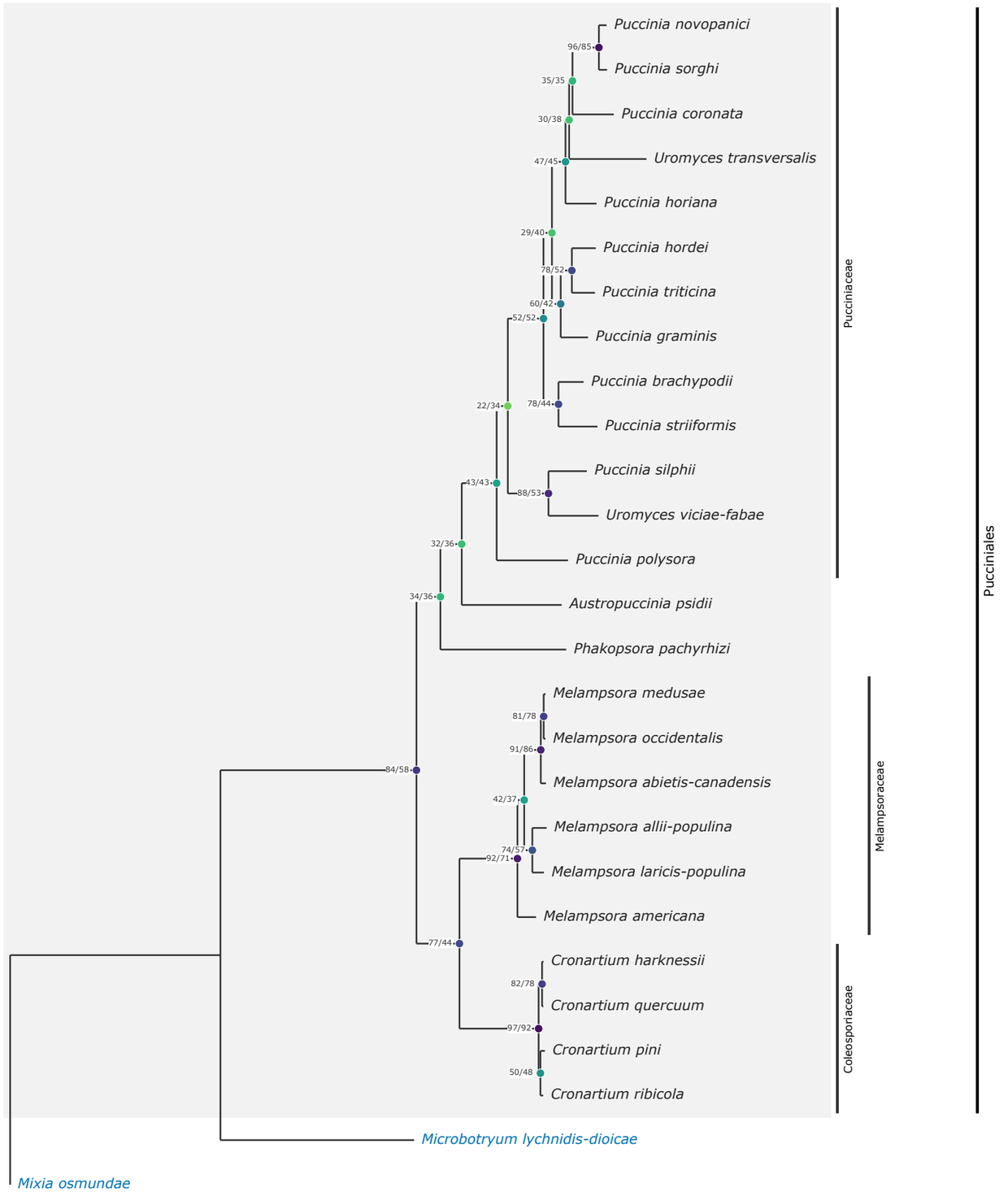
Pucciniales

Supermatrix of 526 BUSCO genes. Jerry Cooper, Nov. 2026

Notes: ~30% of deposited genomes contain excessive contamination. Divergance of allelic loci is also substantial

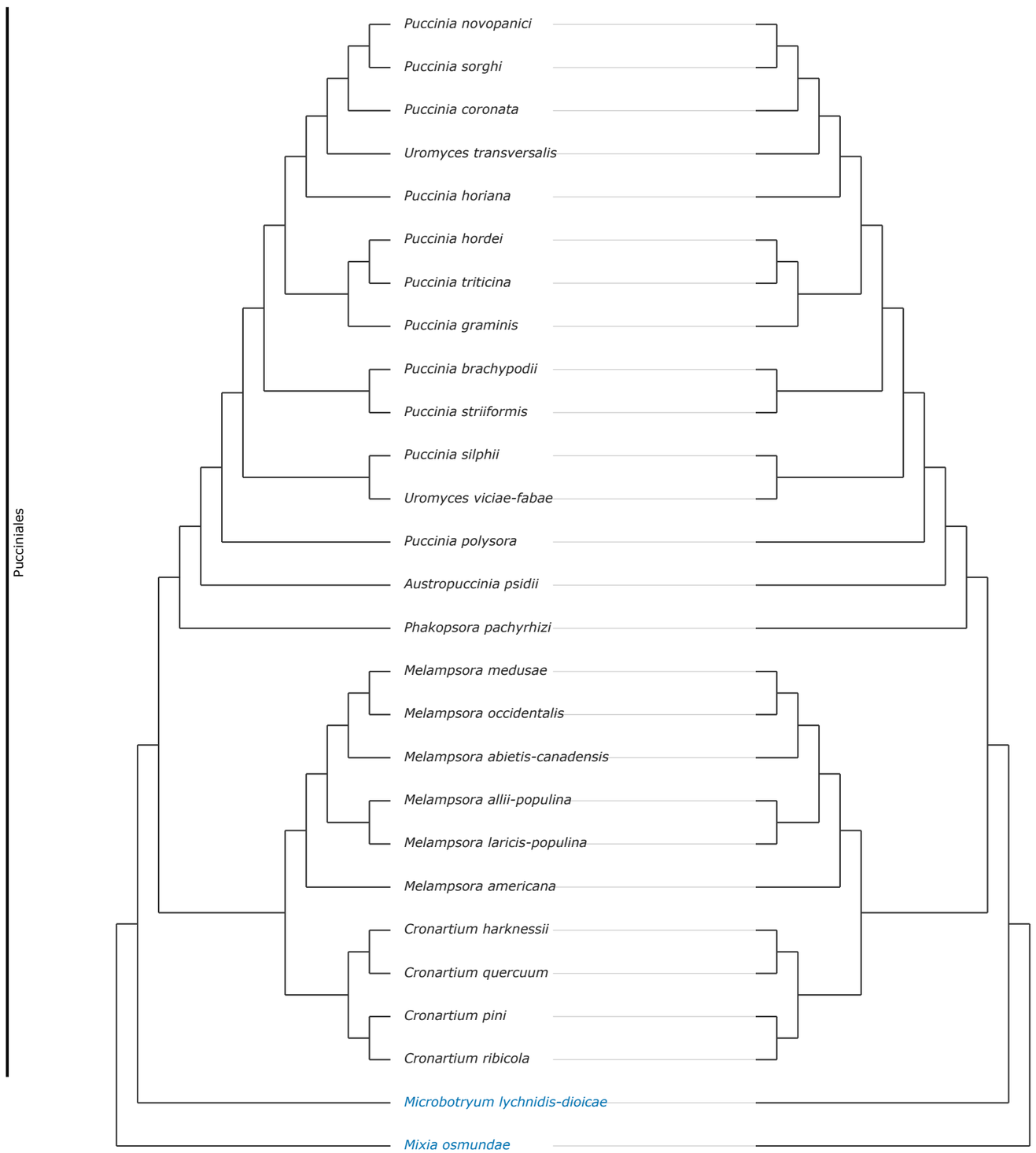
A. Maximum likelihood (IQ-TREE, 526 loci)



ML (concatenation)

B. Coalescent (ASTRAL, 526 gene trees)

ASTRAL (coalescent)



0.05 substitutions/site

node colour: gene concordance factor (gCF, %)

0 20 40 60 80 100

node labels: gCF / sCF (%)
SH-aLRT / UFBoot = 100/100 on every node

outgroup (2 taxa)
other ingroup (25 taxa)

branch absent from the other tree
branch present in both trees
taxon changes position