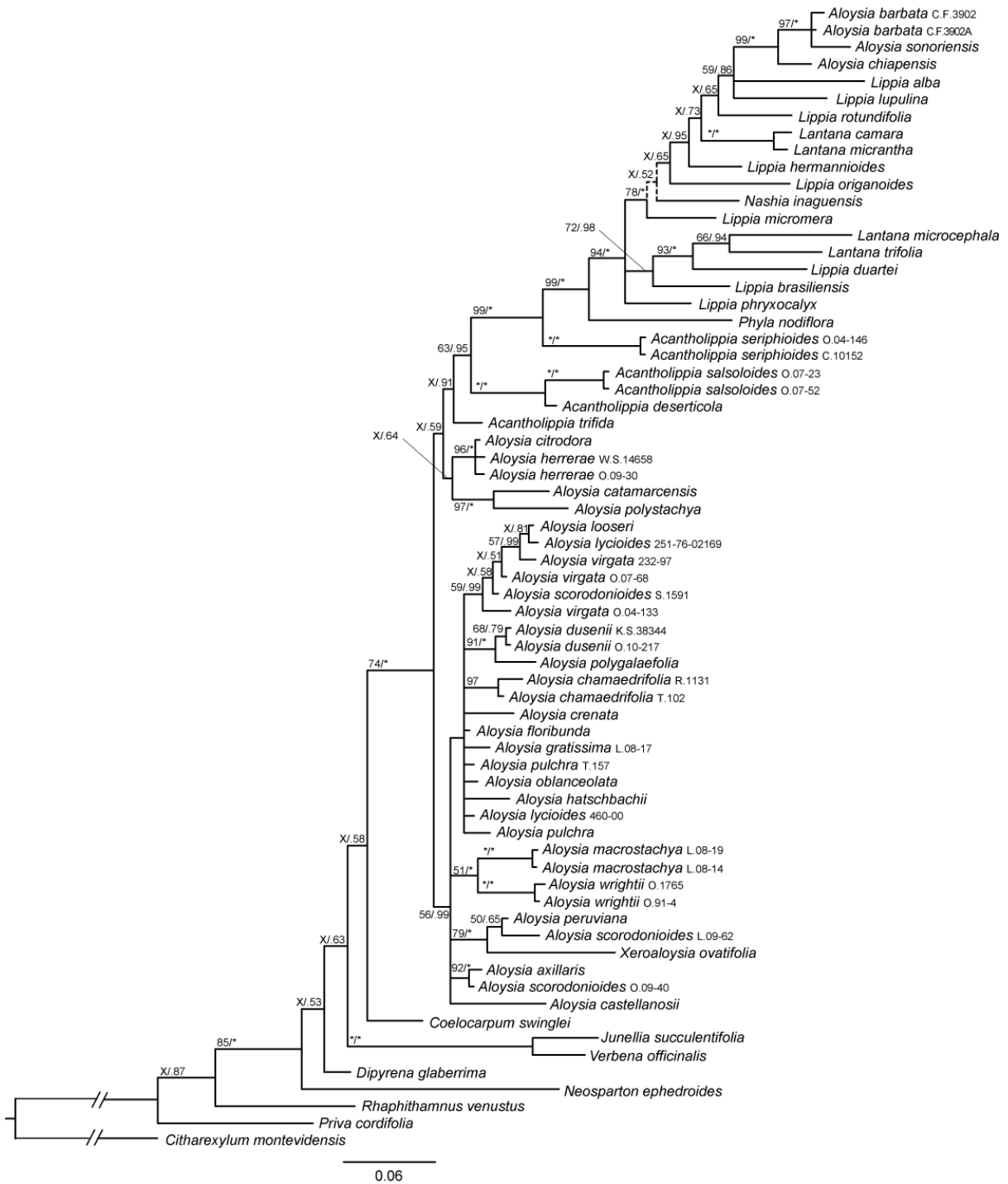
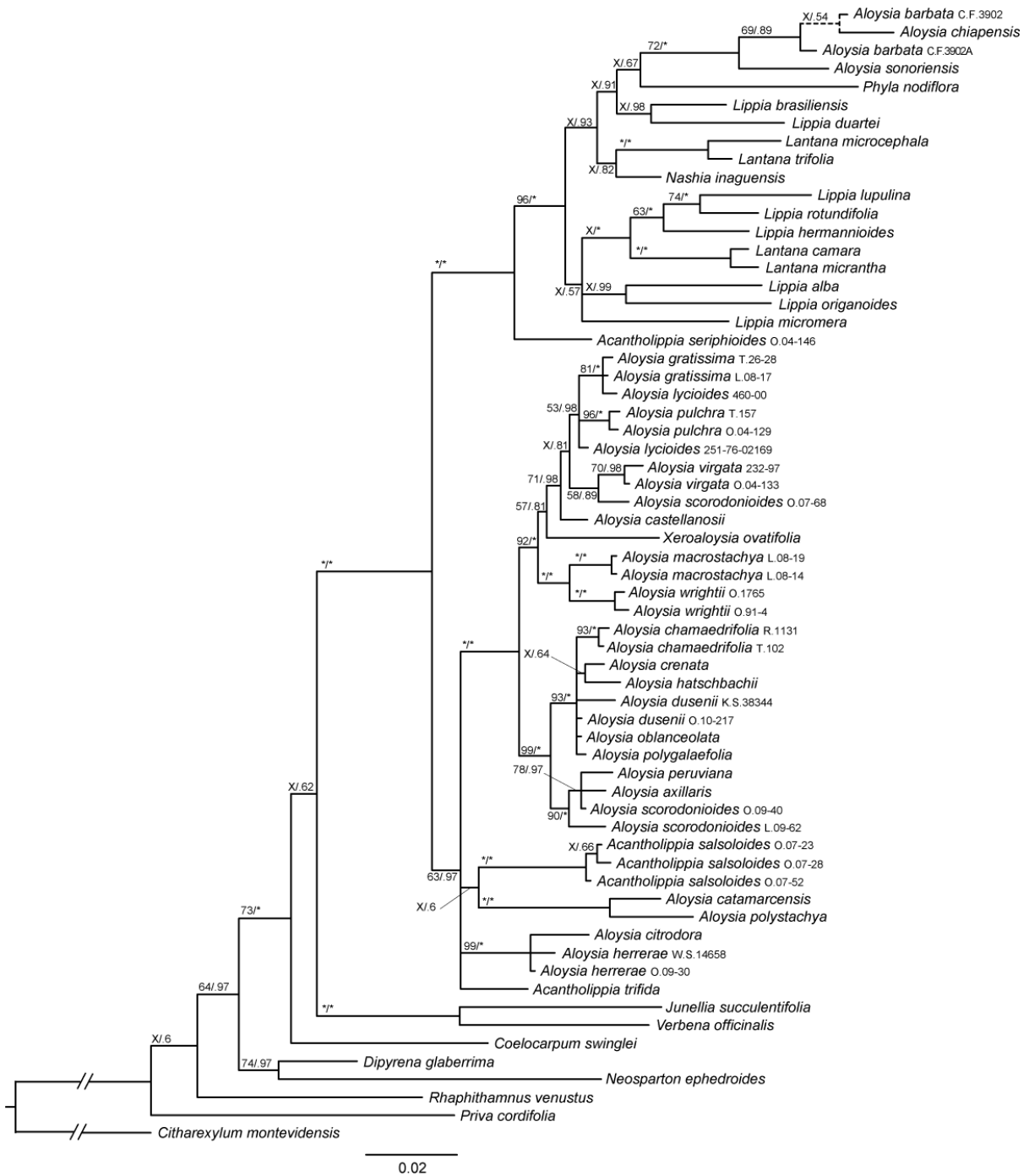


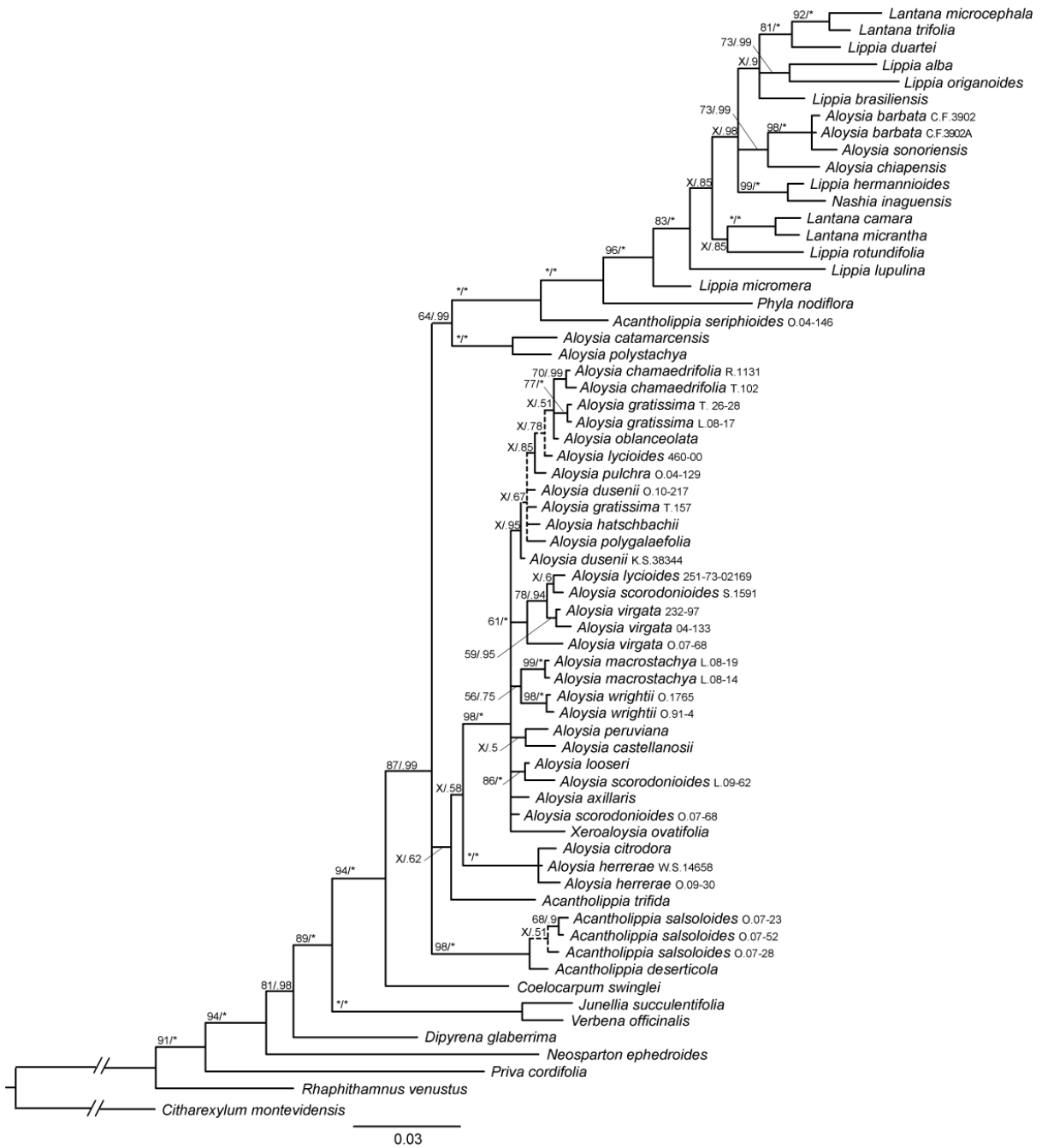
Phylogeny inferred from 4,266 aligned positions of DNA sequence data from 3 chloroplast loci in combination. Topology inferred by ML and Bayesian analyses, branch lengths inferred by Bayesian analysis. Branches are labeled with ML bootstrap values/Bayesian posterior probabilities greater than 50%/0.50. Stars (*) denote 100% support, Xs denote bootstrap values below 50%.



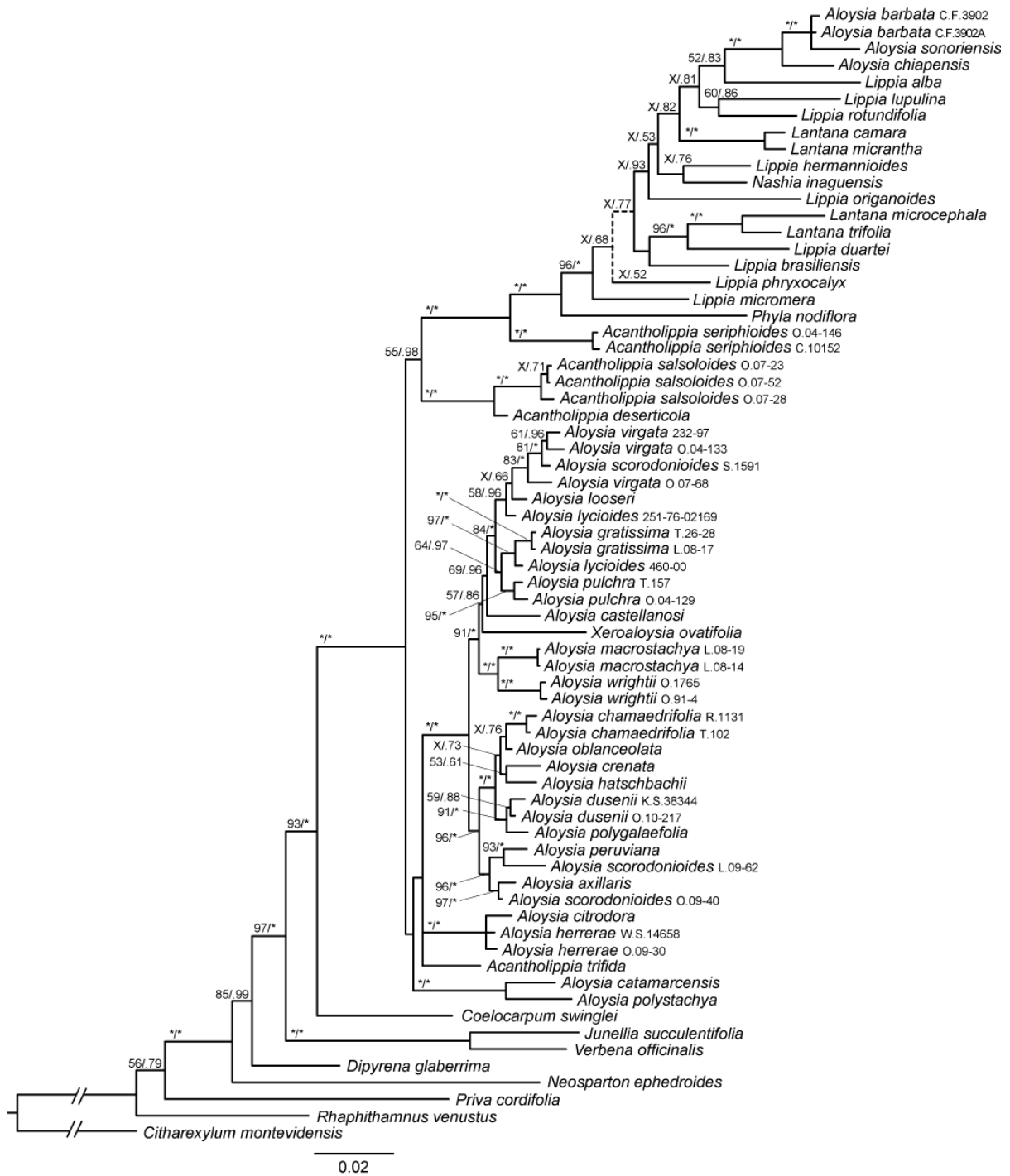
Phylogeny inferred from DNA sequence from nuclear region ETS (514 aligned positions). Topology inferred by ML and Bayesian analyses, branch lengths inferred by Bayesian analysis. Branches are labeled with ML bootstrap values/Bayesian posterior probabilities greater than 50%/0.50. Stars (*) denote 100% support, Xs denote bootstrap values below 50%. Dashed lines indicate disagreement between ML and Bayesian analyses; topology inferred from Bayesian analysis is shown.



Phylogeny inferred from DNA sequence from nuclear region PPR 81 (1,221 aligned positions). Topology inferred by ML and Bayesian analyses, branch lengths inferred by Bayesian analysis. Branches are labeled with ML bootstrap values/Bayesian posterior probabilities greater than 50%/0.50. Stars (*) denote 100% support, Xs denote bootstrap values below 50%. Dashed lines indicate disagreement between ML and Bayesian analyses; topology inferred from Bayesian analysis is shown.



Phylogeny inferred from DNA sequence from nuclear region PPR 123 (1,325 aligned positions). Topology inferred by ML and Bayesian analyses, branch lengths inferred by Bayesian analysis. Branches are labeled with ML bootstrap values/Bayesian posterior probabilities greater than 50%/0.50. Stars (*) denote 100% support, Xs denote bootstrap values below 50%. Dashed lines indicate disagreement between ML and Bayesian analyses; topology inferred from Bayesian analysis is shown.



Phylogeny inferred from 3,060 aligned positions of DNA sequence data from 3 nuclear loci in combination. Topology inferred by ML and Bayesian analyses, branch lengths inferred by Bayesian analysis. Branches are labeled with ML bootstrap values/Bayesian posterior probabilities greater than 50%/0.50. Stars (*) denote 100% support, Xs denote bootstrap values below 50%. Dashed lines indicate disagreement between ML and Bayesian analyses; topology inferred from Bayesian analysis is shown.