File S-III. Results of likelihood mapping analyzes of datasets of different generas and phylogenetic analysis.

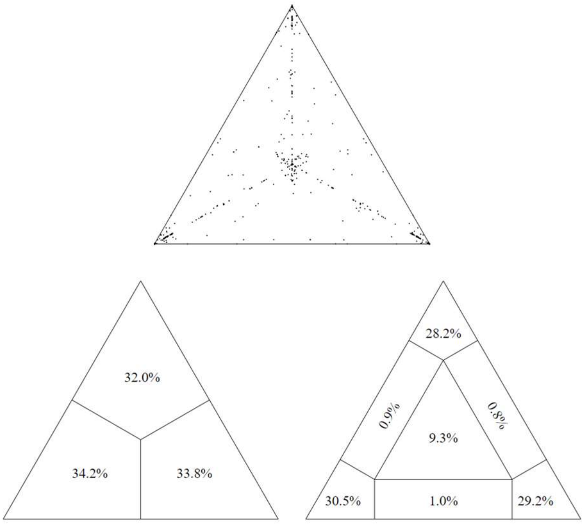


Figure S-III 1. Result of the likelihood mapping analysis of the *Aedeomyia* genus dataset: Input data: 16 sequences with 633 nucleotide sites, constant number of sites: 320 (= 50.6% of all sites). Number of resolved quartets (regions 1 + 2 + 3): 1601 (= 87.97%); number of partially resolved quartets (regions 4 + 5 + 6): 50 (= 2.75%): Number of unresolved quartets (region 7): 169 (= 9.29%).

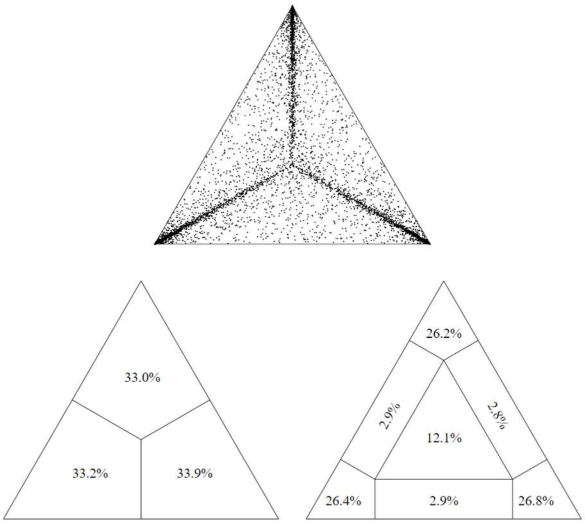


Figure S-III 2. Result of likelihood mapping analysis of the *Aedes* genus dataset: Input data: 173 sequences with 632 nucleotide sites, constant number of sites: 255 (= 40.3% of all sites). Number of resolved quartets (regions 1 + 2 + 3): 7941 (= 79.41%); number of partially resolved quartets (regions 4 + 5 + 6): 850 (= 8.50%); number of unresolved quartets (region 7): 1209 (= 12.09%).

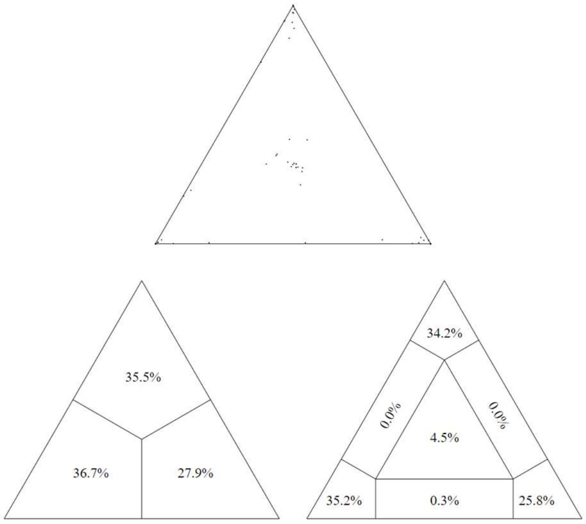


Figure S-III 3. Result of the likelihood mapping analysis of the *Eretmapodites* genus dataset: Input data: 11 sequences with 636 nucleotide sites, constant number of sites: 333 (= 52.4% of all sites). Number of resolved quartets (regions 1 + 2 + 3): 314 (= 95.15%); number of partially resolved quartets (regions 4 + 5 + 6): 1 (= 0.30%); number of unresolved quartets (region 7): 15 (= 4.55%).

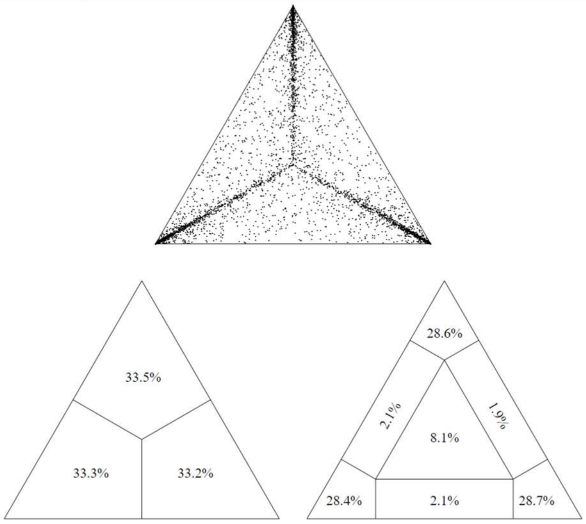


Figure S-III 4. Result of likelihood mapping analysis of the *Culex* and *Lutzia* genera datasets: Input data: 171 sequences with 636 nucleotide sites, constant number of sites: 213 (= 33.5% of all sites). Number of resolved quartets (regions 1 + 2 + 3): 8581 (= 85.81%); number of partially resolved quartets (regions 4 + 5 + 6): 606 (= 6.06%); number of unresolved quartets (region 7): 813 (= 8.13%).

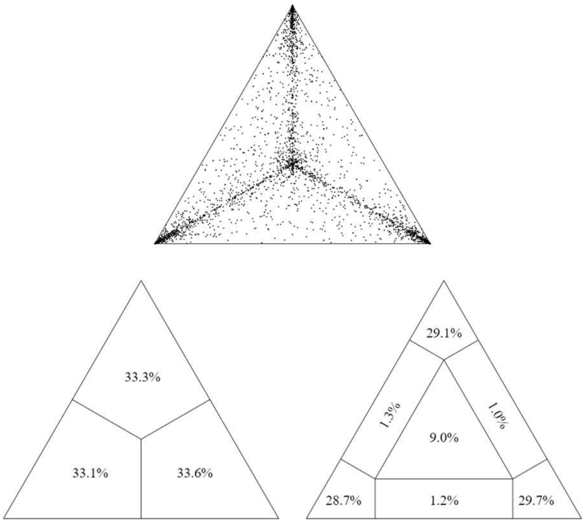


Figure S-III 5. Result of likelihood mapping analysis of the *Coquillettidia* genus dataset: Input data: 27 sequences with 636 nucleotide sites, constant number of sites: 388 (= 61.0% of all sites). Number of resolved quartets (regions 1 + 2 + 3): 8739 (= 87.39%); number of partially resolved quartets (regions 4 + 5 + 6): 357 (= 3.57%); number of unresolved quartets (region 7): 904 (= 9.04%).

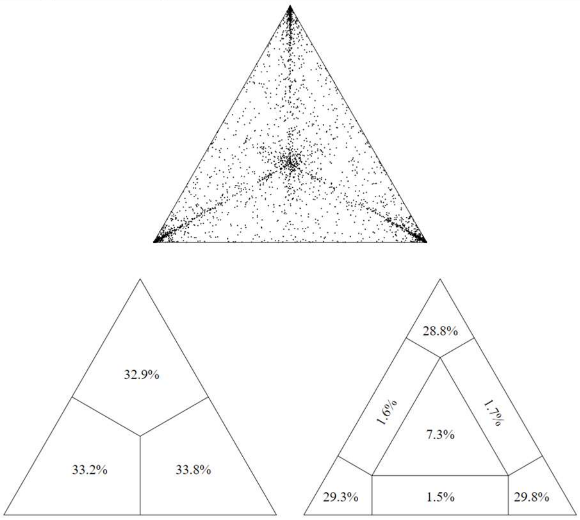


Figure S-III 6. Result of likelihood mapping analysis of the *Mansonia* genus dataset: Input data: 32 sequences with 636 nucleotide sites, constant number of sites: 279 (= 43.9% of all sites). Number of resolved quartets (regions 1 + 2 + 3): 8790 (= 87.90%); number of partially resolved quartets (regions 4 + 5 + 6): 475 (= 4.75%); number of unresolved quartets (region 7): 735 (= 7.35%).

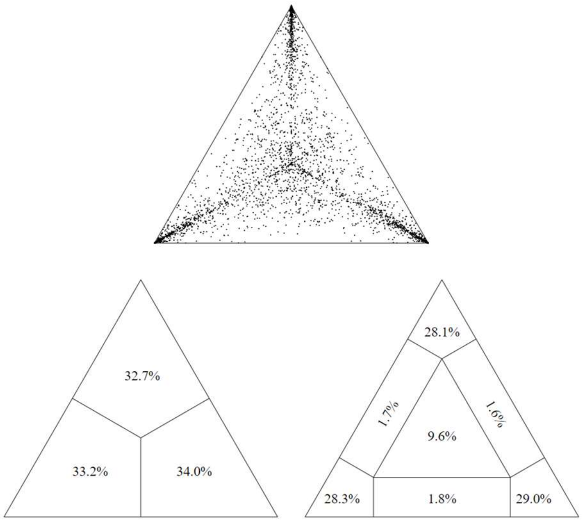


Figure S-III 7. Result of likelihood mapping analysis of the *Ficalbia* and *Mimomyia* genera datasets: Input data: 34 sequences with 636 nucleotide sites, constant number of sites: 235 (= 36.9% of all sites). Number of resolved quartets (regions 1 + 2 + 3): 8534 (= 85.34%); number of partially resolved quartets (regions 4 + 5 + 6): 510 (= 5.10%), number of unresolved quartets (region 7): 956 (= 9.56%).

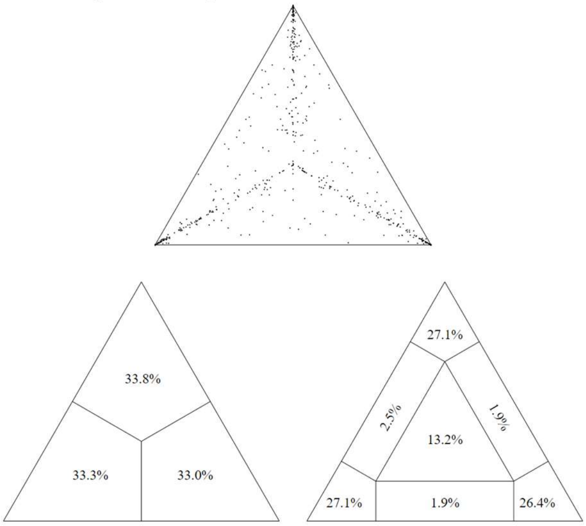


Figure S-III 8. Result of the likelihood mapping analysis of the *Uranotaenia* genus dataset: Input data: 14 sequences with 636 nucleotide sites, constant number of sites: 328 (= 51.6% of all sites). Number of resolved quartets (regions 1 + 2 + 3): 806 (= 80.52%); number of partially resolved quartets (regions 4 + 5 + 6): 63 (= 6.29%); number of unresolved quartets (region 7): 132 (= 13.19%).

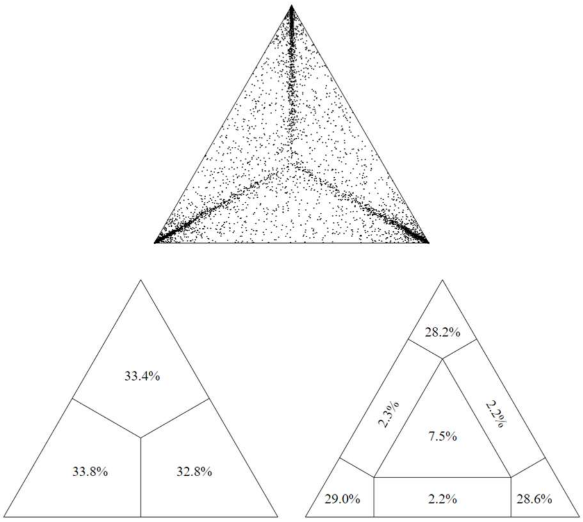


Figure S-III 9. Result of likelihood mapping analysis of the genera datasets *Aedeomyia*, *Aedes*, *Eretmapodites*, *Culex*, *Lutzia*, *Coquillettidia*, *Mansonia*, *Mimomyia* and *Uranotaenia*: Input data: 180 sequences with 632 nucleotide sites, number of constant sites: 164 (= 25.9% of all websites). Number of resolved quartets (regions 1 + 2 + 3): 8573 (= 85.73%); number of partially resolved quartets (regions 4 + 5 + 6): 673 (= 6.73%); number of unresolved quartets (region 7): 754 (= 7.54%).

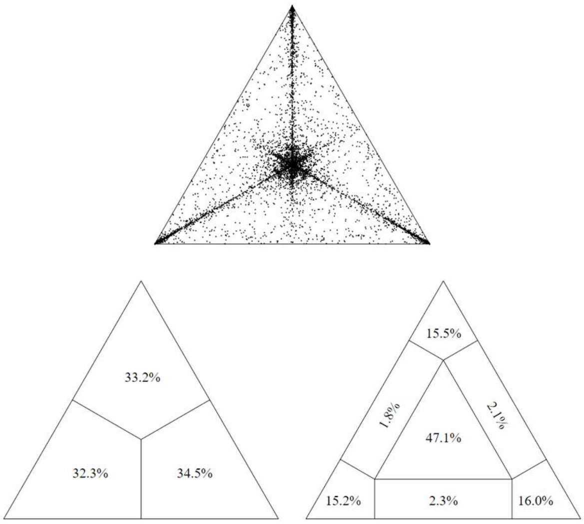


Figure S-III 10. Result of likelihood mapping analysis of the Bitaeniorhynchus complex dataset: Input data: 47 sequences with 653 nucleotide sites, constant number of sites: 323 (= 49.5% of all sites). Number of resolved quartets (regions 1 + 2 + 3): 4667 (= 46.67%); number of partially resolved quartets (regions 4 + 5 + 6): 622 (= 6.22%); number of unresolved quartets (region 7): 4711 (= 47.11%).

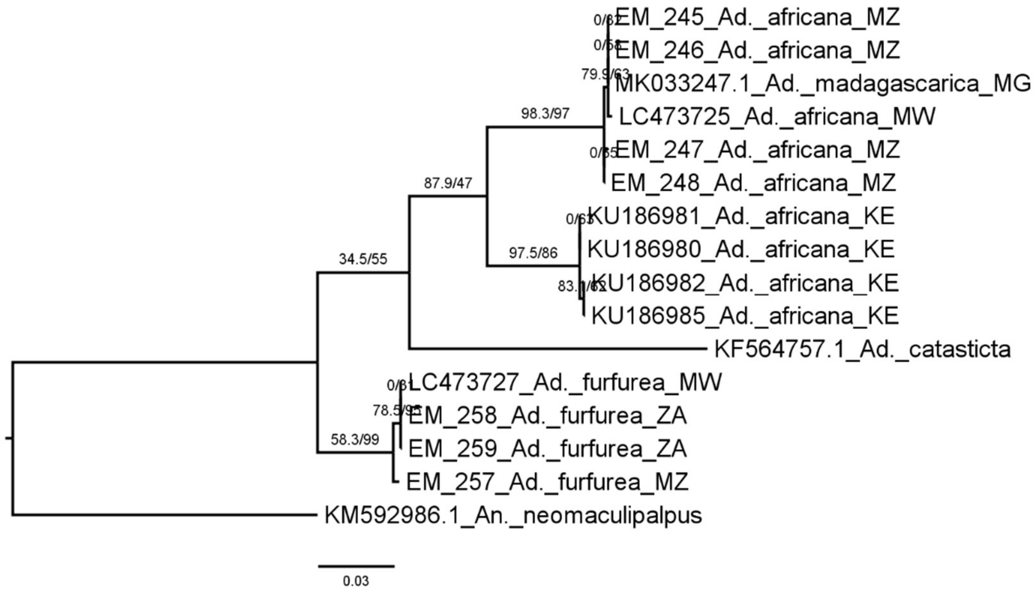


Figure S-III 11. Maximum likelihood tree under the GTR+G model for *Aedeomyia* genus, analysis involved 16 nucleotide sequences with 633 positions in the final dataset, consensus tree probability was -1663,651. Support values for the branches were estimated with aLRT/Bootstrap with 1000 repetitions for each method. The size bar indicates 0.03 replacements per site. The analysis was performed on IQtree.

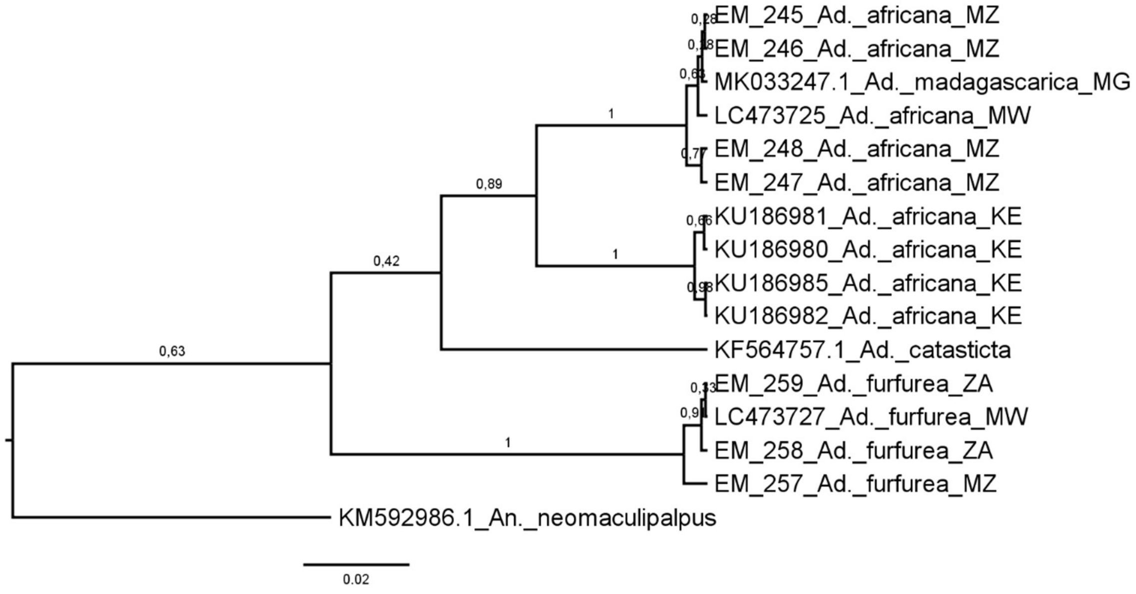
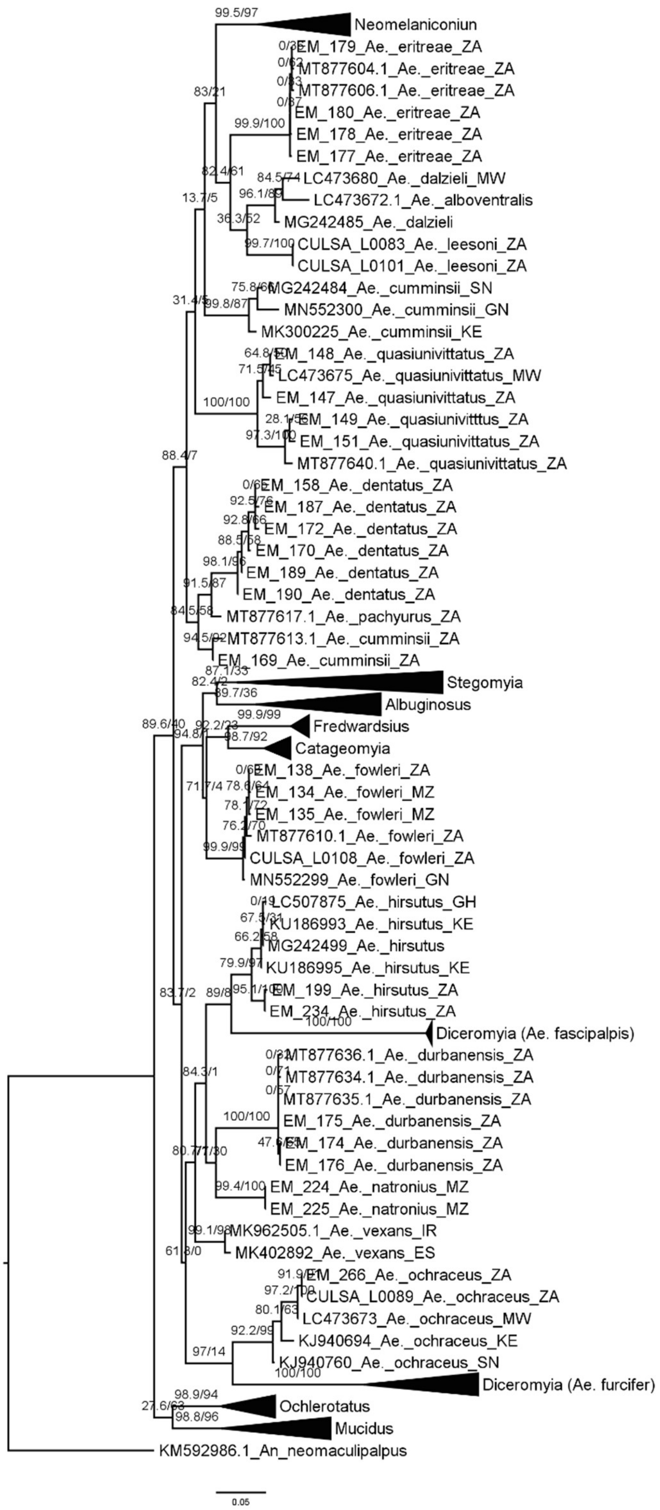


Figure S-III 12. Topology inferred by Bayesian inference under the GTR+G model for the genus *Aedeomyia*, the analysis involved 16 nucleotide sequences with 633 positions in the final dataset. Support values correspond to a posteriori probability. The size bar indicates 0.02 replacements per site. The analysis was done in Beast.

a)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EM_177_Ae._eritreae_ZA
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99.9/100
82.4/61
84.5/74
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96.1/89
13.7/5
36.3/52
MG242485_Ae._dalzieli
99.7/100
CULSA_L0083_Ae._leesoni_ZA
CULSA_L0101_Ae._leesoni_ZA
75.8/66
MG242484_Ae._cumminsii_SN
31.4/5
99.8/87
MN552300_Ae._cumminsii_GN
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64.8
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71.5
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28.1
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97.3/100
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92.5/76
EM_187_Ae._dentatus_ZA
92.8/66
EM_172_Ae._dentatus_ZA
88.5/68
EM_170_Ae._dentatus_ZA
98.1/96
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91.5/87
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Albuginosus
99.9/99
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94.8
92.2/23
Fredwardsius
98.7/92
Catageomyia
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71.7/4
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83.7/2
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95.1/100
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EM_234_Ae._hirsutus_ZA
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71/30
47.6
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100/100
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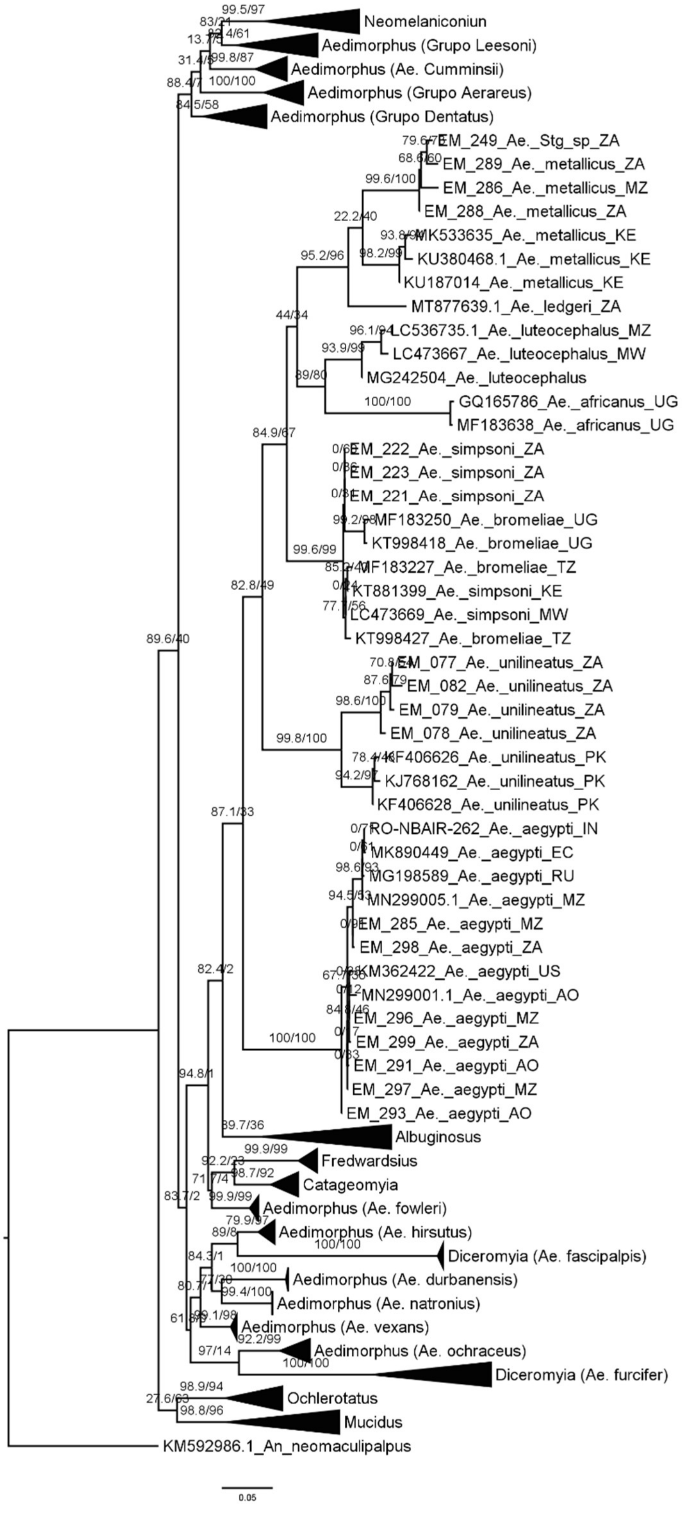
98.8/96
Mucidus
KM592986.1_An_neomaculipalpus
0.05

b)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82.4/61
13.7/5
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31.4/8
99.8/87
Aedimorphus (Ae. Cumminsii)
88.4/7
100/100
Aedimorphus (Grupo Aerareus)
84.5/58
Aedimorphus (Grupo Dentatus)
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98.2/99
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MG242504_Ae._luteocephalus
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EM_297_Ae._aegypti_MZ
EM_293_Ae._aegypti_AO
89.7/36
Albuginosus
99.9/99
92.2/23
Fredwardsius
71.7/4
98.7/92
Catageomyia
83.7/2
99.9/99
Aedimorphus (Ae. fowleri)
79.9/97
89/8
Aedimorphus (Ae. hirsutus)
100/100
Diceromyia (Ae. fascipalpis)
84.3/1
100/100
Aedimorphus (Ae. durbanensis)
80.7/20
99.4/100
Aedimorphus (Ae. natronius)
61.8/2
99.1/98
Aedimorphus (Ae. vexans)
92.2/99
Aedimorphus (Ae. ochraceus)
97/14
100/100
Diceromyia (Ae. furcifer)
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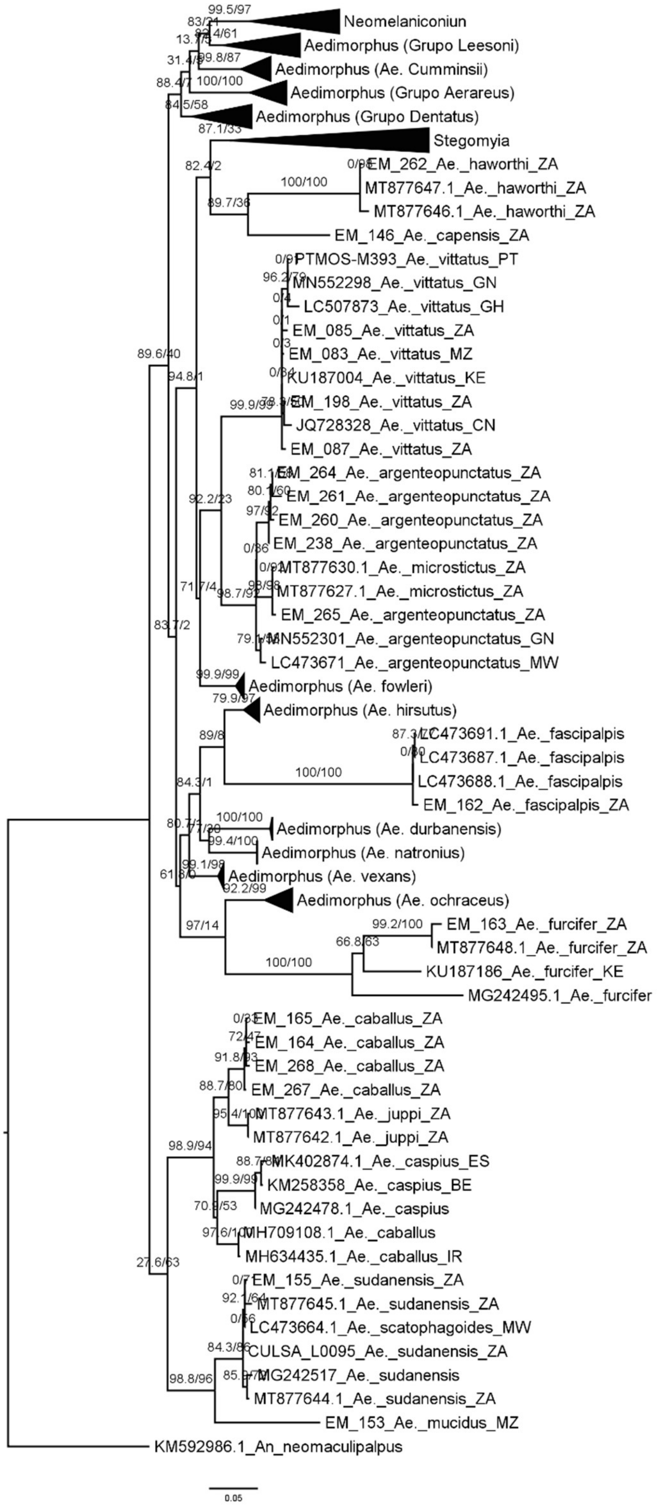
27.6/63
98.8/96
Mucidus
KM592986.1_An_neomaculipalpus
0.05

c)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13.7/5
31.4/9
99.8/87
Aedimorphus (Ae. Cumminsii)
88.4/7
100/100
Aedimorphus (Grupo Aerareus)
84.5/58
Aedimorphus (Grupo Dentatus)
87.1/33
Stegomyia
82.4/2
0/98
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0/4
LC507873_Ae._vittatus_GH
0/1
EM_085_Ae._vittatus_ZA
0/3
EM_083_Ae._vittatus_MZ
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0/84
KU187004_Ae._vittatus_KE
94.8/1
99.9/99
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92.2/23
97/92
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79.9/97
Aedimorphus (Ae. hirsutus)
89/8
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0/80
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84.3/1
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100/100
80.7/1
77/30
Aedimorphus (Ae. durbanensis)
99.4/100
Aedimorphus (Ae. natronius)
99.1/98
61.8/0
Aedimorphus (Ae. vexans)
92.2/99
Aedimorphus (Ae. ochraceus)
99.2/100
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66.8/63
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0/56
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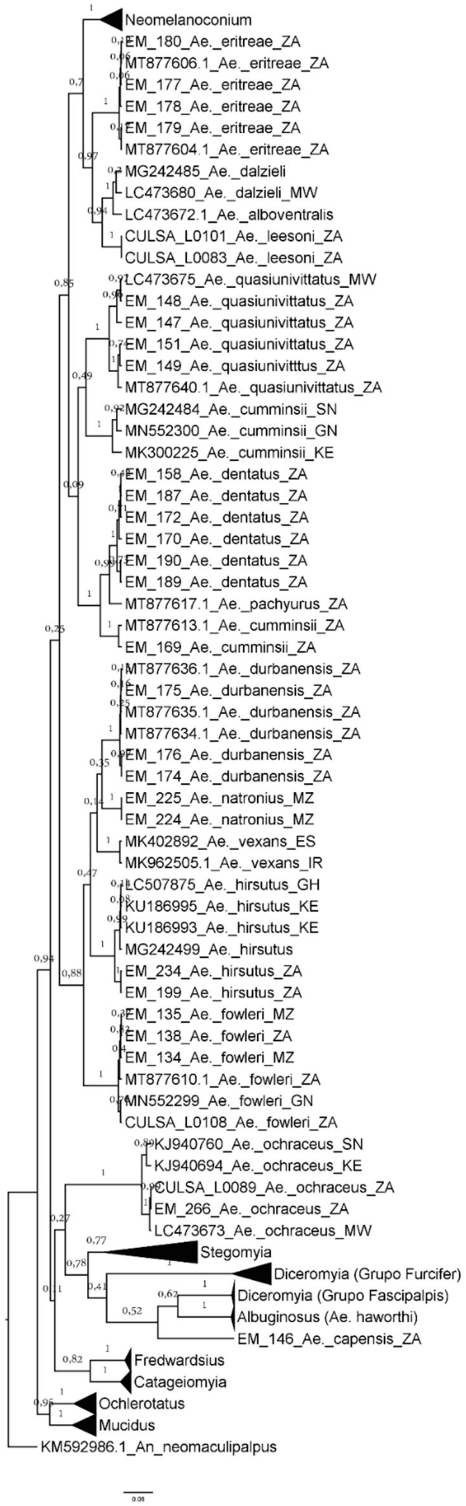
0.05

d)

Figure S-III 13. **a, b, c, d)** Maximum likelihood tree under the GTR+G+I model for *Aedes* genus, analysis involved 173 nucleotide sequences with 632 positions in the final dataset, consensus tree probability was -8262,917. Support values for the branches were estimated with aLRT/Bootstrap with 1000 repetitions for each method. The size bar indicates 0.05 replacements per site. The analysis was performed on IQtree.

a)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KU186995_Ae._hirsutus_KE
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MN552299_Ae._fowleri_GN
CULSA_L0108_Ae._fowleri_ZA
KJ940760_Ae._ochraceus_SN
KJ940694_Ae._ochraceus_KE
CULSA_L0089_Ae._ochraceus_ZA
EM_266_Ae._ochraceus_ZA
LC473673_Ae._ochraceus_MW
Stegomyia
Diceromyia (Grupo Furcifer)
Diceromyia (Grupo Fascipalpis)
Albuginosus (Ae. haworthi)
EM_146_Ae._capensis_ZA
Fredwardsius
Catageiomyia
Ochlerotatus
Mucidus
KM592986.1_An_neomaculipalpus
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0,94
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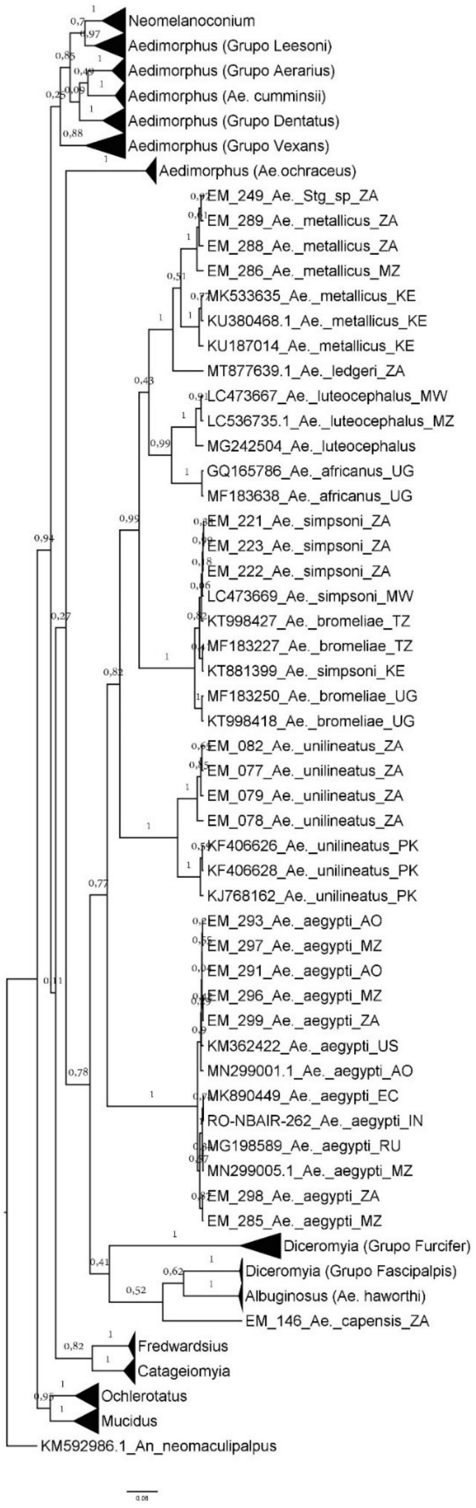
b)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Aedimorphus (Grupo Aerarius)
Aedimorphus (Ae. cumminsii)
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Aedimorphus (Grupo Vexans)
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Diceromyia (Grupo Fascipalpis)
Albuginosus (Ae. haworthi)
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Fredwardsius
Catageiomyia
Ochlerotatus
Mucidus
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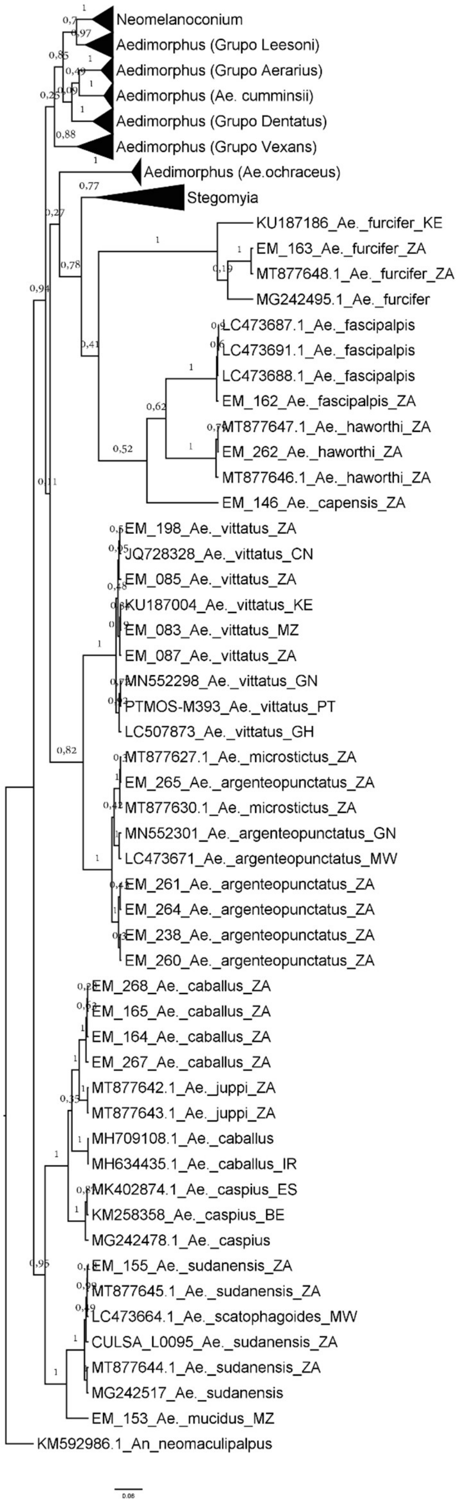
c)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Aedimorphus (Grupo Aerarius)
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Aedimorphus (Grupo Vexans)
Aedimorphus (Ae.ochraceus)
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d)

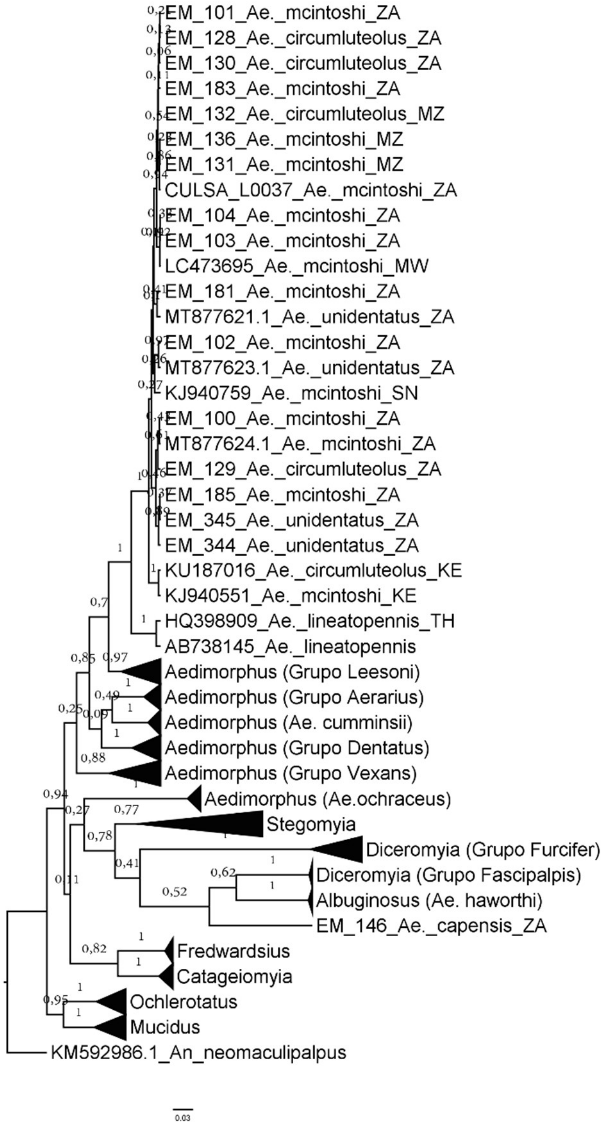


Figure S-III 14. **a, b, c, d)** Topology inferred by Bayesian inference under the GTR+G+1 model for the genus *Aedes*, the analysis involved 173 nucleotide sequences with 632 positions in the final dataset. Support values correspond to a posteriori probability. The size bar indicates 0.03 replacements per site. The analysis was done in Beast.

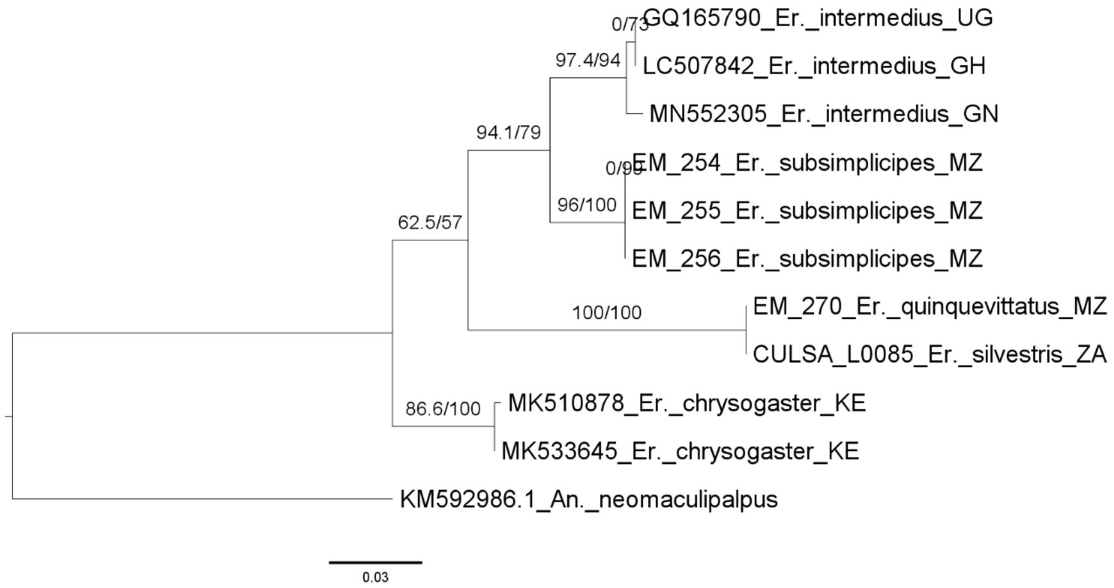


Figure S-III 15. Maximum likelihood tree under the GTR+I model for *Eretmapodites* genus, analysis involved 11 nucleotide sequences with 636 positions in the final dataset, probability of consensus tree was -1680,980. Support values for the branches were estimated with aLRT/Bootstrap with 1000 repetitions for each method. The size bar indicates 0.03 replacements per site. The analysis was performed on IQtree.

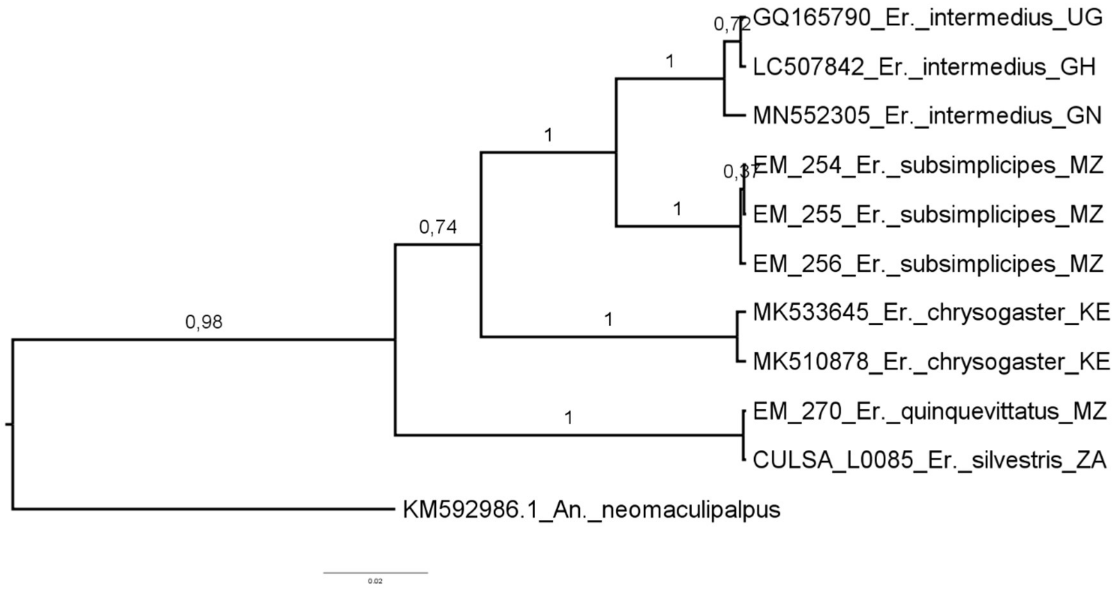
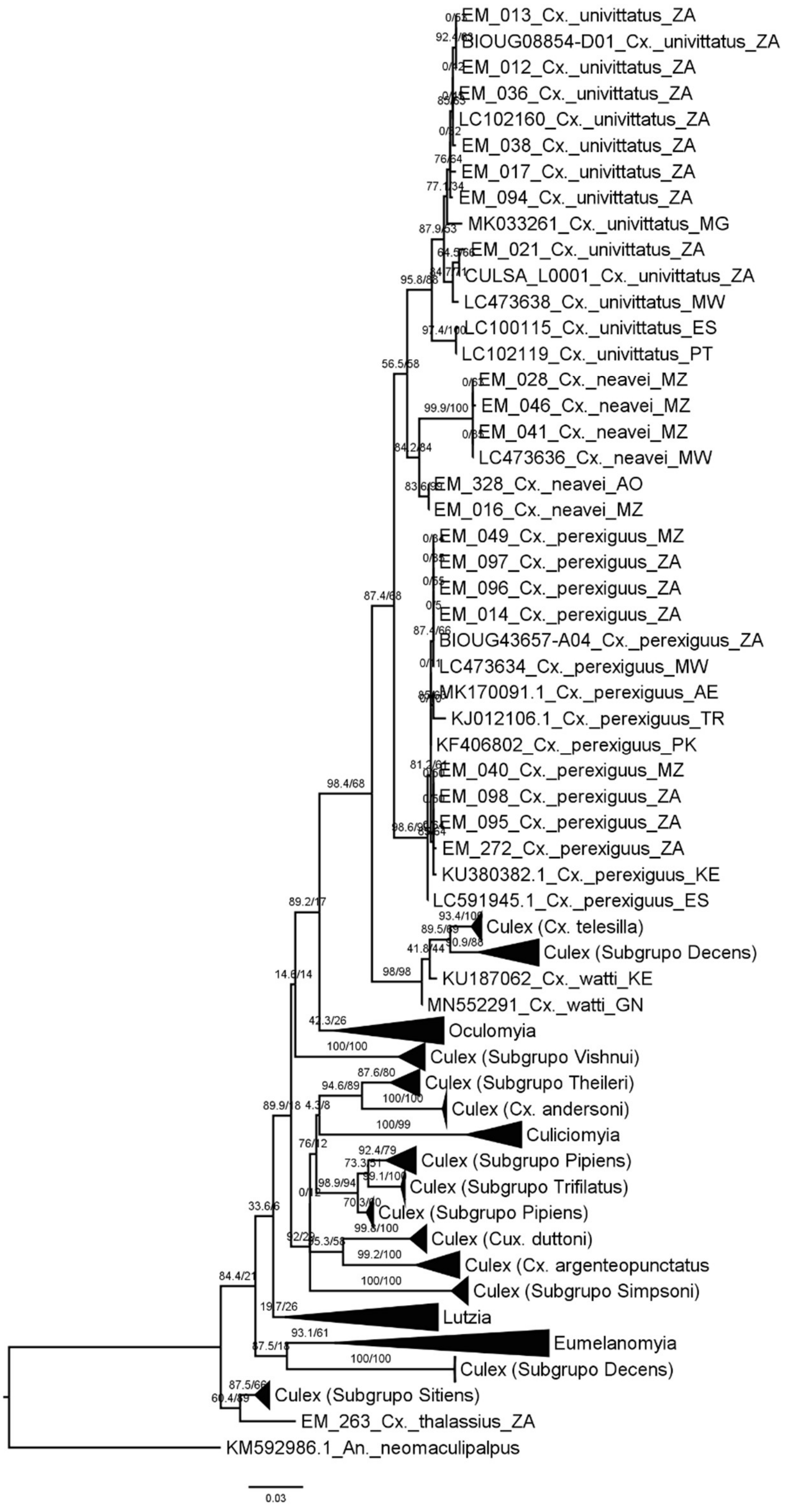


Figure S-III 16. Topology inferred by Bayesian inference under the GTR+1 model for the genus *Eretmapodites*, the analysis involved 11 nucleotide sequences with 636 positions in the final dataset. Support values correspond to a posteriori probability. The size bar indicates 0.02 replacements per site. The analysis was performed using the Beast program.

a)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EM_038_Cx._univittatus_ZA
EM_017_Cx._univittatus_ZA
EM_094_Cx._univittatus_ZA
MK033261_Cx._univittatus_MG
EM_021_Cx._univittatus_ZA
CULSA_L0001_Cx._univittatus_ZA
LC473638_Cx._univittatus_MW
LC100115_Cx._univittatus_ES
LC102119_Cx._univittatus_PT
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EM_046_Cx._neavei_MZ
EM_041_Cx._neavei_MZ
LC473636_Cx._neavei_MW
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EM_016_Cx._neavei_MZ
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EM_095_Cx._perexiguus_ZA
EM_272_Cx._perexiguus_ZA
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LC591945.1_Cx._perexiguus_ES
Culex (Cx. telesilla)
Culex (Subgrupo Decens)
KU187062_Cx._watti_KE
MN552291_Cx._watti_GN
Oculomyia
Culex (Subgrupo Vishnui)
Culex (Subgrupo Theileri)
Culex (Cx. andersoni)
Culiciomyia
Culex (Subgrupo Pipiens)
Culex (Subgrupo Trifilatus)
Culex (Subgrupo Pipiens)
Culex (Cux. duttoni)
Culex (Cx. argenteopunctatus
Culex (Subgrupo Simpsoni)
Lutzia
Eumelanomyia
Culex (Subgrupo Decens)
Culex (Subgrupo Sitiens)
EM_263_Cx._thalassius_ZA
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0/42
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0/52
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64.5/66
95.8/88
97.4/100
56.5/58
0/65
99.9/100
0/85
84.2/84
83.6/95
0/84
0/85
0/55
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87.4/66
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81.2/61
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98/98
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b)


87.4/68
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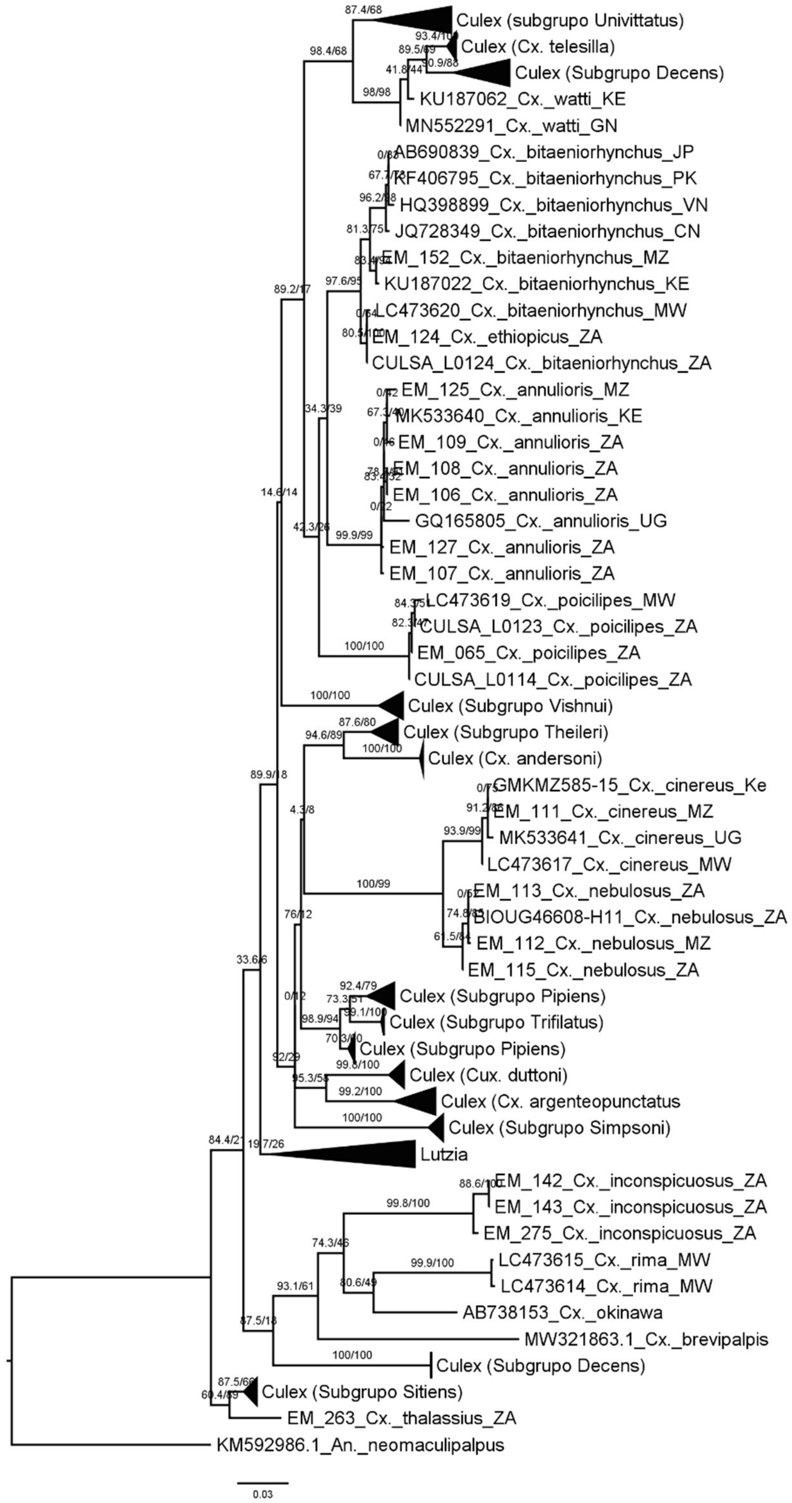
c)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41.8/44
98/98
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95.3/58
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d)

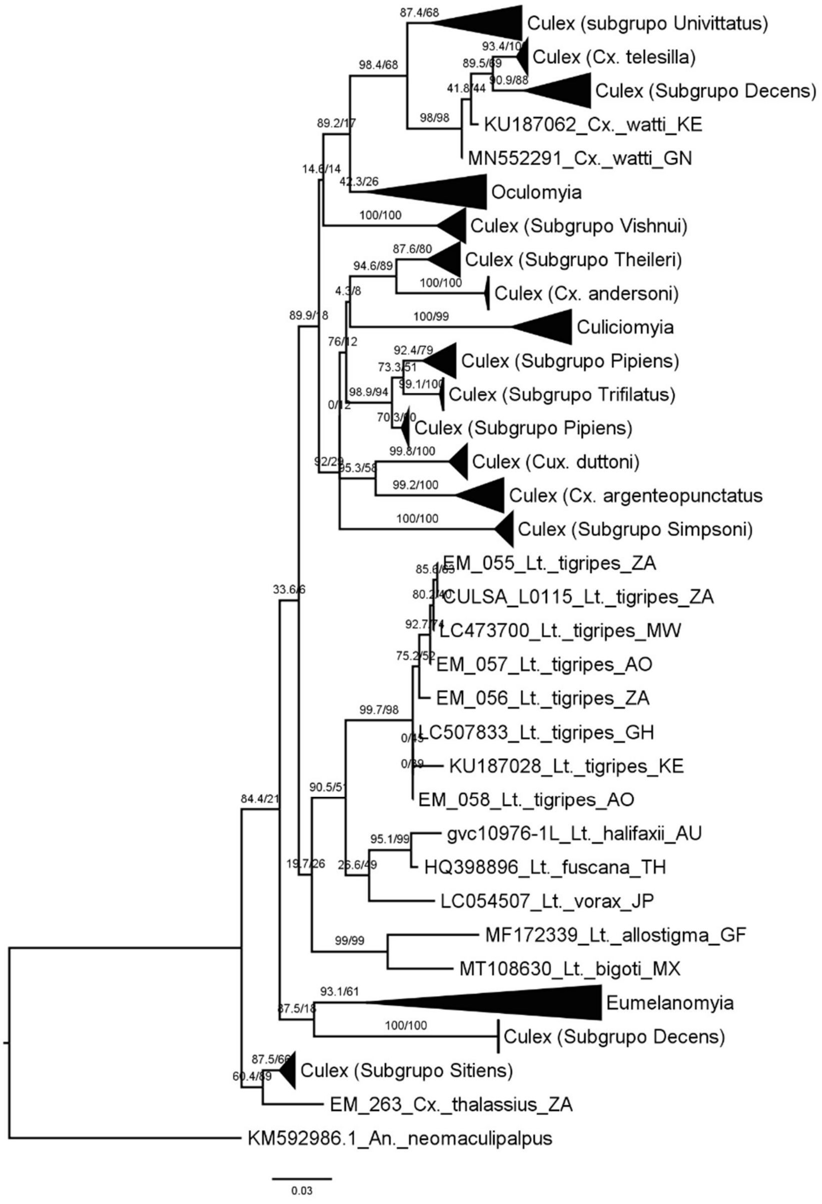
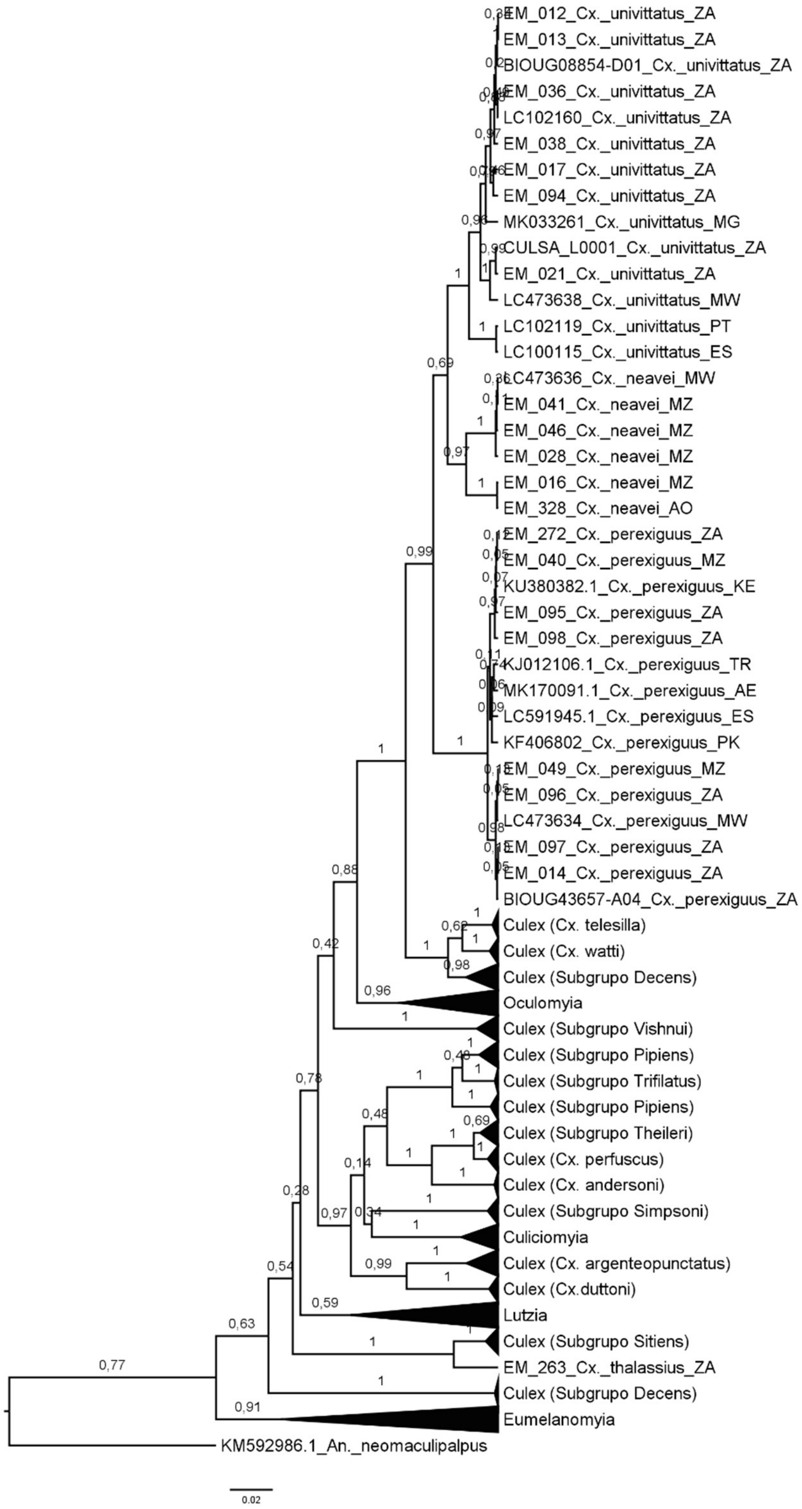


Figure S-III 17. **a, b, c, d)** Maximum likelihood tree under the GTR+G+I model for *Culex* and *Lutzia* genera, analysis involved 171 nucleotide sequences with 636 positions in the final dataset, consensus tree probability was -6105,653. Support values for the branches were estimated with aLRT/Bootstrap with 1000 repetitions for each method. The size bar indicates 0.03 replacements per site. The analysis was performed on IQtree.

a)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Culex (Cx. watti)
Culex (Subgrupo Decens)
Oculomyia
Culex (Subgrupo Vishnui)
Culex (Subgrupo Pipiens)
Culex (Subgrupo Trifilatus)
Culex (Subgrupo Pipiens)
Culex (Subgrupo Theileri)
Culex (Cx. perfuscus)
Culex (Cx. andersoni)
Culex (Subgrupo Simpsoni)
Culiciomyia
Culex (Cx. argenteopunctatus)
Culex (Cx.duttoni)
Lutzia
Culex (Subgrupo Sitiens)
EM_263_Cx._thalassius_ZA
Culex (Subgrupo Decens)
Eumelanomyia
KM592986.1_An._neomaculipalpus
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b)


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1
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KU187062_Cx._watti_KE
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0,98
EM_074_Cx._decens_ZA
MK033250_Cx._decens_MG
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Oculomyia
0,42
0,71
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MF179223_Cx._tritaeniorhynchus
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CULSA_L0055_Cx._tritaeniorhynchus_ZA
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EM_157_Cx._tritaeniorhynchus_ZA
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LC473656_Cx._quinquefasciatus_MW
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EM_340_Cx._quinquefasciatus_ZA
EM_334_Cx._quinquefasciatus_AO
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EM_310_Cx._quinquefasciatus_ZA
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MT506038_Cx._quinquefasciatus_ZA
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HG793522_Cx._pipiens
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EM_303_Cx._pipiens_ZA
EM_302_Cx._pipiens_ZA
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EM_331_Cx._sp_ZA
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0,91
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MT512681_Cx._theileri_ZA
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0,99
LC102115_Cx._theileri_PT
BIOUG49028-H06_Cx._theileri_PK
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LC473663_Cx._perfuscus_MW
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EM_031_Cx._andersoni_ZA
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EM_192_Cx._andersoni_ZA
EM_195_Cx._andersoni_ZA
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0,19
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EM_160_Cx._simpsoni_ZA
EM_026_Cx._simpsoni_MZ
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EM_032_Cx._simpsoni_ZA
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0,55
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Culiciomyia
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LC473630_Cx._duttoni_MW
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KU187073_Cx._duttoni_KE
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0,59
Lutzia
0,49
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MN398411_Cx._sitiens_MY
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MN733806_Cx._sitiens_NC
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JQ728396_Cx._sitiens_CN
EM_263_Cx._thalassius_ZA
0,77
0,18
EM_063_Cx._antennatus_ZA
0,05
EM_060_Cx._antennatus_MZ
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0,18
LC473659_Cx._antennatus_MW
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MK033248_Cx._antennatus_MG
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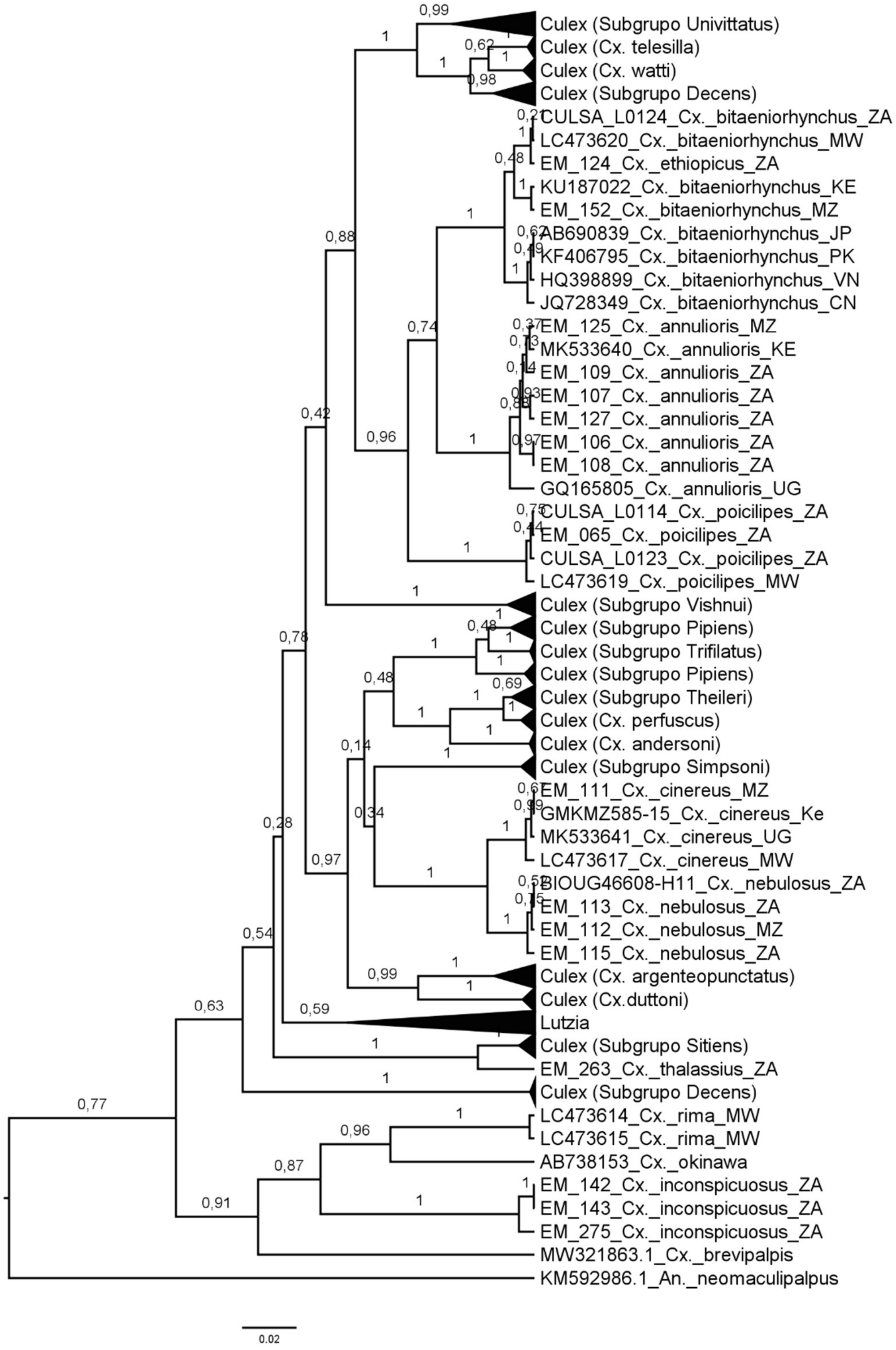
Eumelanomyia
KM592986.1_An._neomaculipalpus
0.02

c)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Culex (Cx. telesilla)
Culex (Cx. watti)
Culex (Subgrupo Decens)
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EM_107_Cx._annulioris_ZA
EM_127_Cx._annulioris_ZA
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EM_108_Cx._annulioris_ZA
GQ165805_Cx._annulioris_UG
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LC473619_Cx._poicilipes_MW
Culex (Subgrupo Vishnui)
Culex (Subgrupo Pipiens)
Culex (Subgrupo Trifilatus)
Culex (Subgrupo Pipiens)
Culex (Subgrupo Theileri)
Culex (Cx. perfuscus)
Culex (Cx. andersoni)
Culex (Subgrupo Simpsoni)
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GMKMZ585-15_Cx._cinereus_Ke
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LC473617_Cx._cinereus_MW
BIOUG46608-H11_Cx._nebulosus_ZA
EM_113_Cx._nebulosus_ZA
EM_112_Cx._nebulosus_MZ
EM_115_Cx._nebulosus_ZA
Culex (Cx. argenteopunctatus)
Culex (Cx.duttoni)
Lutzia
Culex (Subgrupo Sitiens)
EM_263_Cx._thalassius_ZA
Culex (Subgrupo Decens)
LC473614_Cx._rima_MW
LC473615_Cx._rima_MW
AB738153_Cx._okinawa
EM_142_Cx._inconspicuosus_ZA
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KM592986.1_An._neomaculipalpus
0.02

d)

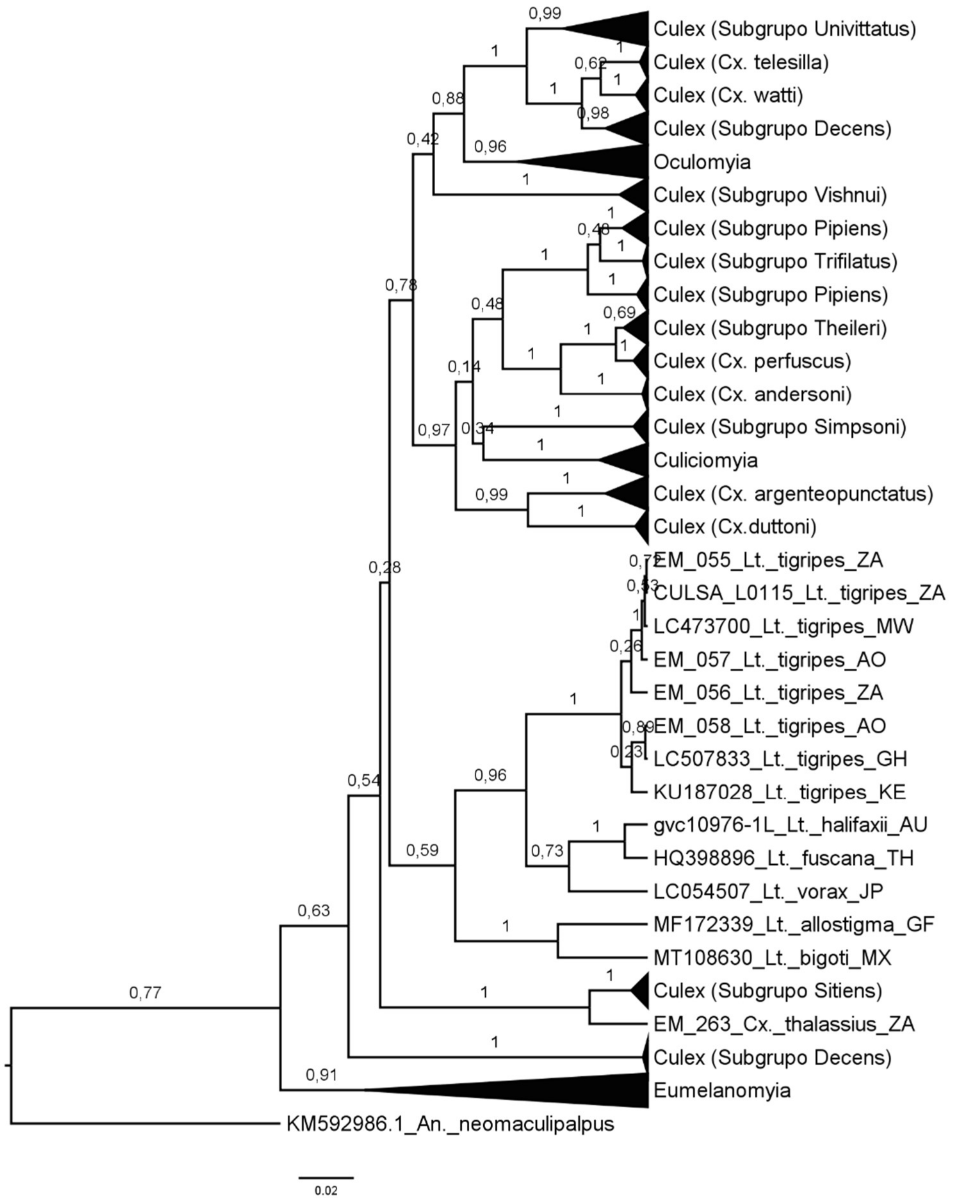

Figure S-III 18. **a, b, c, d)** Topology inferred by Bayesian inference under the GTR+G+1 model for the *Culex* and *Lutzia* genera, the analysis involved 171 nucleotide sequences with 636 positions in the final dataset. Support values correspond to a posteriori probability. The size bar indicates 0.02 replacements per site. The analysis was performed using the Beast program.

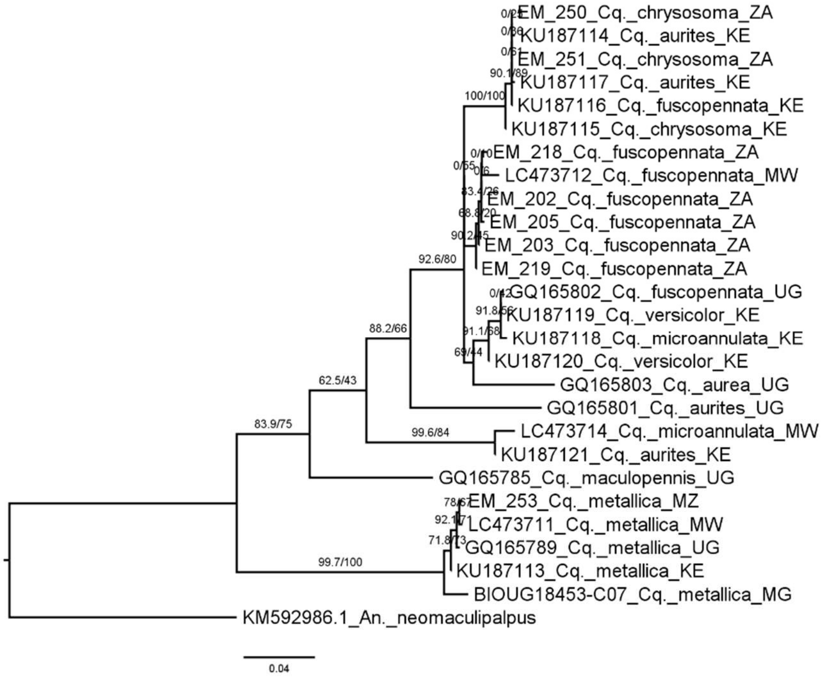

Figure S-III 19. Maximum likelihood tree under the GTR+G model for *Coquillettidia* genus, analysis involved 27 nucleotide sequences with 636 positions in the final dataset, consensus tree probability was -2352,702. Support values for the branches were estimated with aLRT/Bootstrap with 1000 repetitions for each method. The size bar indicates 0.04 replacements per site. The analysis was performed on IQtree.

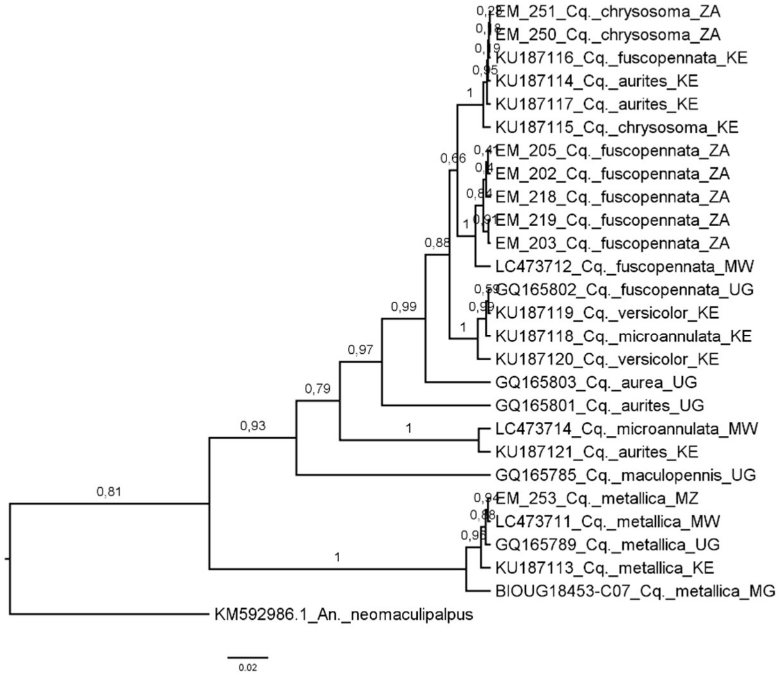

Figure S-III 20. Topology inferred by Bayesian inference under the GTR+G model for the genus *Coquillettidia*, the analysis involved 27 nucleotide sequences with 636 positions in the final dataset. Support values correspond to a posteriori probability. The size bar indicates 0.02 replacements per site. The analysis was performed using the Beast program.

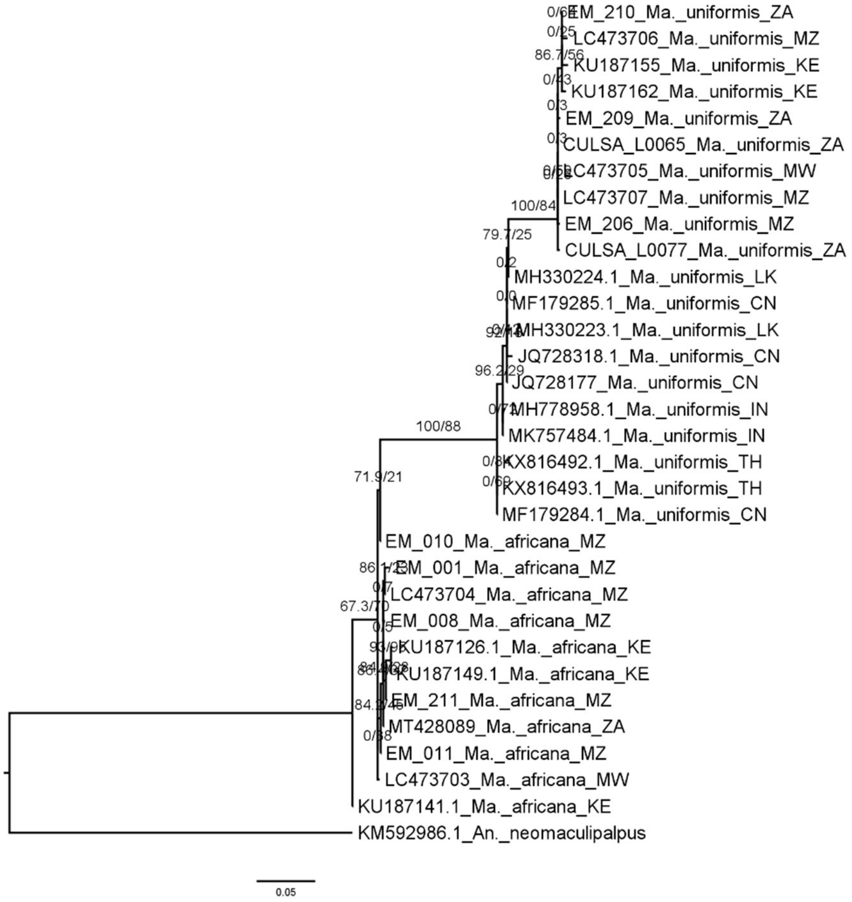

Figure S-III 21. Maximum likelihood tree under the GTR+G model for *Mansonia* genus, analysis involved 32 nucleotide sequences with 636 positions in the final dataset, consensus tree probability was -1779,294. Support values for the branches were estimated with aLRT/Bootstrap with 1000 repetitions for each method. The size bar indicates 0.05 replacements per site. The analysis was performed on IQtree.

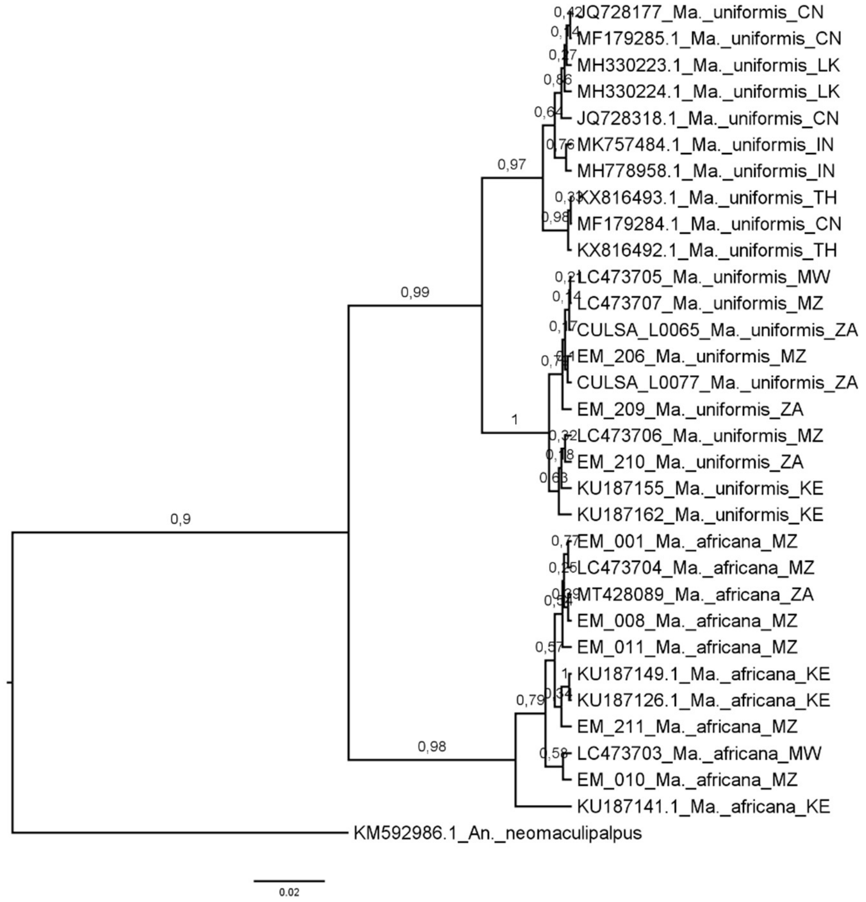

Figure S-III 22. Topology inferred by Bayesian inference under the GTR+G model for the genus *Mansonia*, the analysis involved 32 nucleotide sequences with 636 positions in the final dataset. Support values correspond to a posteriori probability. The size bar indicates 0.02 replacements per site. The analysis was performed using the Beast program.

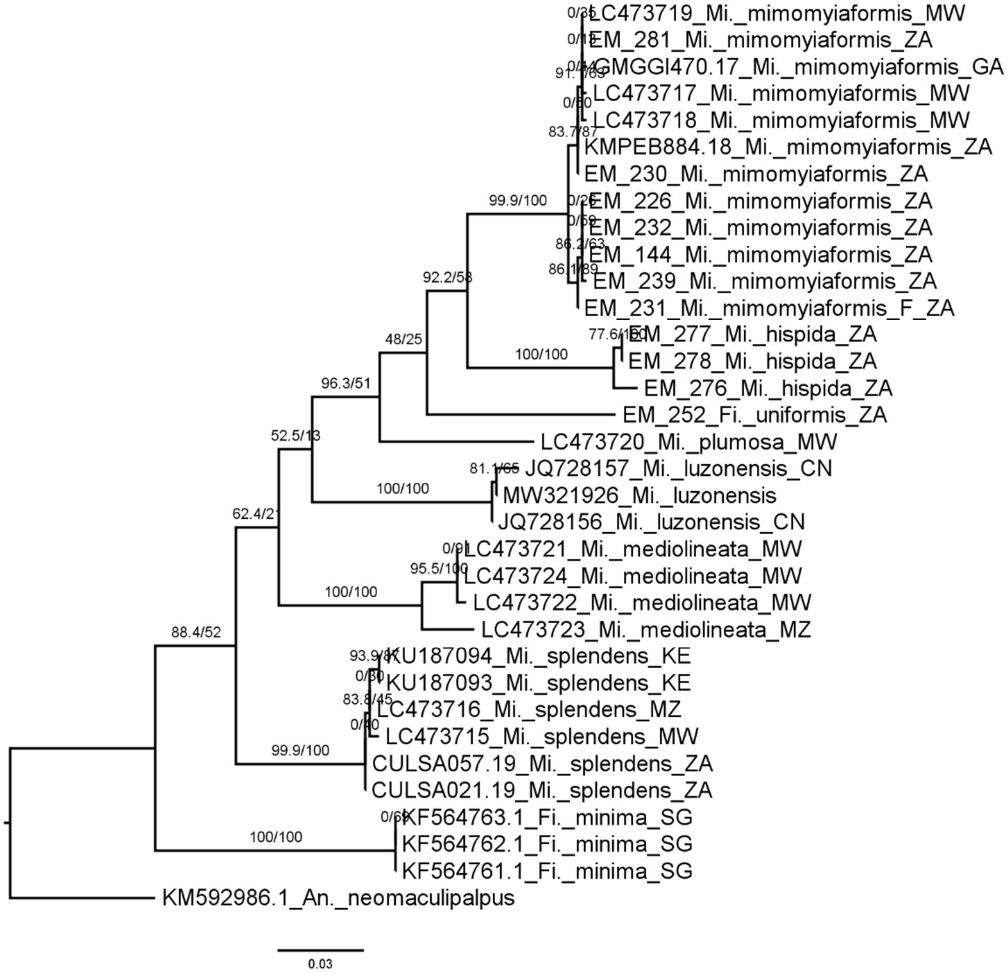

Figure S-III 23. Maximum likelihood tree under the GTR+G model for *Ficalbia* and *Mimomyia* genus, analysis involved 34 nucleotide sequences with 636 positions in the final dataset, consensus tree probability was -2907,251. Support values for the branches were estimated with aLRT/Bootstrap with 1000 repetitions for each method. The size bar indicates 0.03 replacements per site. The analysis was performed on IQtree.

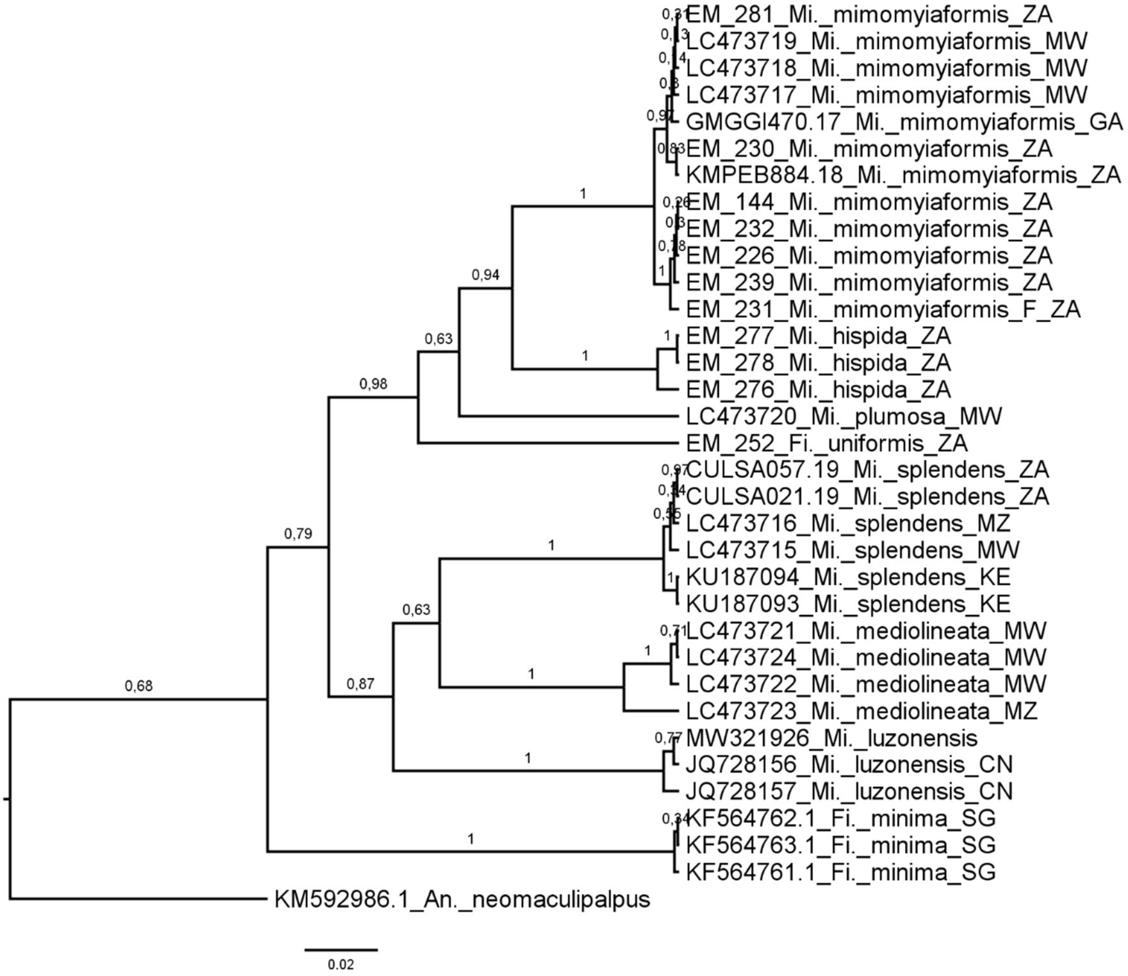

Figure S-III 24. Topology inferred by Bayesian inference under the GTR+G model for the genus *Ficalbia* and *Mimomyia*, the analysis involved 34 nucleotide sequences with 636 positions in the final dataset. Support values correspond to a posteriori probability. The size bar indicates 0.02 replacements per site. The analysis was performed using the Beast program.

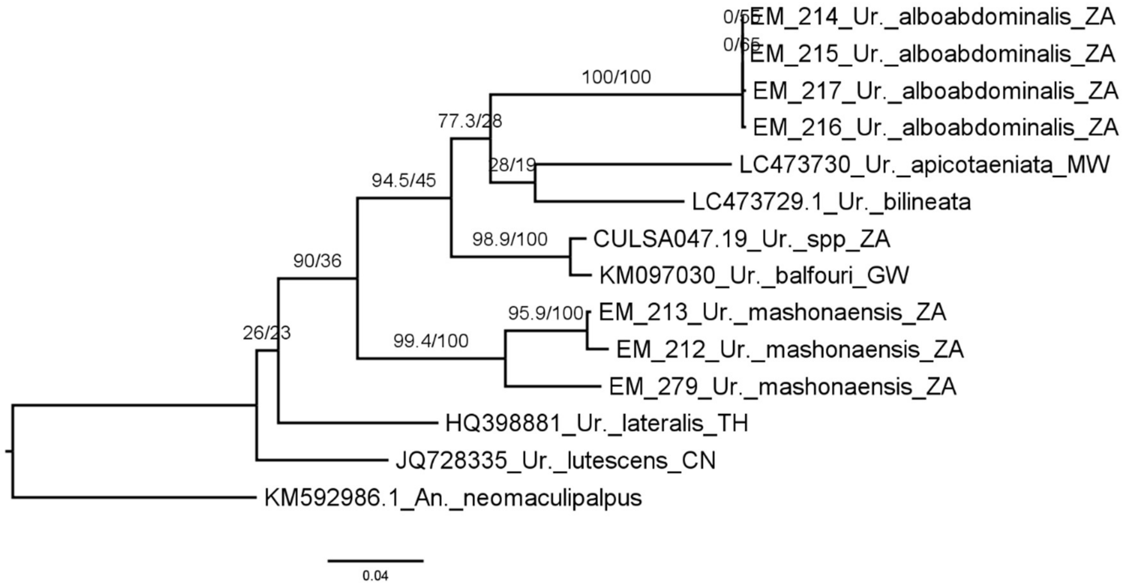

Figure S-III 25. Maximum likelihood tree under the GTR+G model for *Uranotaenia* genus, analysis involved 14 nucleotide sequences with 636 positions in the final dataset, probability of consensus tree was -2516,763. Support values for the branches were estimated with aLRT/Bootstrap with 1000 repetitions for each method. The size bar indicates 0.04 replacements per site. The analysis was performed on IQtree.

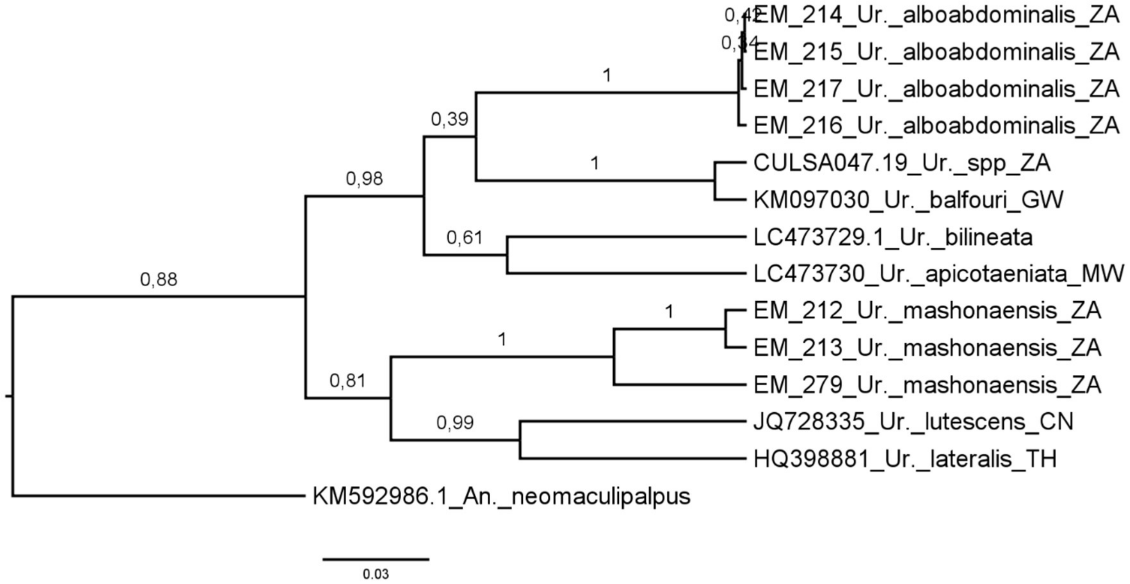

Figure S-III 26. Topology inferred by Bayesian inference under the GTR+G model for the genus *Uranotaenia*, the analysis involved 14 nucleotide sequences with 636 positions in the final dataset. Support values correspond to a posteriori probability. The size bar indicates 0.03 replacements per site. The analysis was performed using the Beast program.

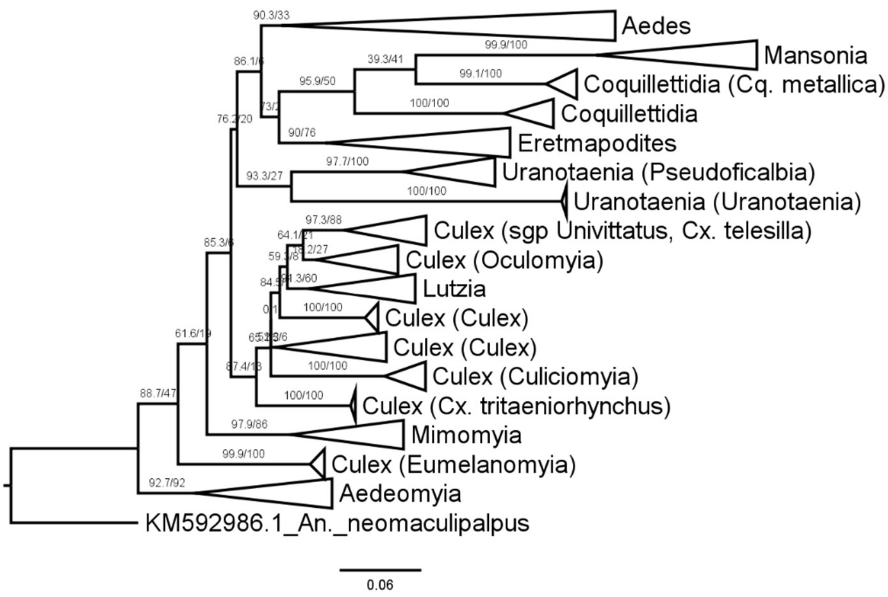

Figure S-III 27. Maximum likelihood tree under the GTR+G+I model for the genera *Aedeomyia*, *Aedes*, *Eretmapodites*, *Culex*, *Lutzia*, *Coquillettidia*, *Mansonia*, *Mimomyia*, *Uranotaenia*, the analysis involved 180 nucleotide sequences with 632 positions in the final data set, consensus tree probability was -11568343. Support values for the branches were estimated with aLRT/Bootstrap with 1000 repetitions for each method. The size bar indicates 0.06 replacements per site. The analysis was performed on IQtree.

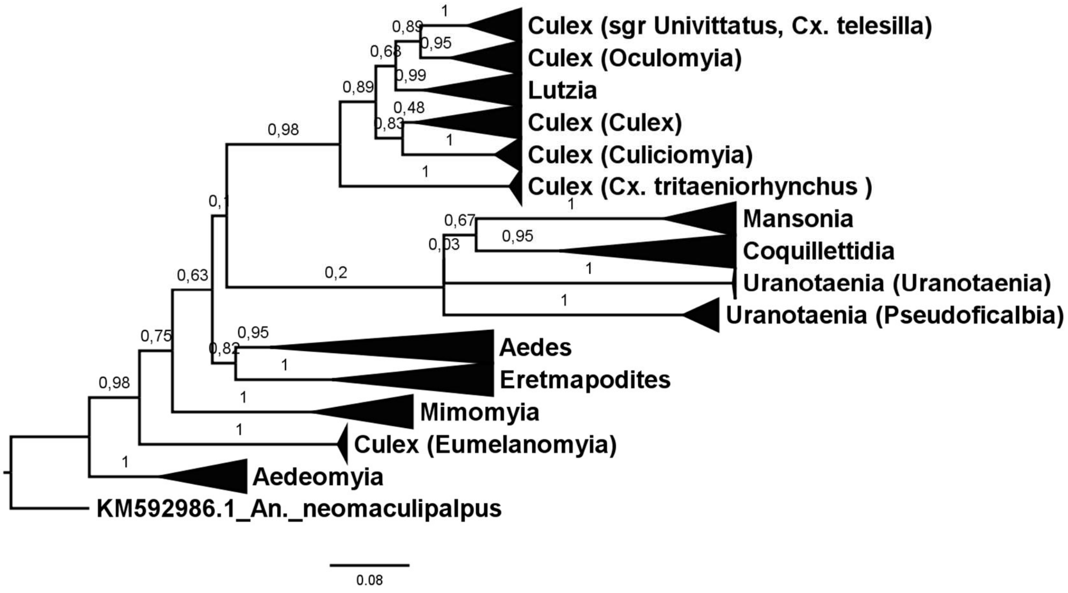

Figure S-III 28. Topology inferred by Bayesian inference under the GTR+G+I model for the genera *Aedeomyia*, *Aedes*, *Eretmapodites*, *Culex*, *Lutzia*, *Coquillettidia*, *Mansonia*, *Mimomyia*, *Uranotaenia*, the analysis involved 180 nucleotide sequences with 632 positions in the final dataset. Support values correspond to a posteriori probability. The size bar indicates 0.08 replacements per site. The analysis was performed using the Beast program.

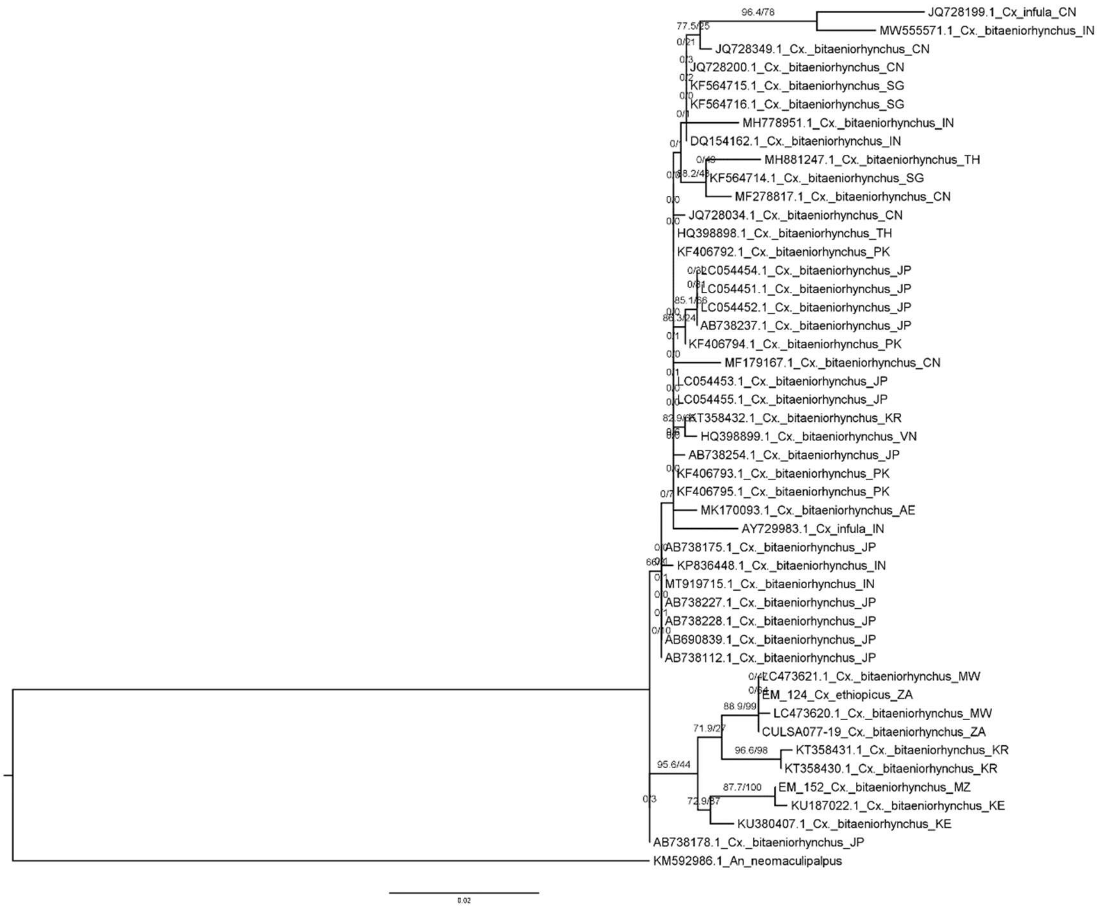

Figure S-III 29. Maximum likelihood tree under the T92+G model for the Bitaeniorhynchus Complex, analysis involved 47 nucleotide sequences with 653 positions in the final dataset, consensus tree probability was -1675,730. Support values for the branches were estimated with aLRT/Bootstrap with 1000 repetitions for each method. The size bar indicates 0.02 replacements per site. The analysis was performed on IQtree.

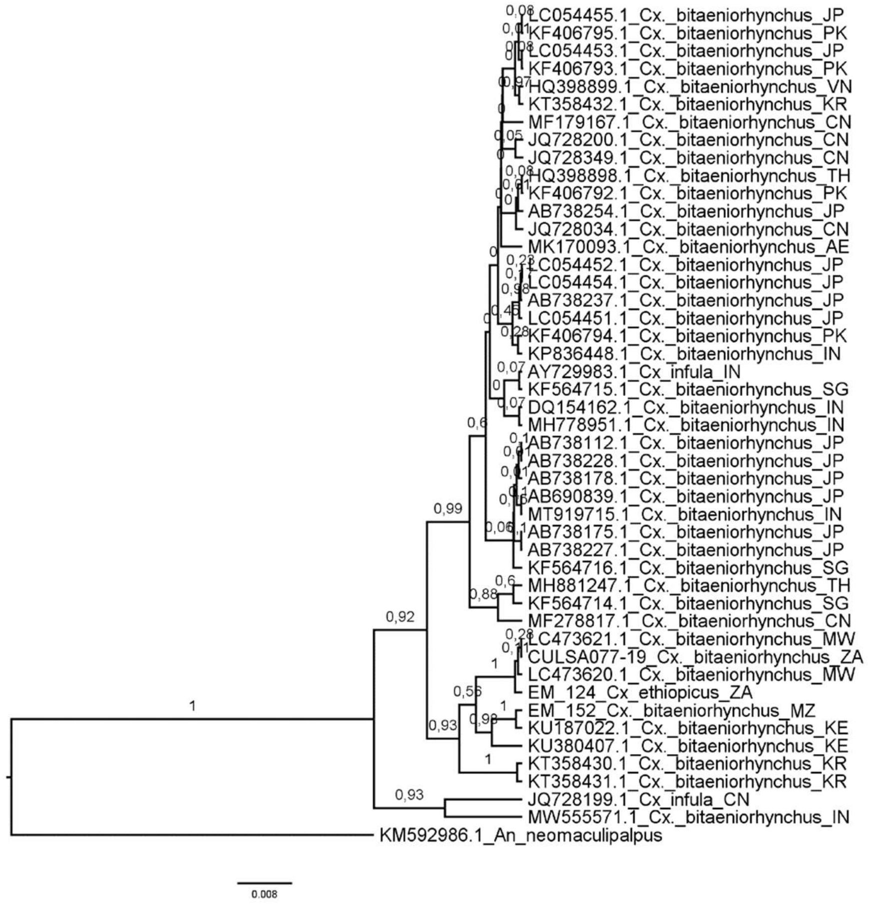

Figure S-III 30. Topology inferred by Bayesian inference under the T92+G model for the Bitaeniorhynchus Complex, the analysis involved 47 nucleotide sequences with 653 positions in the final dataset. Support values correspond to a posteriori probability. The size bar indicates 0.008 replacements per site. The analysis was performed using the Beast program.