

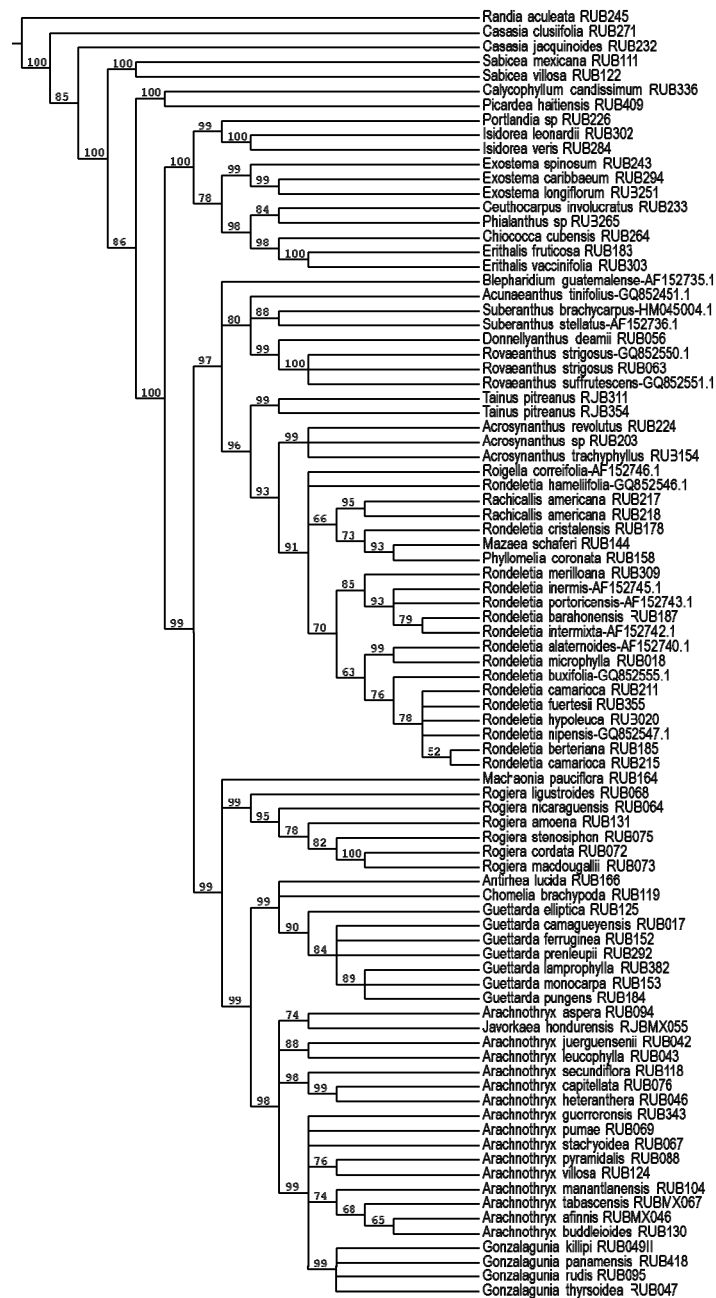
# Willdenowia 47(3) – Electronic supplement

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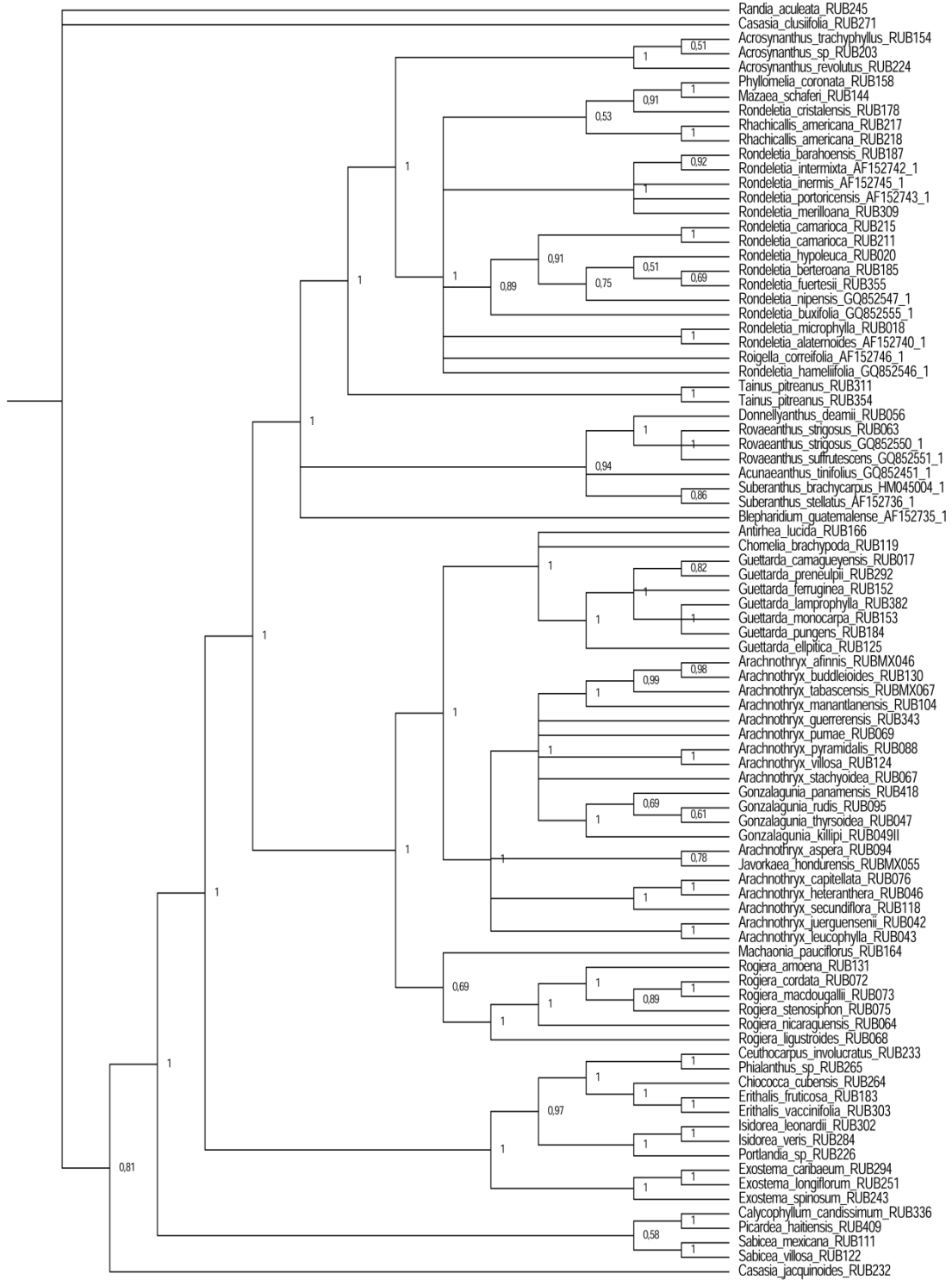
## The new Hispaniolan genus *Tainus* (*Rubiaceae*) constitutes an isolated lineage in the Caribbean biodiversity hotspot

Electronic supplement to: Torres-Montúfar A., Borsch T., Fuentes S., Clase T., Peguero B. & Ochoterena H. 2017: The new Hispaniolan genus *Tainus* (*Rubiaceae*) constitutes an isolated lineage in the Caribbean biodiversity hotspot. – Willdenowia 47: 259–270. doi: <https://doi.org/10.3372/wi.47.47309>

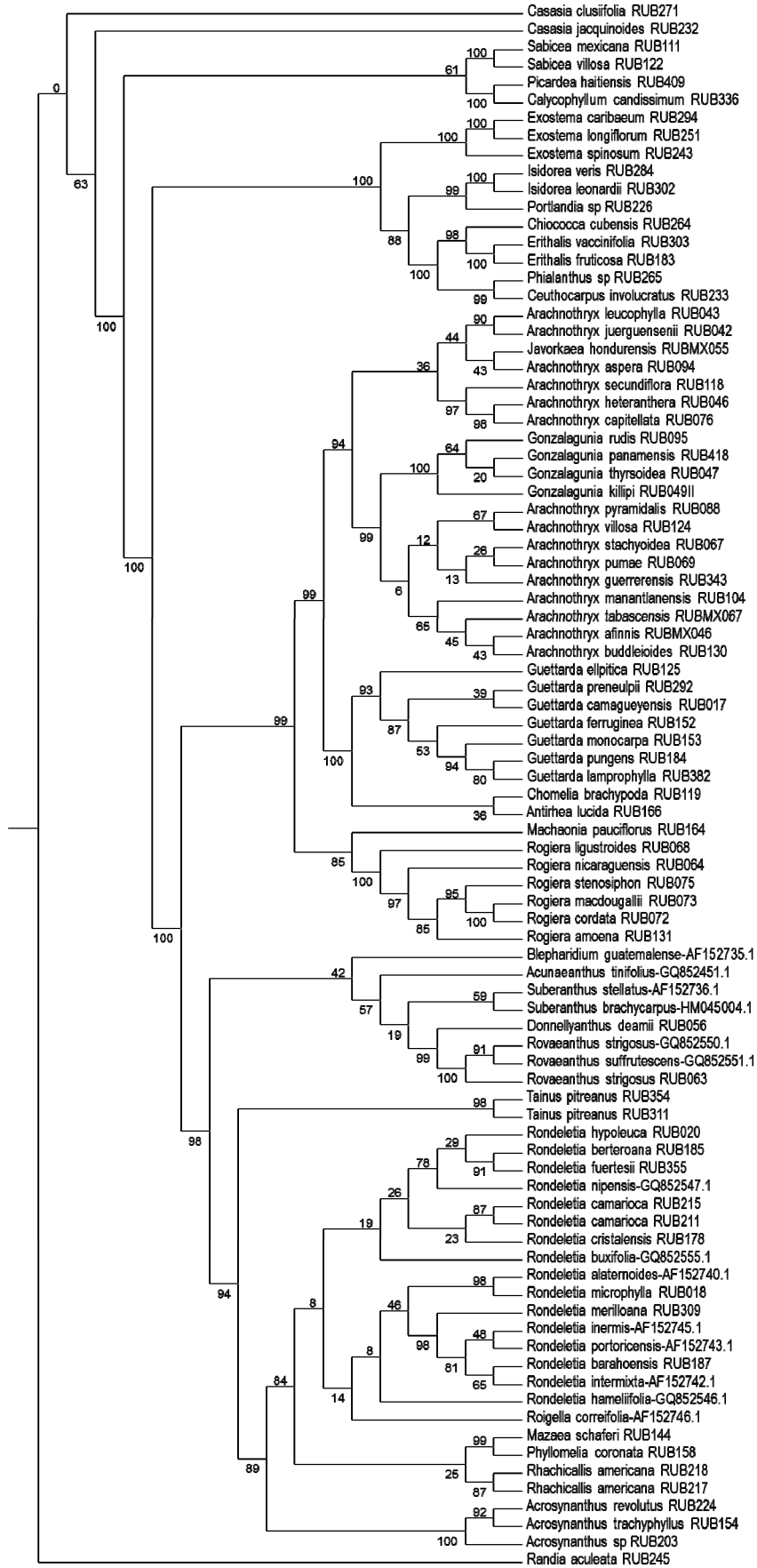
### Appendix 2. Phylogenetic trees



1. Parsimony tree. Consensus tree (L = 1702, Ci = 0.61, Ri = 0.84) from more than 1500 most parsimonious trees (L = 1681, Ci = 0.62, Ri = 0.84). Jackknife values are shown.



2. Bayesian tree. Posterior probabilities are shown.



3. Maximum likelihood best tree. Model of substitution: GTR+G+I. Likelihood score:  $-ln = 7248.75198$ . Bootstrap values are shown.

### Appendix 3. Lists of microstructural characters

#### 1. List of microstructural characters and their aligned positions found in the *trnK-matK* region coded as absent/present unless otherwise stated

##### Gaps

1. 7
2. 54–55
3. 55
4. 65
5. 91
6. 134–135
7. 190
8. 259–260
9. 260
10. 279–287
11. 283
12. 300
13. 316
14. 409
15. 510–515
16. 520–521
17. 568–572
18. 638
19. 900
20. 936
21. 958
22. 1017
23. 1236–1244
24. 1847
25. 1927
26. 2270–2283
27. 2319
28. 2369–2377
29. 2389
30. 2581

##### SSRs

1. 145–148: AATT
2. 180–181: TT
3. 330–339: GT (3 repeats = 0; 4 repeats = 1; 5 repeats = 2)
4. 360–363: TGAT
5. 458–467: ACTAAAAATG
6. 504–509: GTTTAT
7. 556–567: CTAGAATACTTT
8. 689–694: CAACAA
9. 1228–1233: TGGAAT
10. 1247–1252: ATGATA
11. 1642–1647: ATAAAA
12. 2050–2055: TTGAAA
13. 2144–2164: CAAGAACTTCTTCTACTTTTT
14. 2297–2302: GACAAA
15. 2350–2361: double GTAAT
16. 2592–2596: TTATT
17. 2736–2741: TTTCTA

**2. List of microstructural characters and their aligned positions found in the *petD* region coded as absent/present**

**Gaps**

1. 38
2. 115
3. 116
4. 193
5. 317–324
6. 377
7. 441–450
8. 459–465
9. 488–492
10. 493–497
11. 603
12. 689
13. 694
14. 725
15. 825
16. 861
17. 884–888
18. 903–907
19. 914–916
20. 914–931
21. 948–952
22. 1004

**SSRs**

1. 24–31: TTGGAGAA
2. 167–172: TTGAAG
3. 268–269: AA
4. 309–131: CGTAA
5. 328–332: AGAGG
6. 421–425: ATAAT
7. 426–434: CAGTATAAT
8. 506–526: AAAATAGAGTTATCTATTCA
9. 536–540: CTTAA
10. 548–563: CTTACTTAAGATTTAA
11. 687–688: GT
12. 776–778: AGT
13. 781–785: TGTA
14. 864–865: AA

**Inversions**

1. 135–152: TGTCAAATAAATAATATT/AATATTATTTATTTGACA
2. 466–472: AATAGAG/CTCTATT
3. 473–487: CTAATAAATAATATAG/CTATATTTTTTTTAG
4. 827–833: TTCTTT/AAAGAA

**3. List of microstructural characters and their aligned positions found in the *trnL-F* region coded as absent/present****Gaps**

1. 30
2. 86–89
3. 166–174
4. 227–230
5. 231–232
6. 264
7. 442
8. 527
9. 541–542
10. 617
11. 618
12. 646–653
13. 802–811


**SSRs**

1. 252–262: CAATACTATAT
2. 269–273: CAAAT
3. 389–392: TGAT
4. 426–430: TTTTC
5. 483–493: TTCTACATGCT
6. 667–671: CTCTT
7. 683–692: GAAATAGATC
8. 696–715: TCTCTTAGAAATAGATCTTGG
9. 731–734: CTTT
10. 753–754: GT
11. 755–757: TGT
12. 762–771: TCTTGTTATA
13. 787–791: ATACA
14. 792–798: CAATACA

**Inversion**

1. 420–422: TTC/GAA

**Willdenowia**

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