6
B ortho	1	2	0

A terminal branches are estimated under RAxML-NG T92+F+FreeRate. RTT z-scores are sensitive to small MAD; ranks/clade flags should be read together.

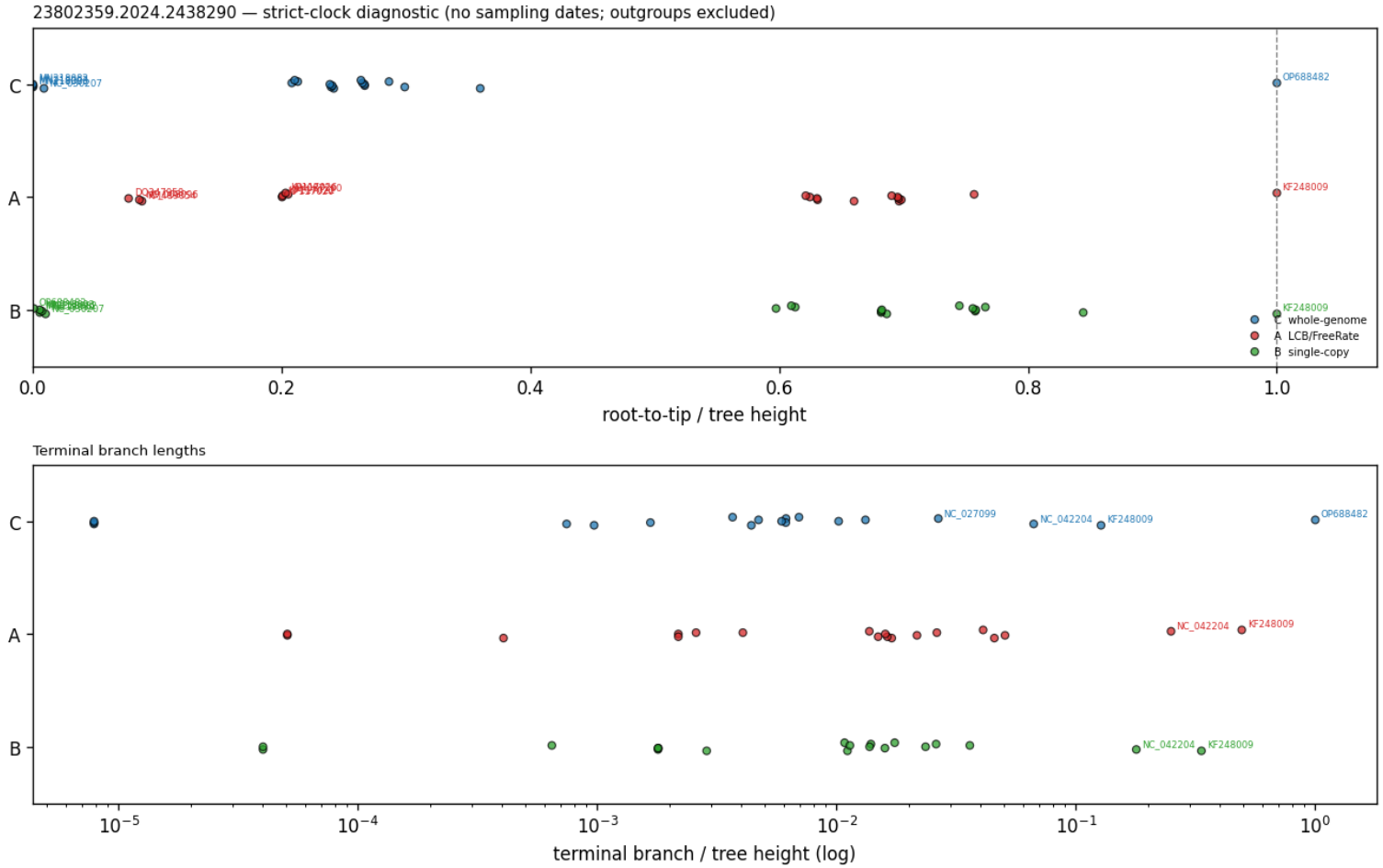
23802359.2024.2438290

The complete chloroplast genome of Solanum melongena ‘Yunqie 9’

Status: Verified (B name-based fallback; self-contradictory M&M;). Rooted at KR078313; OP688482 highlighted; long branch reproduced and disappeared. B is a name-based fallback (20 taxa); OrthoFinder unavailable. M&M; says CDS + MEGA K2P, Results says 21 whole plastomes aligned with MAFFT, and the caption says 21 complete plastomes; the exact Figure 3 matrix is not specified.



23802359.2024.2438290 - strict-clock branch-length diagnostic



method	RTT outliers	terminal outliers	flagged clades
C naive	5	5	3
A FreeRate	8	3	6
B ortho	6	3	3

A terminal branches are estimated under RAxML-NG T92+F+FreeRate. RTT z-scores are sensitive to small MAD; ranks/clade flags should be read together.

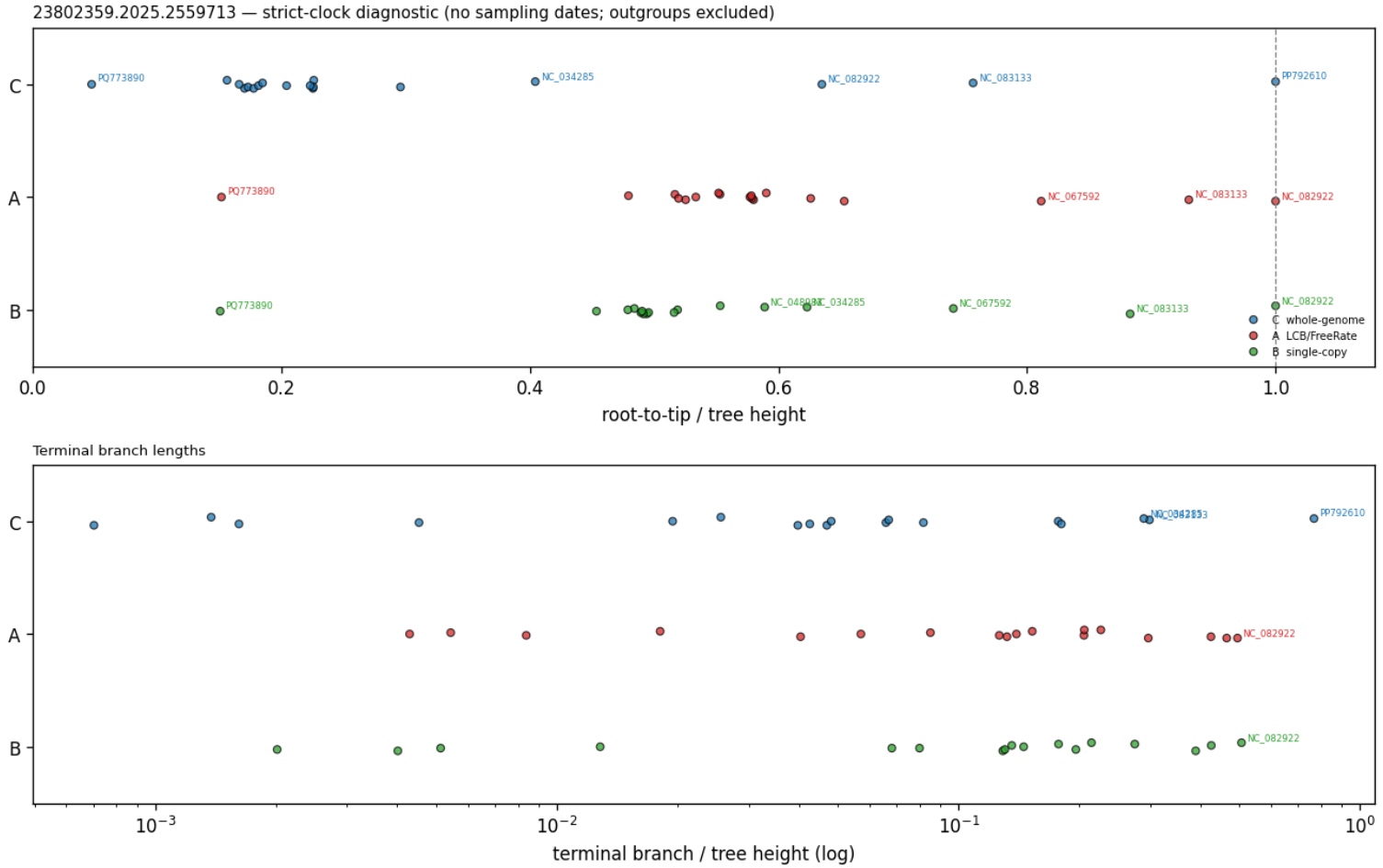
23802359.2025.2559713

The complete chloroplast genome of Hiptage benghalensis (L.) Kurz and its phylogenetic analysis in malpighiaceae

Status: Verified (B name-based fallback). PP792610 highlighted; long branch reproduced and disappeared. PP792610 had 0 CDS; tblastn recovered 47 CDS; Bname=19 taxa/79 genes.



23802359.2025.2559713 - strict-clock branch-length diagnostic



method	RTT outliers	terminal outliers	flagged clades
C naive	5	3	4
A FreeRate	4	1	2
B ortho	6	1	3

A terminal branches are estimated under RAxML-NG T92+F+FreeRate. RTT z-scores are sensitive to small MAD; ranks/clade flags should be read together.

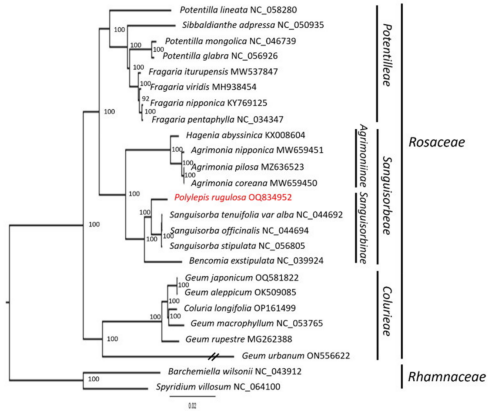
23802359.2025.2528566

The complete plastome sequence of Polylepis rugulosa Bitter 1911 (Rosaceae), an endangered tree species native of the Andean cordillera of South America

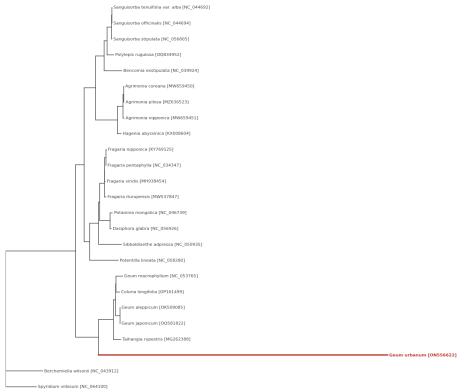
Status: Verified. ON556622 highlighted; long branch reproduced and disappeared.

23802359.2025.2528566 | The complete plastome sequence of Polylepis rugulosa Bitter 1911 (Rosaceae), an endangered tree species native of the Andean cordillera of South America

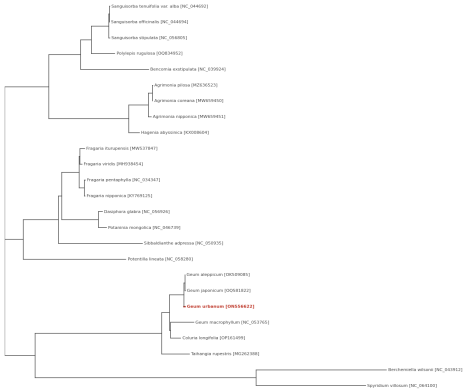
Paper tree: TMDN_A_2528566_F0003_C.jpg



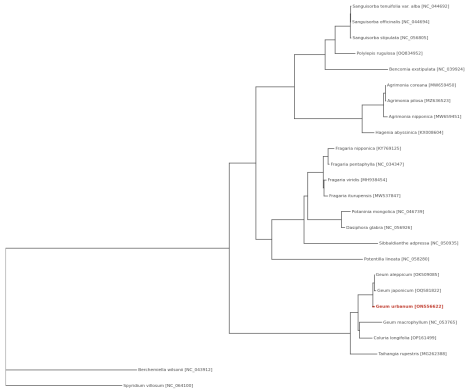
C: whole-genome MAFFT + trimAl + IQ-TREE | n=25



A: SibeliaZ LCB + RAxML-NG T92+FreeRate | n=25

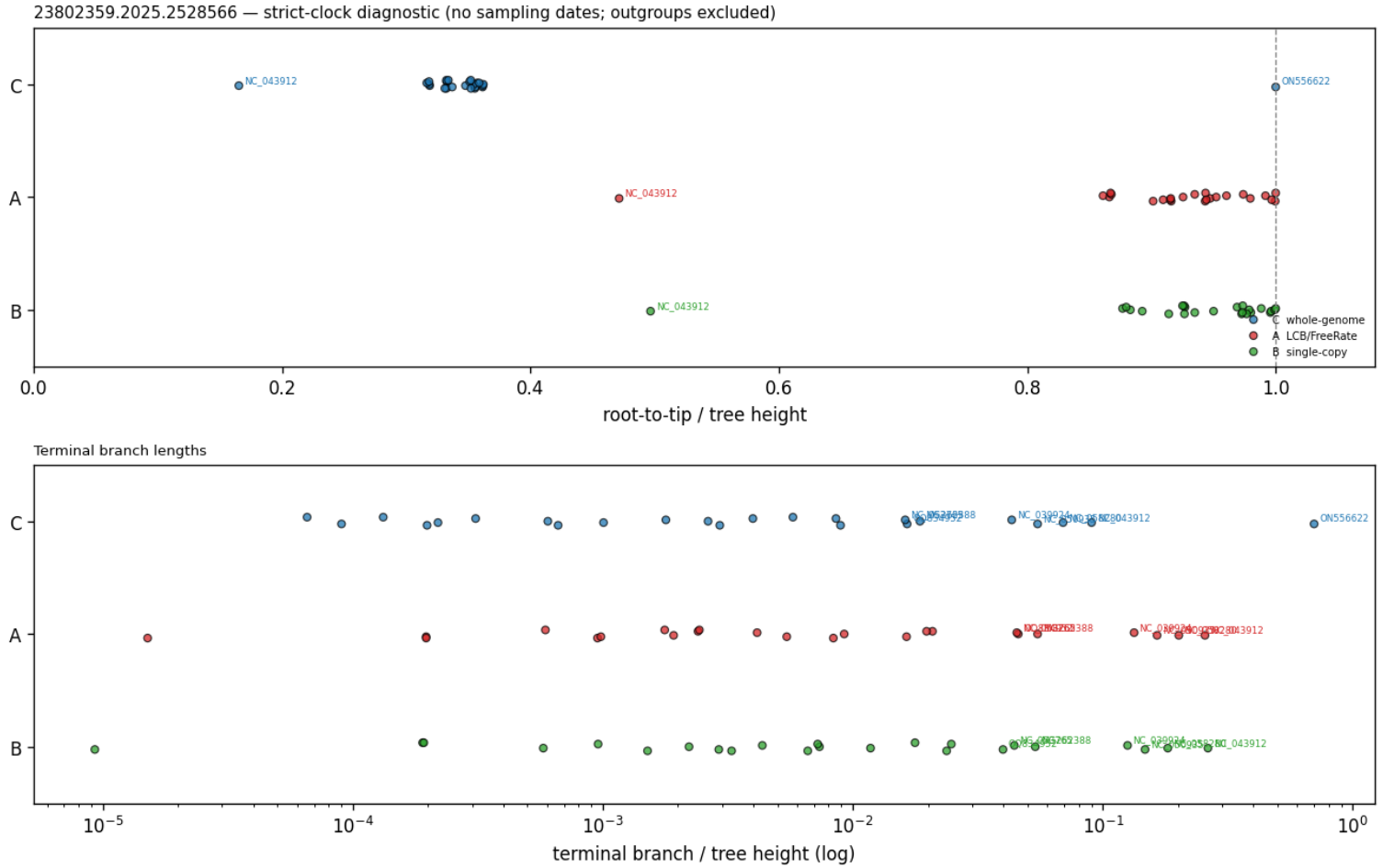


B: single-copy orthologs + IQ-TREE TESTMERGE | n=25



Tip labels: organism [accession]. Paper panel is the published tree image; C/A/B are reproduced from the audited dataset and rerooted on the paper's stated outgroup(s). Branch lengths are as output by each method. Red = curated long-branch taxon/clade (or automatic outlier where uncurated).

23802359.2025.2528566 - strict-clock branch-length diagnostic



method	RTT outliers	terminal outliers	flagged clades
C naive	2	8	1
A FreeRate	1	7	0
B ortho	1	7	0

A terminal branches are estimated under RAxML-NG T92+F+FreeRate. RTT z-scores are sensitive to small MAD; ranks/clade flags should be read together.

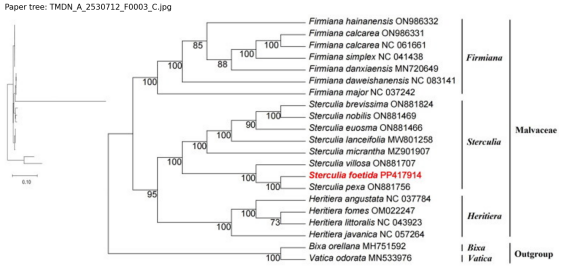
23802359.2025.2530712

The first complete chloroplast genome sequence of Sterculia foetida Linnaeus (Malvaceae) and a comparative phylogenetic analysis

Status: Verified (root fixed). Rooted at MH751592 + MN533976; MZ901907 highlighted; long branch reproduced and disappeared; B is a name-based fallback (21 taxa, 84 genes).

23802359.2025.2530712 | The first complete chloroplast genome sequence of Sterculia foetida Linnaeus (Malvaceae) and a comparative phylogenetic analysis

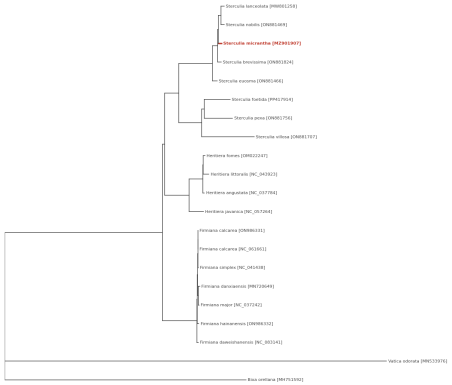
Paper tree: TMDN_A_2530712_F0003_C.jpg



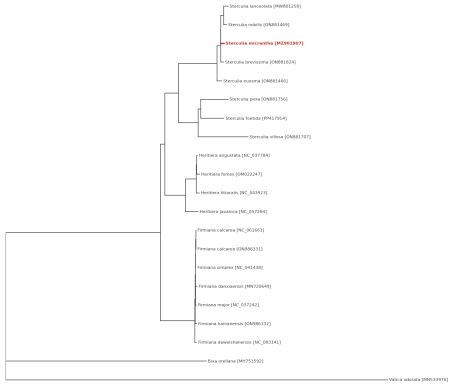
C: whole-genome MAFFT + trimAl + IQ-TREE | n=21 | rooted at MH751592, MN533976



A: SibeliaZ LCB + RAxML-NG T92+FreeRate | n=21 | rooted at MH751592, MN533976

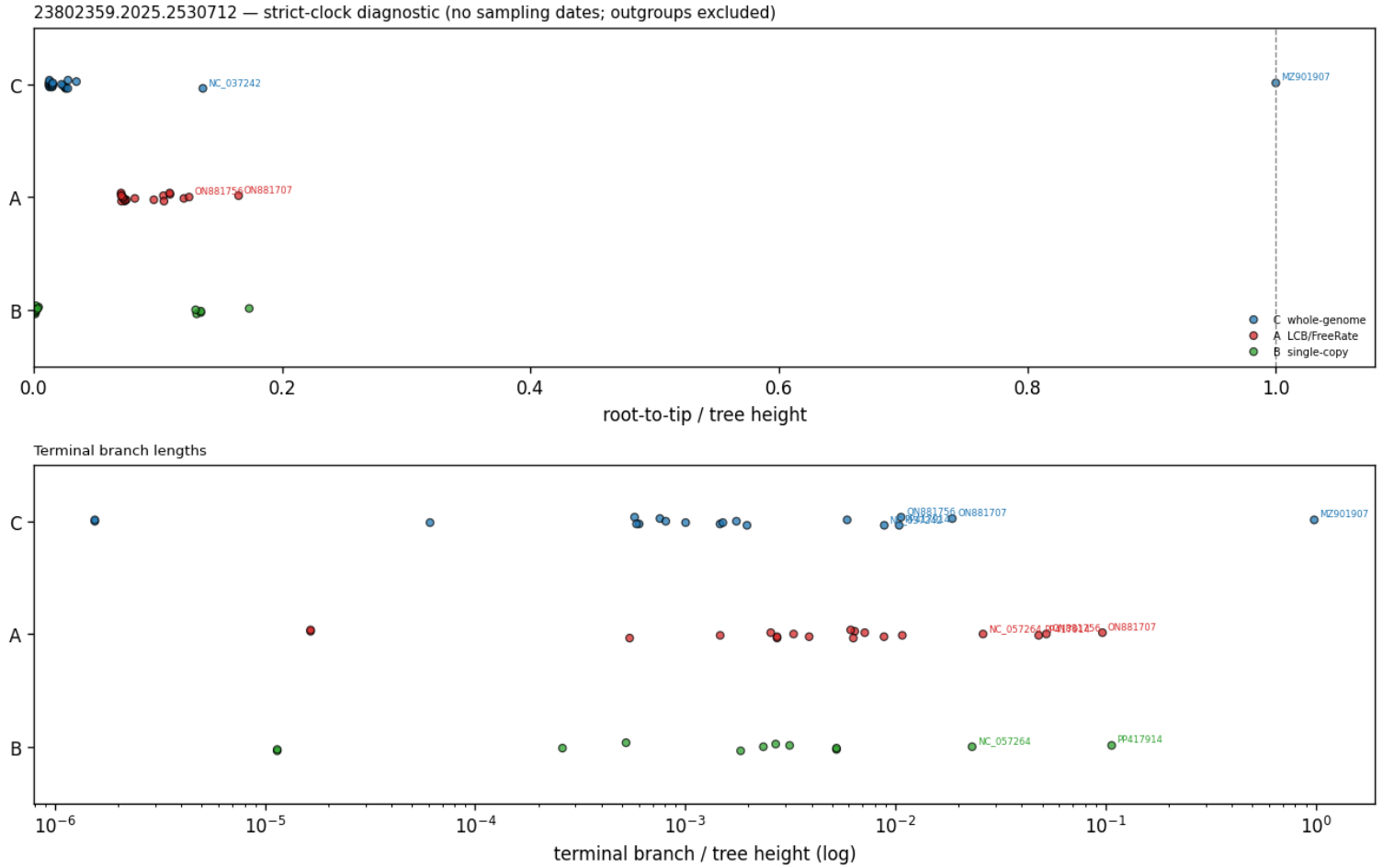


B: name-based single-copy (fallback) | n=21 | rooted at MH751592, MN533976



Tip labels: organism [accession]. Paper panel is the published tree image; C/A/B are reproduced from the audited dataset and rerooted on the paper's stated outgroup(s). Branch lengths are as output by each method. Red = curated long-branch taxon/clade (or automatic outlier where uncurated).

23802359.2025.2530712 - strict-clock branch-length diagnostic



method	RTT outliers	terminal outliers	flagged clades
C naive	4	7	4
A FreeRate	4	6	3
B ortho	2	4	2

A terminal branches are estimated under RAxML-NG T92+F+FreeRate. RTT z-scores are sensitive to small MAD; ranks/clade flags should be read together.

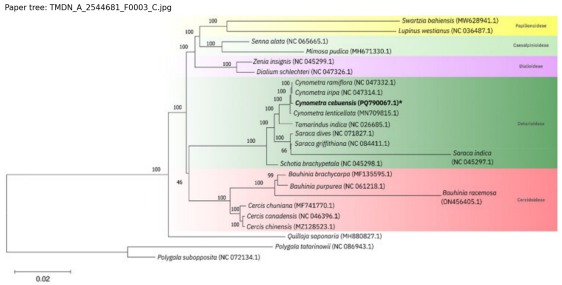
23802359.2025.2544681

The complete chloroplast genome of Cynometra cebuensis F. Seid. (Fabaceae), a critically endangered endemic plant from Cebu, Philippines

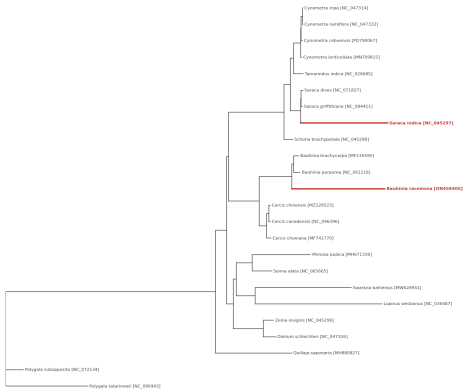
Status: Verified (root fixed). Rooted at NC_086943 + NC_072134; ON456405 + NC_045297 highlighted; long branch reproduced and disappeared; B is a name-based fallback (24 taxa, 78 genes).

23802359.2025.2544681 | The complete chloroplast genome of Cynometra cebuensis F. Seid. (Fabaceae), a critically endangered endemic plant from Cebu, Philippines

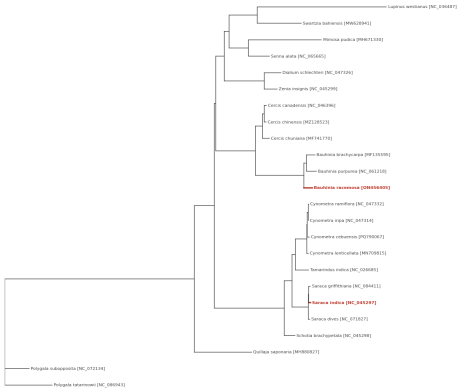
Paper tree: TMDN_A_2544681_F0003_C.jpg



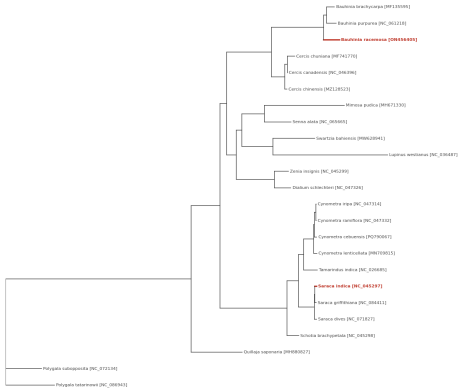
C: whole-genome MAFFT + trimAl + IQ-TREE | n=24 | rooted at NC_086943, NC_072134



A: SibeliaZ LCB + RAxML-NG T92+FreeRate | n=24 | rooted at NC_086943, NC_072134

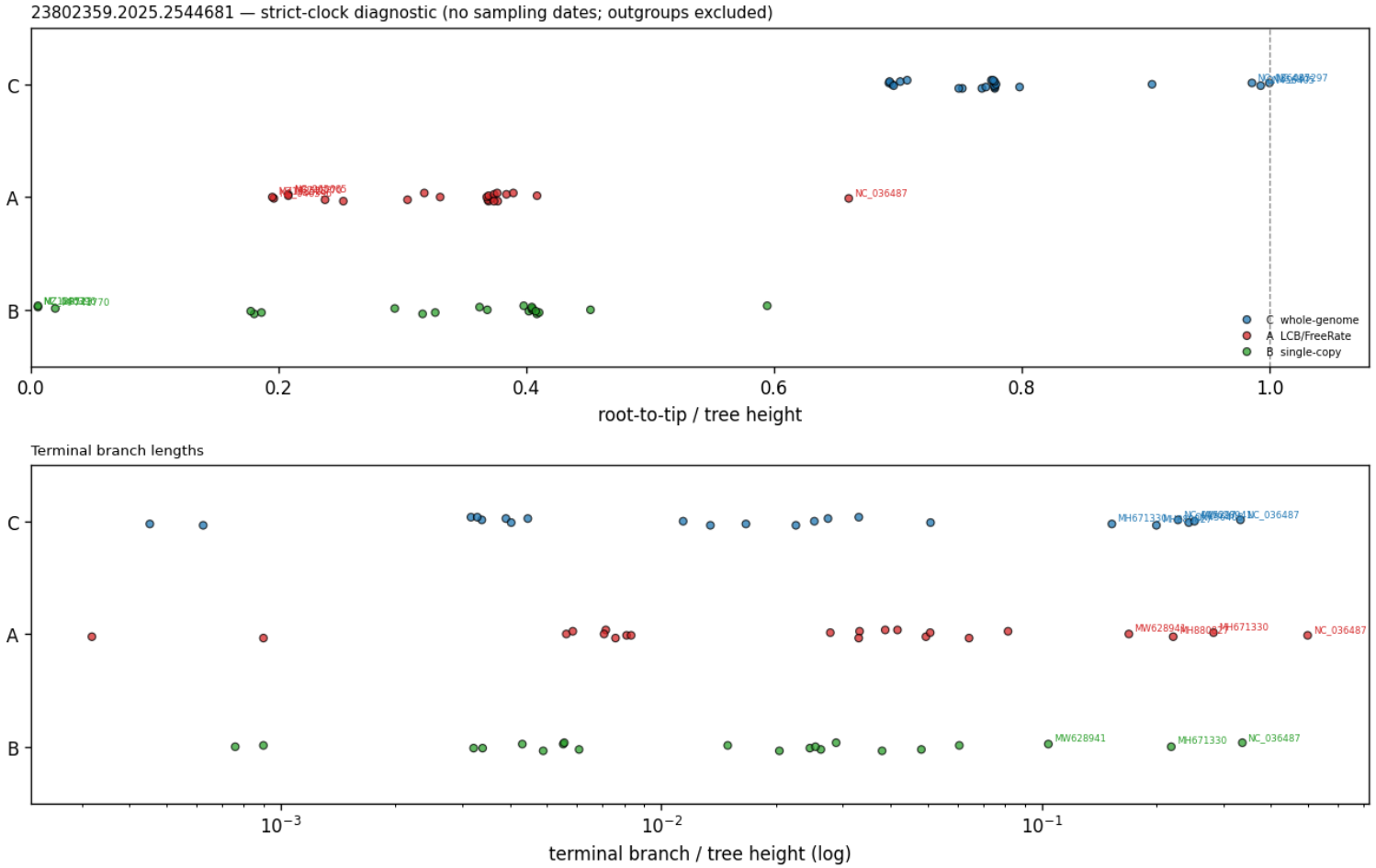


B: name-based single-copy (fallback) | n=24 | rooted at NC_086943, NC_072134



Tip labels: organism [accession]. Paper panel is the published tree image; C/A/B are reproduced from the audited dataset and rerooted on the paper's stated outgroup(s). Branch lengths are as output by each method. Red = curated long-branch taxon/clade (or automatic outlier where uncurated).

23802359.2025.2544681 - strict-clock branch-length diagnostic



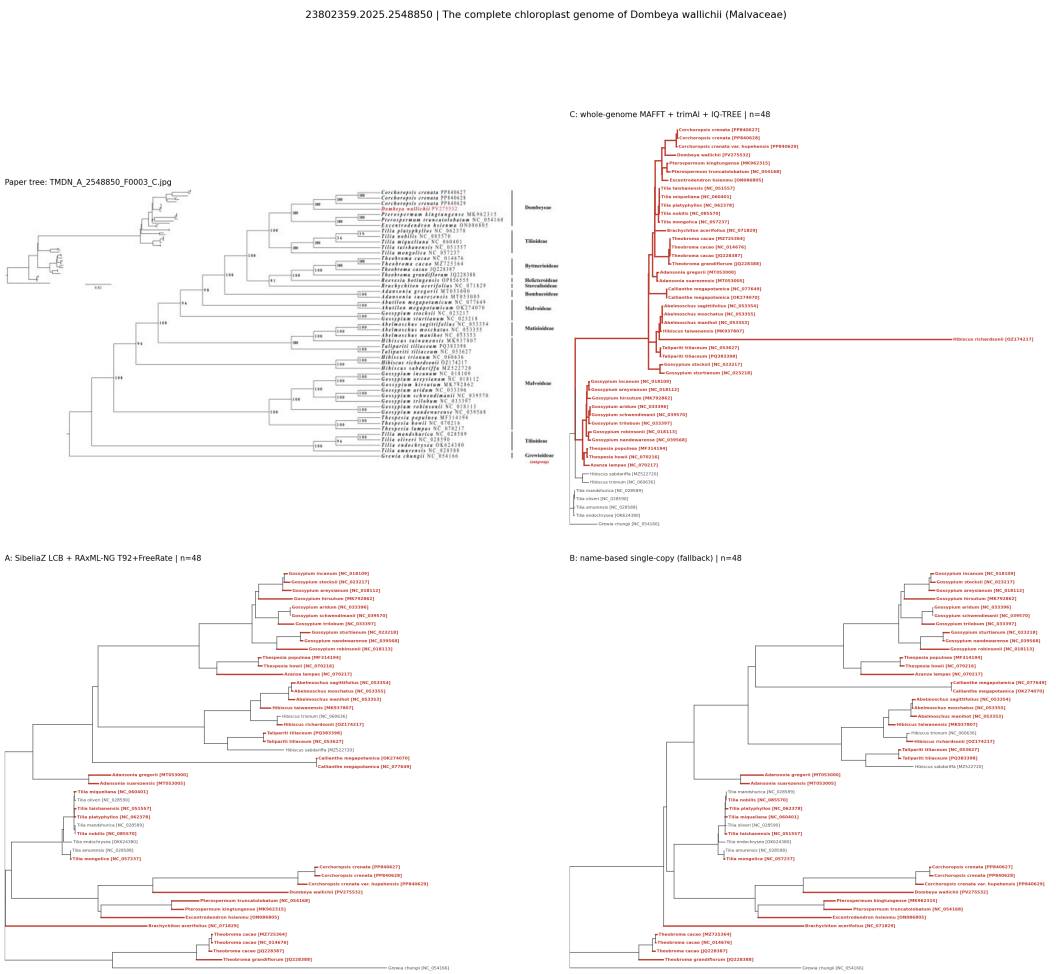
method	RTT outliers	terminal outliers	flagged clades
C naive	5	7	3
A FreeRate	7	5	9
B ortho	5	4	4

A terminal branches are estimated under RAxML-NG T92+F+FreeRate. RTT z-scores are sensitive to small MAD; ranks/clade flags should be read together.

23802359.2025.2548850

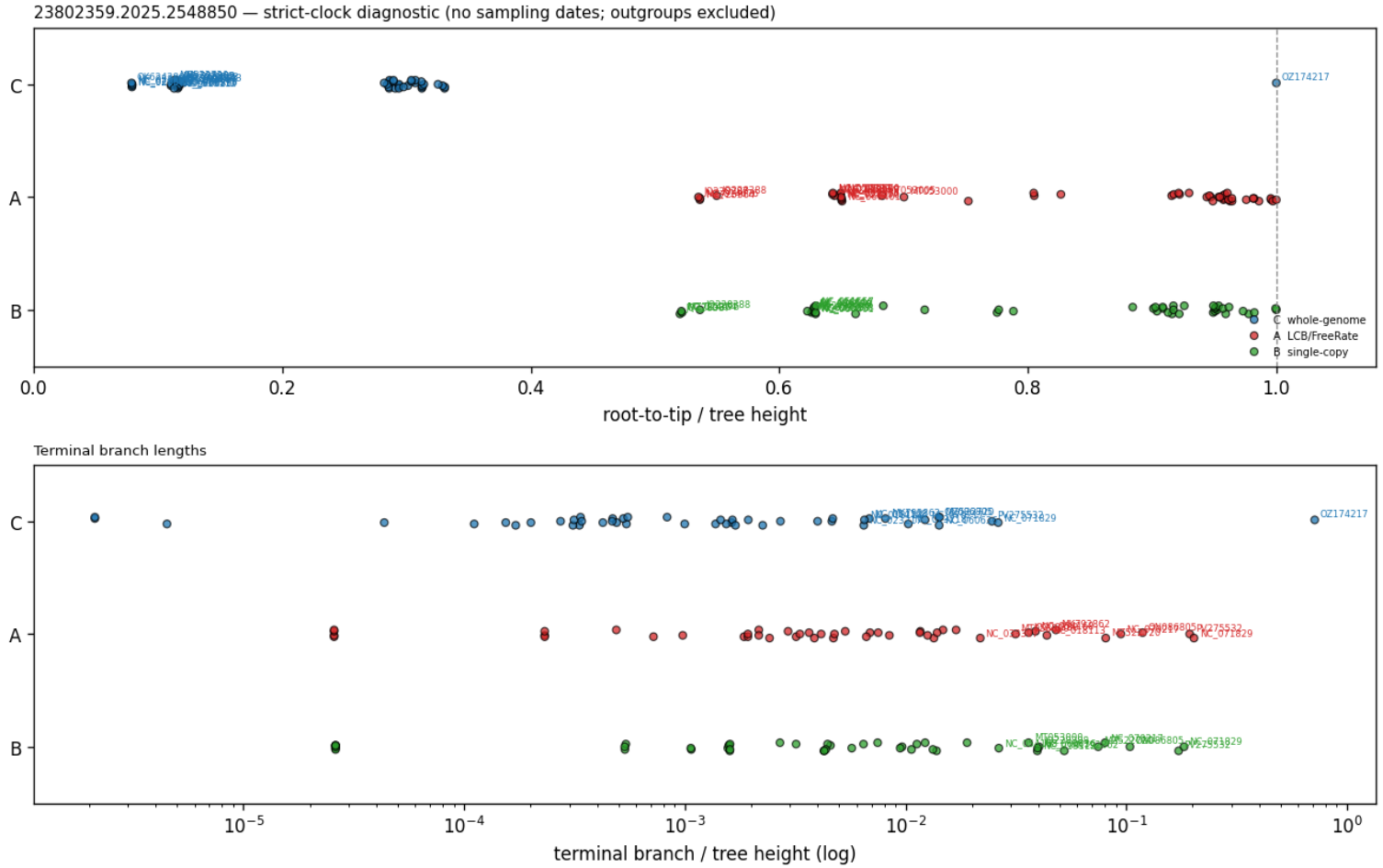
The complete chloroplast genome of Dombeya wallichii (Malvaceae)

Status: Verified. Gossypium-Corchoropsis clade highlighted; long branch reproduced and disappeared; B is a name-based fallback (48 taxa, 84 genes).



Tip labels: organism [accession]. Paper panel is the published tree image; C/A/B are reproduced from the audited dataset and rerooted on the paper's stated outgroup(s). Branch lengths are as output by each method. Red = curated long-branch taxon/clade (or automatic outlier where uncurated).

23802359.2025.2548850 - strict-clock branch-length diagnostic



method	RTT outliers	terminal outliers	flagged clades
C naive	18	12	17
A FreeRate	15	11	16
B ortho	13	11	14

A terminal branches are estimated under RAxML-NG T92+F+FreeRate. RTT z-scores are sensitive to small MAD; ranks/clade flags should be read together.

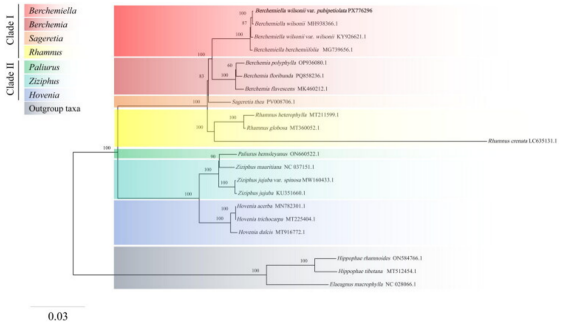
23802359.2026.2635835

Phylogenomic insights from the complete chloroplast genome of Berchemiella wilsonii var. pubipetiolata H. Qian (Rhamnaceae) from Zhejiang

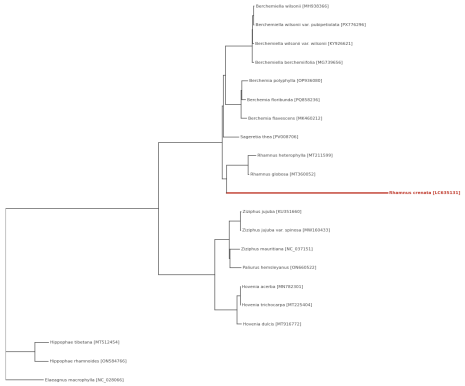
Status: Verified (root fixed). Rooted at NC_028066 + ON584766 + MT512454; LC635131 highlighted; long branch reproduced and disappeared.

23802359.2026.2635835 | Phylogenomic insights from the complete chloroplast genome of Berchemiella wilsonii var. pubipetiolata H. Qian (Rhamnaceae) from Zhejiang

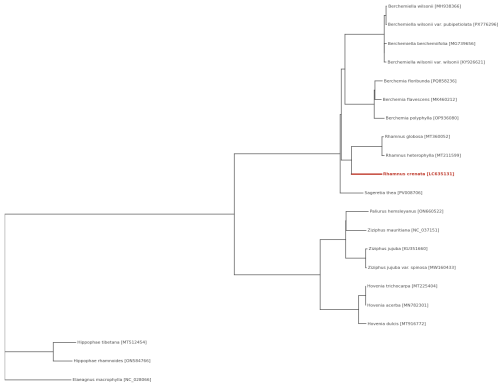
Paper tree: TMDN_A_2635835_F0003_C.jpg



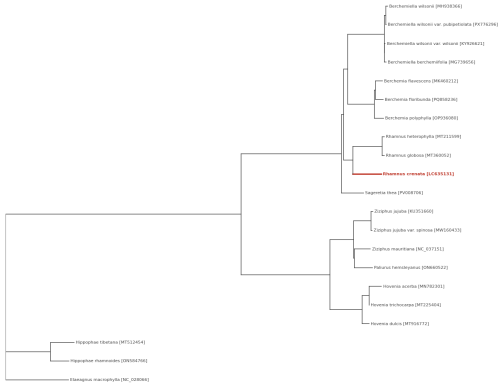
C: whole-genome MAFFT + trimAl + IQ-TREE | n=21 | rooted at NC_028066, ON584766, MT512454



A: SibeliaZ LCB + RAxML-NG T92+FreeRate | n=21 | rooted at NC_028066, ON584766, MT512454

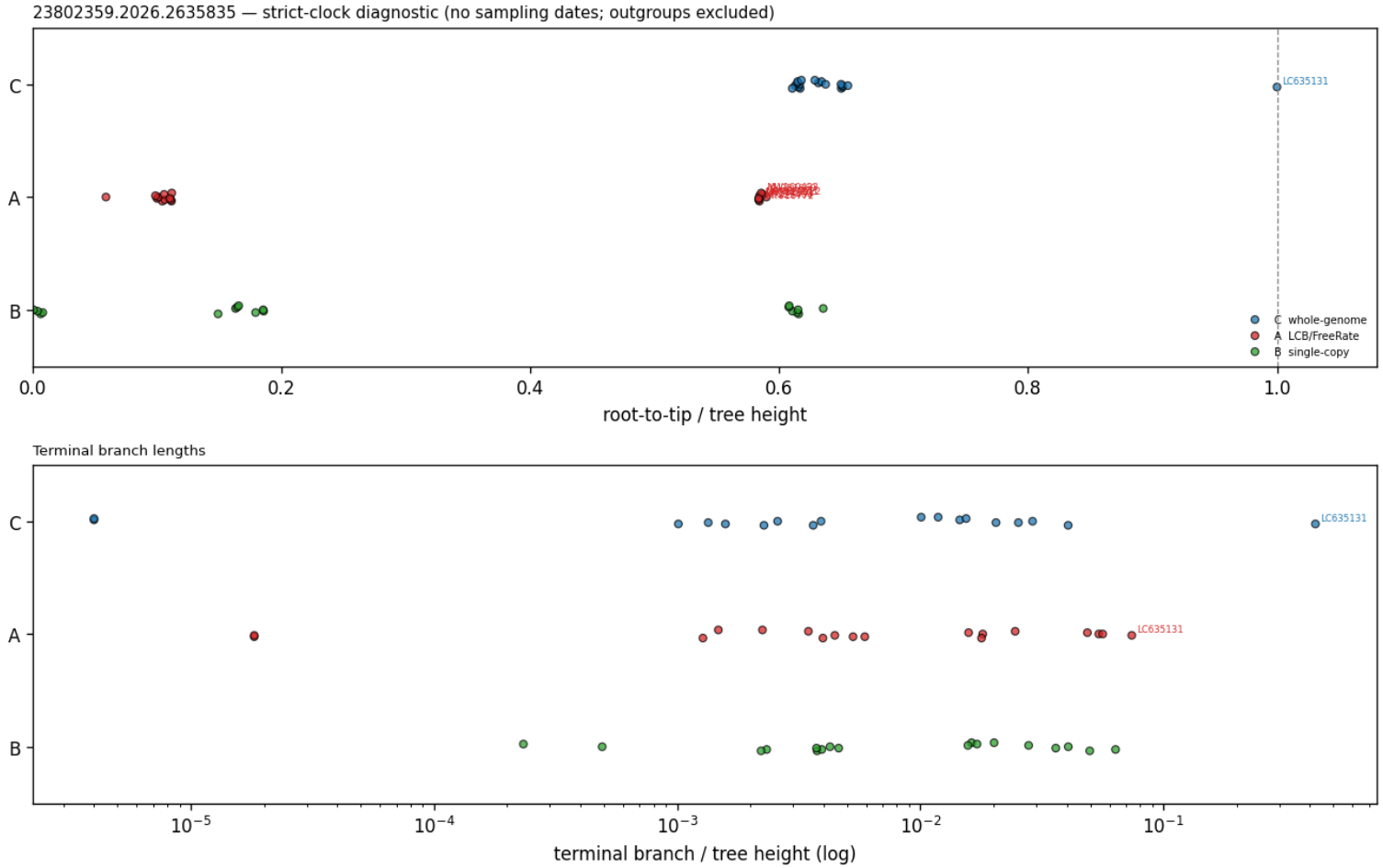


B: single-copy orthologs + IQ-TREE TESTMERGE | n=21 | rooted at NC_028066, ON584766, MT512454



Tip labels: organism [accession]. Paper panel is the published tree image; C/A/B are reproduced from the audited dataset and rerooted on the paper's stated outgroup(s). Branch lengths are as output by each method. Red = curated long-branch taxon/clade (or automatic outlier where uncurated).

23802359.2026.2635835 - strict-clock branch-length diagnostic



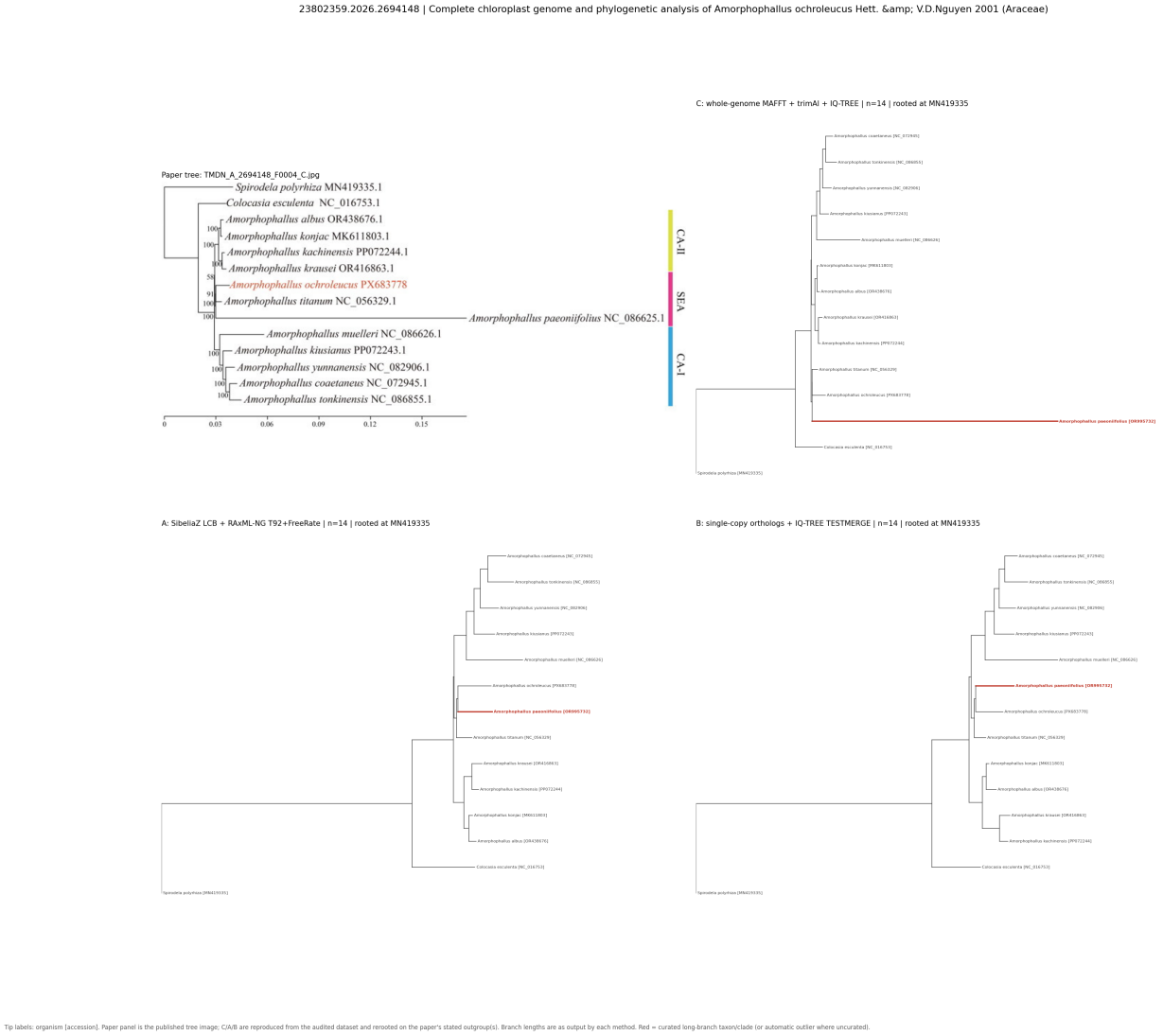
method	RTT outliers	terminal outliers	flagged clades
C naive	4	2	1
A FreeRate	10	2	10
B ortho	3	1	2

A terminal branches are estimated under RAxML-NG T92+F+FreeRate. RTT z-scores are sensitive to small MAD; ranks/clade flags should be read together.

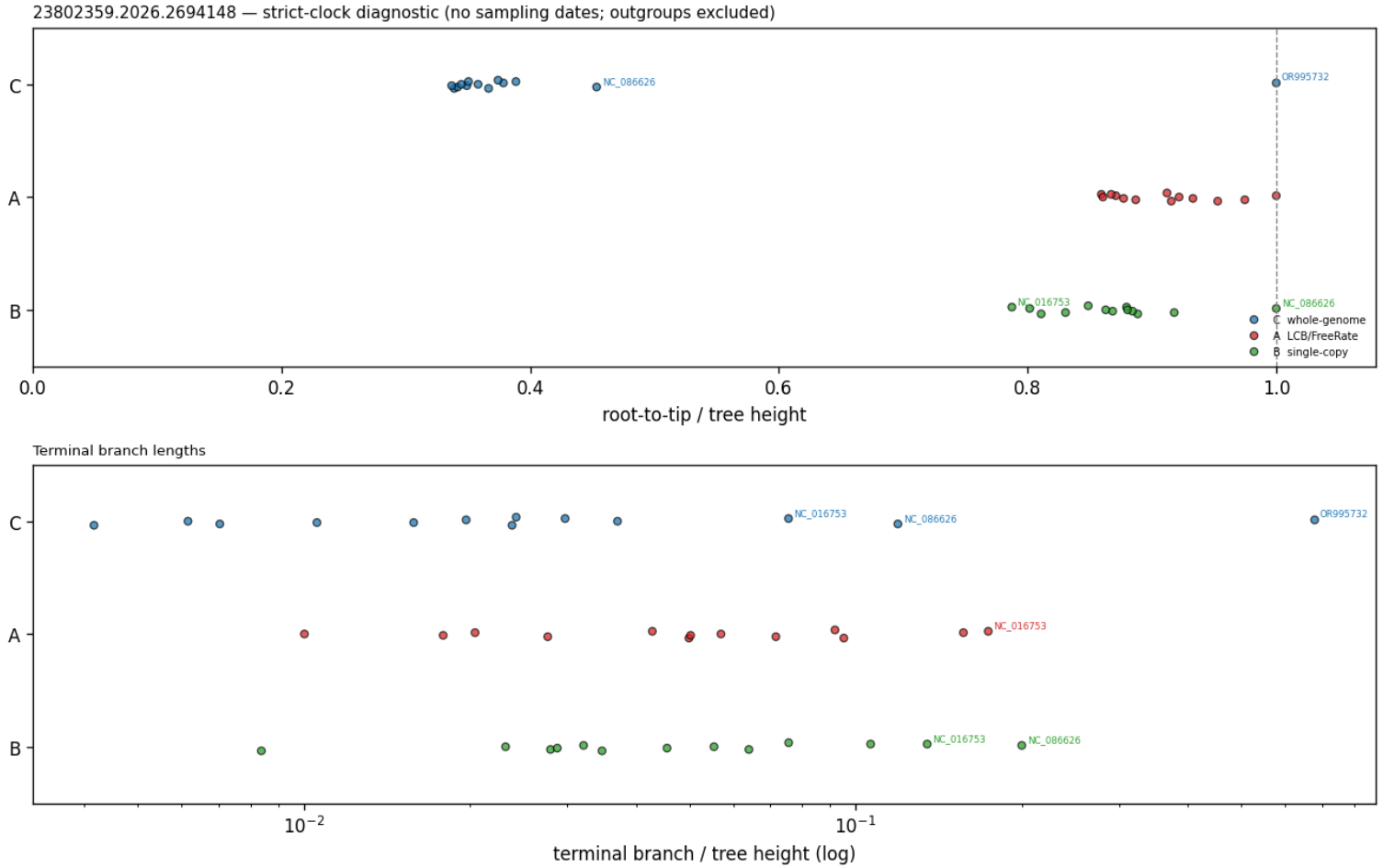
23802359.2026.2694148

Complete chloroplast genome and phylogenetic analysis of Amorphophallus ochroleucus Hett. & V.D.Nguyen 2001 (Araceae)

Status: Verified (root/accession note). Rooted at MN419335; OR995732 highlighted; NC_086625 is the RefSeq version of OR995732 (identical, 176,258 bp).



23802359.2026.2694148 - strict-clock branch-length diagnostic



method	RTT outliers	terminal outliers	flagged clades
C naive	2	3	0
A FreeRate	0	1	0
B ortho	2	2	0

A terminal branches are estimated under RAxML-NG T92+F+FreeRate. RTT z-scores are sensitive to small MAD; ranks/clade flags should be read together.

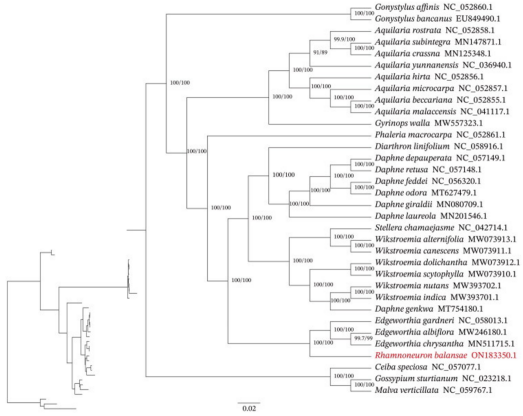
23802359.2026.2694188

The complete chloroplast genome of Rhamnoneuron balansae, the only species of Rhamnoneuron (Thymelaeaceae)

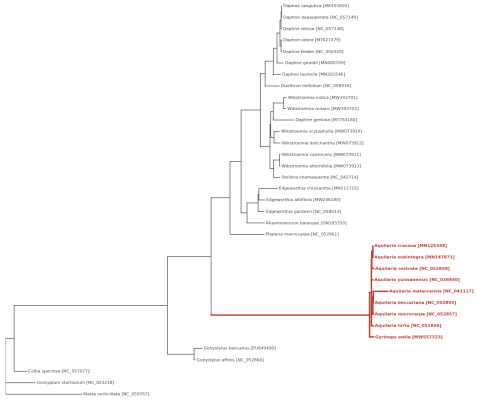
Status: Verified. Rooted at NC_059767 + NC_023218 + NC_057077; 9-taxon Aquilaria/Gyrinops clade highlighted; overall clade shortened and internal NC_041117 branch disappeared.

23802359.2026.2694188 | The complete chloroplast genome of Rhamnoneuron balansae, the only species of Rhamnoneuron (Thymelaeaceae)

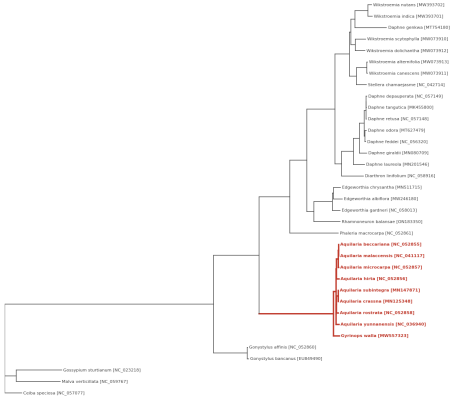
Paper tree: TMDN_A_2694188_F0003_C.jpg



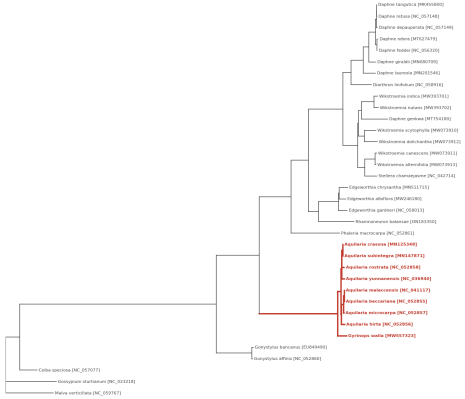
C: whole-genome MAFFT + trimAl + IQ-TREE | n=35 | rooted at NC_059767, NC_023218, NC_057077



A: SibeliaZ LCB + RAxML-NG T92+FreeRate | n=35 | rooted at NC_059767, NC_023218, NC_057077

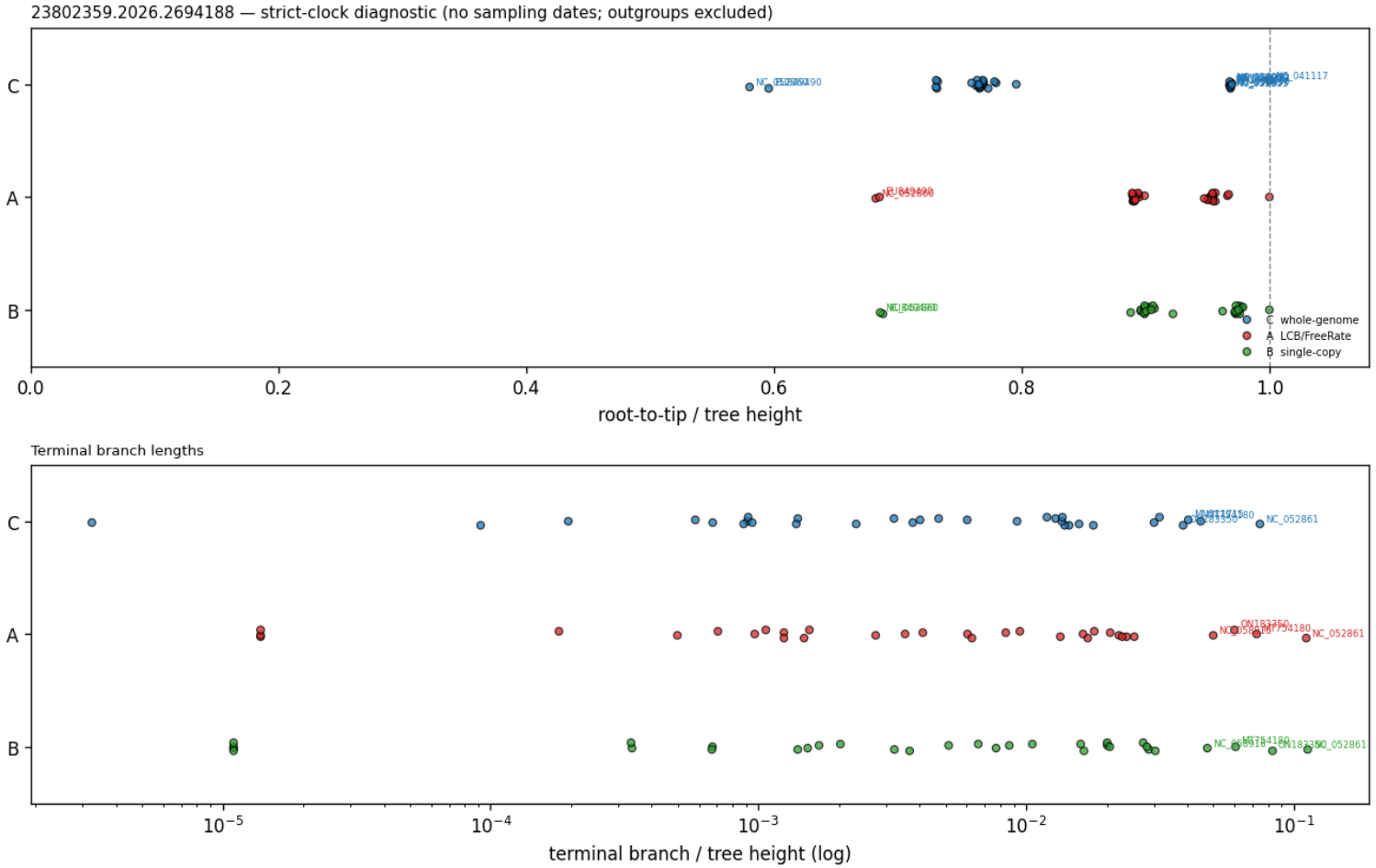


B: single-copy orthologs + IQ-TREE TESTMERGE | n=35 | rooted at NC_059767, NC_023218, NC_057077



Tip labels: organism [accession]. Paper panel is the published tree image; C/A/B are reproduced from the audited dataset and rerooted on the paper's stated outgroup(s). Branch lengths are as output by each method. Red = curated long-branch taxon/clade (or automatic outlier where uncurated).

23802359.2026.2694188 - strict-clock branch-length diagnostic



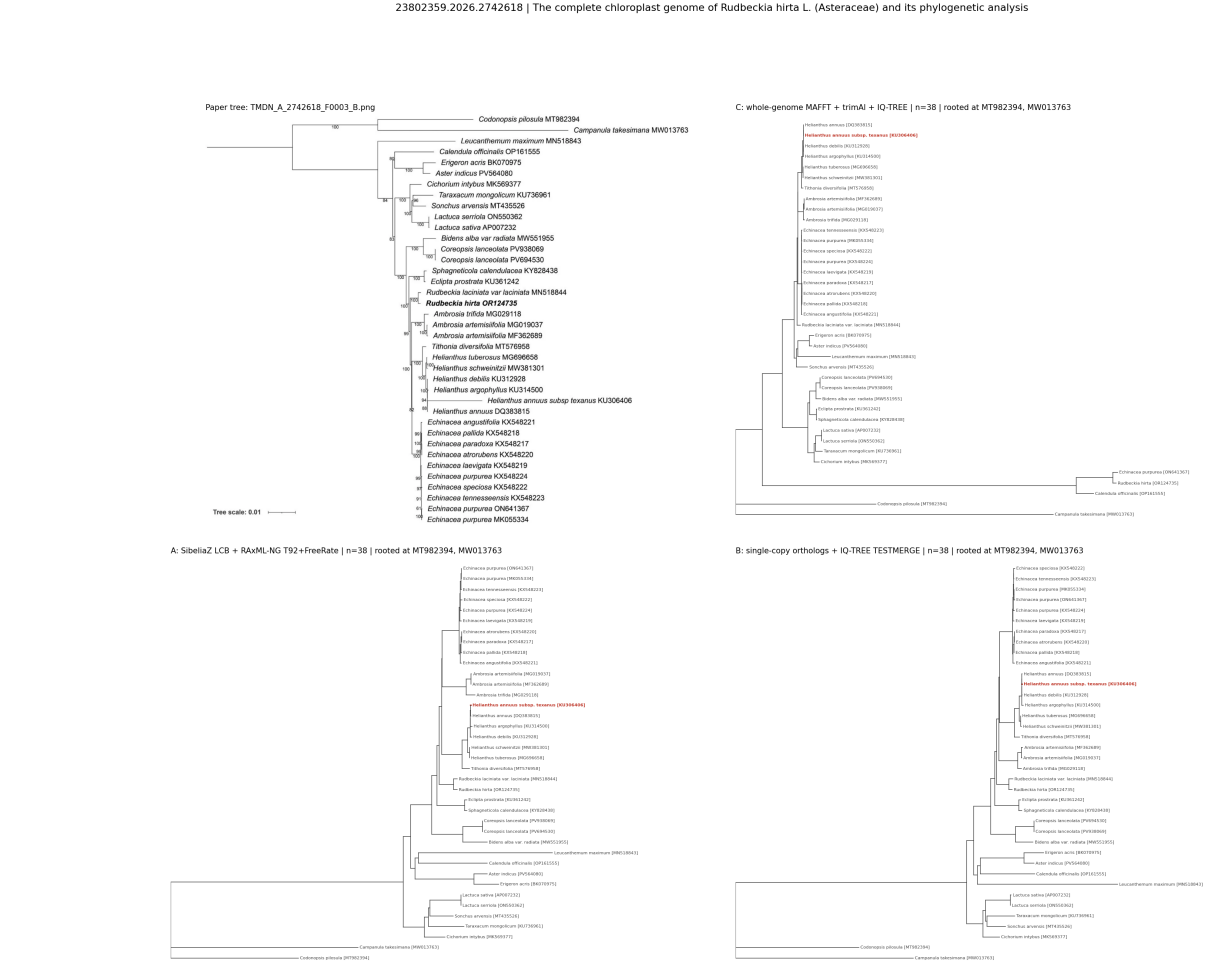
method	RTT outliers	terminal outliers	flagged clades
C naive	13	5	11
A FreeRate	4	6	1
B ortho	4	6	1

A terminal branches are estimated under RAxML-NG T92+F+FreeRate. RTT z-scores are sensitive to small MAD; ranks/clade flags should be read together.

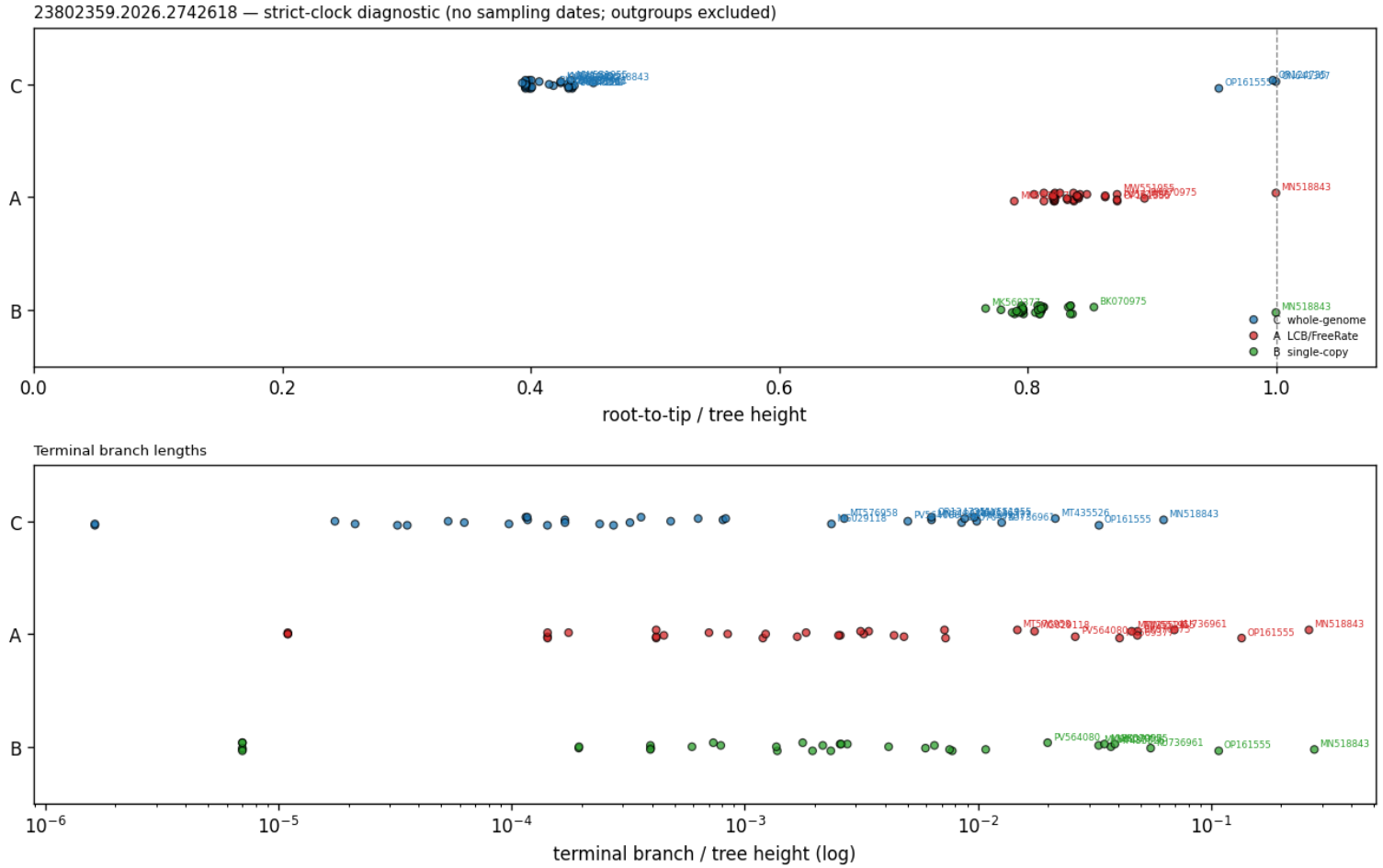
23802359.2026.2742618

The complete chloroplast genome of Rudbeckia hirta L. (Asteraceae) and its phylogenetic analysis

Status: Verified (paper figure restored). Rooted at MT982394 + MW013763; KU306406 highlighted; paper long branch is not reproduced by C/A/B. Paper M&M; is whole-plastome MAFFT + TVM+F+G4, not CDS.



23802359.2026.2742618 - strict-clock branch-length diagnostic



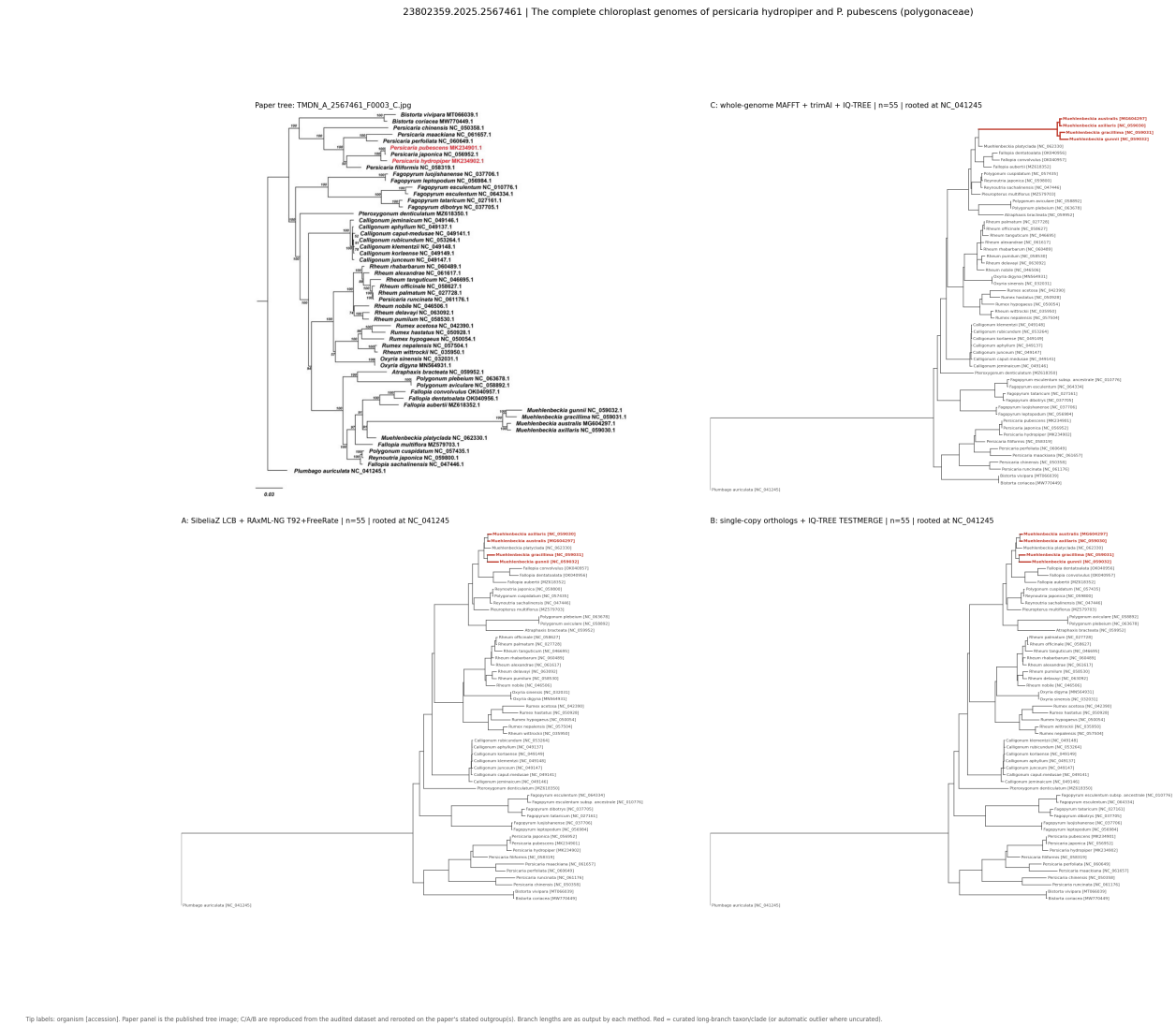
method	RTT outliers	terminal outliers	flagged clades
C naive	15	14	15
A FreeRate	7	11	5
B ortho	4	9	6

A terminal branches are estimated under RAxML-NG T92+F+FreeRate. RTT z-scores are sensitive to small MAD; ranks/clade flags should be read together.

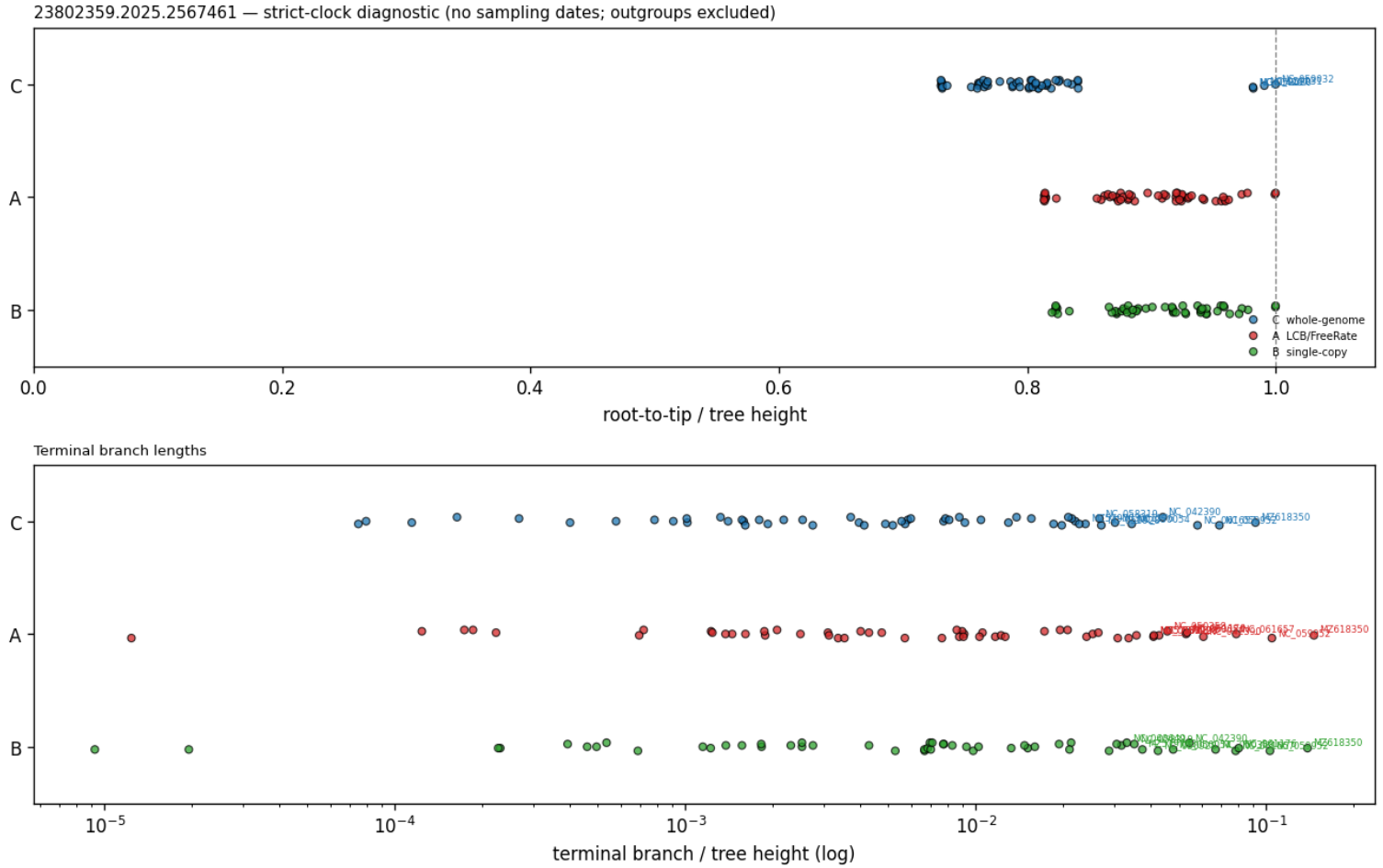
23802359.2025.2567461

The complete chloroplast genomes of persicaria hydropiper and P. pubescens (polygonaceae)

Status: Verified (highlight corrected). Muehlenbeckia clade MG604297 + NC_059030/031/032 highlighted; long branch reproduced and disappeared.



23802359.2025.2567461 - strict-clock branch-length diagnostic



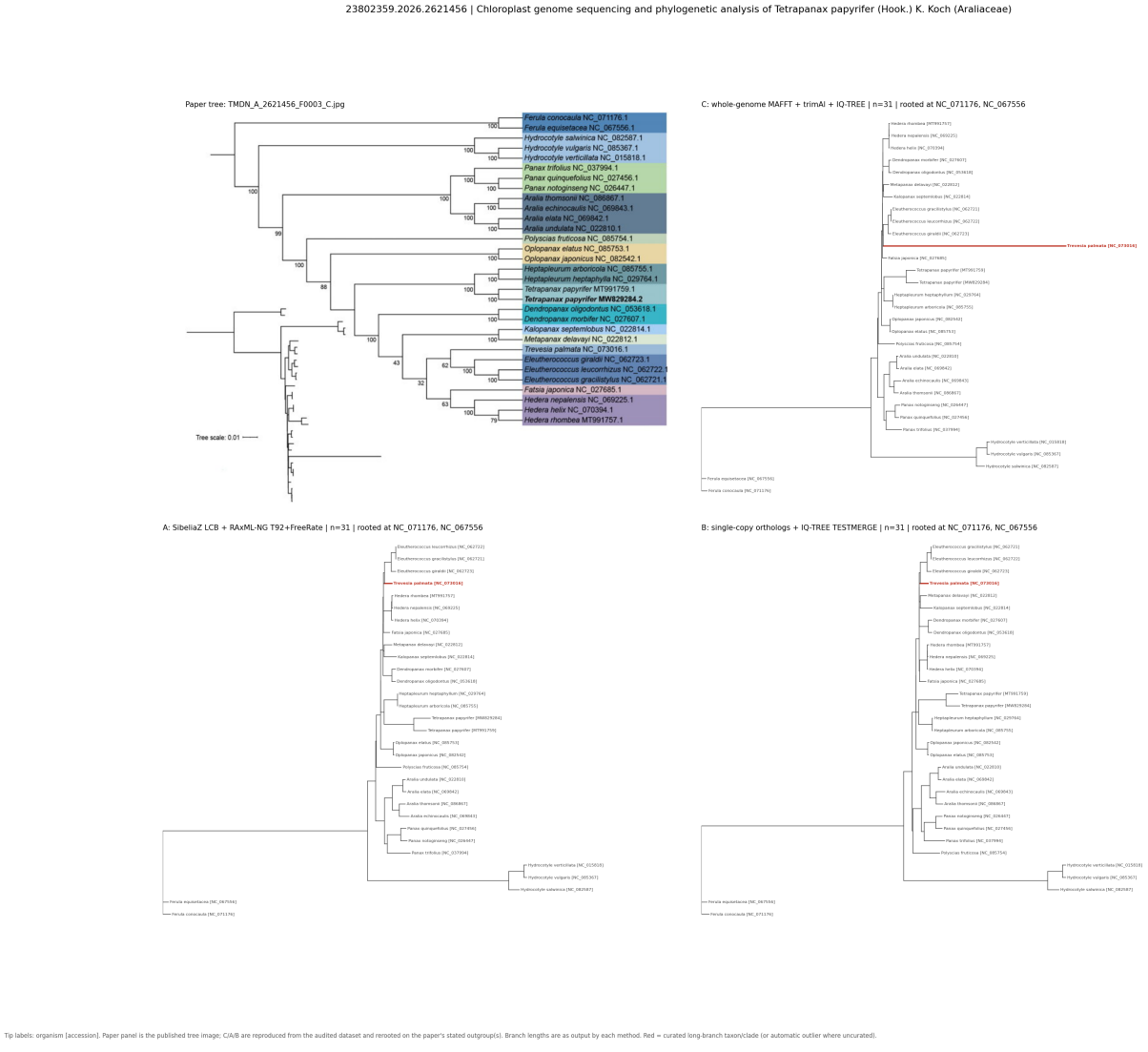
method	RTT outliers	terminal outliers	flagged clades
C naive	4	9	8
A FreeRate	0	10	5
B ortho	0	11	8

A terminal branches are estimated under RAxML-NG T92+F+FreeRate. RTT z-scores are sensitive to small MAD; ranks/clade flags should be read together.

23802359.2026.2621456

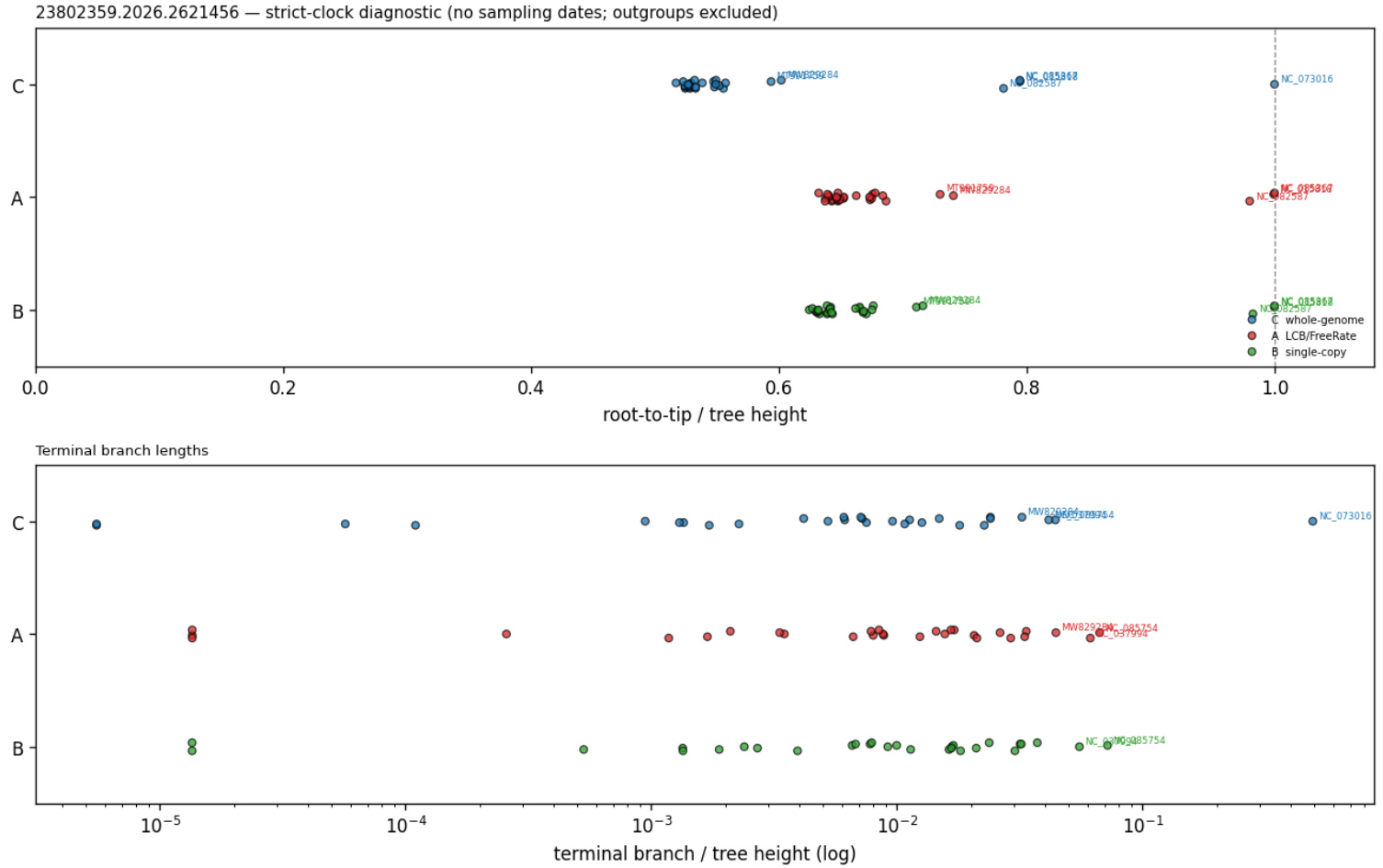
Chloroplast genome sequencing and phylogenetic analysis of Tetrapanax papyrifer (Hook.) K. Koch (Araliaceae)

Status: Verified. Long branch reproduced and disappeared.



Tip labels: organism [accession]. Paper panel is the published tree image; C/A/B are reproduced from the audited dataset and rerooted on the paper's stated outgroup(s). Branch lengths are as output by each method. Red = curated long-branch taxon/clade (or automatic outlier where uncurated).

23802359.2026.2621456 - strict-clock branch-length diagnostic



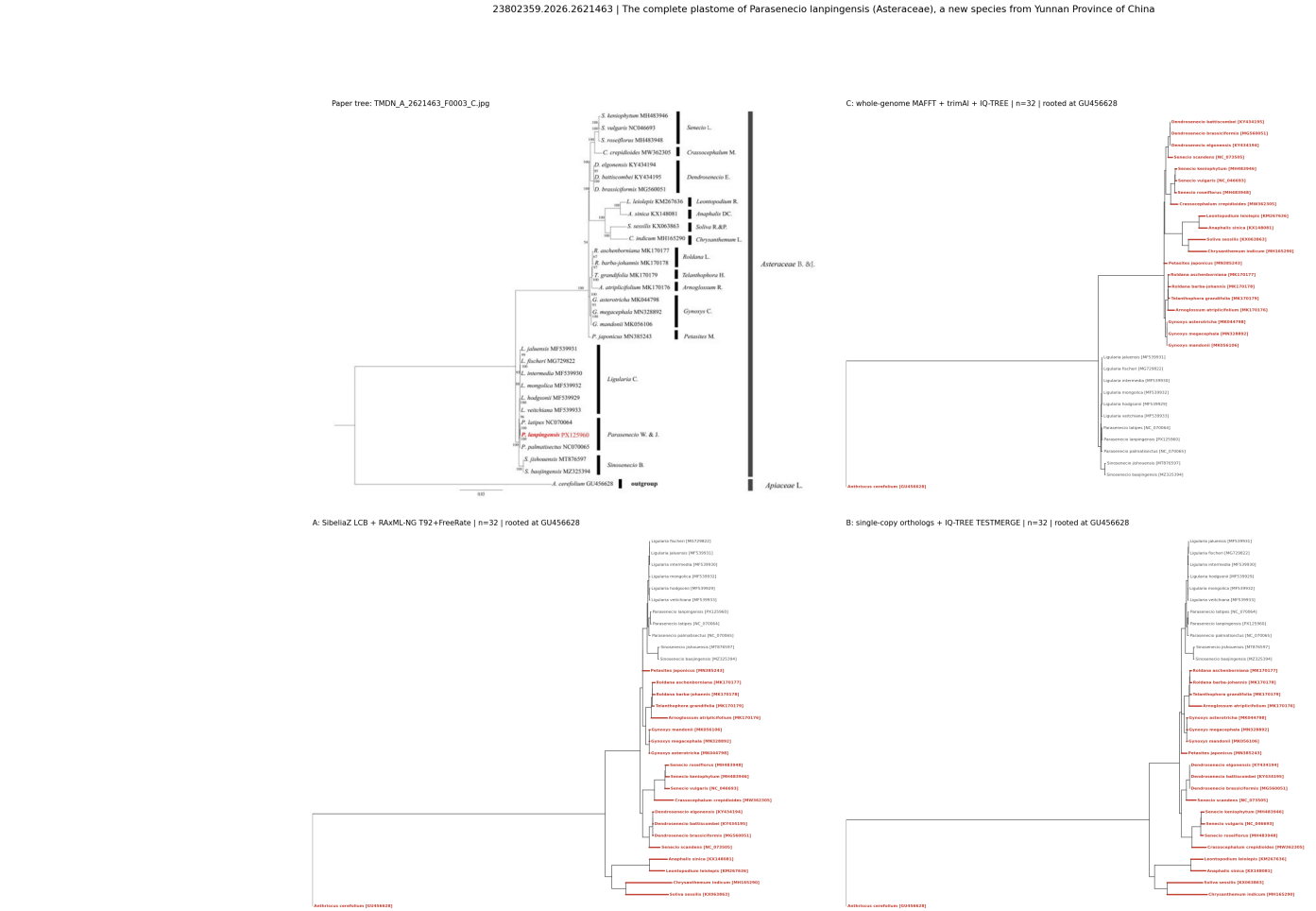
method	RTT outliers	terminal outliers	flagged clades
C naive	7	4	4
A FreeRate	6	3	4
B ortho	6	2	4

A terminal branches are estimated under RAxML-NG T92+F+FreeRate. RTT z-scores are sensitive to small MAD; ranks/clade flags should be read together.

23802359.2026.2621463

The complete plastome of Parasenecio lanpingensis (Asteraceae), a new species from Yunnan Province of China

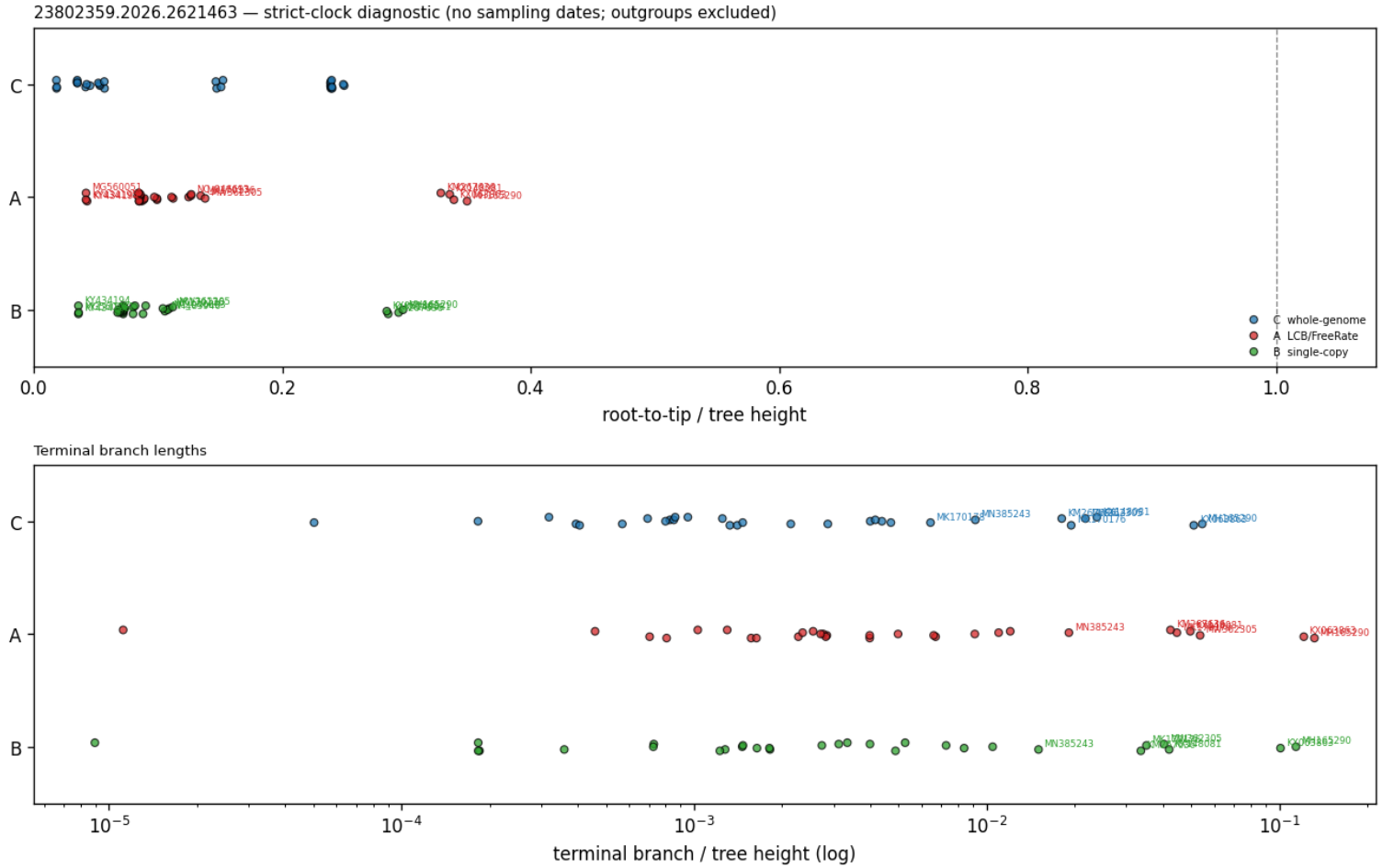
Status: Verified. Rooted at GU456628; NC_073505 highlighted; long branch reproduced and disappeared.



Note: the paper text's MT123456 is a Beilong virus record; the paper figure labels GU456628 (Anthriscus cerefolium) as the outgroup. C/A/B are rooted at GU456628.

Tip labels: organism [accession]. Paper panel is the published tree image; C/A/B are reproduced from the audited dataset and rerooted on the paper's stated outgroup(s). Branch lengths are as output by each method. Red = curated long-branch taxon/clade (or automatic outlier where uncurated).

23802359.2026.2621463 - strict-clock branch-length diagnostic



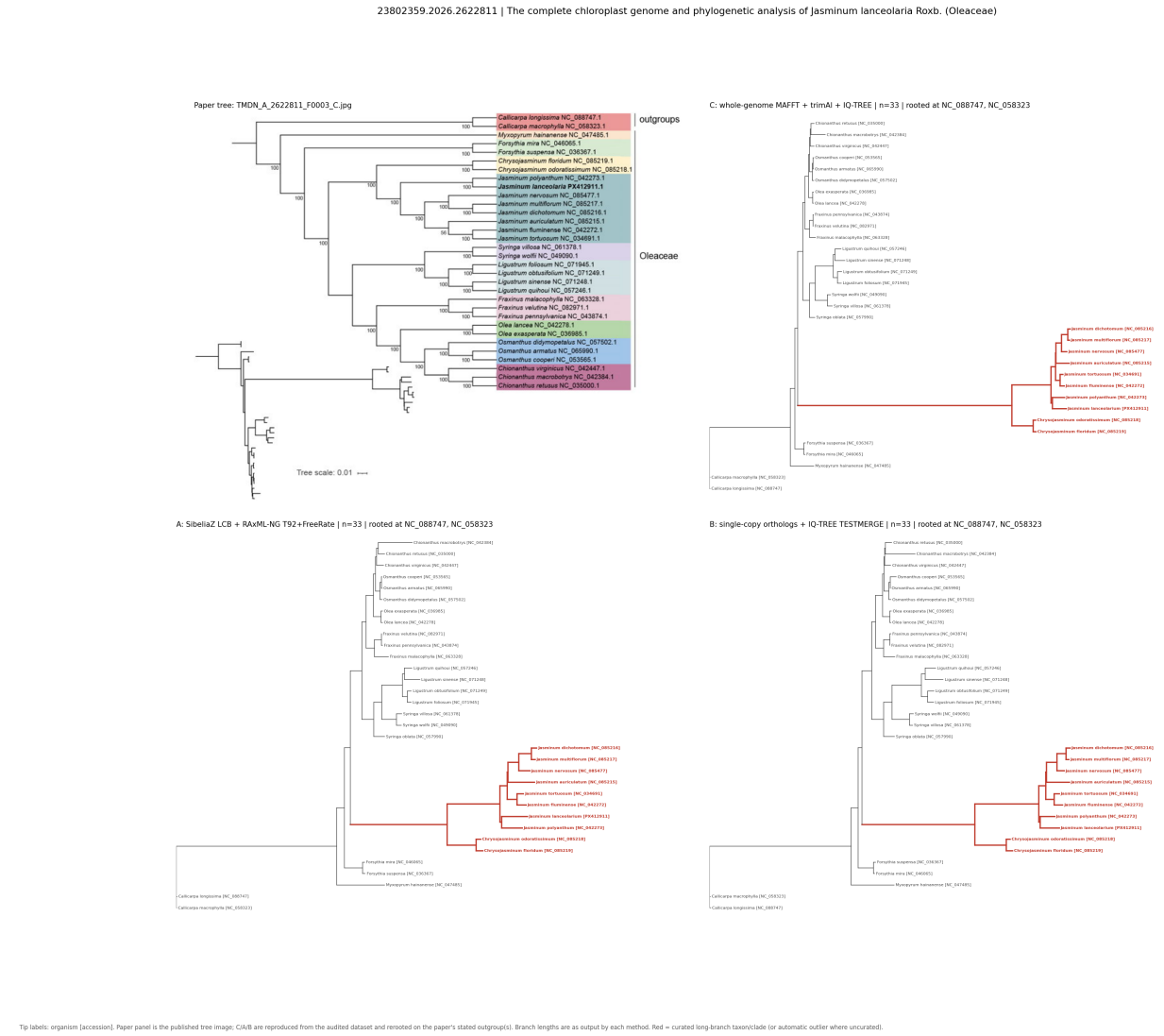
method	RTT outliers	terminal outliers	flagged clades
C naive	1	9	4
A FreeRate	11	8	7
B ortho	12	8	9

A terminal branches are estimated under RAxML-NG T92+F+FreeRate. RTT z-scores are sensitive to small MAD; ranks/clade flags should be read together.

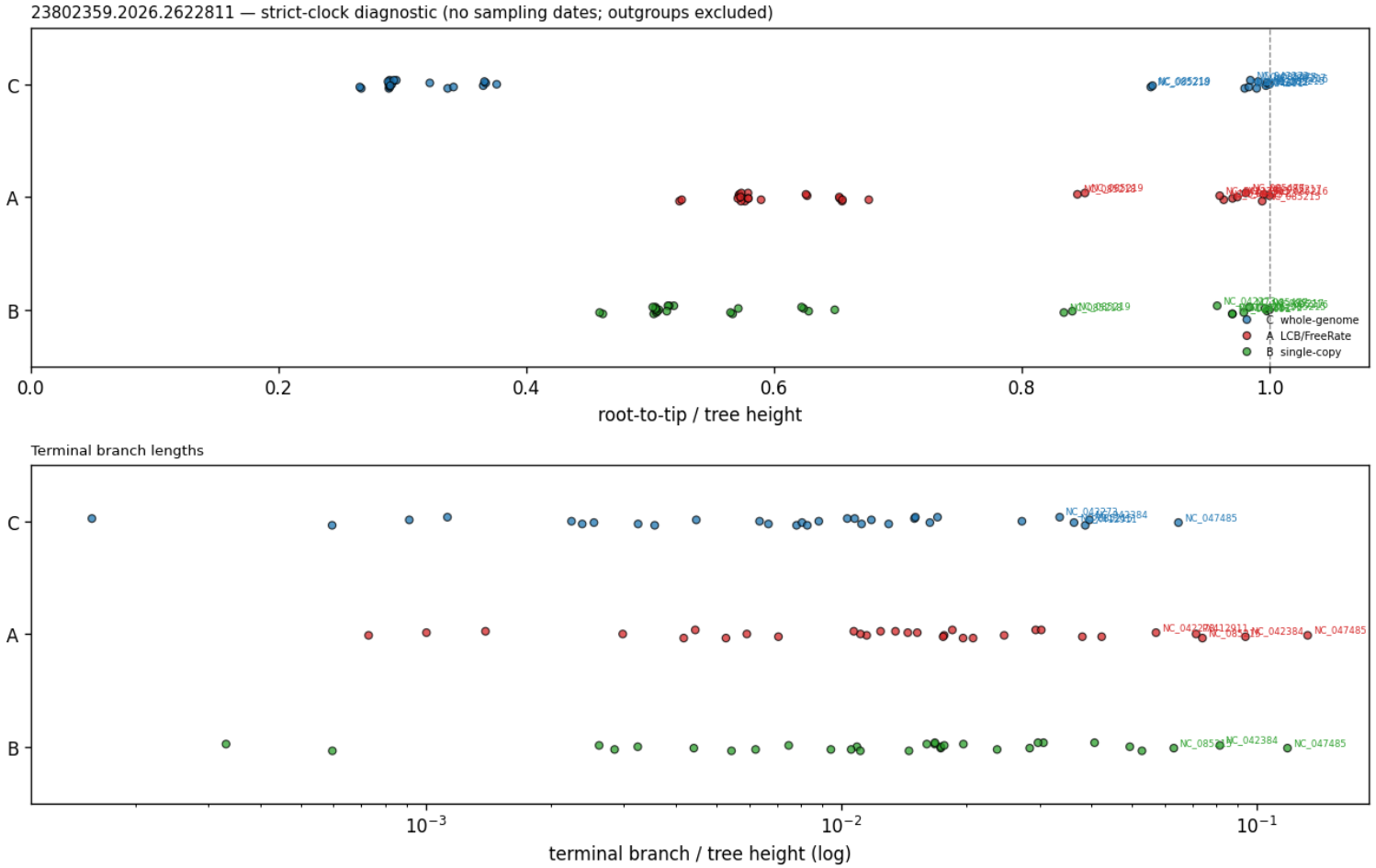
23802359.2026.2622811

The complete chloroplast genome and phylogenetic analysis of Jasminum lanceolaria Roxb. (Oleaceae)

Status: Verified (local-clock). Long branch shortened to an acceptable local-clock range.



23802359.2026.2622811 - strict-clock branch-length diagnostic



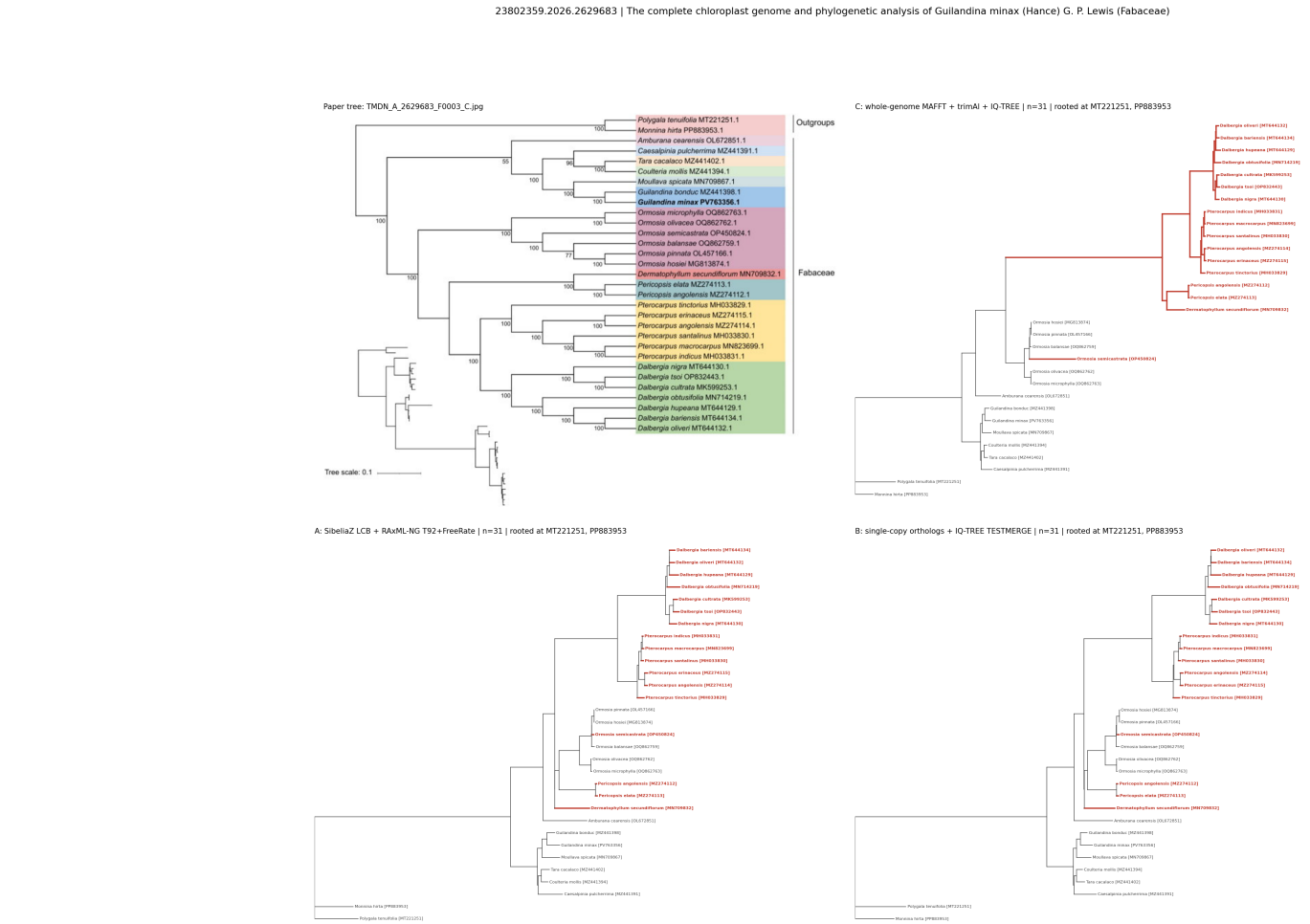
method	RTT outliers	terminal outliers	flagged clades
C naive	11	5	9
A FreeRate	11	5	9
B ortho	11	3	9

A terminal branches are estimated under RAxML-NG T92+F+FreeRate. RTT z-scores are sensitive to small MAD; ranks/clade flags should be read together.

23802359.2026.2629683

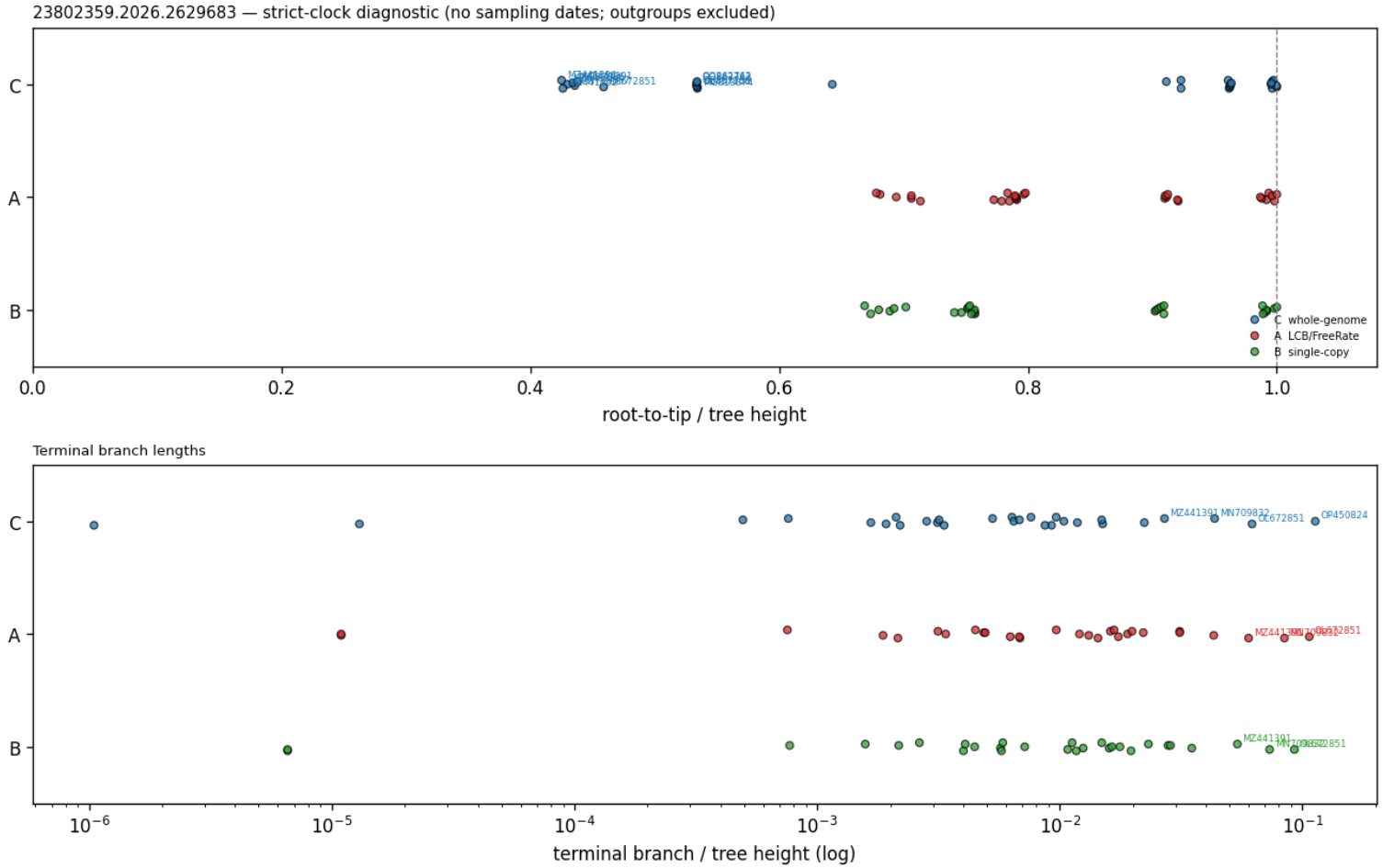
The complete chloroplast genome and phylogenetic analysis of Guilandina minax (Hance) G. P. Lewis (Fabaceae)

Status: Verified (local-clock). Long branch shortened to an acceptable local-clock range.



Tip labels: organism [accession]. Paper panel is the published tree image; C/A/B are reproduced from the audited dataset and rerooted on the paper's stated outgroup(s). Branch lengths are as output by each method. Red = curated long-branch taxon/clade (or automatic outlier where uncurated).

23802359.2026.2629683 - strict-clock branch-length diagnostic



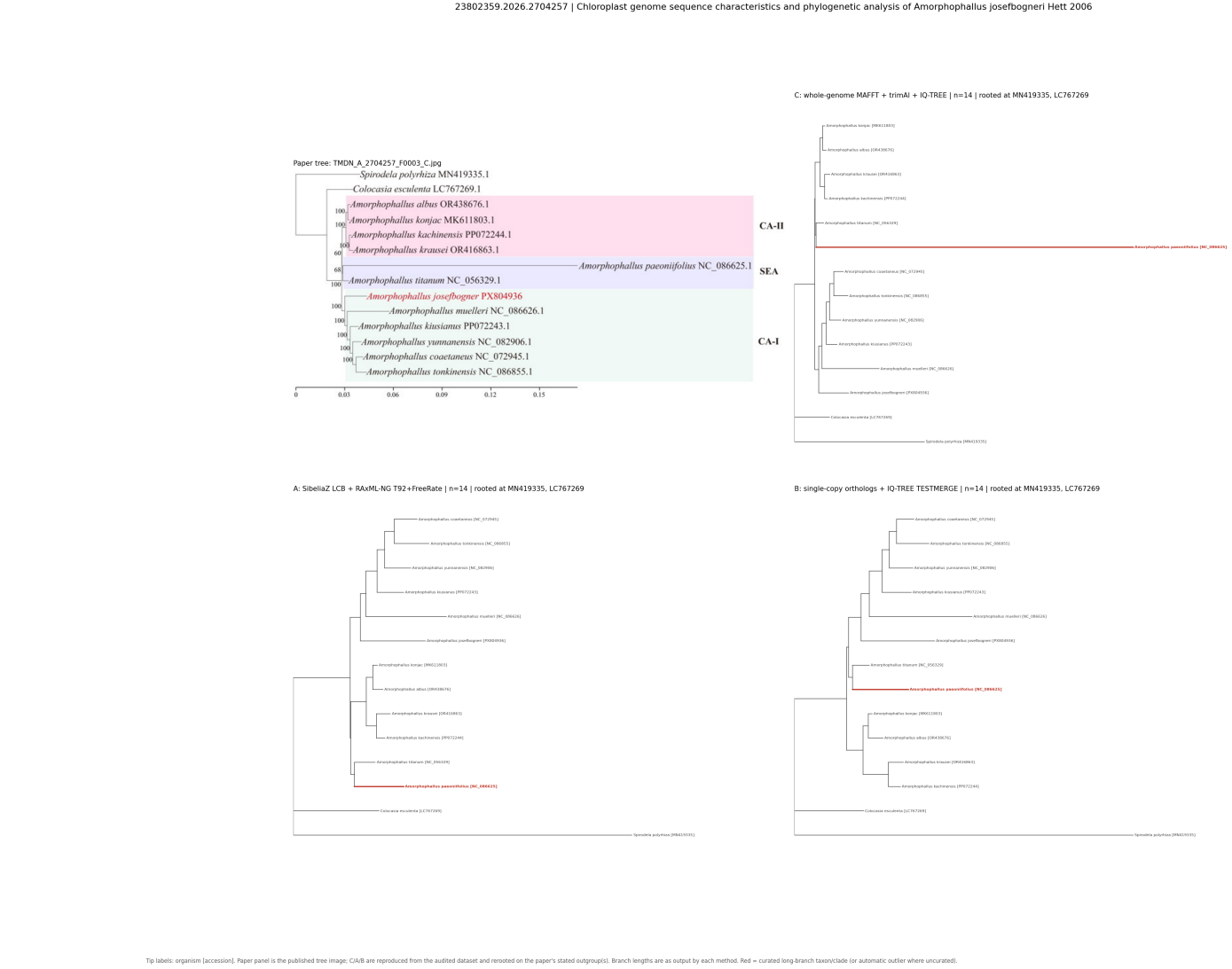
method	RTT outliers	terminal outliers	flagged clades
C naive	13	5	11
A FreeRate	1	4	0
B ortho	1	4	0

A terminal branches are estimated under RAxML-NG T92+F+FreeRate. RTT z-scores are sensitive to small MAD; ranks/clade flags should be read together.

23802359.2026.2704257

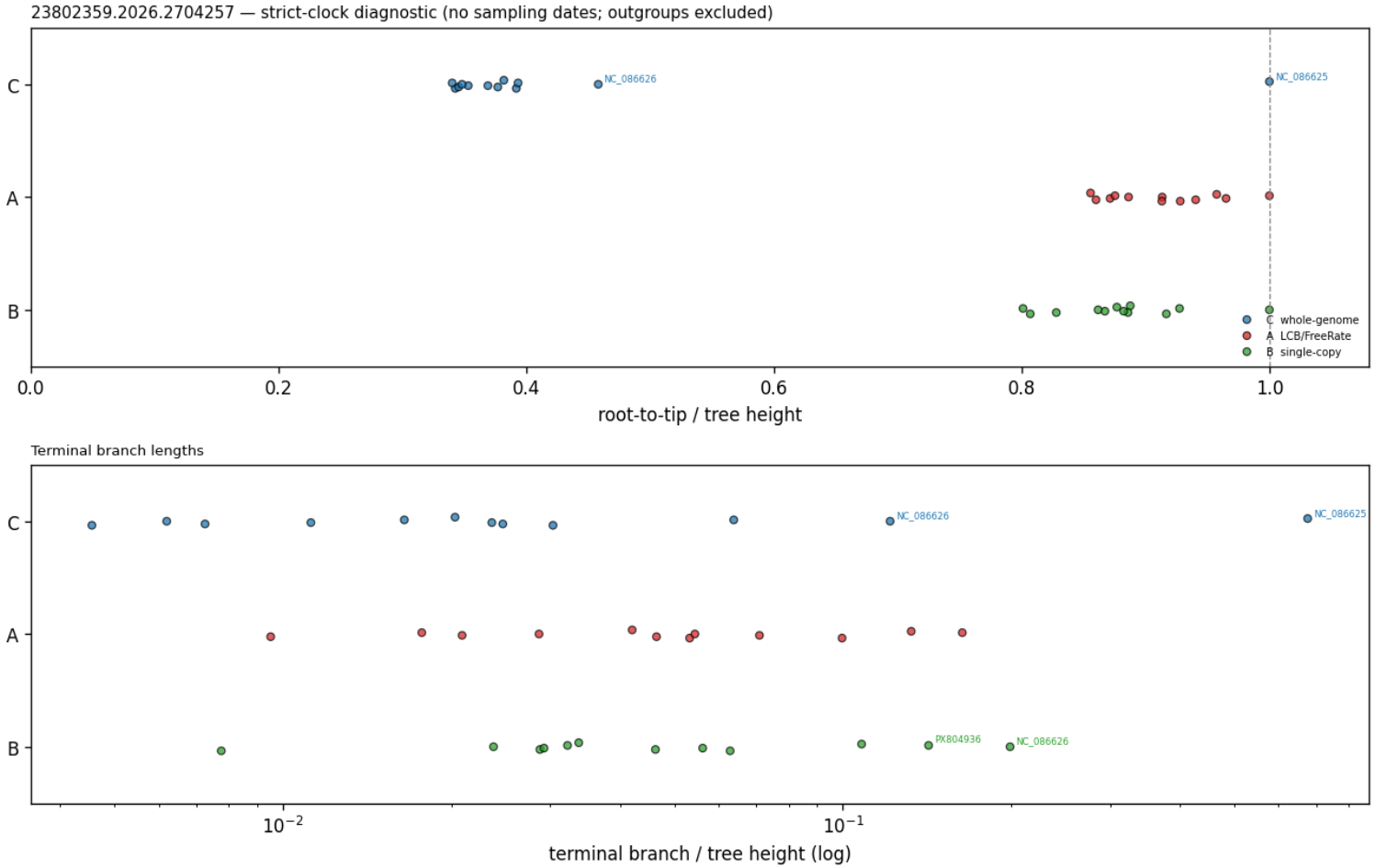
Chloroplast genome sequence characteristics and phylogenetic analysis of Amorphophallus josefbogneri Hett 2006

Status: Verified. NC_086625 long branch reproduced and disappeared; A-B topology identical.



Tip labels: organism [accession]. Paper panel is the published tree image; C/A/B are reproduced from the audited dataset and rerooted on the paper's stated outgroup(s). Branch lengths are as output by each method. Red = curated long-branch taxon/clade (or automatic outlier where uncurated).

23802359.2026.2704257 - strict-clock branch-length diagnostic



method	RTT outliers	terminal outliers	flagged clades
C naive	2	2	0
A FreeRate	0	1	0
B ortho	0	3	0

A terminal branches are estimated under RAxML-NG T92+F+FreeRate. RTT z-scores are sensitive to small MAD; ranks/clade flags should be read together.

RF triangle summary (unrooted, normalized)

Pairwise RF distances among C (naive whole-genome), A (LCB + RAxML-NG T92+F+FreeRate), and B (single-copy orthologs). Values are normalized by the maximum possible RF for the shared taxon set. All 38 analysed archived cases are shown; the reclassified case 2284410 and the CDS/PCG-based exclusions are not included.

dataset	n	C-A unrooted	C-B unrooted	A-B unrooted
23802359.2023.2274619	17	0.143	0.071	0.143
23802359.2023.2275827	20	0.353	0.412	0.353
23802359.2023.2281029	39	0.000	0.028	0.028
23802359.2023.2282225	35	0.094	0.094	0.125
23802359.2023.2288889	19	0.125	0.125	0.000
23802359.2023.2290844	26	0.000	0.000	0.000
23802359.2023.2294896	19	0.125	0.188	0.188
23802359.2023.2301012	15	0.000	0.000	0.000
23802359.2024.2306203	23	0.250	0.250	0.250
23802359.2024.2306207	15	0.833	0.833	0.000
23802359.2024.2309262	29	0.077	0.231	0.154
23802359.2024.2324928	20	0.412	0.353	0.059
23802359.2024.2347508	32	0.172	0.172	0.000
23802359.2024.2378966	27	0.375	0.375	0.083
23802359.2024.2383680	27	0.125	0.167	0.125
23802359.2024.2412239	26	0.043	0.043	0.000
23802359.2024.2420842	13	0.100	0.200	0.100
23802359.2024.2420847	14	0.727	0.727	0.091
23802359.2024.2432370	29	0.000	0.000	0.000
23802359.2024.2437099	21	0.056	0.056	0.000
23802359.2025.2466604	12	0.667	0.667	0.000
23802359.2025.2505249	24	0.476	0.571	0.571
23802359.2024.2438290	20	0.176	0.176	0.176
23802359.2025.2559713	19	0.438	0.438	0.188

dataset	n	C-A unrooted	C-B unrooted	A-B unrooted
23802359.2025.2528566	25	0.136	0.136	0.000
23802359.2025.2530712	21	0.389	0.444	0.056
23802359.2025.2544681	24	0.095	0.143	0.048
23802359.2025.2548850	48	0.578	0.578	0.111
23802359.2026.2635835	21	0.167	0.167	0.000
23802359.2026.2694148	14	0.182	0.182	0.000
23802359.2026.2694188	35	0.000	0.031	0.031
23802359.2026.2742618	38	0.543	0.543	0.171
23802359.2025.2567461	55	0.077	0.038	0.058
23802359.2026.2621456	31	0.107	0.143	0.107
23802359.2026.2621463	32	0.241	0.207	0.172
23802359.2026.2622811	33	0.000	0.000	0.000
23802359.2026.2629683	31	0.107	0.107	0.000
23802359.2026.2704257	14	0.000	0.091	0.091

Excluded from the main cohort: 2290339, 2294894, 2294898 and 2357681 (CDS/PCG-based original analyses). All other completed datasets are included.