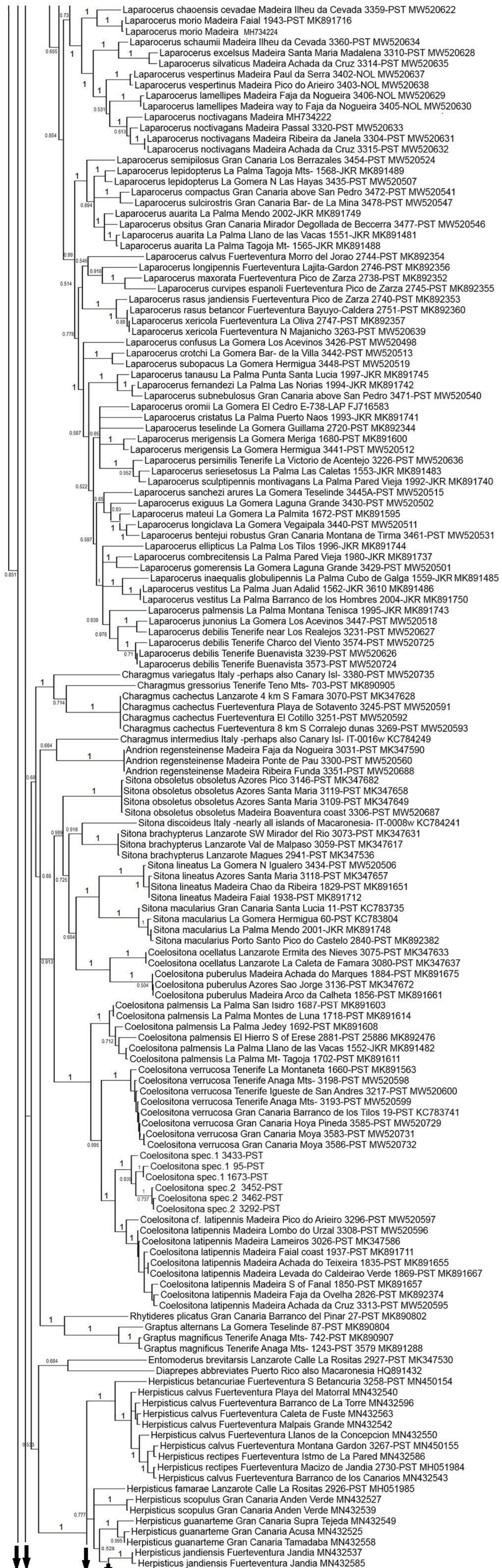
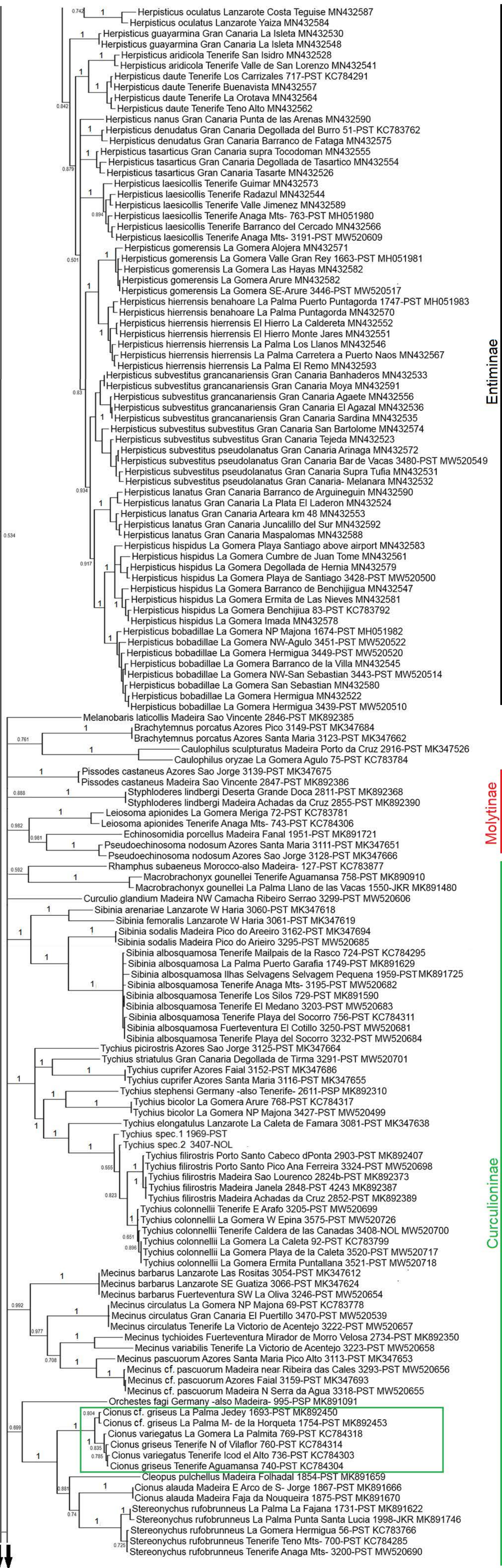




**Fig. 2** Bayesian 50% majority rule consensus tree built from mitochondrial CO1 gene sequence (658 bp) for 468 species of 1388 samples of the Macaronesian Curculionidea. Posterior probability values are indicated next to the respective nodes. Species / Island / Location / Collector's number / Genbank acc. no. The species and species groups marked in colour are discussed in the article.



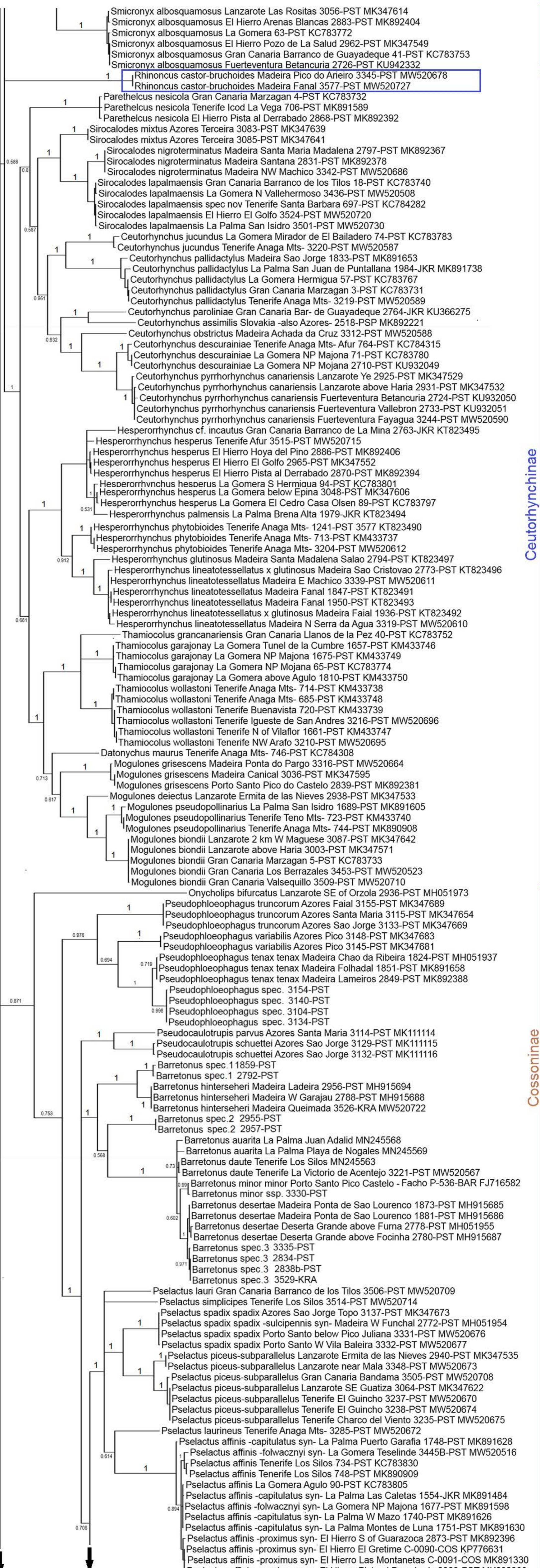
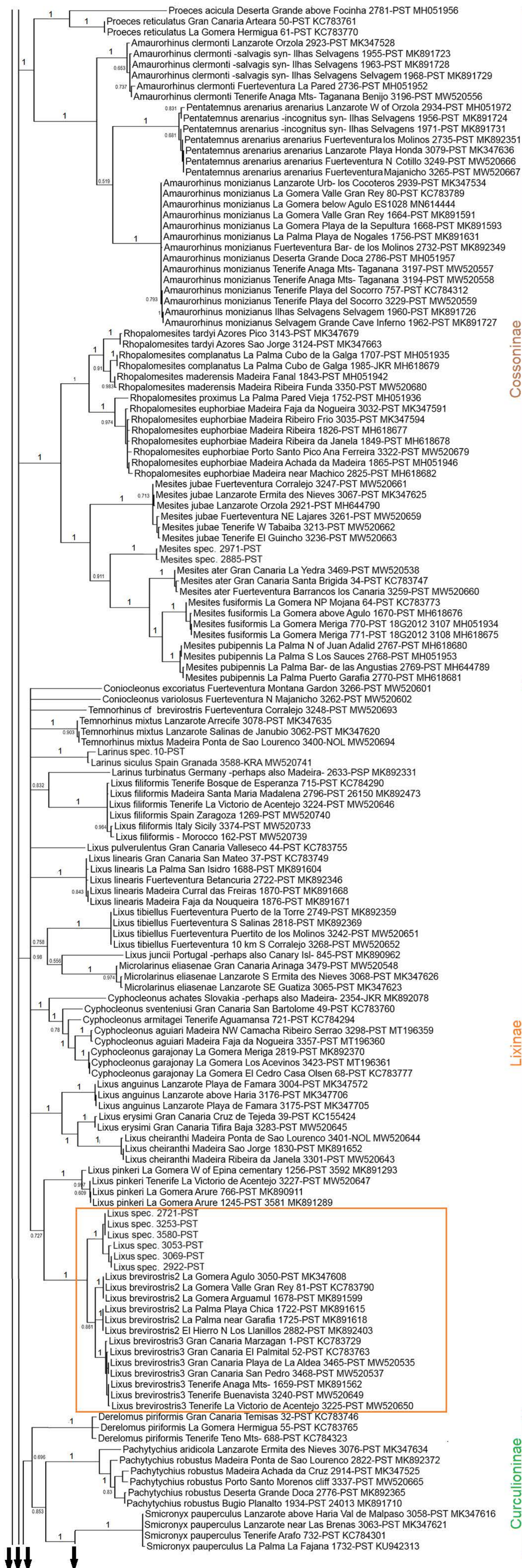
Entiminae

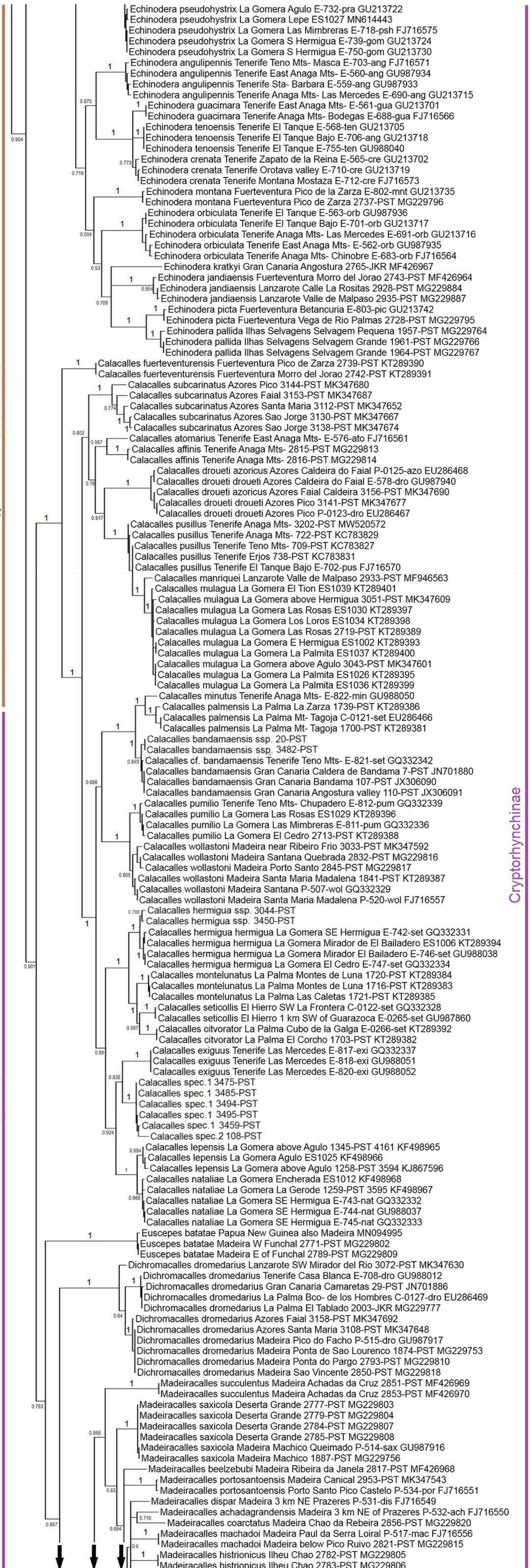
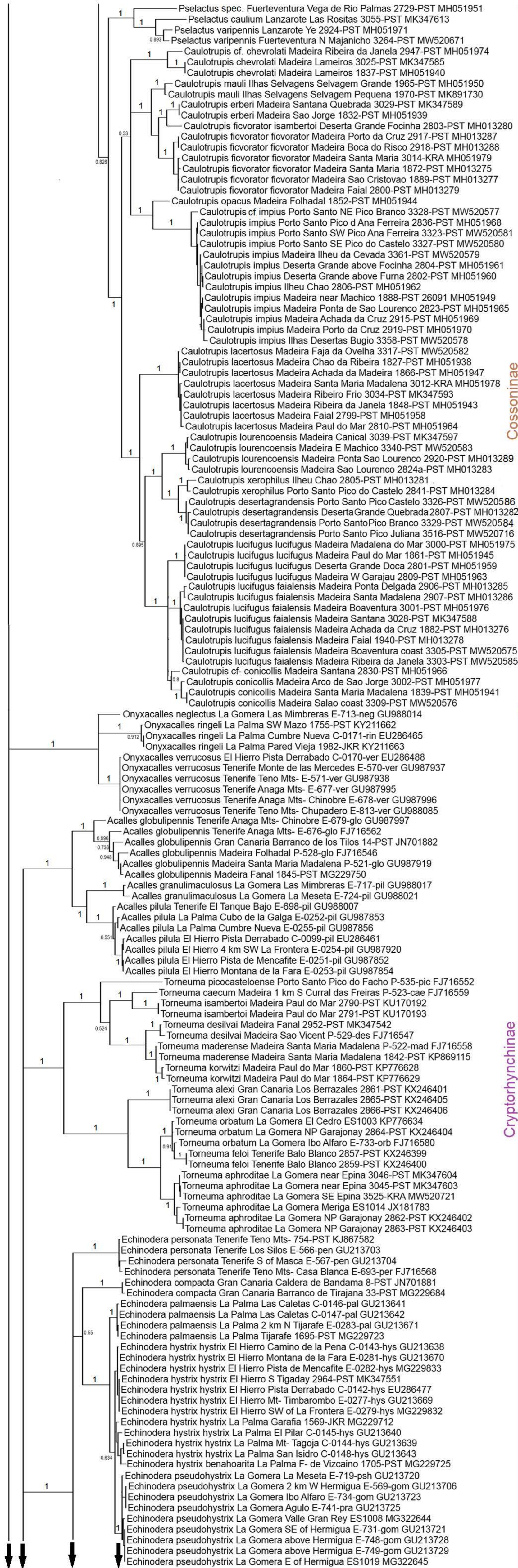


Entiminae

Molytinae

Curculioninae

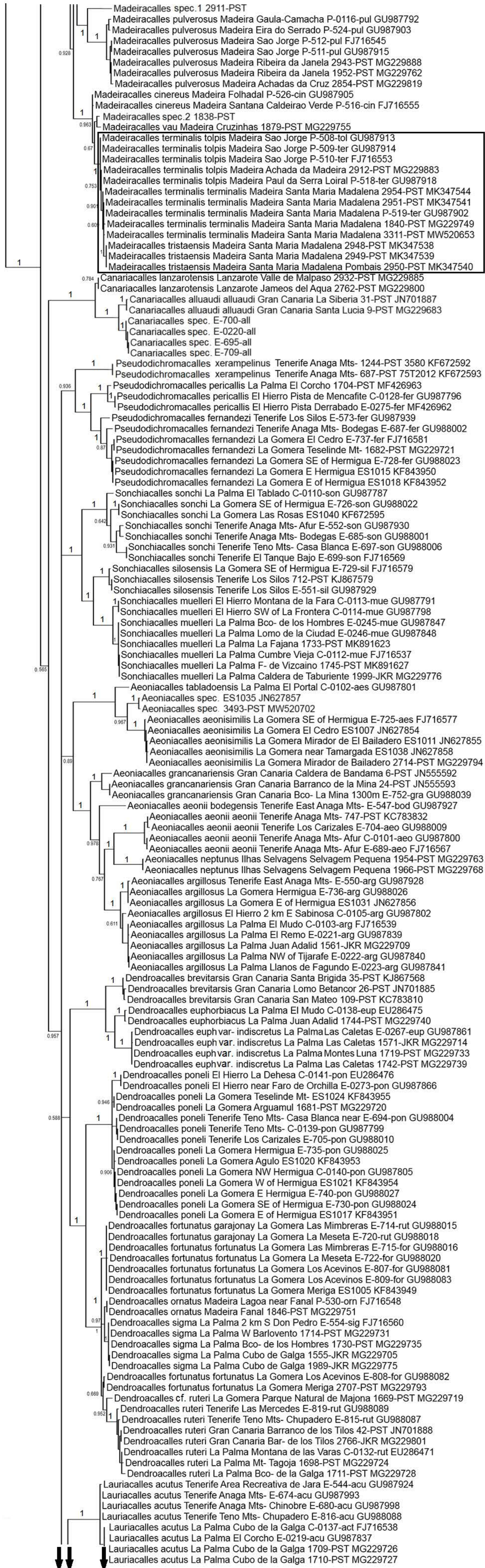




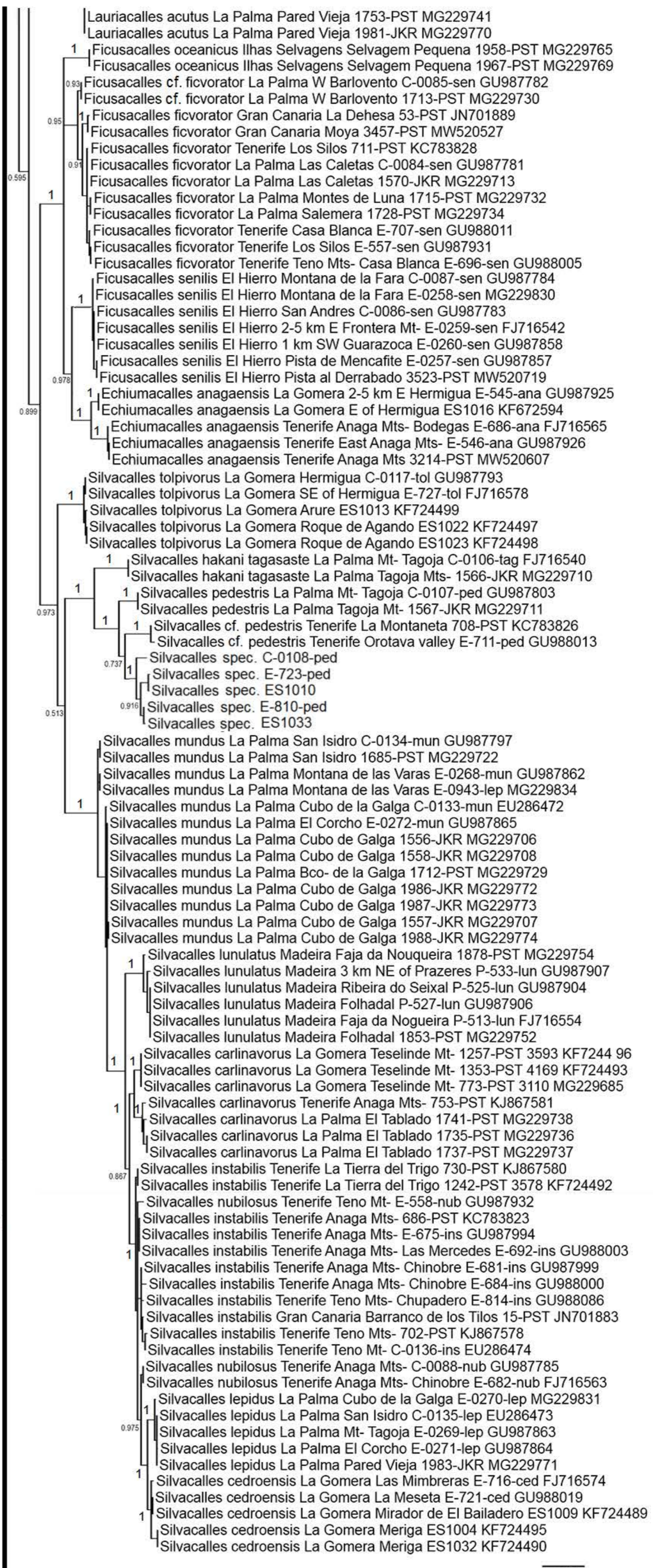
Cossoninae

Cryptorhynchinae

Cryptorhynchinae



Cryptorhynchinae



Cryptorhynchinae

**Fig. 2** Bayesian 50% majority rule consensus tree built from mitochondrial CO1 gene sequence (658 bp) for 468 species of 1388 samples of the Macaronesian Curculionidae. Posterior probability values are indicated next to the respective nodes. Species / Island / Location / Collector's number / Genbank acc. no. The species and species groups marked in colour are discussed in the article.