

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

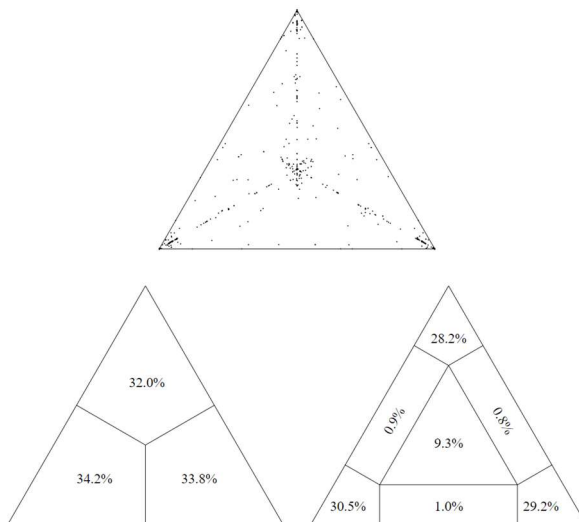


Figure S-III 1. Result of the likelihood mapping analysis of the *Aedeomyia* genus dataset: Input data: 16 sequences with 633 nucleotide sites, constant number of sites: 320 (= 50.6% of all sites). Number of resolved quartets (regions 1 + 2 + 3): 1601 (= 87.97%); number of partially resolved quartets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

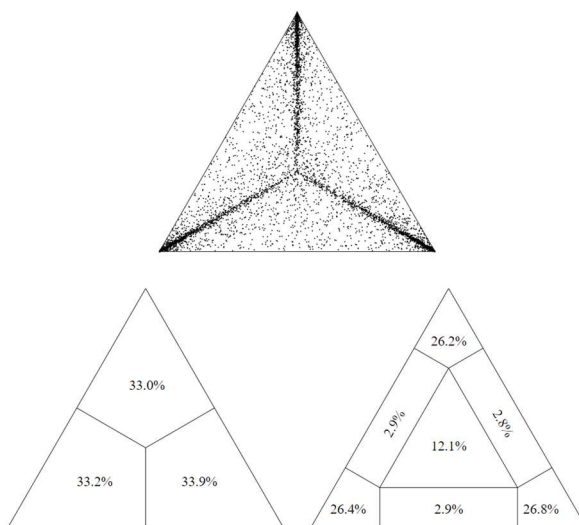


Figure S-III 2. Result of likelihood mapping analysis of the *Aedes* genus dataset: Input data: 173 sequences with 632 nucleotide sites, constant number of sites: 255 (= 40.3% of all sites). Number of resolved quartets (regions 1 + 2 + 3): 7941 (= 79.41%); number of partially resolved quartets (regions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

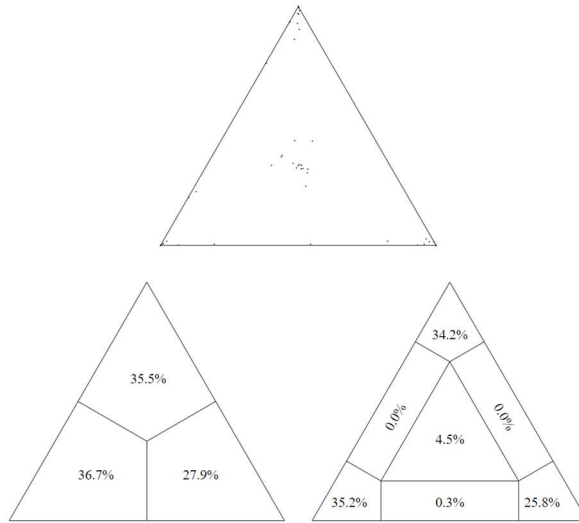


Figure S-III 3. Result of the likelihood mapping analysis of the *Eretmapodites* genus dataset: Input data: 11 sequences with 636 nucleotide sites, constant number of sites: 333 (= 52.4% of all sites). Number of resolved quartets (regions 1 + 2 + 3): 314 (= 95.15%); number of partially resolved quartets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

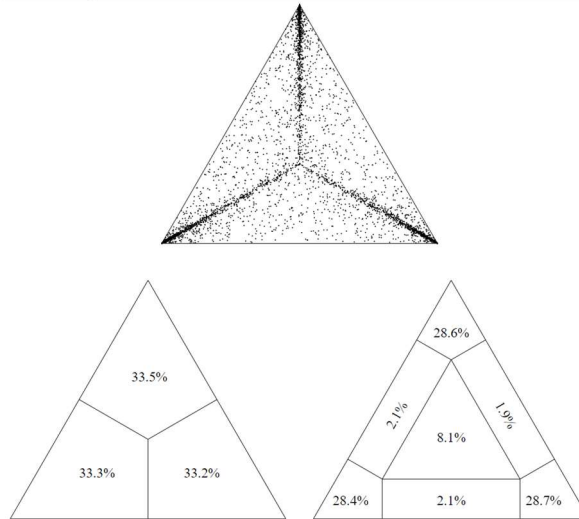


Figure S-III 4. Result of likelihood mapping analysis of the *Culex* and *Lutzia* genera datasets: Input data: 171 sequences with 636 nucleotide sites, constant number of sites: 213 (= 33.5% of all sites). Number of resolved quartets (regions 1 + 2 + 3): 8581 (= 85.81%); number of partially resolved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

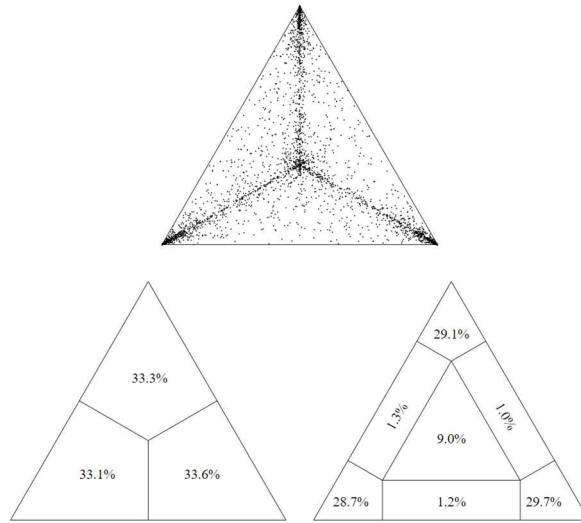


Figure S-III 5. Result of likelihood mapping analysis of the *Coquillettidia* genus dataset: Input data: 27 sequences with 636 nucleotide sites, constant number of sites: 388 (= 61.0% of all sites). Number of resolved quartets (regions 1 + 2 + 3): 8739 (= 87.39%); number of partially resolved quartets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

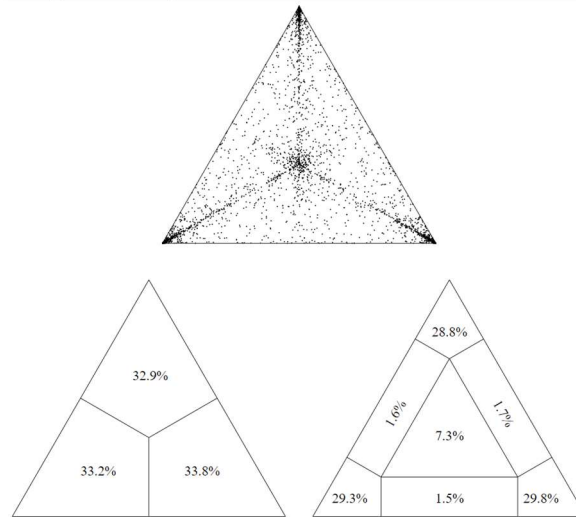


Figure S-III 6. Result of likelihood mapping analysis of the *Mansonia* genus dataset: Input data: 32 sequences with 636 nucleotide sites, constant number of sites: 279 (= 43.9% of all sites). Number of resolved quartets (regions 1 + 2 + 3): 8790 (= 87.90%); number of partially resolved quartets (regions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

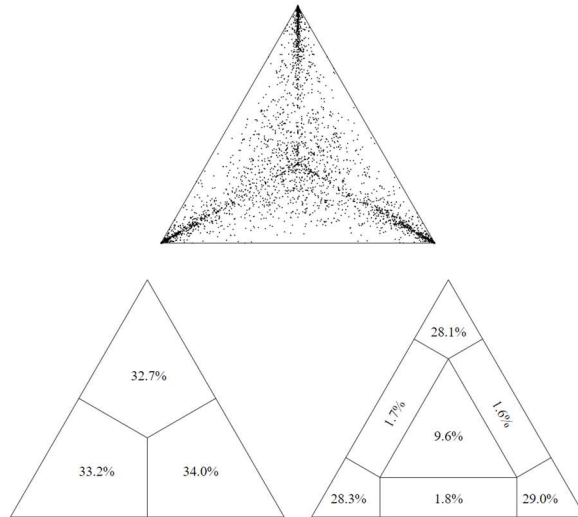


Figure S-III 7. Result of likelihood mapping analysis of the *Ficalbia* and *Mimomyia* genera datasets: Input data: 34 sequences with 636 nucleotide sites, constant number of sites: 235 (= 36.9% of all sites). Number of resolved quartets (regions 1 + 2 + 3): 8534 (= 85.34%); number of partially resolved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

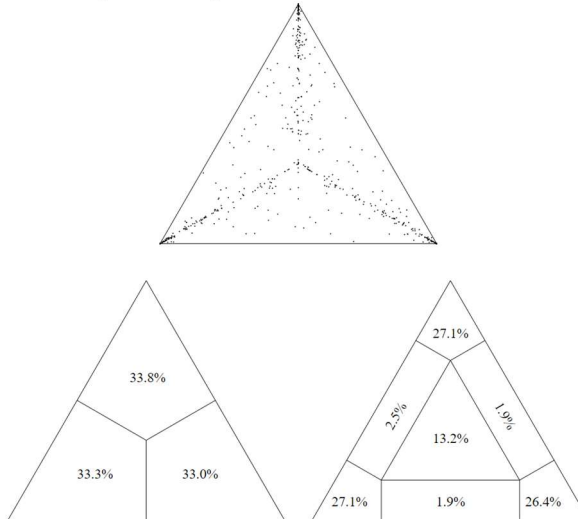


Figure S-III 8. Result of the likelihood mapping analysis of the *Uranotaenia* genus dataset: Input data: 14 sequences with 636 nucleotide sites, constant number of sites: 328 (= 51.6% of all sites). Number of resolved quartets (regions 1 + 2 + 3): 806 (= 80.52%); number of partially resolved quartets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

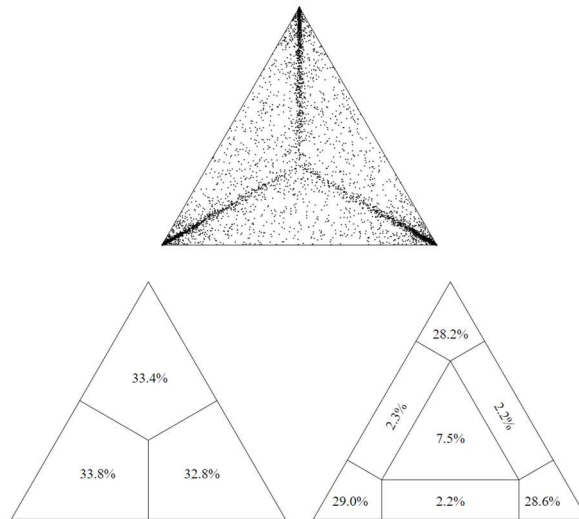


Figure S-III 9. Result of likelihood mapping analysis of the genera datasets *Aedeomyia*, *Aedes*, *Eretmapodites*, *Culex*, *Lutzia*, *Coquillettia*, *Mansonia*, *Mimomyia* and *Uranotaenia*: Input data: 180 sequences with 632 nucleotide sites, number of constant sites: 164 (= 25.9% of all websites). 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%).

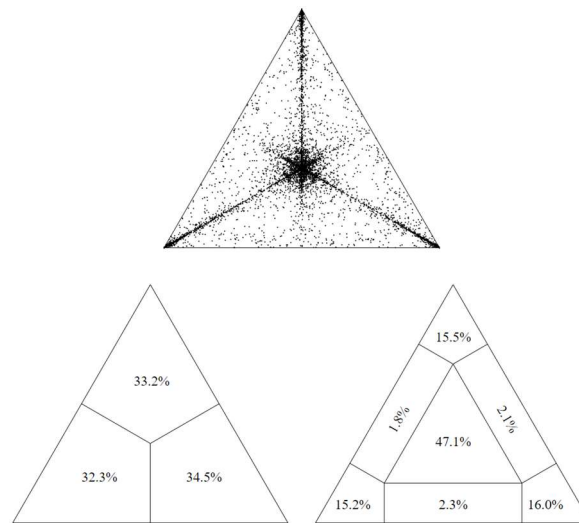


Figure S-III 10. Result of likelihood mapping analysis of the *Bitaniorhynchus* complex dataset: Input data: 47 sequences with 653 nucleotide sites, constant number of sites: 323 (= 49.5% of all sites). Number of resolved quartets (regions 1 + 2 + 3): 4667 (= 46.67%); number of partially resolved quartets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

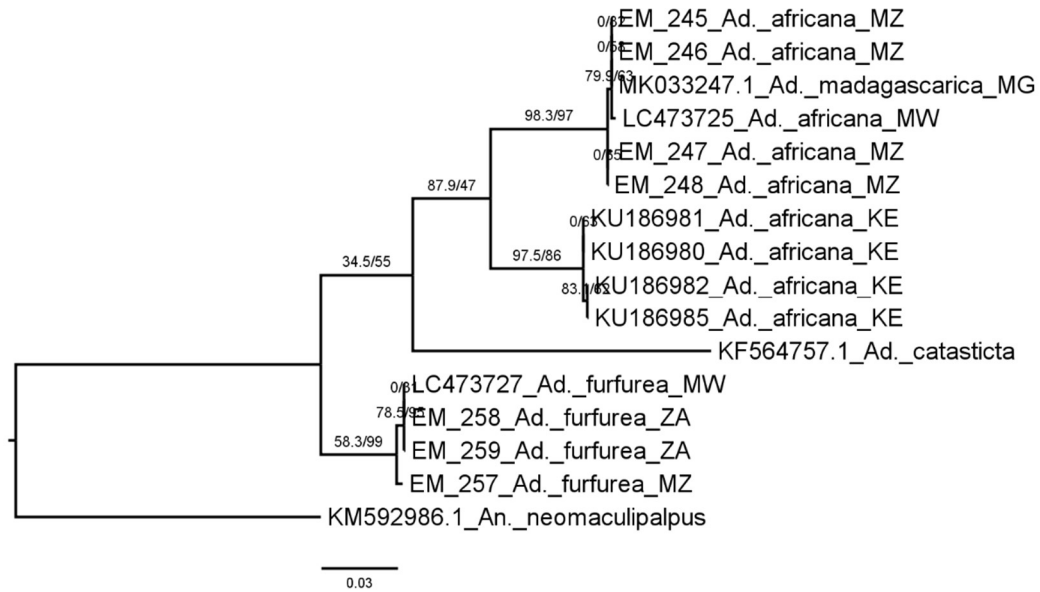


Figure S-III 11. Maximum likelihood tree under the GTR+G model for *Aedeomyia* genus, analysis involved 16 nucleotide sequences with 633 positions in the final dataset, consensus tree probability was -1663,651. Support values for the branches were estimated with aLRT/Bootstrap with 1000 repetitions for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

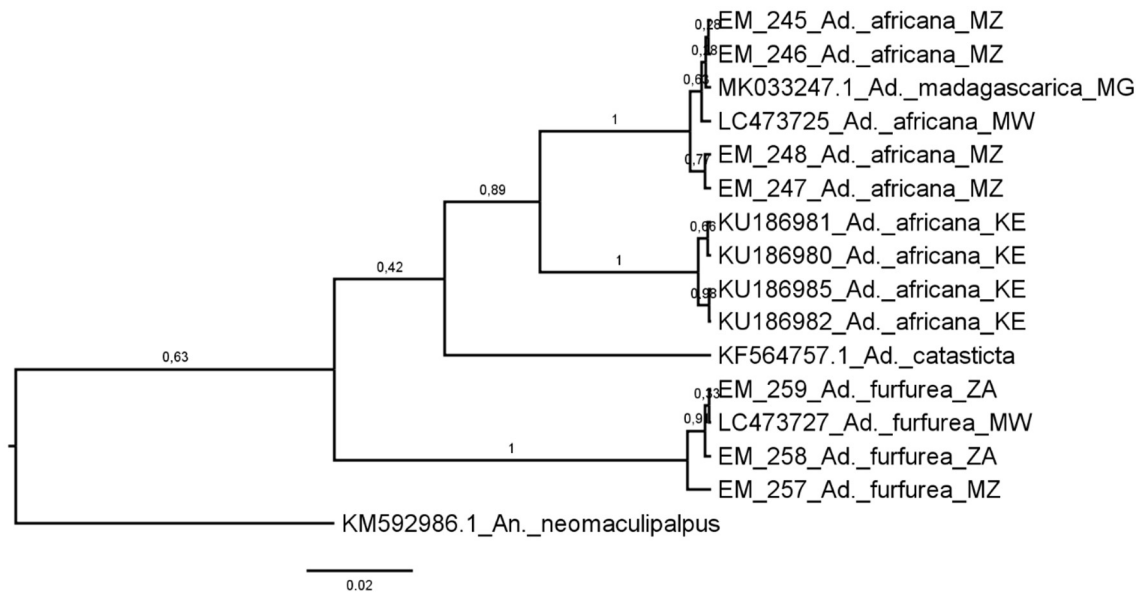
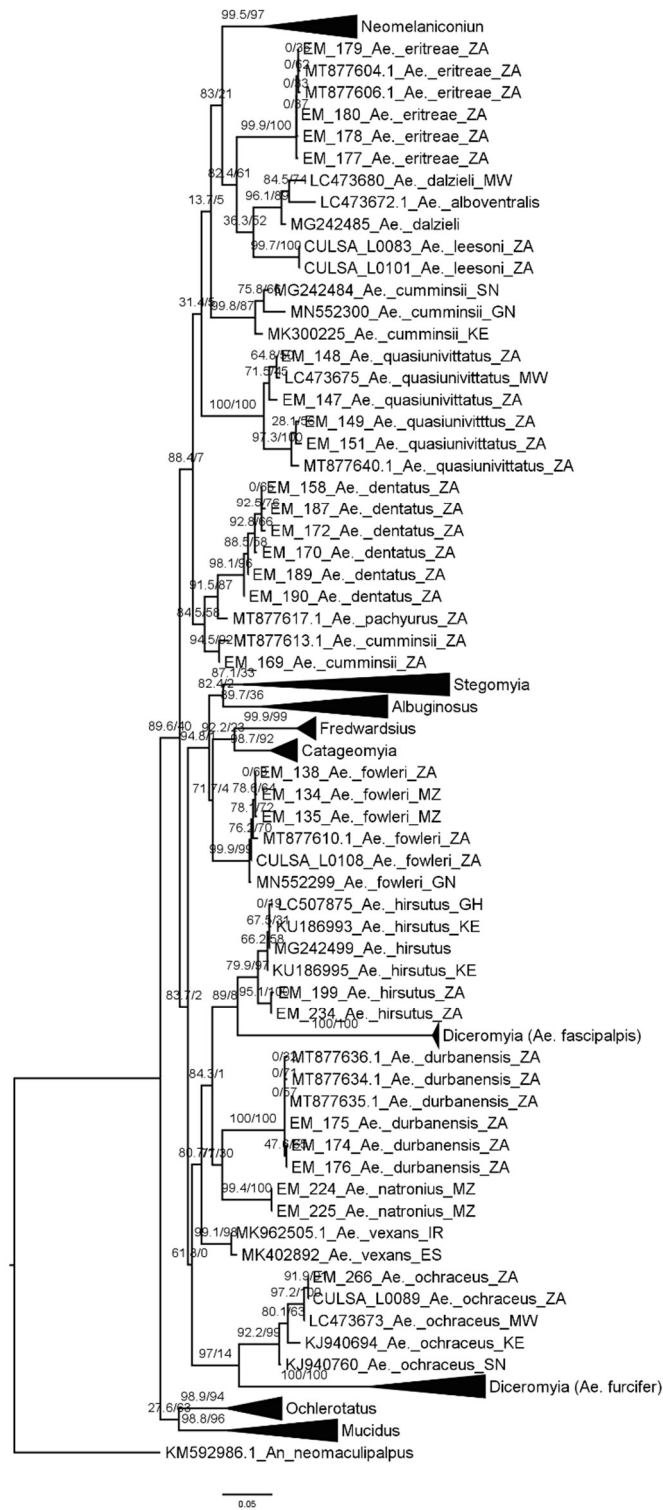
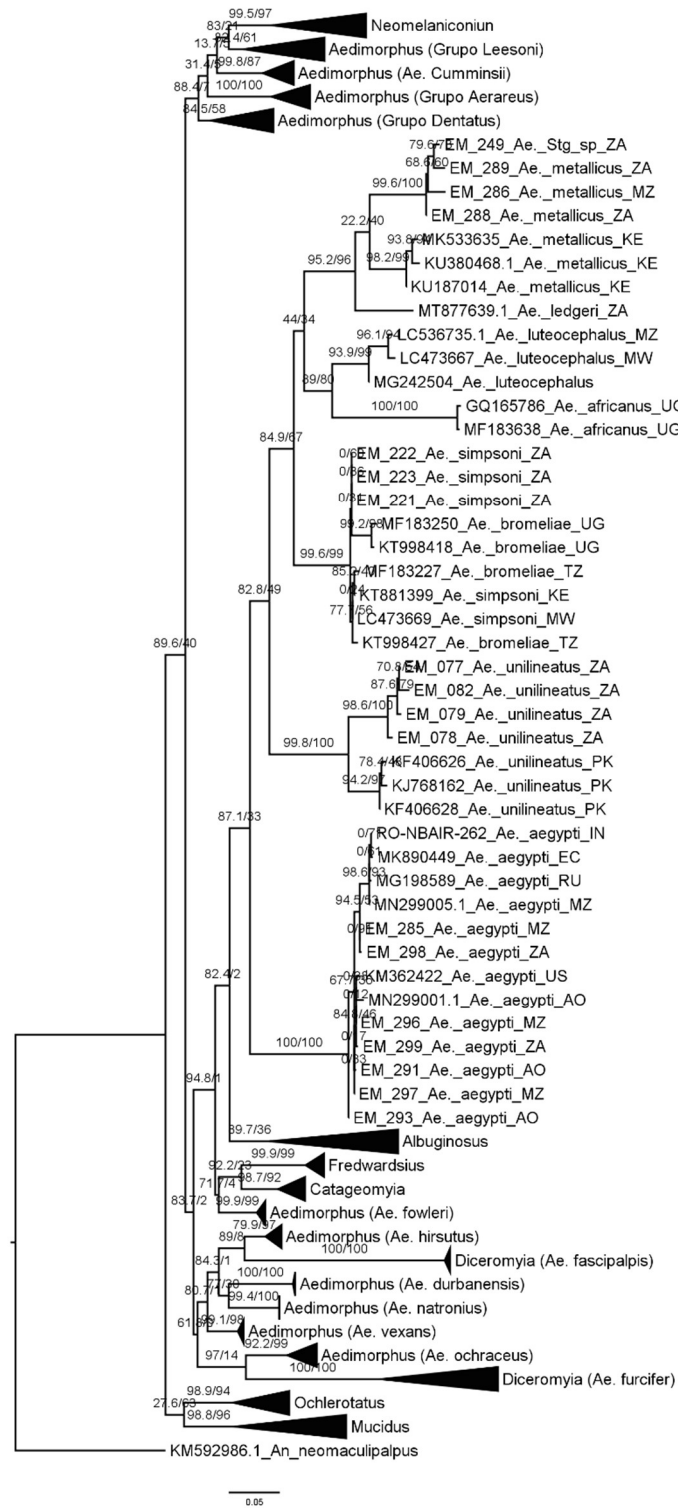


Figure S-III 12. Topology inferred by Bayesian inference under the GTR+G model for the genus *Aedeomyia*, the analysis involved 16 nucleotide sequences with 633 positions in the final dataset. Support values correspond to a posteriori probability. The size bar indicates 0.02 replacements per site. The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

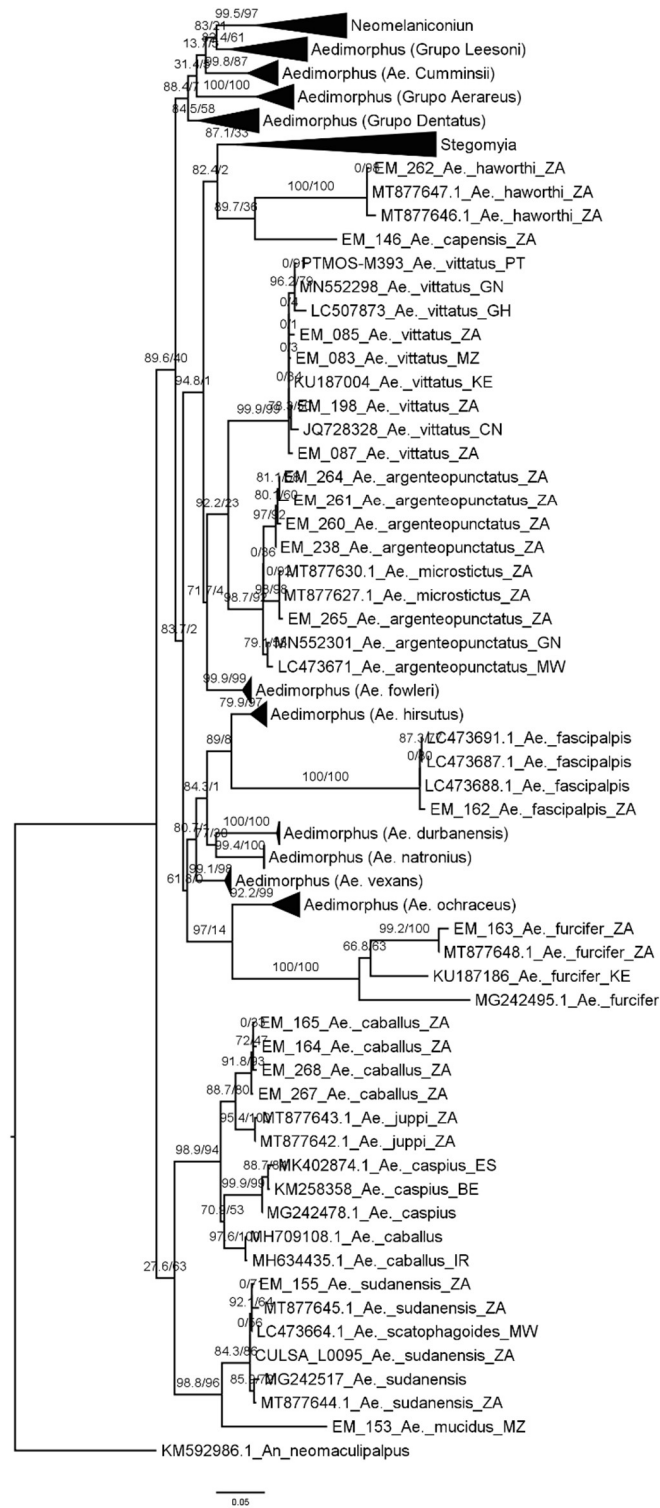
a)



b)



c)



d)

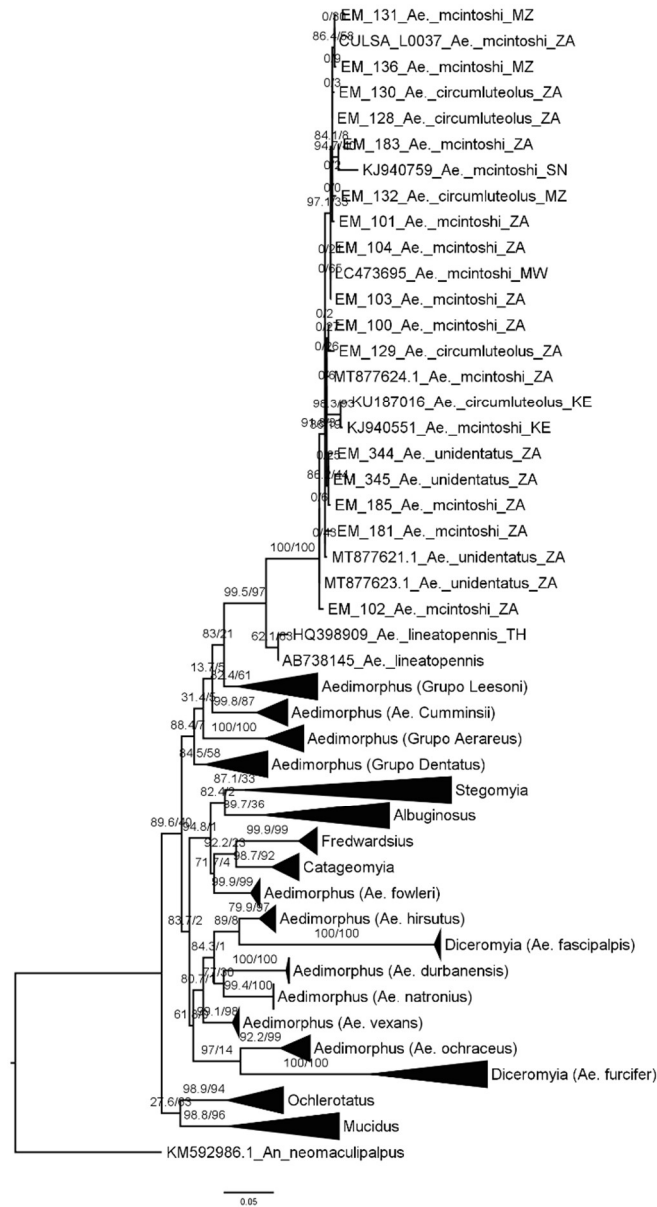
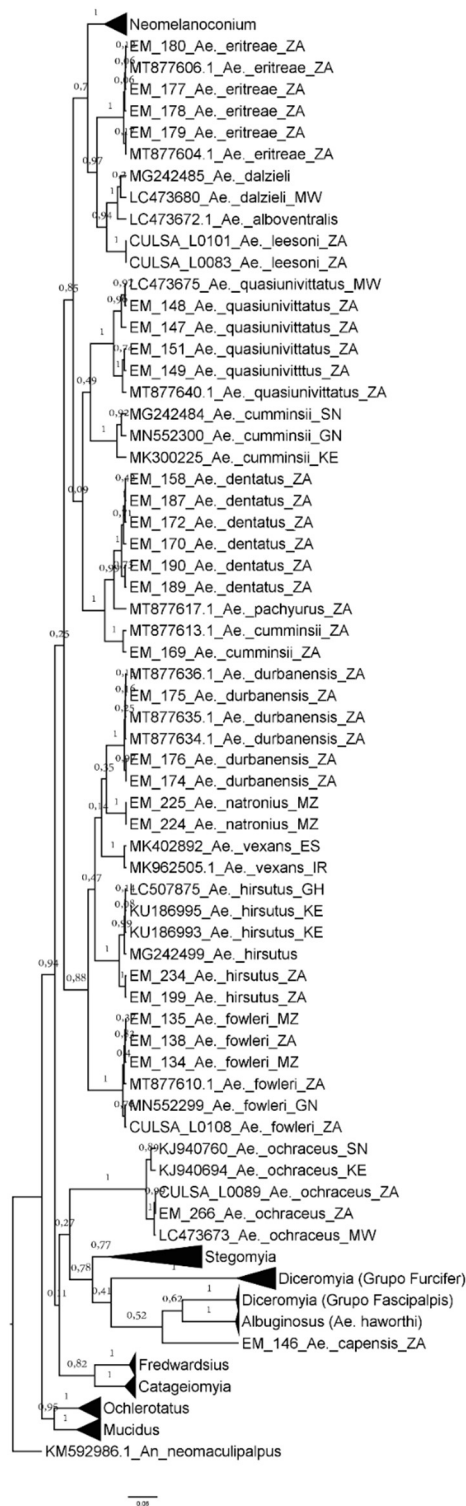
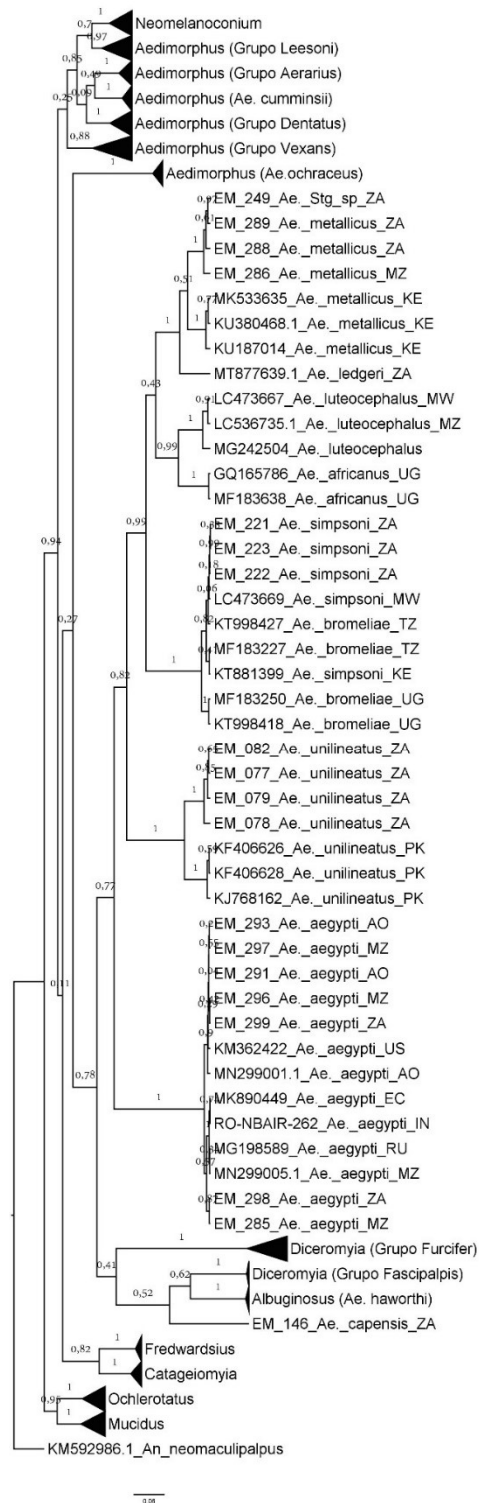


Figure S-III 13. a, b, c, d) Maximum likelihood tree under the GTR+G+I model for *Aedes* genus, analysis involved 173 nucleotide sequences with 632 positions in the final dataset, consensus tree probability was -8262,917. Support values for the branches were estimated with aLRT/Bootstrap with 1000 repetitions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

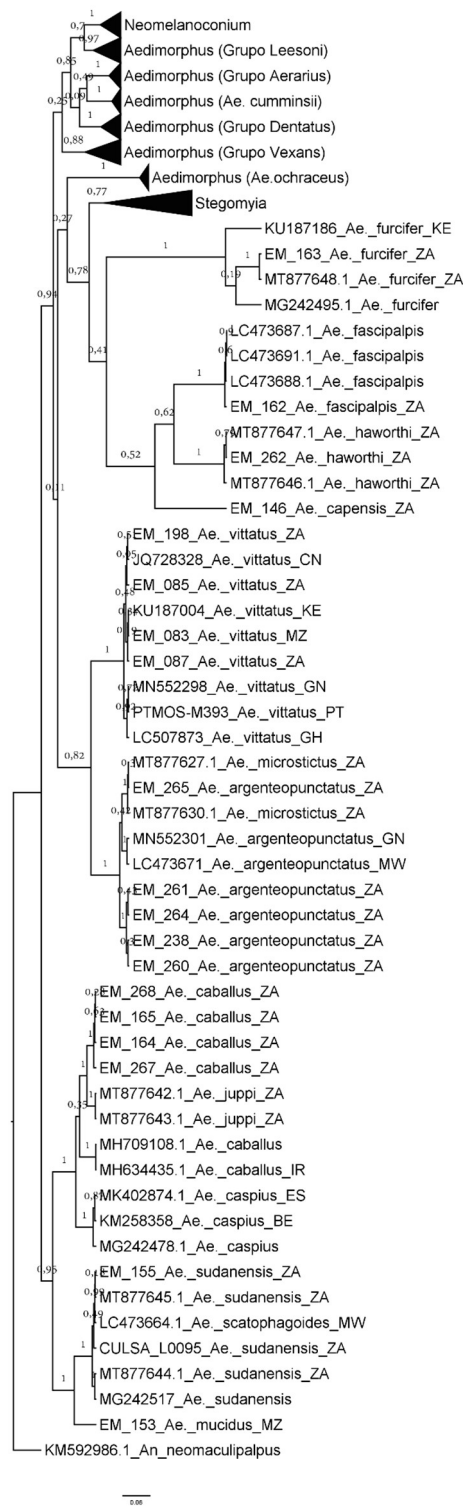
a)



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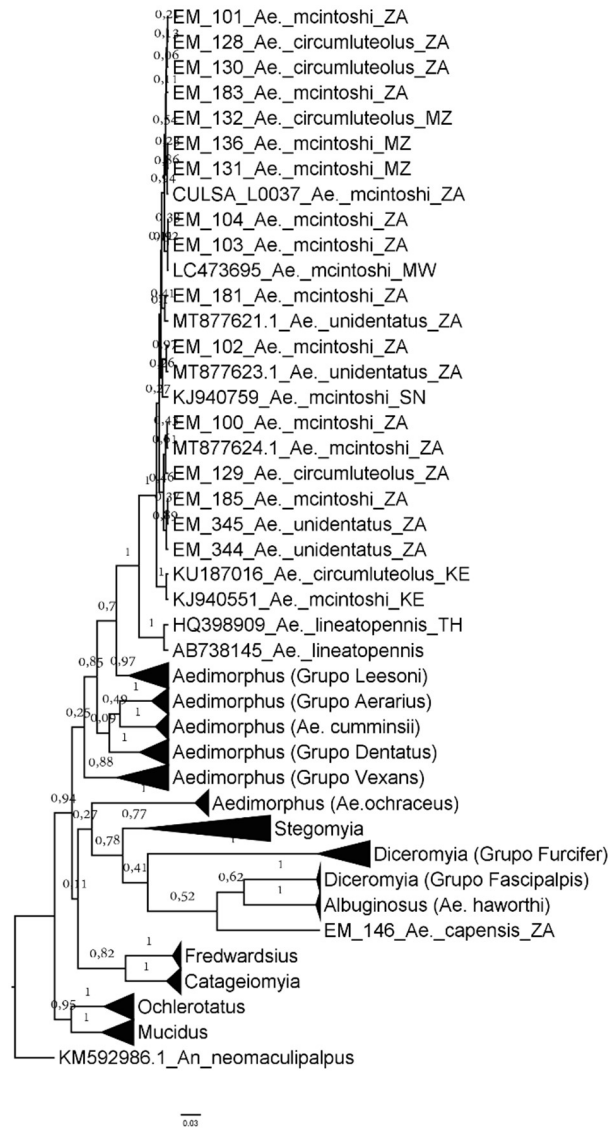


Figure S-III 14.

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.

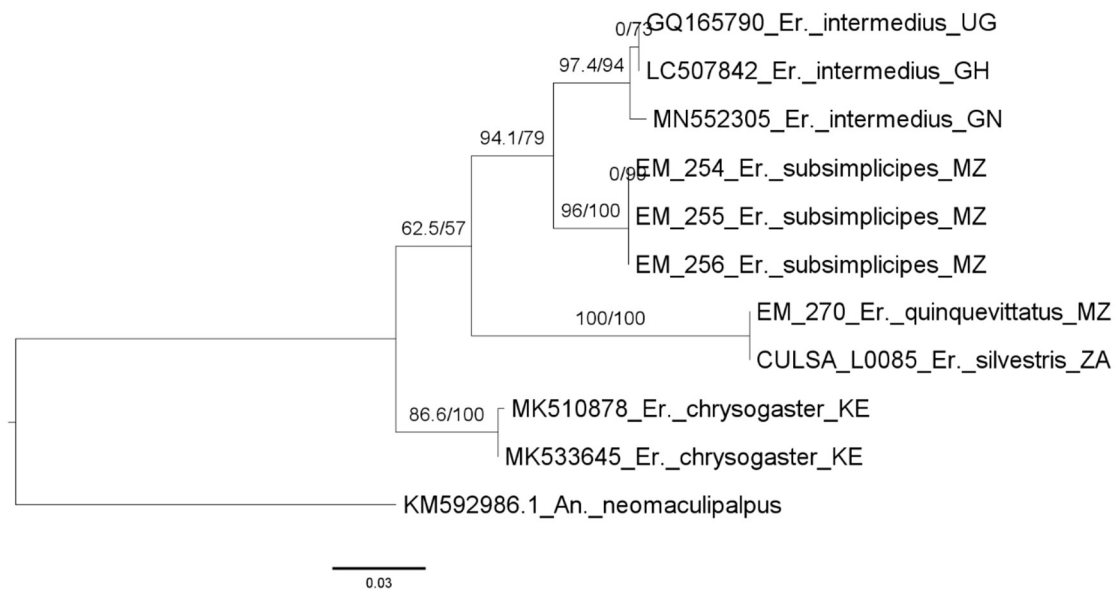


Figure S-III 15. Maximum likelihood tree under the GTR+I model for *Eretmapodites* genus, analysis involved 11 nucleotide sequences with 636 positions in the final dataset, probability of consensus tree was -1680,980. Support values for the branches were estimated with aLRT/Bootstrap with 1000 repetitions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

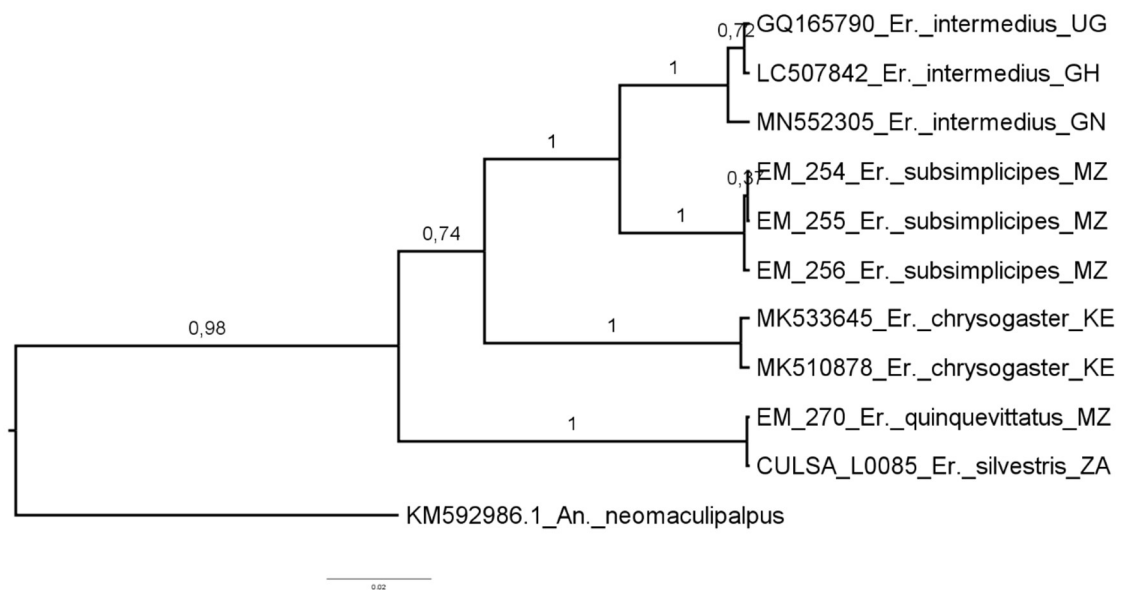
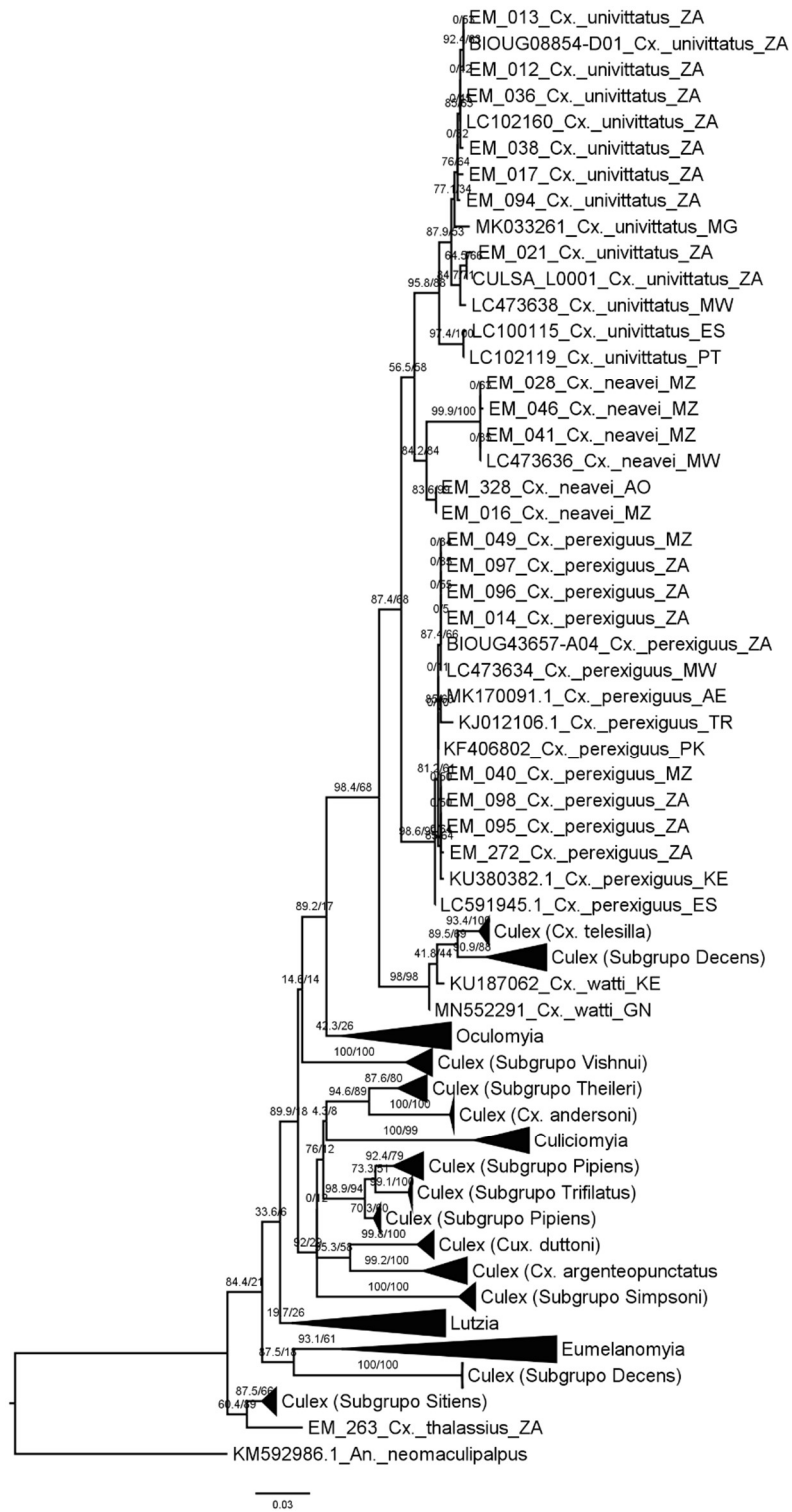


Figure S-III 16. Topology inferred by Bayesian inference under the GTR+I model for the genus *Eretmapodites*, the analysis involved 11 nucleotide sequences with 636 positions in the final dataset. Support values correspond to a posteriori probability. The size bar indicates 0.02 replacements per site.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

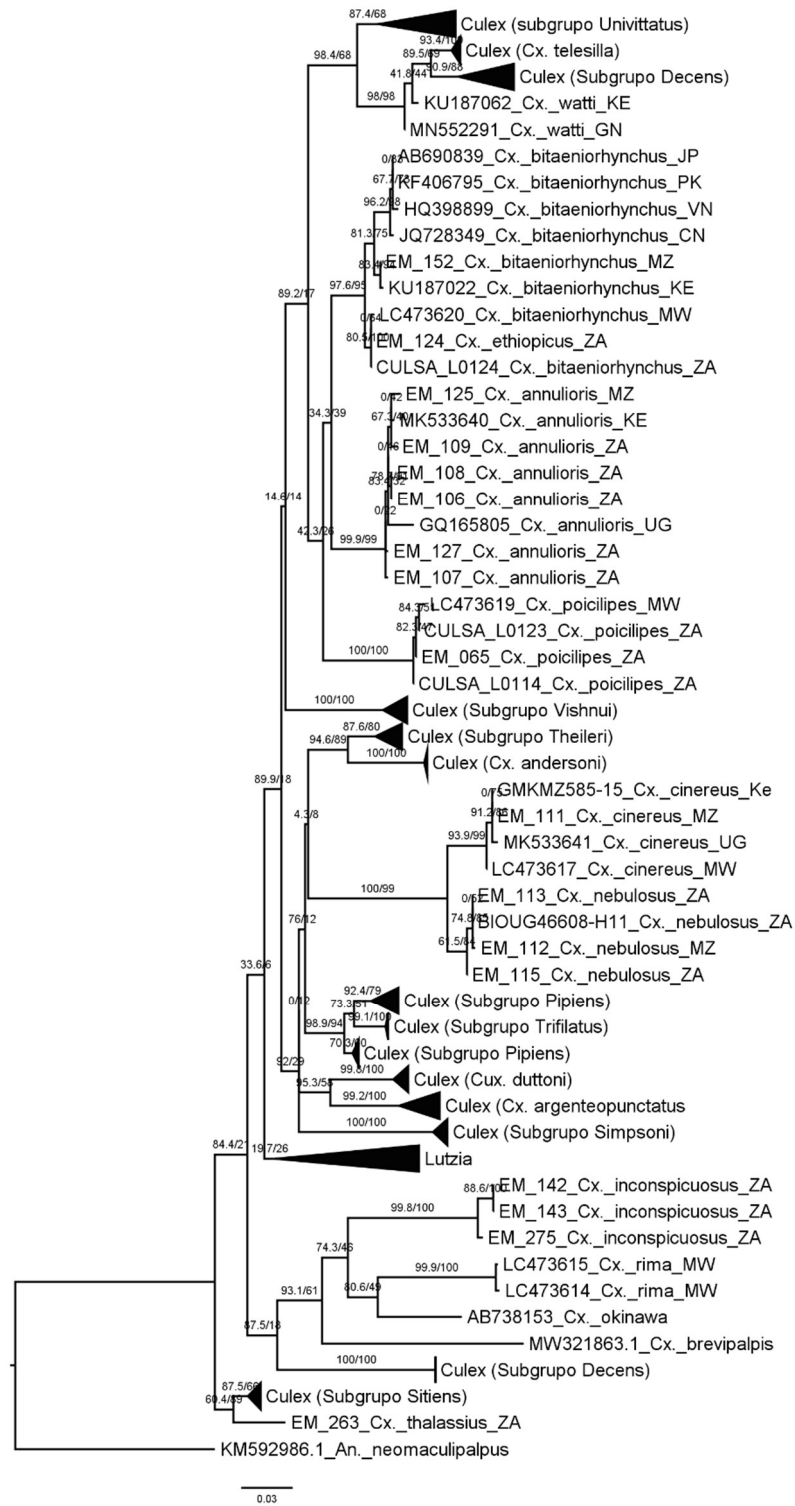
a)



b)



c)



d)

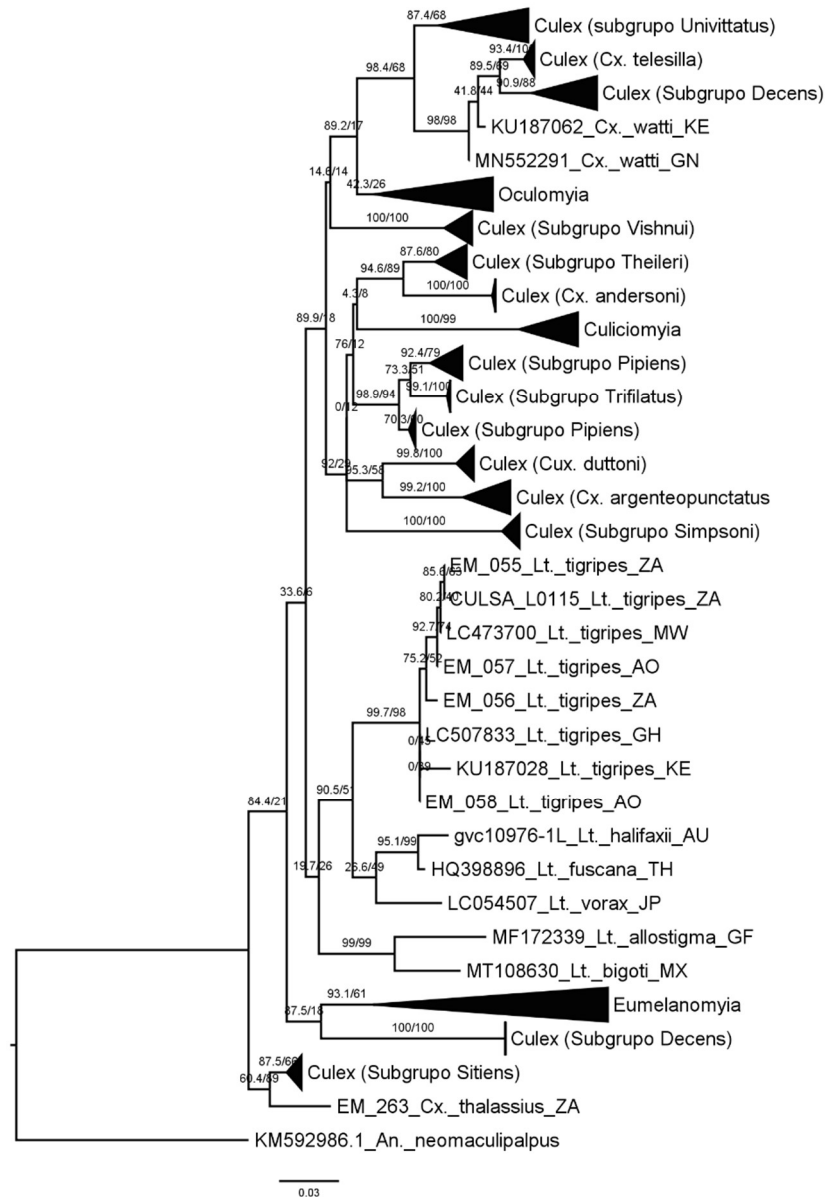
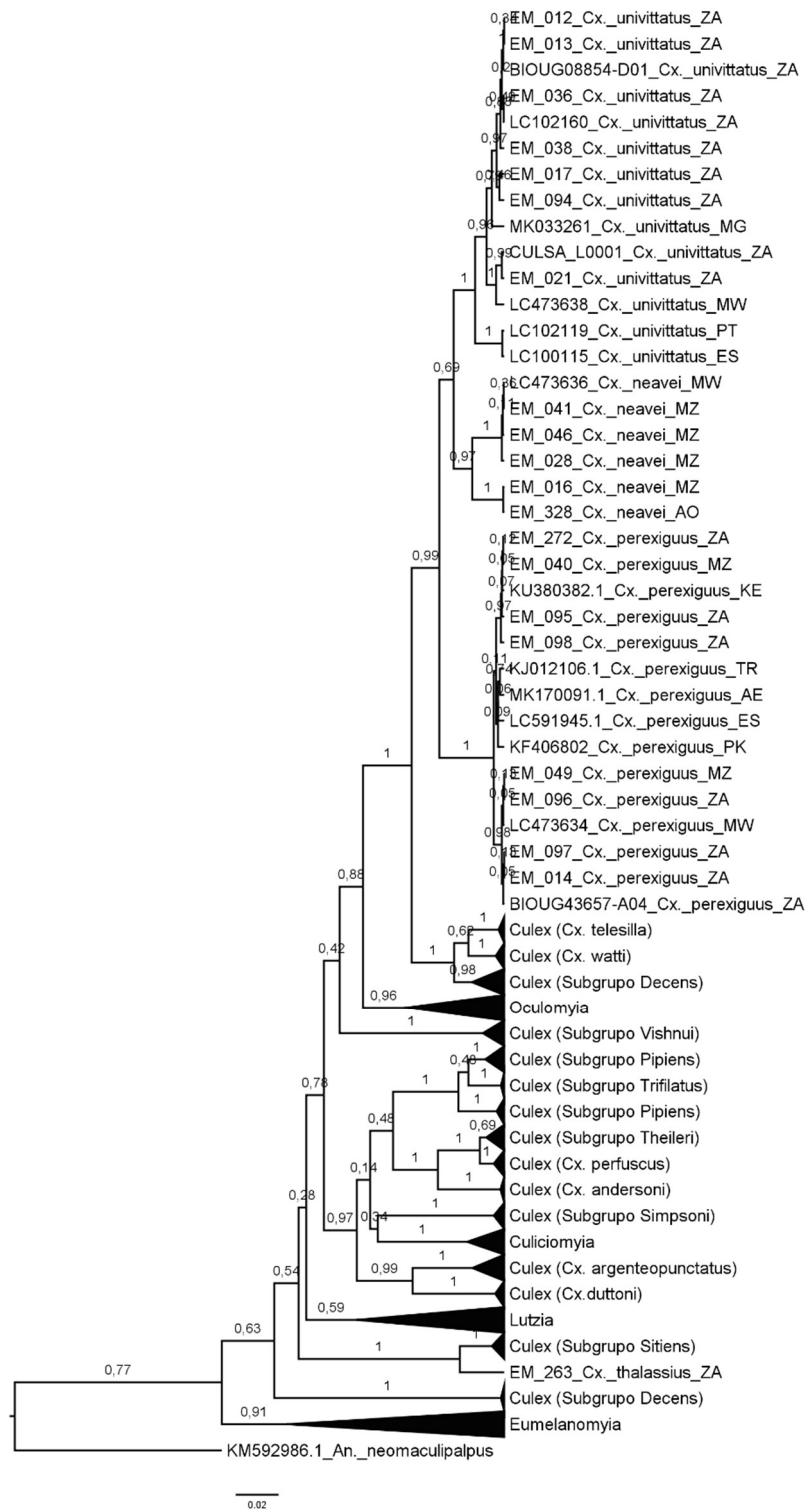
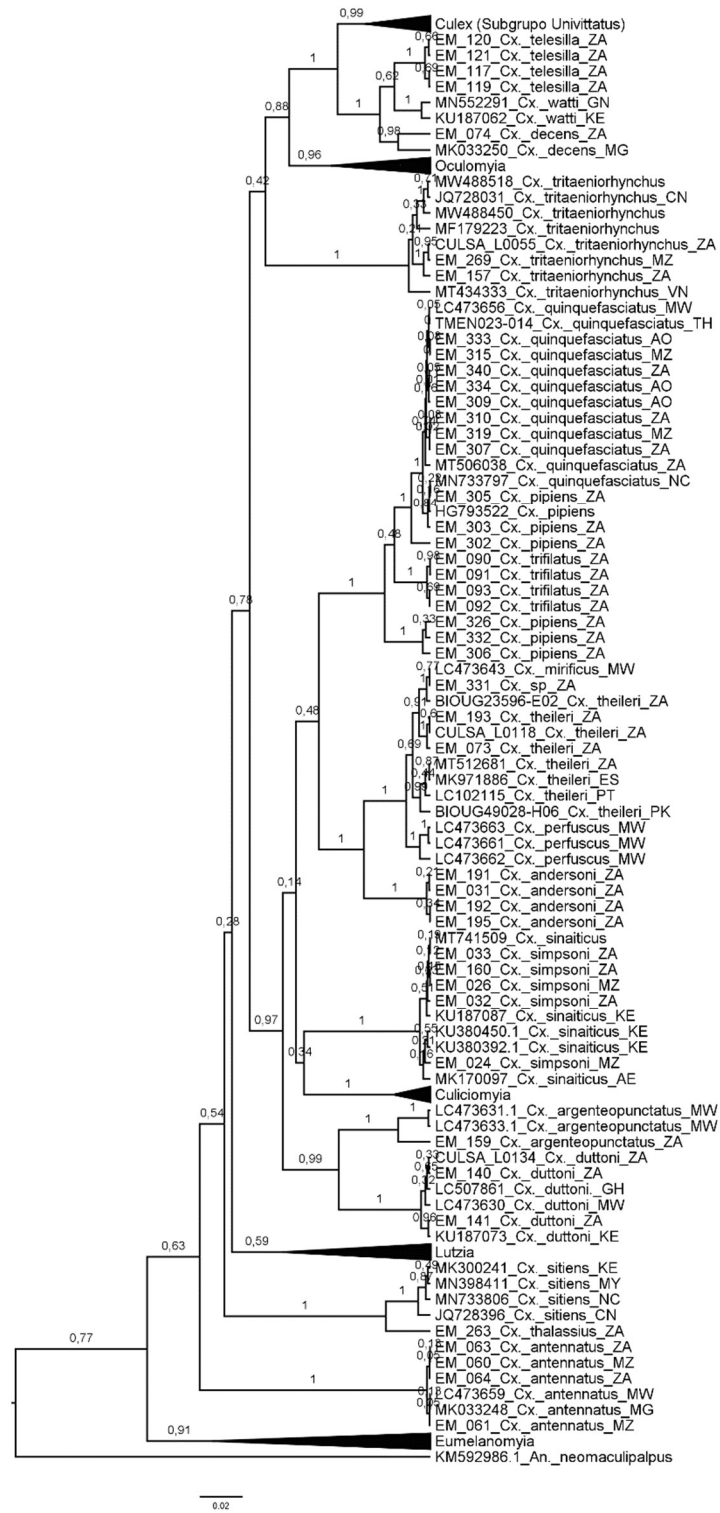


Figure S-III 17. a, b, c, d) Maximum likelihood tree under the GTR+G+I model for *Culex* and *Lutzia* genera, analysis involved 171 nucleotide sequences with 636 positions in the final dataset, consensus tree probability was -6105,653. Support values for the branches were estimated with aLRT/Bootstrap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

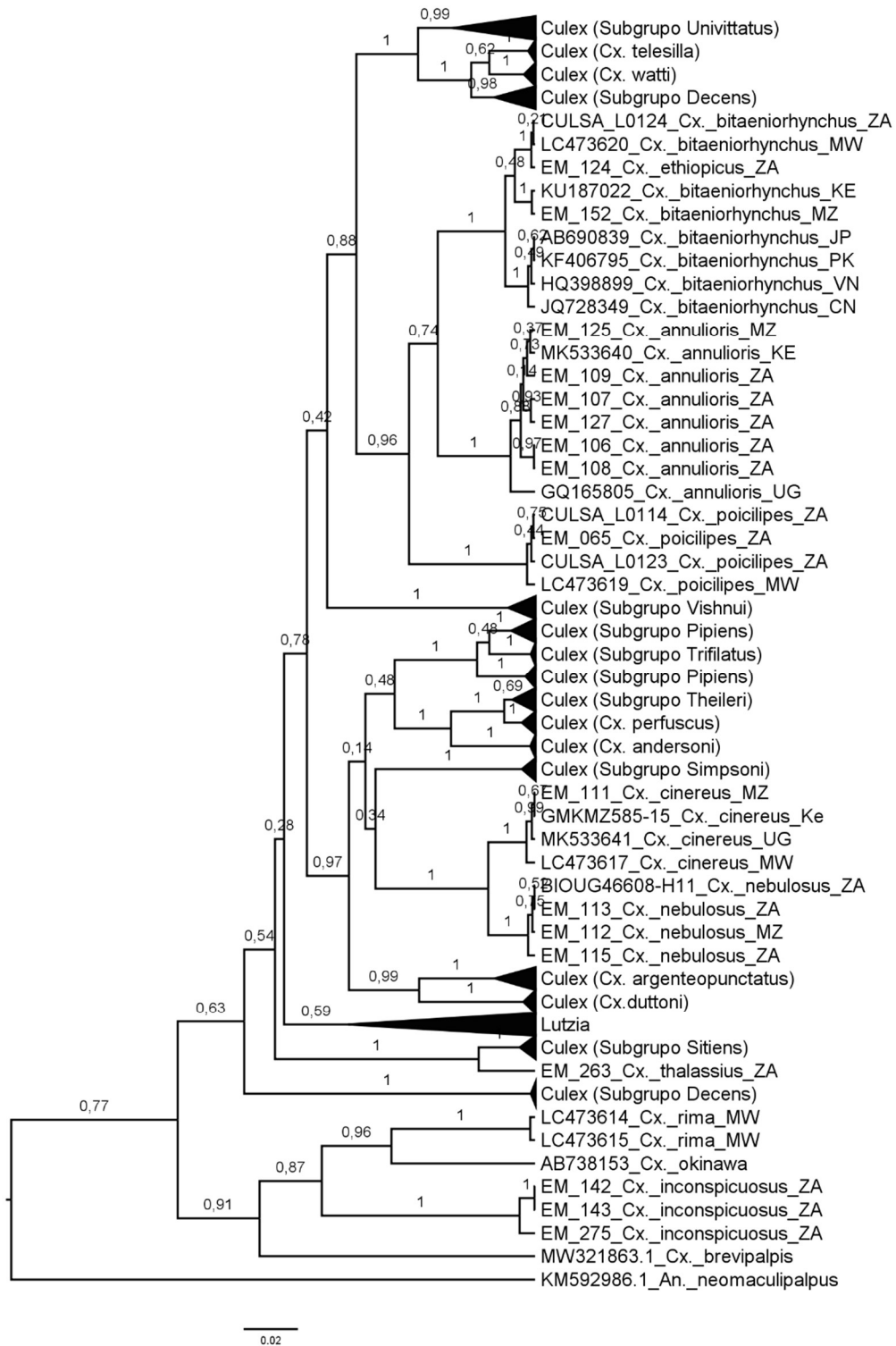
a)



b)



c)



d)

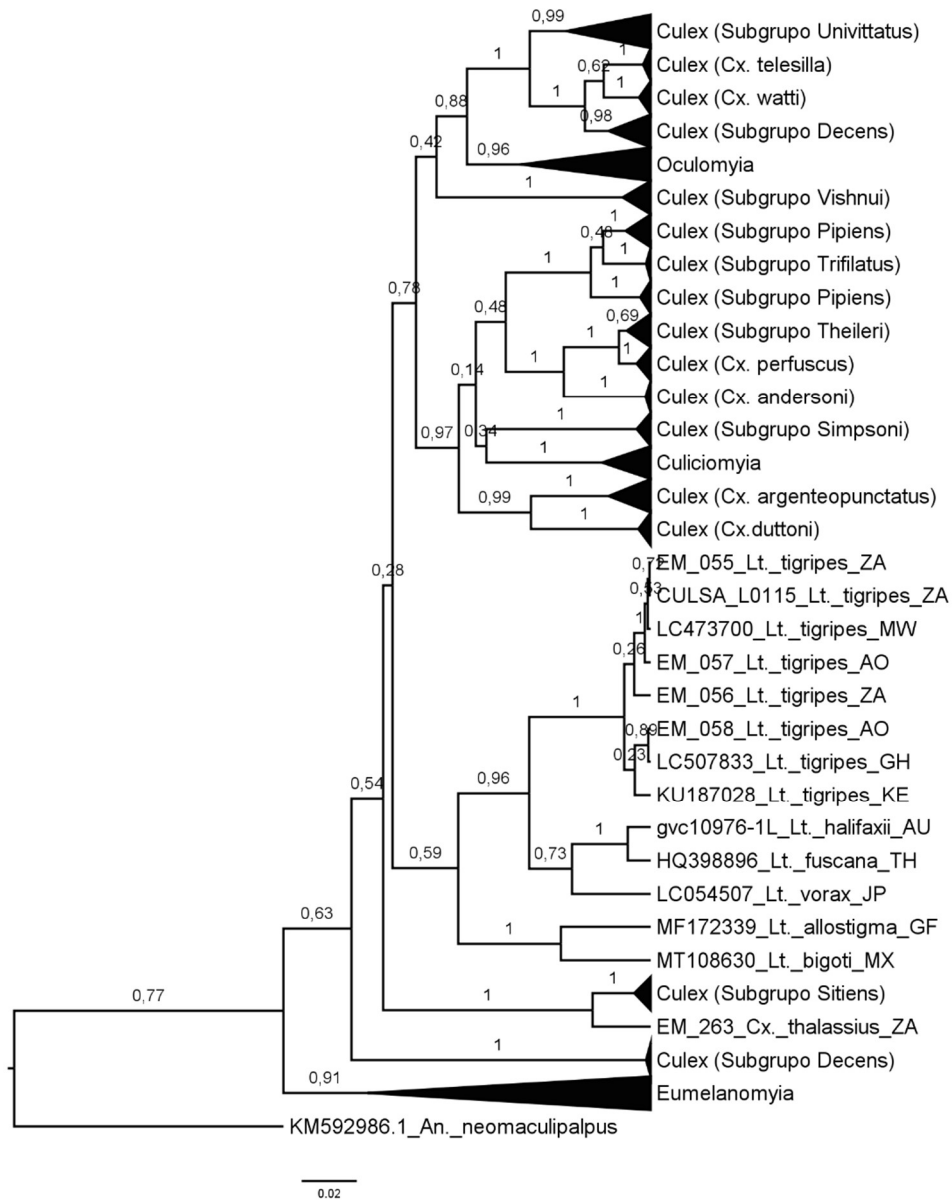


Figure S-III 18. a, b, c, d) Topology inferred by Bayesian inference under the GTR+G+1 model for the *Culex* and *Lutzia* genera, the analysis involved 171 nucleotide sequences with 636 positions in the final dataset. Support values correspond to a posteriori probability. The size bar indicates 0.02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

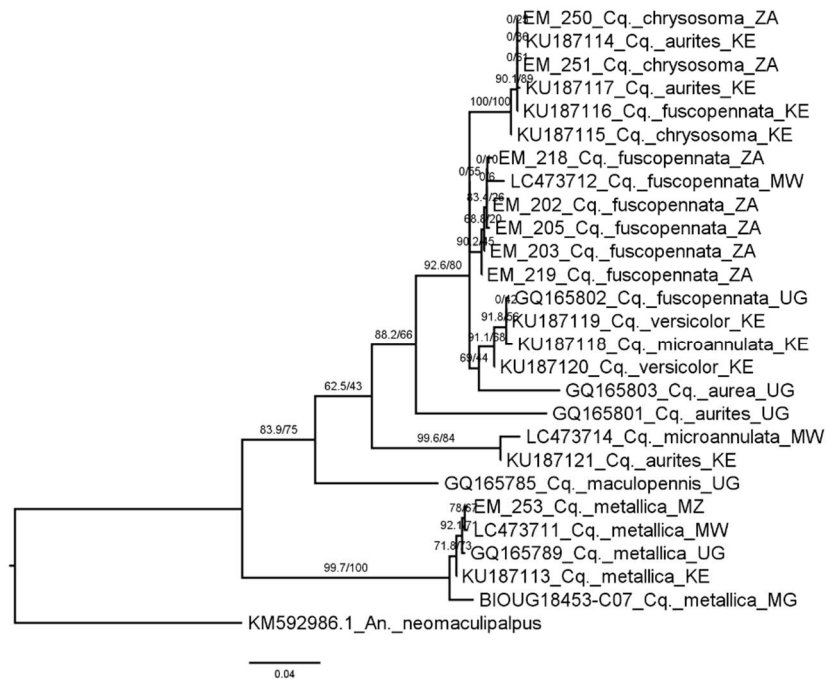


Figure S-III 19. Maximum likelihood tree under the GTR+G model for *Coquillettidia* genus, analysis involved 27 nucleotide sequences with 636 positions in the final dataset, consensus tree probability was -2352,702. Support values for the branches were estimated with aLRT/Bootstrap with 1000 repetitions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

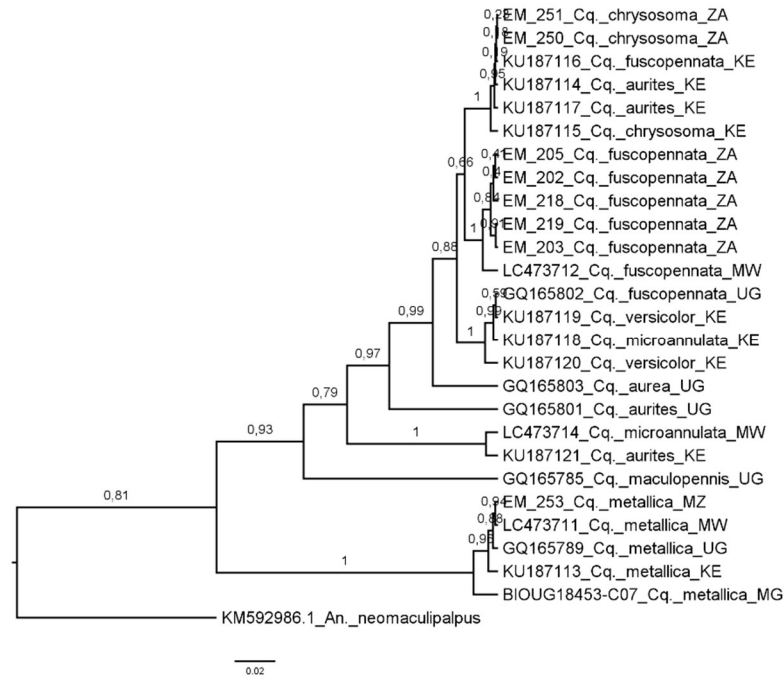


Figure S-III 20. Topology inferred by Bayesian inference under the GTR+G model for the genus *Coquillettidia*, the analysis involved 27 nucleotide sequences with 636 positions in the final dataset. Support values correspond to a posteriori probability. The size bar indicates 0.02 replacements per site.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

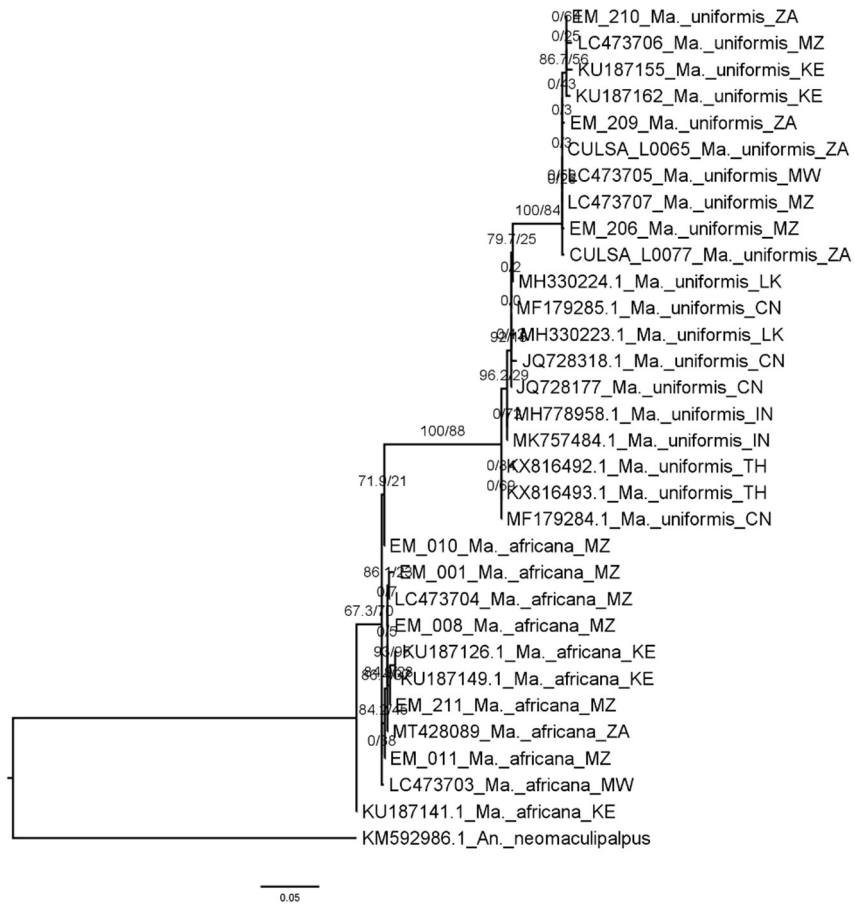


Figure S-III 21. Maximum likelihood tree under the GTR+G model for *Mansonia* genus, analysis involved 32 nucleotide sequences with 636 positions in the final dataset, consensus tree probability was -1779,294. Support values for the branches were estimated with aLRT/Bootstrap with 1000 repetitions for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

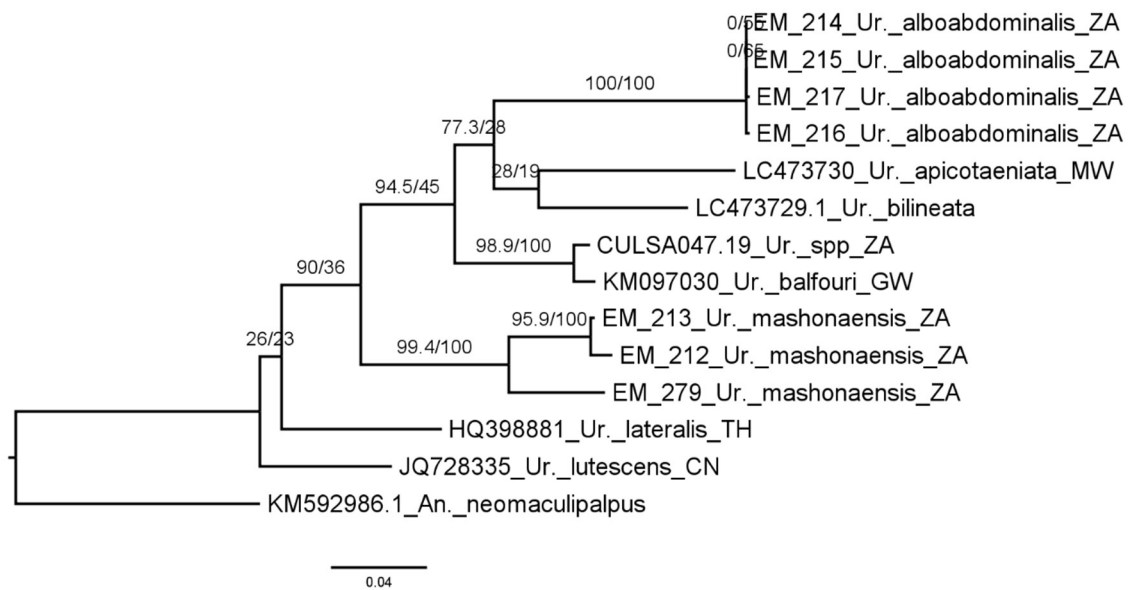


Figure S-III 25. Maximum likelihood tree under the GTR+G model for *Uranotaenia* genus, analysis involved 14 nucleotide sequences with 636 positions in the final dataset, probability of consensus tree was -2516,763. Support values for the branches were estimated with aLRT/Bootstrap with 1000 repetitions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

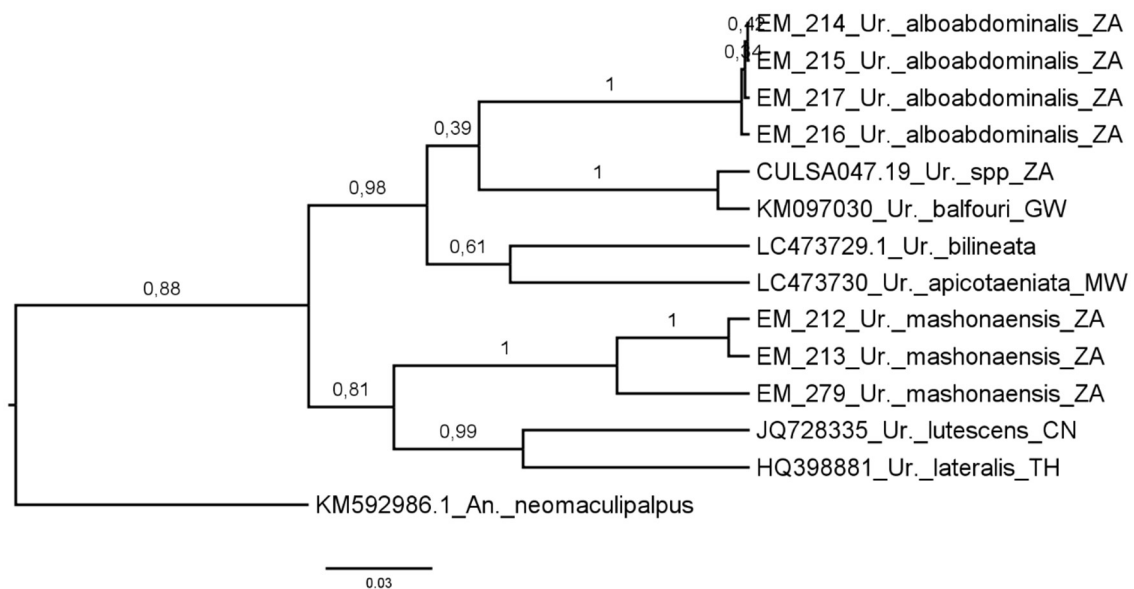


Figure S-III 26. Topology inferred by Bayesian inference under the GTR+G model for the genus *Uranotaenia*, the analysis involved 14 nucleotide sequences with 636 positions in the final dataset. Support values correspond to a posteriori probability. The size bar indicates 0.03 replacements per site.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

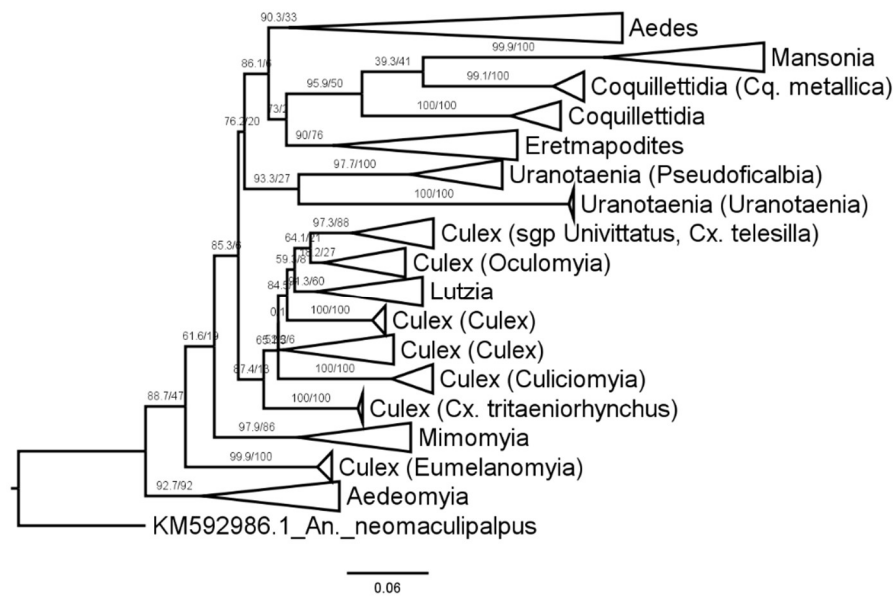


Figure S-III 27. Maximum likelihood tree under the GTR+G+I model for the genera *Aedeomyia*, *Aedes*, *Eretmapodites*, *Culex*, *Lutzia*, *Coquillettidia*, *Mansonia*, *Mimomyia*, *Uranotaenia*, the analysis involved 180 nucleotide sequences with 632 positions in the final data set, consensus tree probability 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.

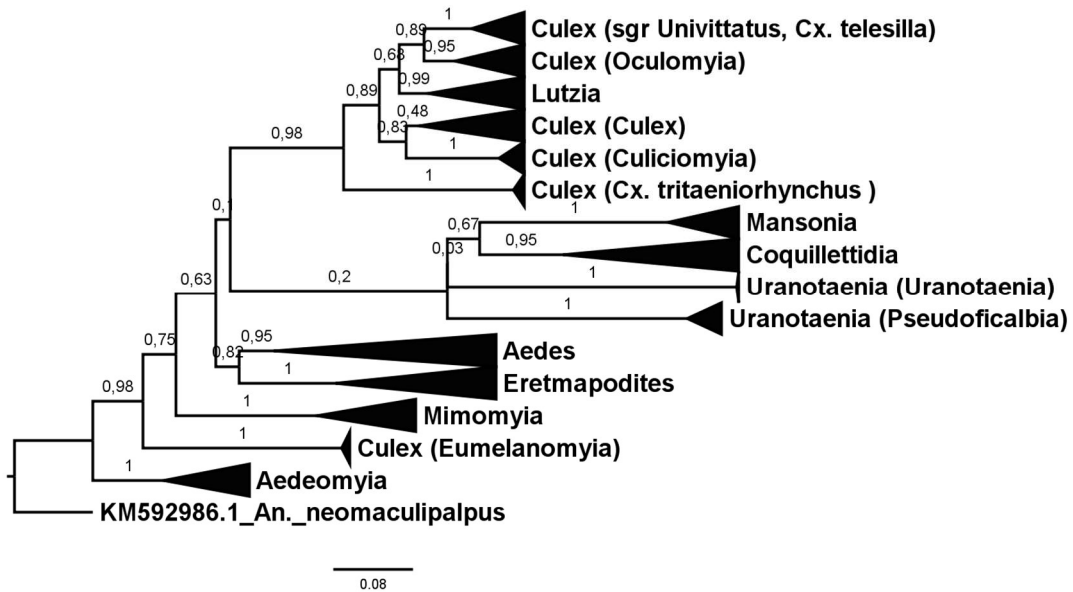


Figure S-III 28. Topology inferred by Bayesian inference under the GTR+G+I model for the genera *Aedeomyia*, *Aedes*, *Eretmapodites*, *Culex*, *Lutzia*, *Coquillettidia*, *Mansonia*, *Mimomyia*, *Uranotaenia*, the analysis involved 180 nucleotide sequences with 632 positions in the final dataset. Support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

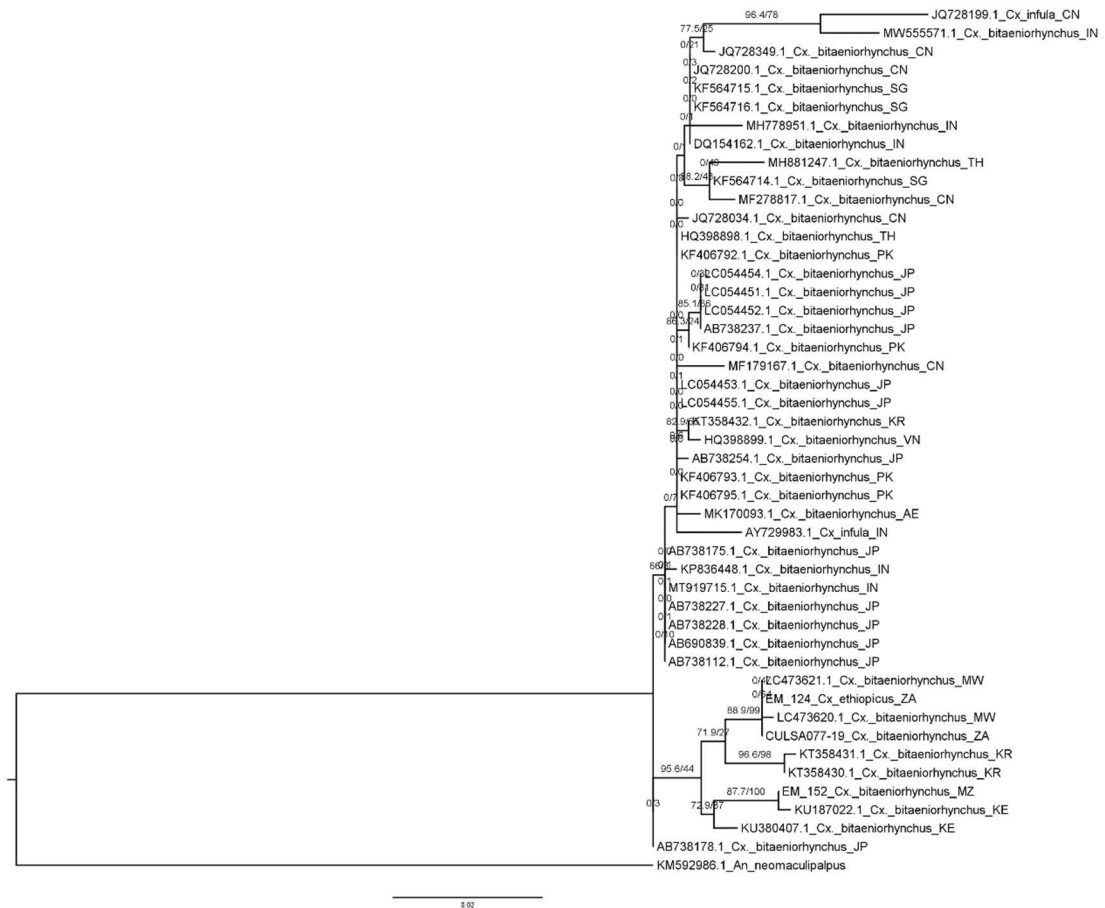


Figure S-III 29. Maximum likelihood tree under the T92+G model for the Bitaniorhynchus Complex, analysis involved 47 nucleotide sequences with 653 positions in the final dataset, consensus tree probability was -1675,730. Support values for the branches were estimated with aLRT/Bootstrap with 1000 repetitions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

