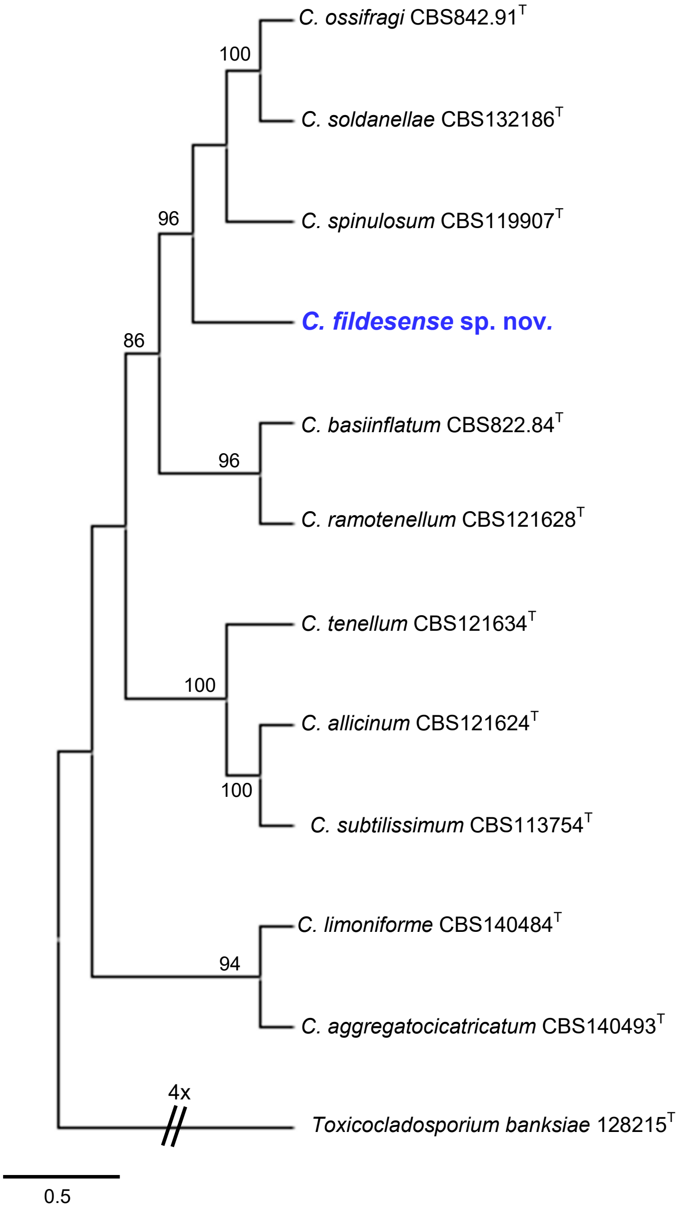
Fungal Planet 1006 – *Cladosporium fildesense*



FP1006 Maximum likelihood (ML) phylogeny of *C. fildesense* and related species within *C. herbarum* complex was inferred from the combined analysis of ITS, *actA* and *tef1* sequences (Bensch et al. 2015). Alignments and ML analyses were performed with MegaX (Kumar et al. 2018). Model used was HKY + G + I. Bootstrap support values (> 50 %) are shown at the nodes (bootstrap iterations = 1 000). The tree was rooted using combined ITS and *actA* sequences from *Toxicocladosporium banksiae* CBS 128215 (type strain).