This package contains 5 files:

**1. SequenceAligments\_Memecylon\_Trimmed\_introns.fasta**

This file contains concatenated alignment of 87 introns**.** First, these introns were individually aligned using MAFFT v7.215 (Katoh and Standley 2013), with the default gap opening penalty. The alignments were then trimmed using trimAl v1.2 (Capella-Gutiérrez et al. 2009) with a gap threshold of 0.9. Then the genes were concatenated using Phyx v8.2.0 (Brown et al. 2017). The code of the samples and names of taxa are provided at the beginning of the sequence.

**2. Partition\_file.txt**

This is the partition scheme generated using Phyx v8.2.0 (Brown et al. 2017) when concatenating the intron alignment. The names of the genes are provided in Amarasinghe et al., 2021. Type of sequence, trimal90\_name\_of\_Gene, and position are provided in the partition file respectively.

3. **RAxML\_bipartitions.from\_trimmed\_concatenated\_introns**

This file contains the species tree resulted from the concatenated alignment. Maximum Likelihood analyses of the concatenated dataset were repeated as in (2) to generate this phylogeny.

4. **Gene\_trees.tre**

Gene trees were generated for each of the individual gene alignments using Maximum Likelihood (ML) in RAxML v8 (Stamatakis 2014), with 500 rapid bootstrap pseudoreplicates combined with a ML tree search using the GTRGAMMA model. 87 gene trees generated from introns are provided here.

**5. ASTAL\_Memecylon.tre**

This is the coalescent species tree. Here, 87 ML gene trees (derived from introns) generated from RAxML were input to ASTRAL-III v5.0.3 (Zhang et al. 2018). Both the code of the samples and names of taxa are available in this tree.