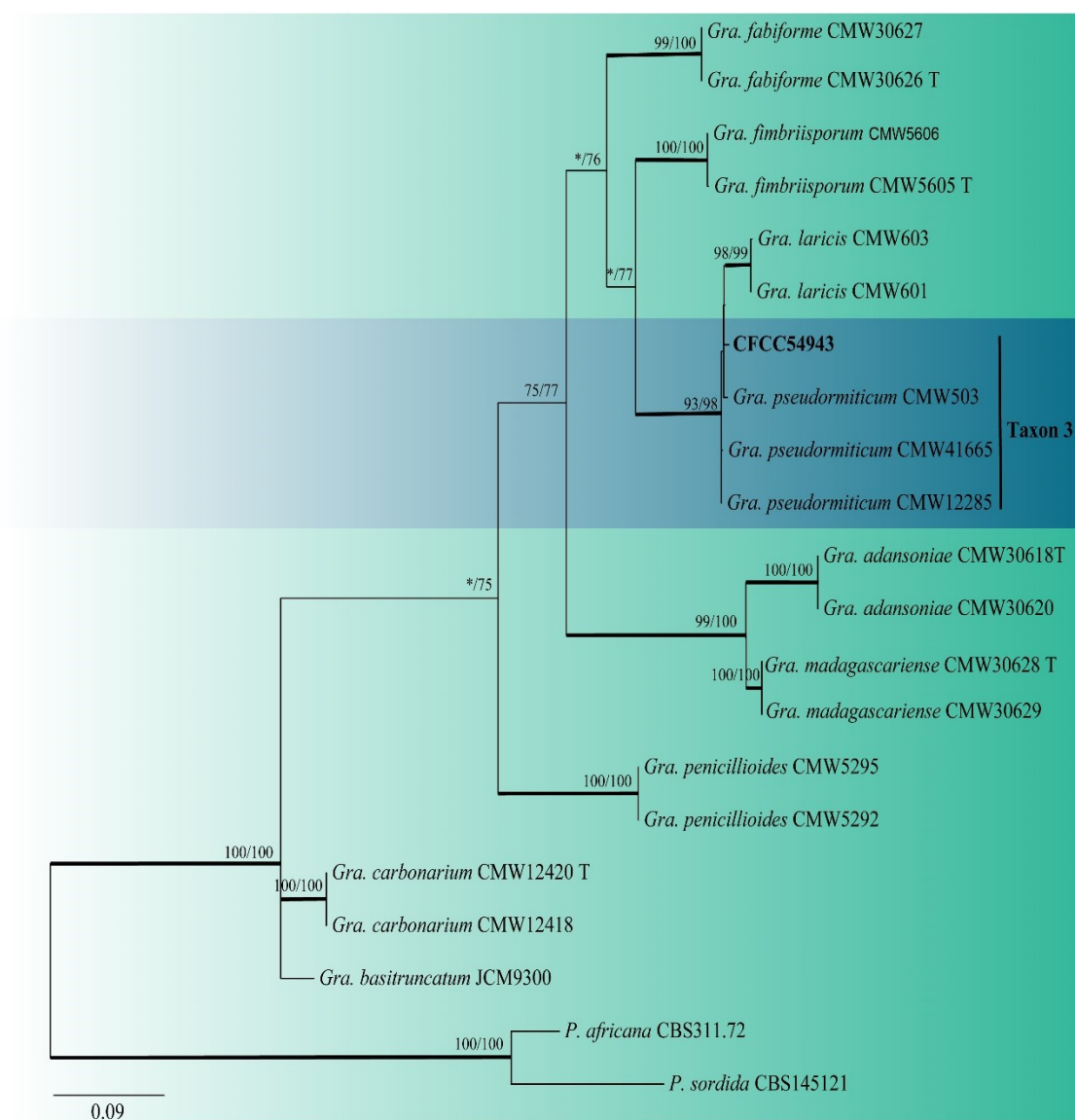


Supplementary Figure S1. ML tree of *Esteya* and related taxa (Taxon 1) generated from the combined (LSU+TUB2) sequence data. Novel sequences obtained in this study are presented in bold typeface. Bold branches indicate posterior probability values ≥ 0.9 . Bootstrap values $\geq 70\%$ for ML and MP are indicated above branches.



Supplementary Figure S2. ML tree of *Graphium* (Taxon 3) generated from the combined (ITS+tEF1- α) sequence data. Novel sequences obtained in this study are presented in bold typeface. Bold branches indicate posterior probability values ≥ 0.9 . Bootstrap values $\geq 70\%$ for ML and MP are indicated above branches. Bootstrap values $< 70\%$ are indicated by *.