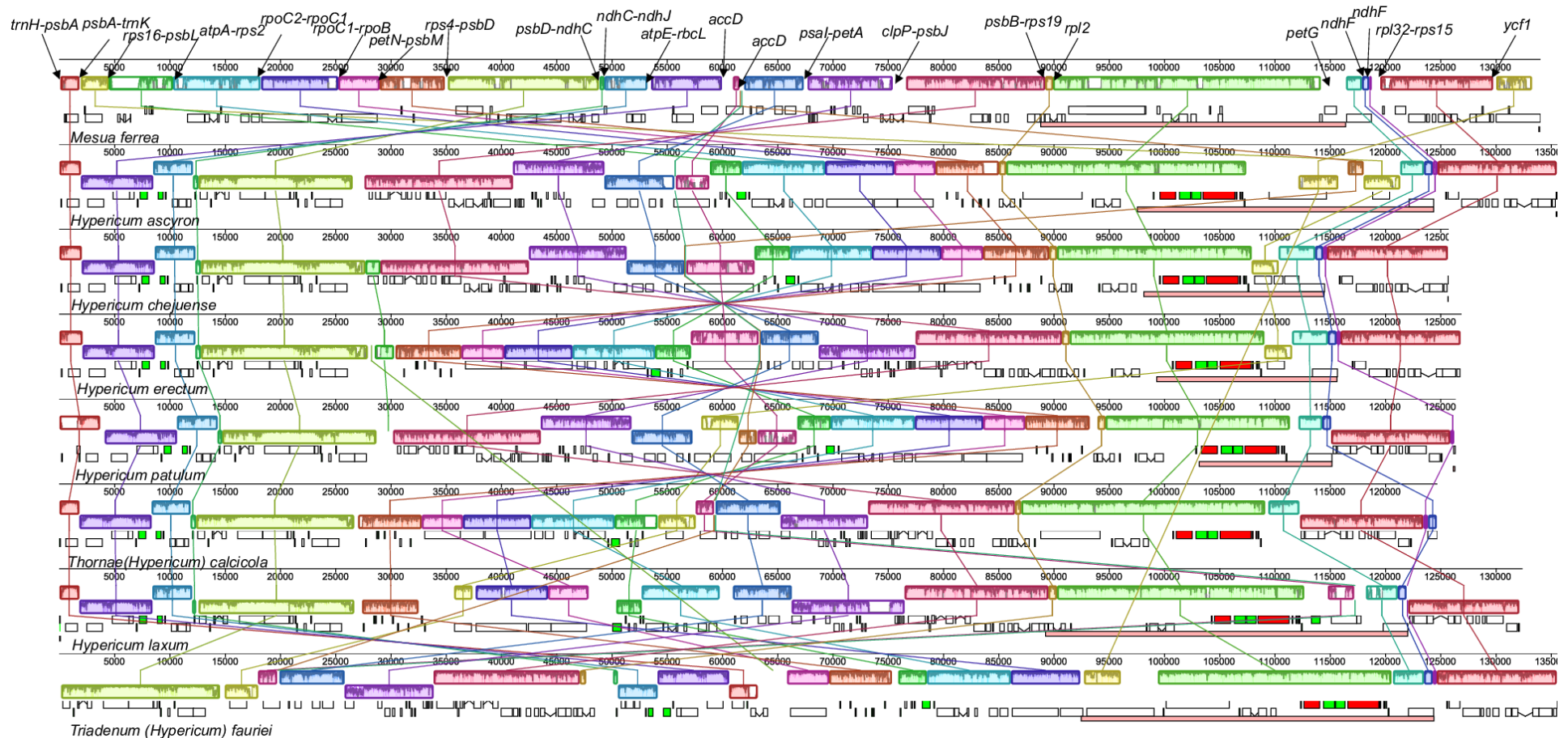
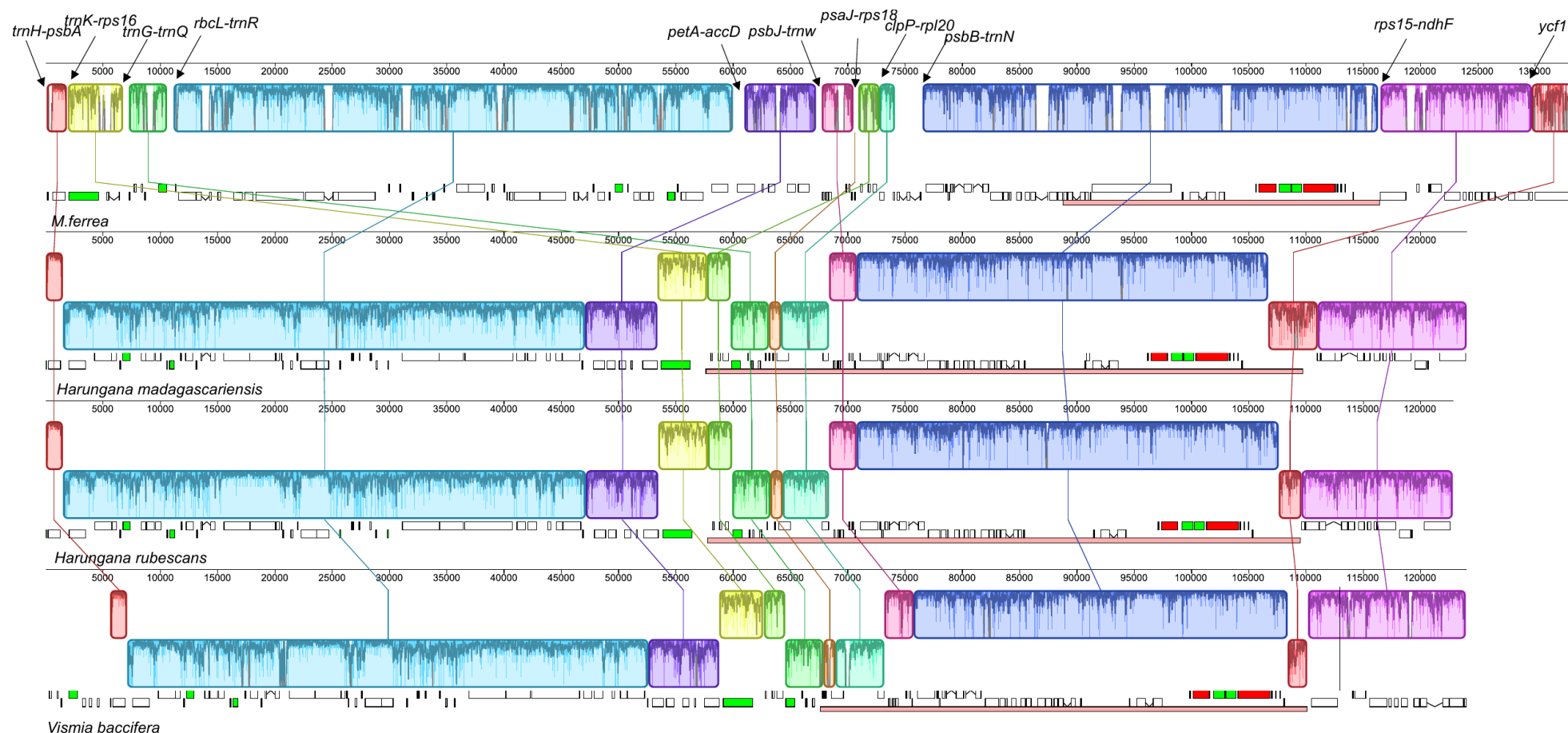


S.No	Family	Tribe	Genus	Origin	Habit	Species studied	Data collected	Voucher
1	Hypericaceae Juss.	Hypericeae Choisy.	Hypericum L.	Africa to Worldwide and invasive	Trees, Shrubs, annuals, and perennials	<i>H. ascyron</i>	Gyeongsan, South Korea	YNH-0013112
2						<i>H. erectum</i>	Chojung mountain, South Korea	YNH-0013113
3						<i>H. laxum</i>	Pusan., South Korea	YNH-0013114
4						<i>H. patulum</i>	Jiri mountain, South Korea	YNH-0013115
5						<i>H. chejuense</i>	Jeju island, , South Korea	YNH-0013116
6			Triadenum Raf.	North American and Eastern Asia	Herb	<i>T. faurei</i>	Jeju island, south Korea.	YNH-0013117
7			Thornea Breedlove & E.M.McClint.,	Central America, Chiapas & northern Guatemala	Trees or Shrub	<i>T. matudae</i>	Taxes University Herbarium. USA.	TU-1115544
8		Cratoxyleae Bentham & J. D. Hooker	Cratoxylum Blume.	Indochina, Malaysia, and Thailand.	Shrub or Trees	<i>C. maingayi</i>	KEW DNA-bank, UK	13946-DNA
9			Eliea Cambess.	Madagascar, Africa.	Shrub	<i>E. articulate</i>	Missouri botanical garden, England.	MO-3026272
10		Vismieae Choisy.	Harungana Lam.	Africa (Madagascar) and South America	Trees	<i>H. madagascariensis</i>	Missouri botanical garden, England.	MO-3021438
11						<i>H. rubescens</i> Syn: (<i>Vismia rubescens</i>)	KEW DNA-bank, UK	25978- DNA
12			Vismia Vandt.	Africa ((Madagascar) and South America	Trees or Shrubs	<i>V. baccifera</i>	Taxes University Herbarium, USA.	TU-0318098
14	Clusiaceae Lindl. (Guttiferae)	Symphonieae Choisy.	Moronobea Aubl.	Madagascar, Africa. Amazon Rainforest, South America.	Tree	<i>M. riparia</i>	Taxes University Herbarium, USA.	TU-0052687
15		Garcinieae Syn: (<i>Rheedia</i>)	Garcinia intermedia	South America and west indies and Madagascar, Africa.	Tree	<i>G. intermedia</i> \ Syn: (<i>Rheedia edulis</i>)	Taxes University Herbarium, USA.	TU-0315507

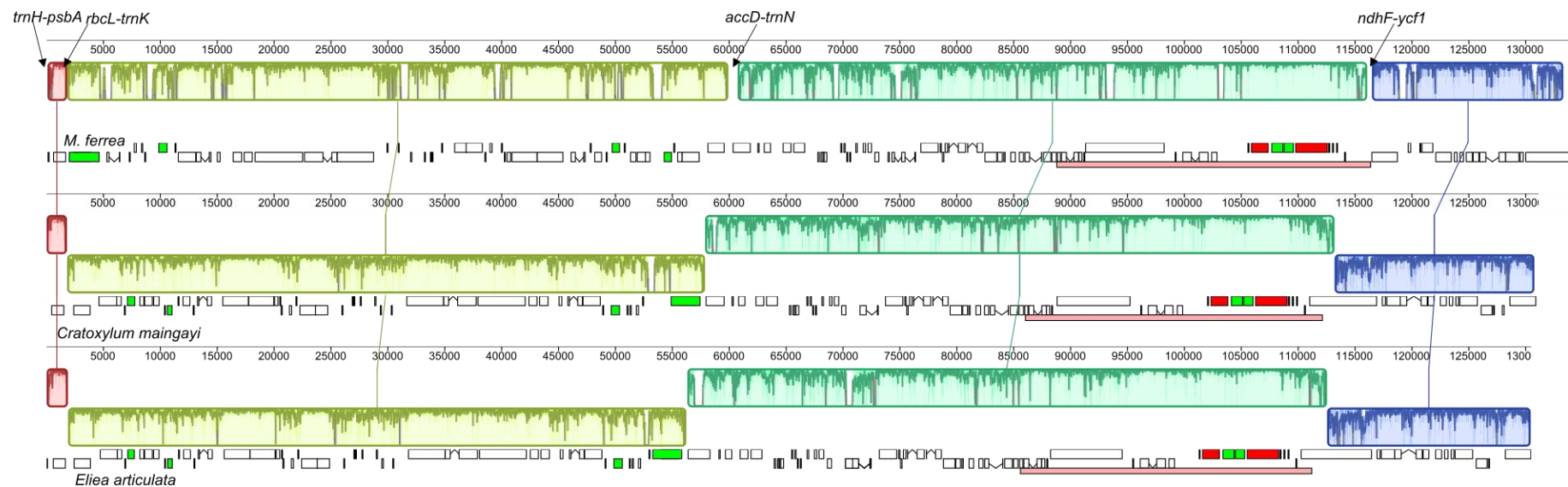
Supplementary Table 1. List of the 15 Hypericaceae species analyzed in this study, including their geographic origins, used for plastome sequencing and comparative analyses.



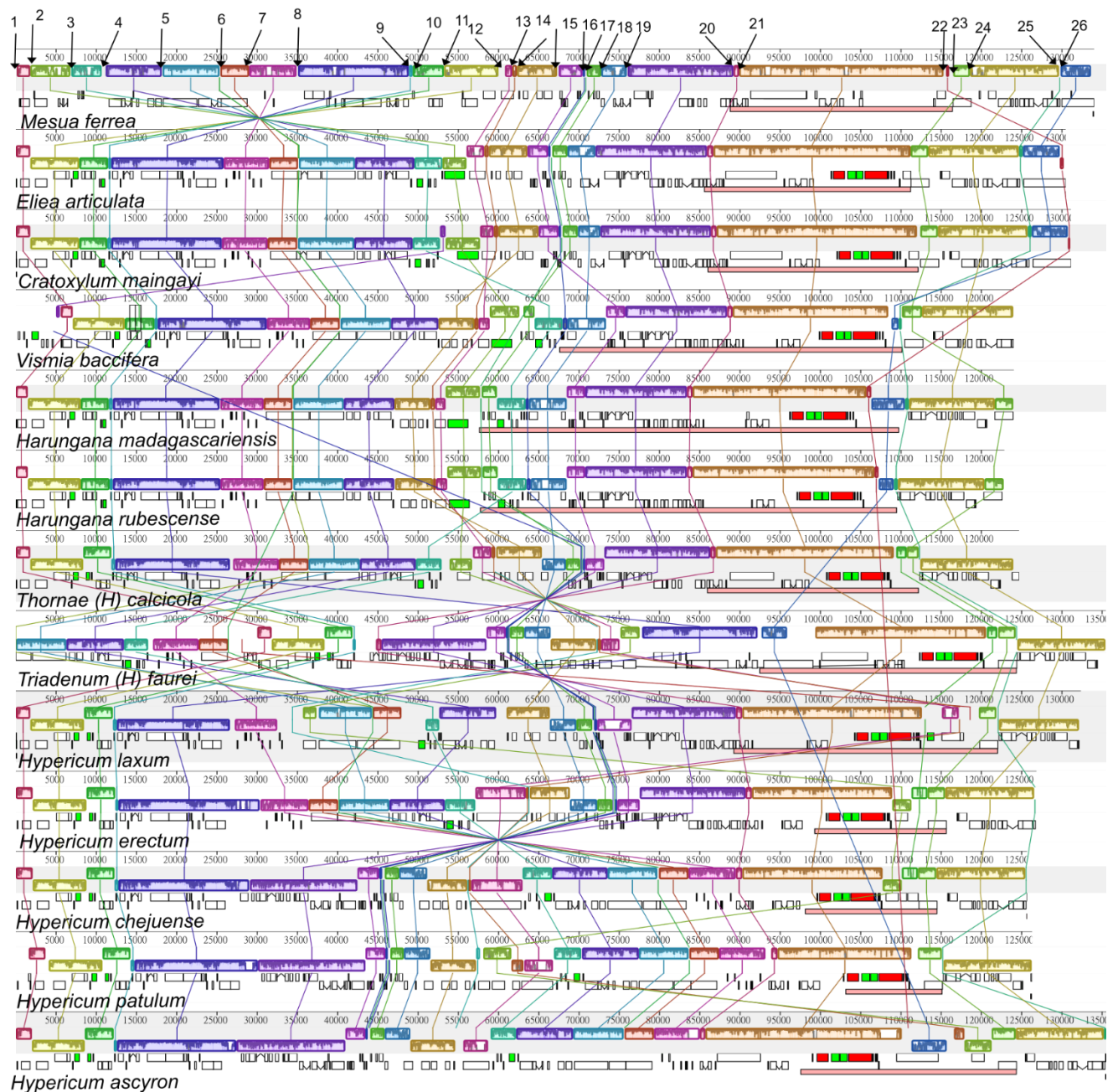
Supplementary Figure 1. Genome rearrangements in the plastomes of Hypericeae species visualized using progressiveMauve. Locally collinear blocks (LCBs) represent conserved syntenic regions across plastid genomes of Hypericeae species and are color-coded. Vertical lines within each block indicate gene boundaries, while the height of the colored blocks represents sequence conservation. Inversions, translocations, and boundary shifts are indicated by the rearranged positions of homologous LCBs among species. Notably, *Hypericum ascyron* shows significant plastome restructuring compared to *Mesua* members. The alignment highlights lineage-specific plastome rearrangements within the tribe, suggesting dynamic structural evolution.



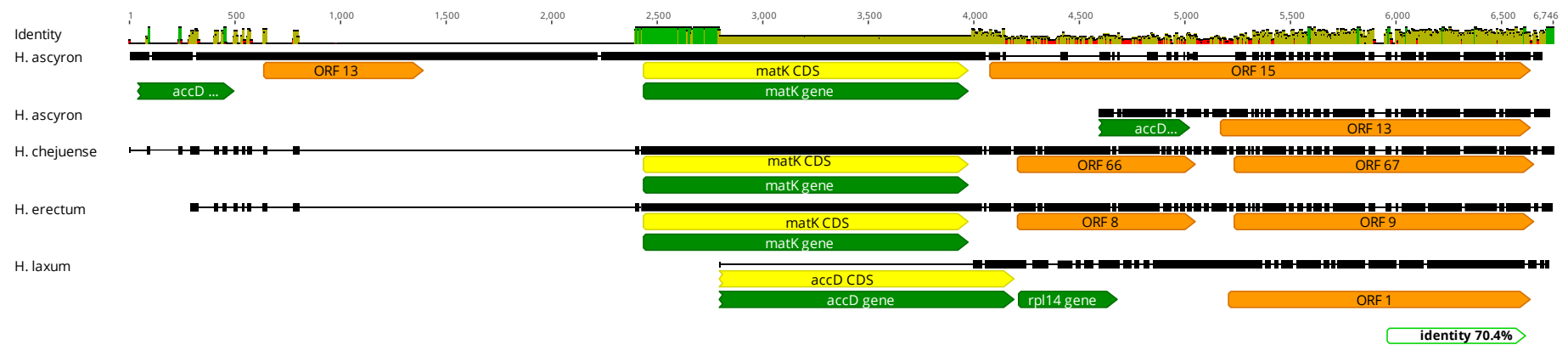
Supplementary Figure 2. Genome rearrangements in the plastomes of *Vismieae* species visualized using progressiveMauve. Locally collinear blocks (LCBs) represent conserved syntenic regions across plastid genomes of Hypericeae species and are color-coded. Vertical lines within each block indicate gene boundaries, while the height of the colored blocks represents sequence conservation. Inversions, translocations, and boundary shifts are indicated by the rearranged positions of homologous LCBs among species. Notably, *Hypericum ascyron* shows significant plastome restructuring compared to other *Mesua* members. The alignment highlights lineage-specific plastome rearrangements within the tribe, suggesting dynamic structural evolution.



Supplementary Figure 3. Genome rearrangements in the plastomes of *Cratoxyleae* species visualized using progressiveMauve. Locally collinear blocks (LCBs) represent conserved syntenic regions across plastid genomes of Hypericeae species and are color-coded. Vertical lines within each block indicate gene boundaries, while the height of the colored blocks represents sequence conservation. Inversions, translocations, and boundary shifts are indicated by the rearranged positions of homologous LCBs among species. Notably, *Hypericum ascyron* shows significant plastome restructuring compared to other *Mesua* members. The alignment highlights lineage-specific plastome rearrangements within the tribe, suggesting dynamic structural evolution.



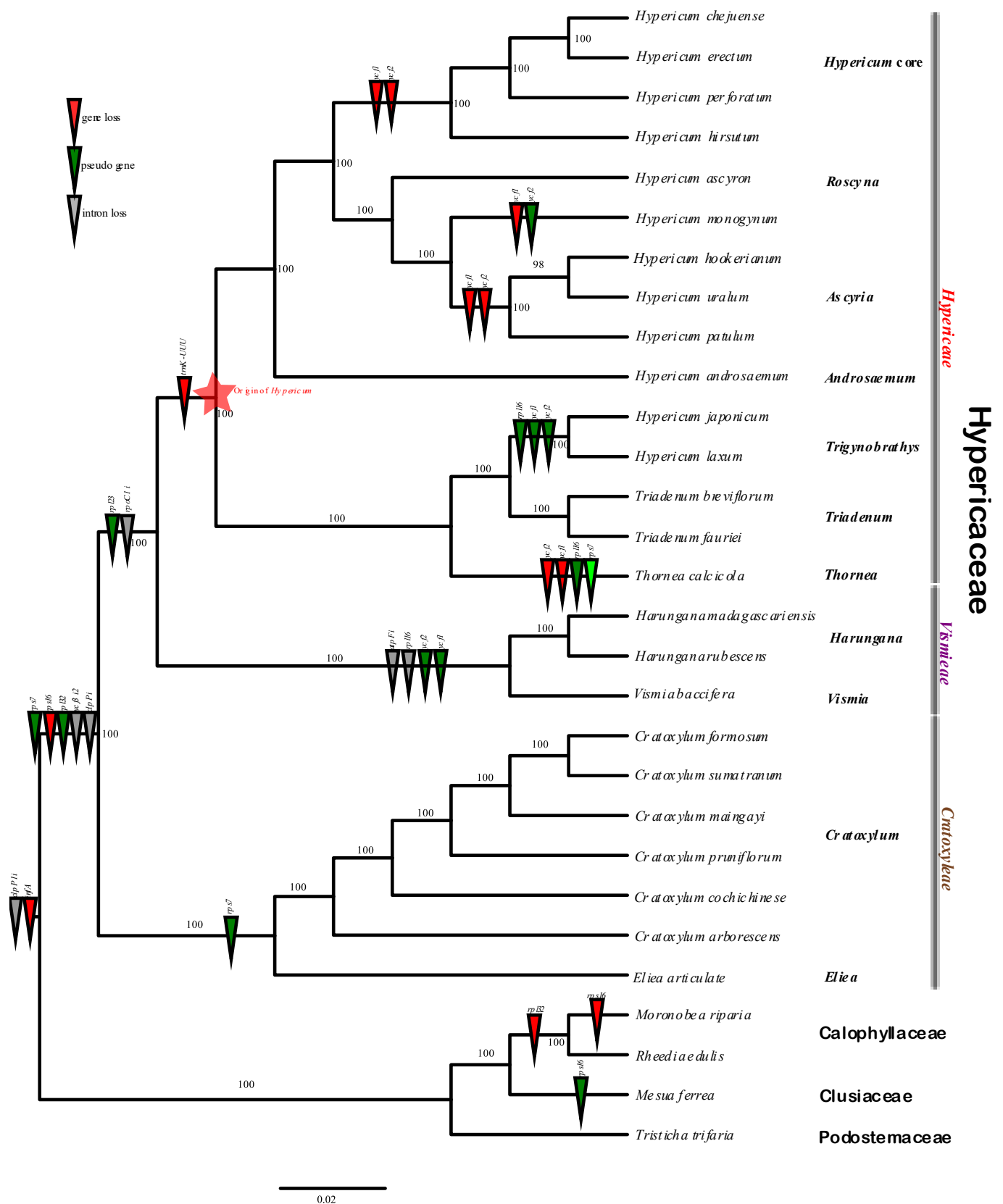
Supplementary Figure 4. The mauve genome alignment against *Mesua* and to the *Hypericaceae* family species. The numbering from 1-26, a Local colinear blocks from tribe to tribe. Locally collinear blocks (LCBs) represent conserved syntenic regions across plastid genomes of Hypericeae species and are color-coded. Vertical lines within each block indicate gene boundaries, while the height of the colored blocks represents sequence conservation. Inversions, translocations, and boundary shifts are indicated by the rearranged positions of homologous LCBs among species. Notably, *Hypericum ascyron* shows significant plastome restructuring compared to other *Mesua* members. The alignment highlights lineage-specific plastome rearrangements within the tribe, suggesting dynamic structural evolution.



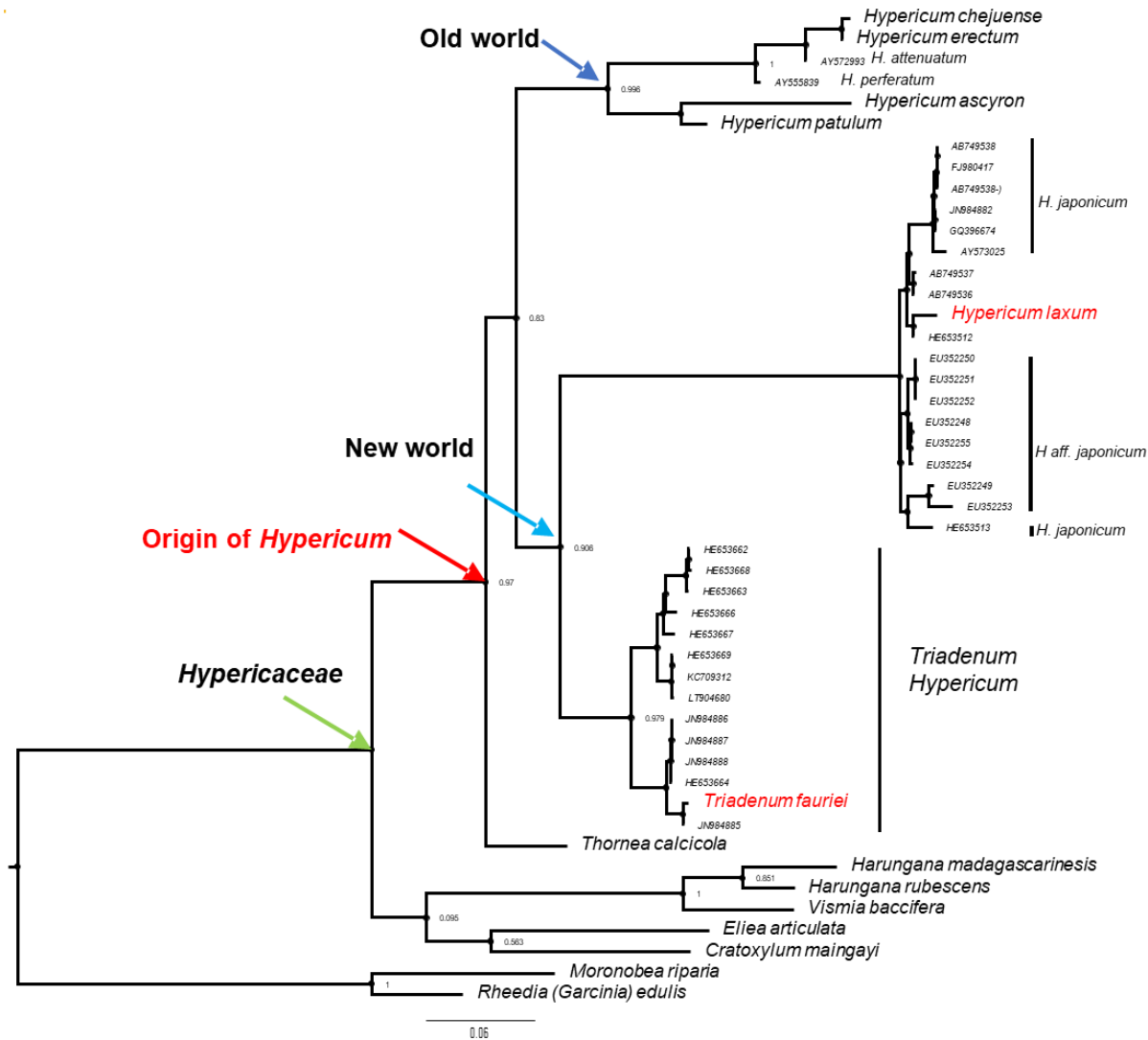
Supplementary Figure 5. Only Translocated *matK* and *accD* found with unknown ORF either partial or complete unknown ORF in *Hypericum* genus alone.



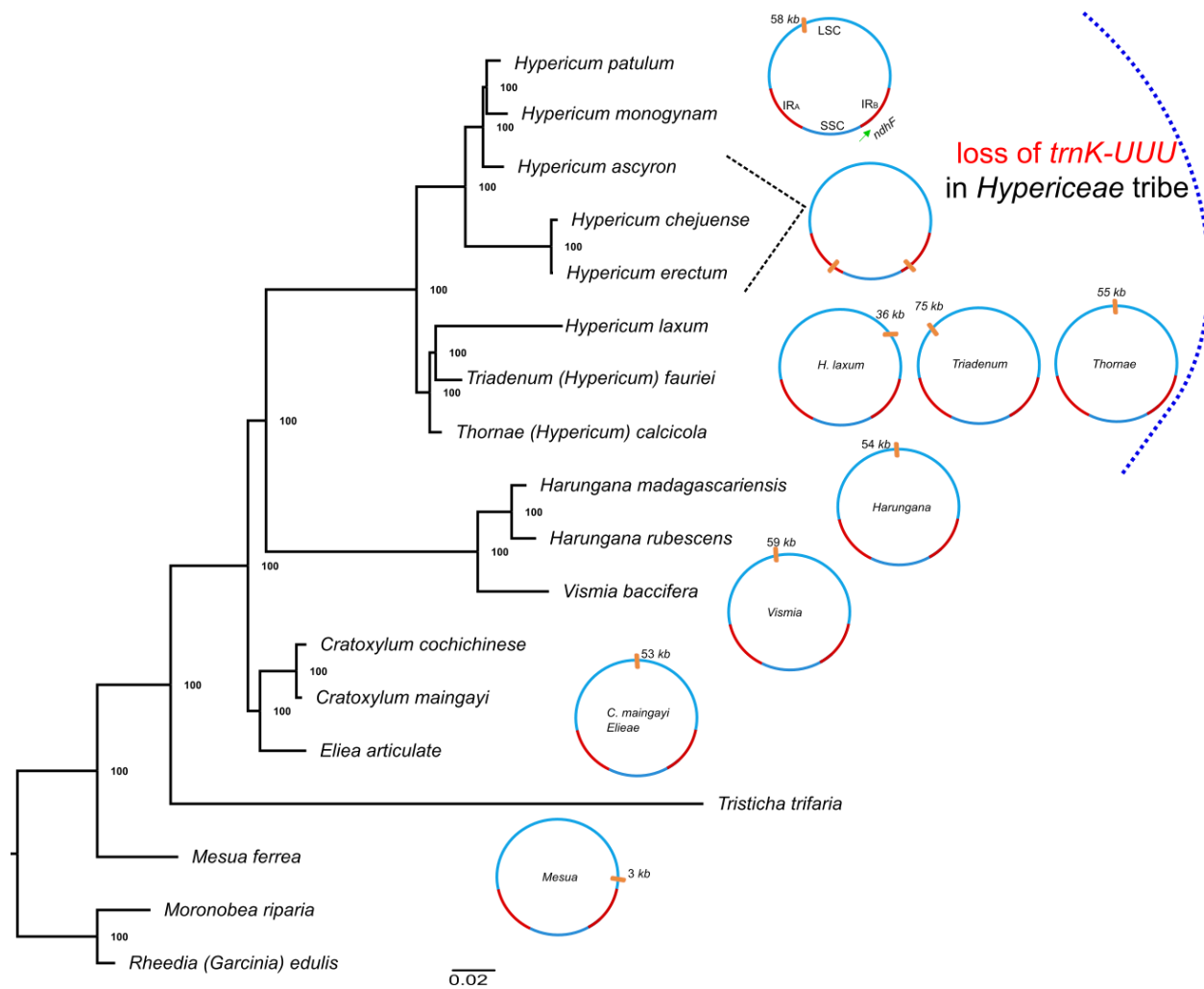
Supplementary Figure 6. tRNA loss in Hypericeae tribe in comparison to the Vismieae and Cratoxyleae tribe of Hypericaceae.



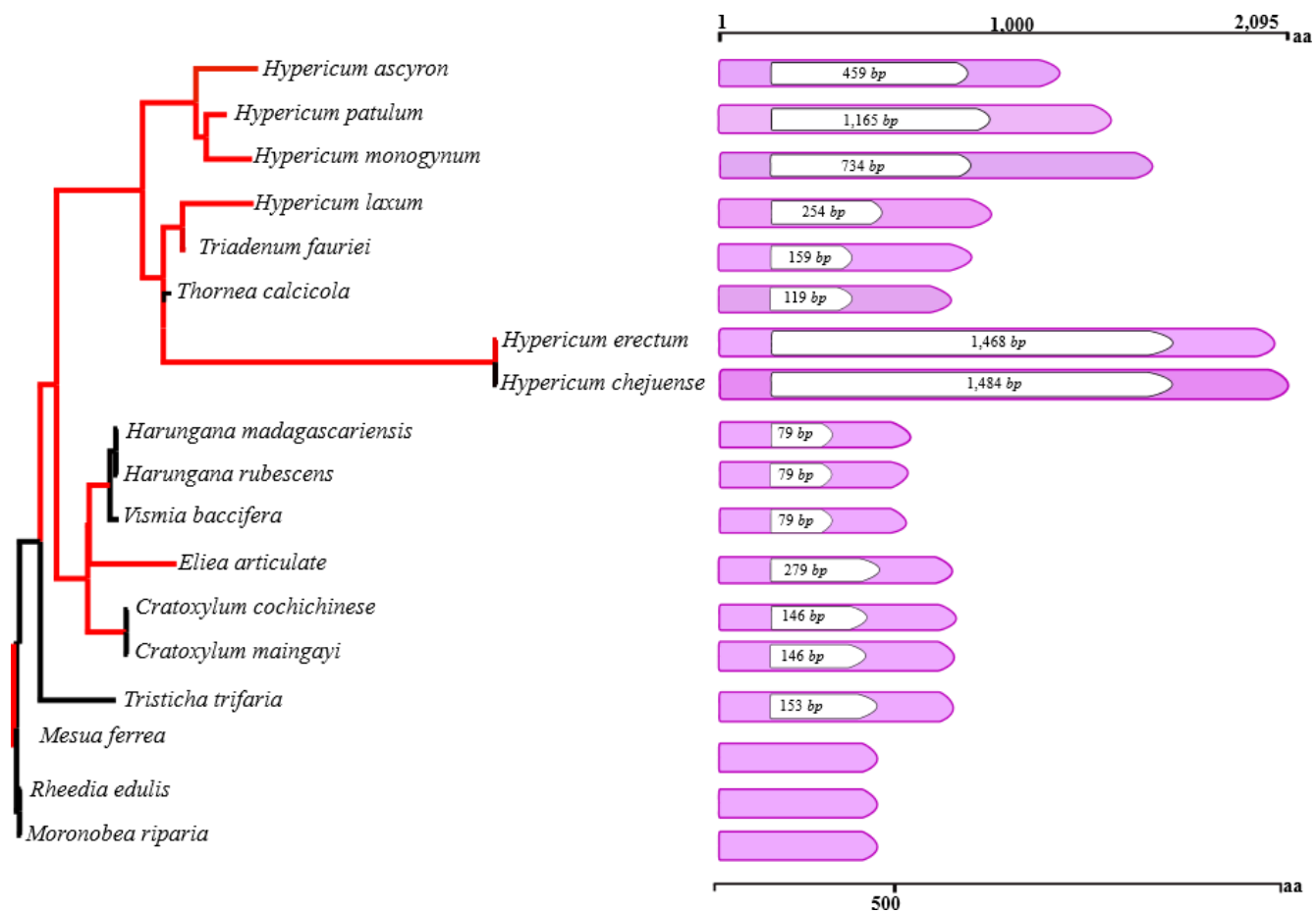
Supplementary Figure 7. Stepwise loss of specific plastid genes and introns along the evolutionary transition from Podostemaceae to Hypericaceae.



Supplementary Figure 8. ITS phylogenetic tree relationship of *Hypericum laxum* and *Triadenum Faurei* position between new vs old world.

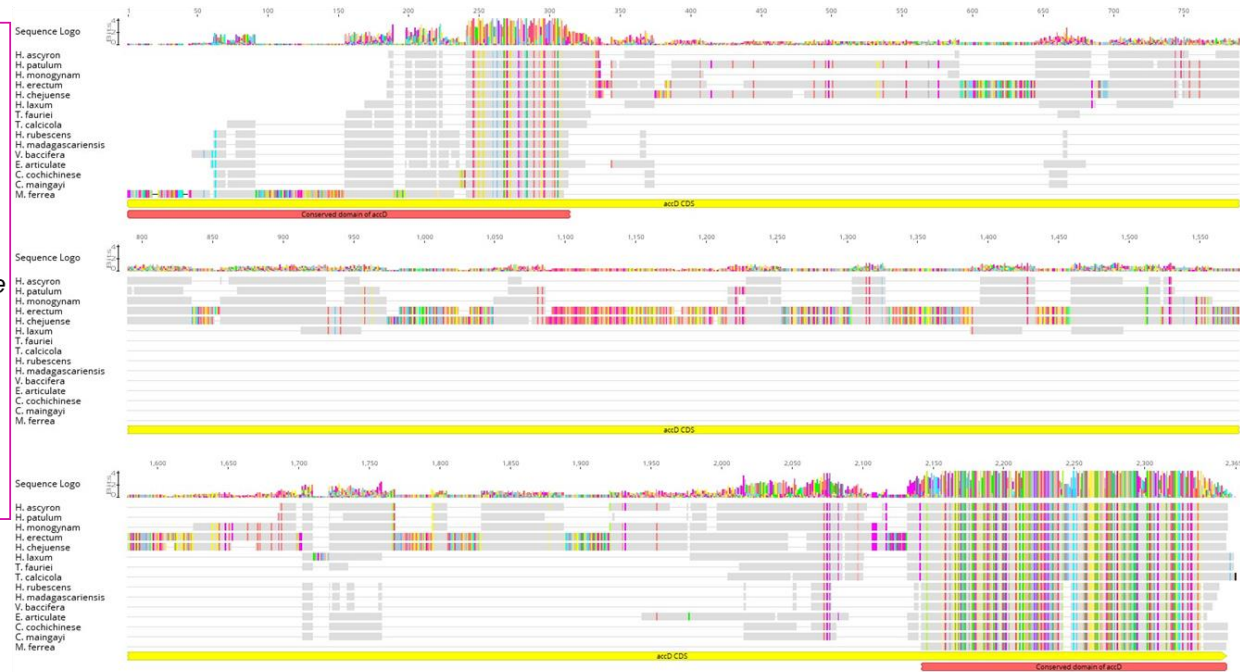
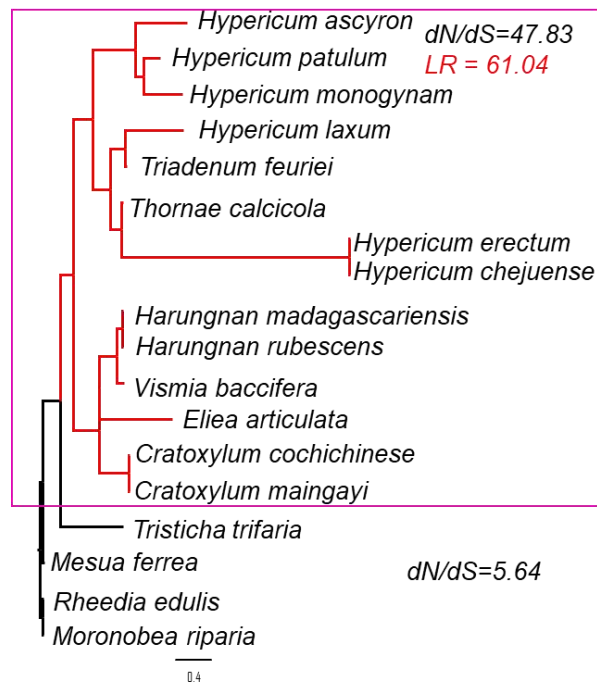


Supplementary Figure 9. Relocation of the free-standing *matK* gene and identification of its breakage point position in the circular plastomes of species within the Hypericeae tribe.



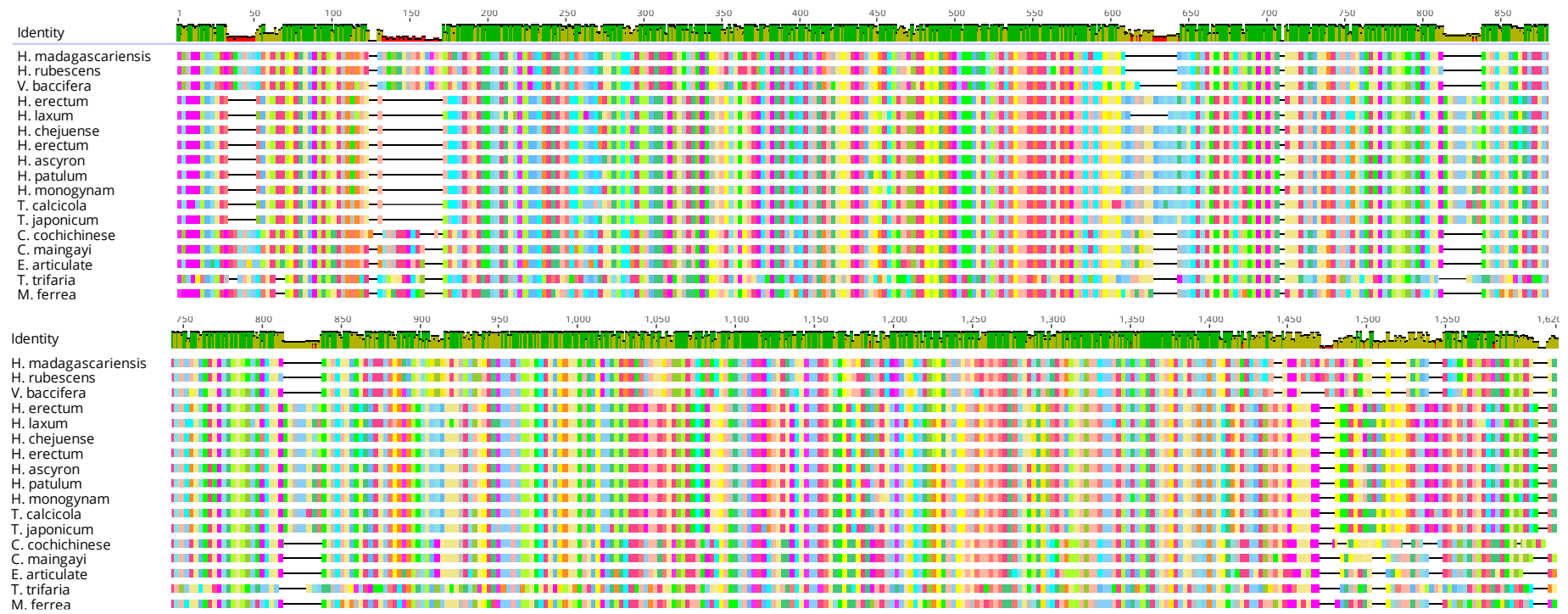
Supplementary Figure 10. Variable-length insertions of random sequences in the *accD* gene among Hypericaceae species, ranging from 79 bp to insertions encoding up to 1,436 amino acids.

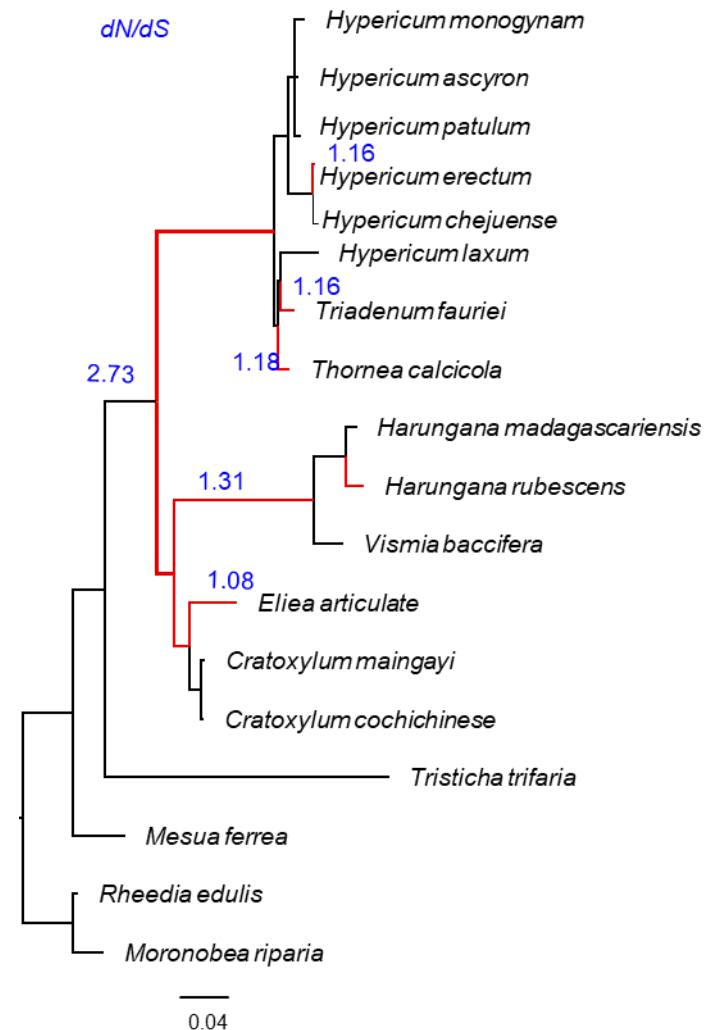
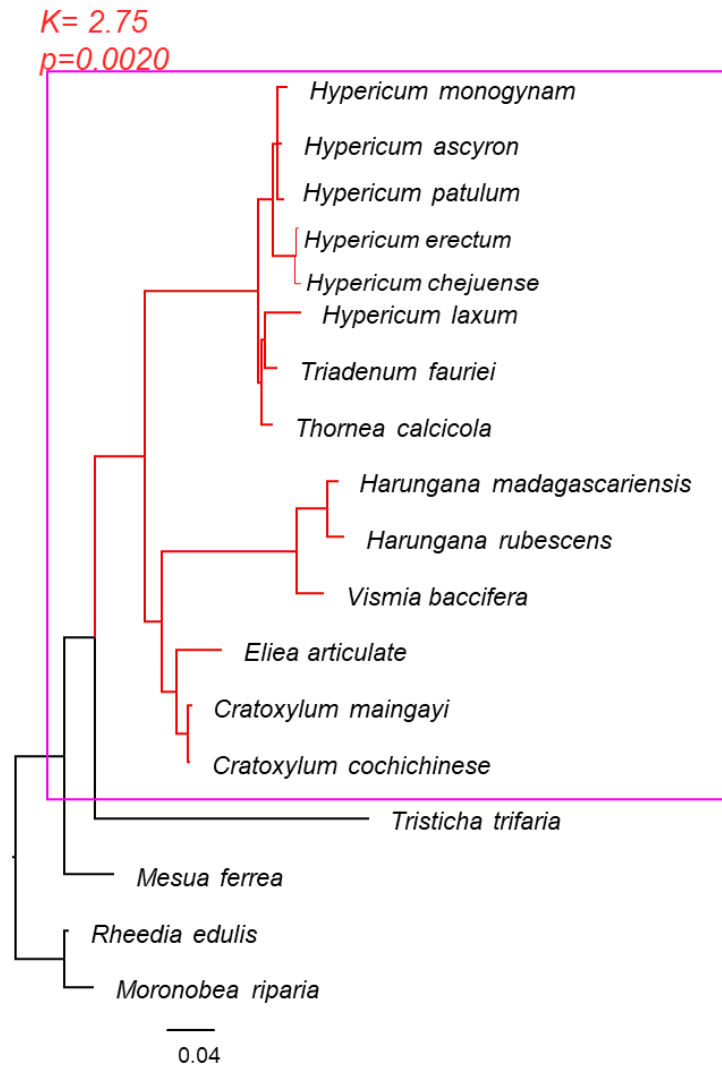
$K = 2.75$
 $p = 0.0000^{**}$



Supplementary Figure 11. RELAX analysis of the *accD* gene across Hypericaceae, with AICc = 55,274.65 and log-likelihood = -27,515. The results indicate selection intensification in species belonging to the Hypericeae tribe.

Supplementary Figure 13. Adaptive Branch-Site REL (aBSREL) analysis of the *matK* gene across Hypericaceae. The model (AICc = 16,127.38; log L = 7,962.65) detected episodic positive selection in specific branches, particularly within the Hypericeae tribe.





Supplementary Figure 14. RELAX and aBSREL analyses of the *matK* gene conducted in a phylogenetic framework. The results ($\log L = -8,024.39$; $AICc = 16,151.36$) indicate that the designated test group (Hyp) exhibits signatures of episodic positive selection.



Supplementary Figure 15. Results of adaptive Branch-Site REL (aBSREL) analysis of the *clpP* gene. Branches highlighted in red represent lineages inferred to be under episodic positive selection based on the full adaptive model.

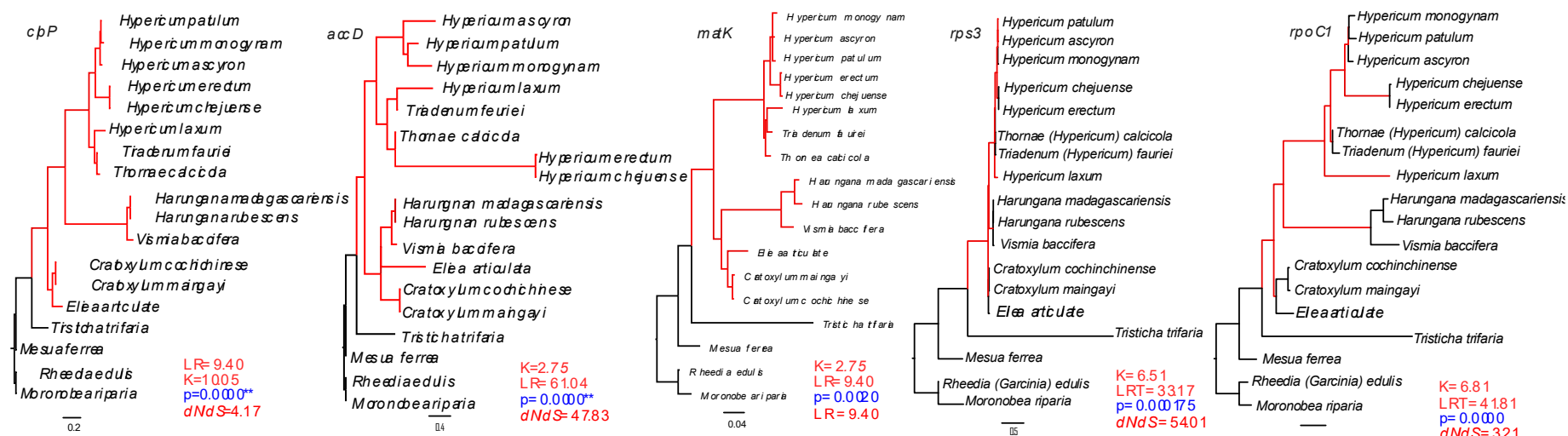
ABSRAL								
gene	node	LRT	dN/dS	Full adaptive model	<i>dN</i>	<i>dS</i>	P-value	BRANCH
<i>rpoA</i>	Node12	11.13377	1.034032	8.800139	8.794013	0.006127	0.001316	Branch leads to <i>Hypericum</i> genus
	Node6	12.87216	0.929769	2646.61	2646.592	0.018273	0.000548	Branch leads to <i>Vismieae</i> tribe
	Node7	12.73453	0.788571	0.130307	0.126824	0.003483	0.000587	Branch leads to <i>Harungana</i> genus
<i>rpoC2</i>	Node11	10.78871	0.556744	0.067508	0.055539	0.011969	0.001567	Branch leads to <i>Hypericeae</i> tribe

Supplementary Table 2. Evidence of positive selection in plastid genes of Hypericaceae species as detected by the aBSREL model. The table includes key parameters from the analysis: LRT: Likelihood ratio test, AICc; Akaike information criterion, *p*-posterior probability, K- Co-efficient, dN/dS- Ratio of non-synonymous to synonymous substitution rates.

RELAX								
gene	selection	K	p	LRT	wHyp	wRef	AICc alternative	AICc null
<i>cemA</i>	intensification	5.24	0.0000**	23.34	0.9973	0.3334	7661.6	7682.9
<i>rpl33</i>	intensification	4.52	0.00312	8.73	0.3478	0.4066	2201.1	2207.6
<i>rpl36</i>	intensification	6.24	0.0090	6.73	0.1509	0.7948	1125.4	1129.6
<i>rps3</i>	intensification	6.51	0.0000**	33.17	0.4664	0.2866	8629.7	8646.4
<i>rps12</i>	intensification	11.1	0.0000**	25.09	0.5671	0.1245	2995.6	3018.6
<i>rpoC1</i>	intensification	6.81	0.0000**	41.81	0.9195	0.3022	13271.8	13311.6

Supplementary Table 3. Positive selection detected in plastid genes of Hypericaceae species based on the RELAX model.

The table summarizes model parameters used to assess shifts in selection intensity: LRT: Likelihood ratio test, AICc; Akaike information criterion, p-posterior probability, K- Co-efficient, dN/dS - Ratio of non-synonymous to synonymous substitution rates.



Supplementary Figure 16. Detection of selection intensity shifts in plastid genes of Hypericaceae species using the RELAX model.

Red-highlighted branches indicate lineages under intensified selection. Each panel represents a different plastid gene (*clpP*, *accD*, *matK*, *rps3*, and *rpoC1*), with associated RELAX model parameters shown below each tree.