Supplementary material to:

Barrios-Izás M.A., Morrone J.J., Grebennikov V.V. & Andújar C. 2026: Mitogenomic evidence reveals convergent evolution of minute eyeless soil-dwelling weevils in Mesoamerica and the Mediterranean (Coleoptera: Curculionidae). — *Eur. J. Entomol.* 123: 291–300. Figs S1–S8.

Fig. S1. Bayesian majority-rule consensus tree of Curculionoidea inferred with PhyloBayes from the DNA15 dataset.

Fig. S2. Bayesian majority-rule consensus tree of Curculionoidea inferred with PhyloBayes from the DNA13 dataset.

Fig. S3. Bayesian majority-rule consensus tree of Curculionoidea inferred with PhyloBayes from the AA13 dataset. This tree is the topology presented in the main text.

Fig. S4. Maximum likelihood tree of Curculionoidea inferred with RAxML from the DNA15 dataset.

Fig. S5. Maximum likelihood tree of Curculionoidea inferred with RAxML from the DNA15 dataset.

Fig. S6. Maximum likelihood tree of Curculionoidea inferred with RAxML from the DNA13 dataset.

Fig. S7. Maximum likelihood tree of Curculionoidea inferred with RAxML from the DNA13 dataset.

Fig. S8. Maximum likelihood tree of Curculionoidea inferred with RAxML from the AA13 dataset.

Fig. S1. Bayesian majority-rule consensus tree of Curculionoidea inferred with PhyloBayes from the DNA15 dataset (13 protein-coding genes and 2 rRNA genes; 13,140 bp). Analyses were conducted under a GTR-CAT model using two independent chains run for 5,000 generations; the first 2,000 generations were discarded as burn-in. Posterior probabilities are indicated at nodes.



Fig. S2. Bayesian majority-rule consensus tree of Curculionoidea inferred with PhyloBayes from the DNA13 dataset (13 protein-coding genes; 11,045 bp). Analyses were conducted under a GTR-CAT model using two independent chains run for 5,000 generations; the first 2,000 generations were discarded as burn-in. Posterior probabilities are indicated at nodes.



Fig. S3. Bayesian majority-rule consensus tree of Curculionoidea inferred with PhyloBayes from the AA13 dataset (amino acid sequences of the 13 mitochondrial protein-coding genes; 3,669 AAs; invertebrate mitochondrial code). Analyses were conducted under a GTR-CAT model using two independent chains run for 5,000 generations; the first 2,000 generations were discarded as burn-in. Posterior probabilities are indicated at nodes. This tree is the topology presented in the main text.

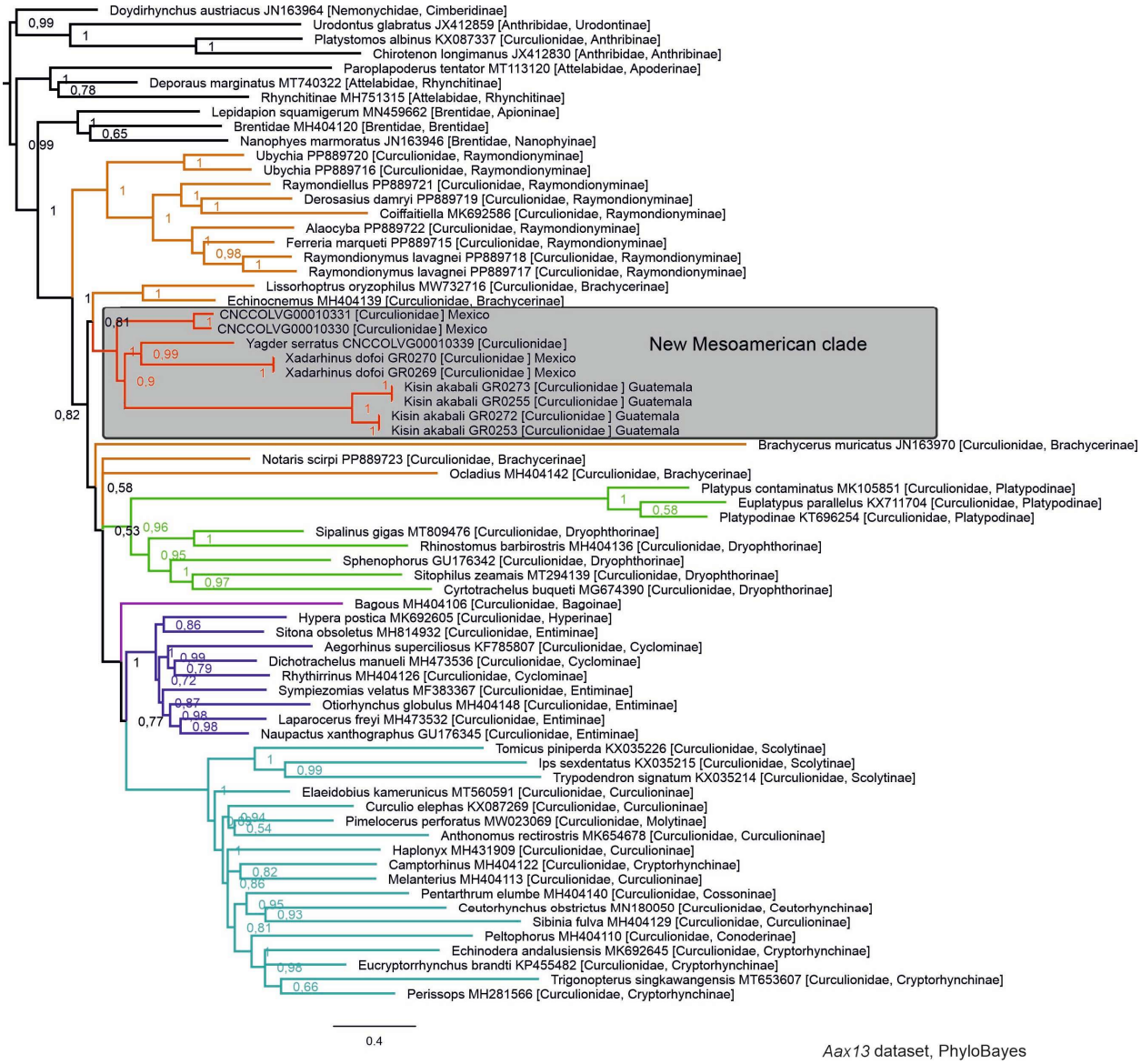


Fig. S4. Maximum likelihood tree of Curculionoidea inferred with RAxML from the DNA15 dataset (13 PCGs + 2 rRNA genes; 13,140 bp), applying gene and codon partitioning. Each partition was analyzed under an independent GTR model, using the CAT approximation during tree searches and GAMMA for final optimization. The best-scoring tree was selected from 100 searches with randomized parsimony starting trees. Node support values correspond to 500 bootstrap replicates.



Fig. S5. Maximum likelihood tree of Curculionoidea inferred with RAxML from the DNA15 dataset (13 PCGs + 2 rRNA genes; 13,140 bp), applying gene partitioning. Each partition was analyzed under an independent GTR model, using the CAT approximation during tree searches and GAMMA for final optimization. The best-scoring tree was selected from 100 searches with randomized parsimony starting trees. Node support values correspond to 500 bootstrap replicates.



Fig. S6. Maximum likelihood tree of Curculionoidea inferred with RAxML from the DNA13 dataset (13 protein-coding genes; 11,045 bp), applying gene and codon partitioning. Each partition was analyzed under an independent GTR model, using the CAT approximation during tree searches and GAMMA for final optimization. The best-scoring tree was selected from 100 searches with randomized parsimony starting trees. Node support values correspond to 500 bootstrap replicates.

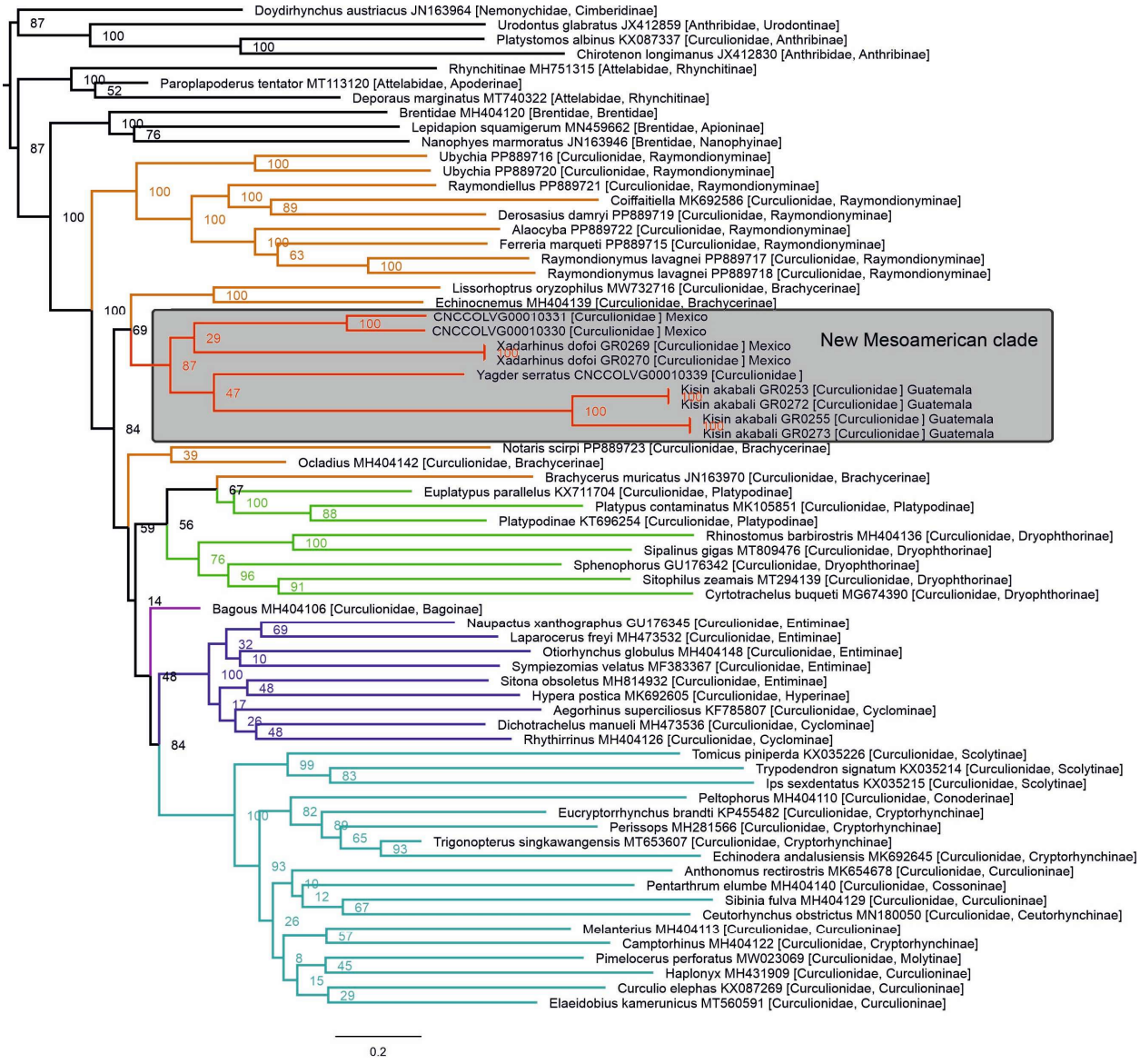


Fig. S7. Maximum likelihood tree of Curculionoidea inferred with RAxML from the DNA13 dataset (13 protein-coding genes; 11,045 bp), applying gene partitioning. Each partition was analyzed under an independent GTR model, using the CAT approximation during tree searches and GAMMA for final optimization. The best-scoring tree was selected from 100 searches with randomized parsimony starting trees. Node support values correspond to 500 bootstrap replicates.



Fig. S8. Maximum likelihood tree of Curculionoidea inferred with RAxML from the AA13 dataset (amino acid sequences of the 13 mitochondrial protein-coding genes; 3,669 AAs), applying gene partitioning. Each partition was analyzed under an independent GTR model, using the CAT approximation during tree searches and GAMMA for final optimization. The best-scoring tree was selected from 100 searches with randomized parsimony starting trees. Node support values correspond to 500 bootstrap replicates.

