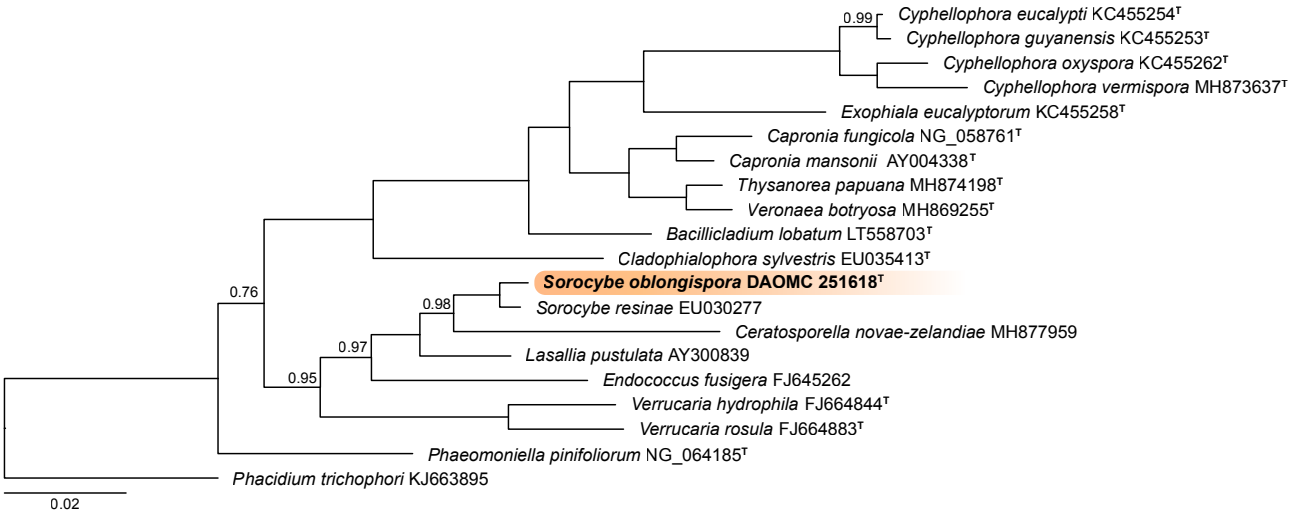
Fungal Planet 1032 – *Sorocybe oblongispora*



FP1032 Bayesian inference (BI) phylogenetic tree based on LSU sequences. The BI analysis was performed with MrBayes v. 3.2.6 using the best-fit nucleotide substitution model (GTR+G) estimated by the Akaike Information Criterion (AIC) using jModelTest v. 2.1.10, with a sampling frequency every 500 generations, three runs consisting of four chains (three heated, one cold), an automated stop value of 0.01, and the first 25 % of the trees discarded as burn-in. Posterior probabilities < 1 are presented in branch nodes. GenBank accession numbers follow the species name and sequences derived from ex-types are denoted with a superscript (T). The novel species is indicated in **bold** and highlighted in an orange box.