

Supplementary materials

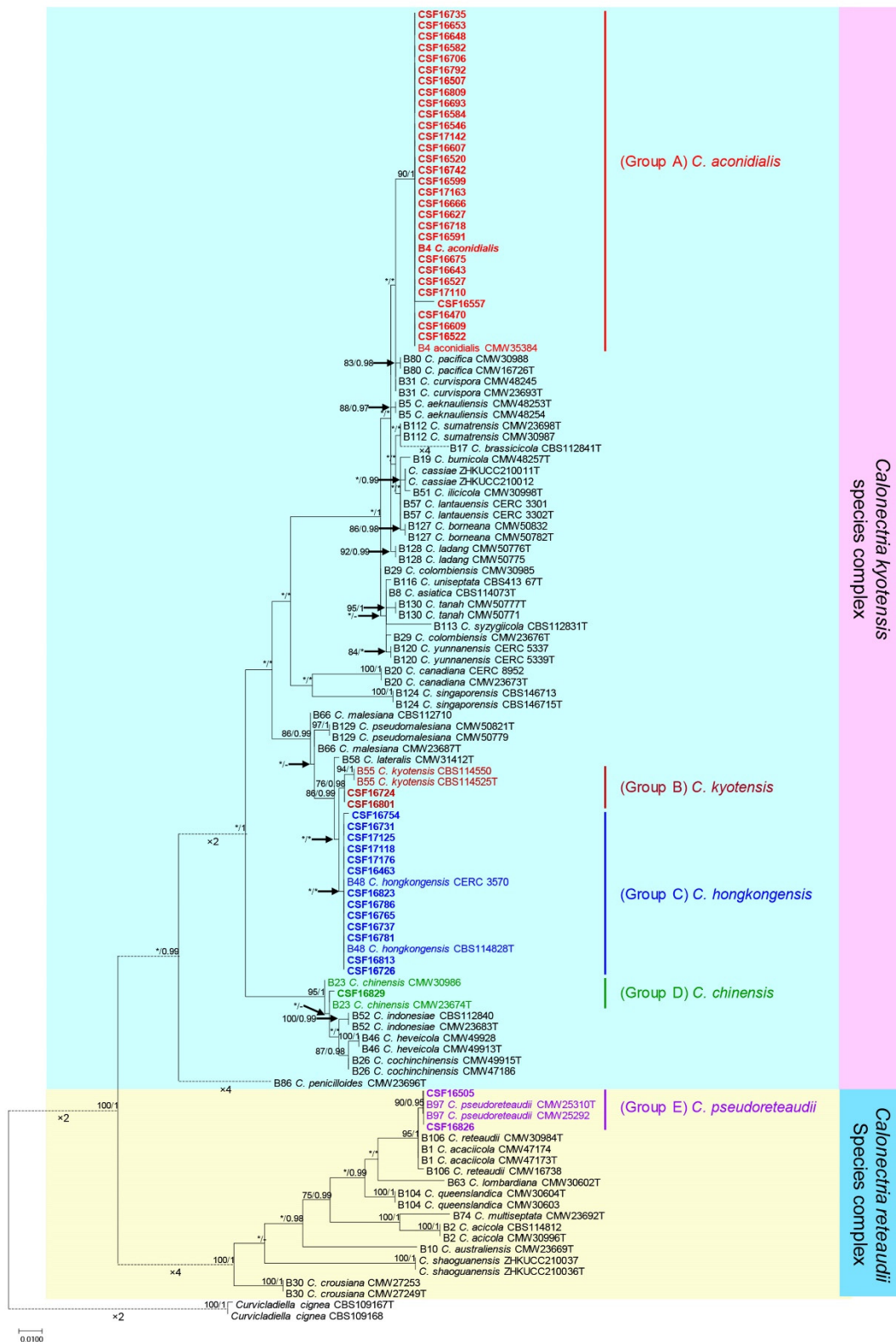
Supplementary Figure S1. Phylogenetic tree of *Calonectria* species based on maximum likelihood (ML) analyses of the *tef1* gene sequences in this study. Bootstrap support value $\geq 70\%$ for ML and posterior probabilities values ≥ 0.95 for Bayesian inference (BI) analyses are presented above the branches as follows: ML/BI. Bootstrap values $< 70\%$ or probabilities values < 0.95 are marked with “*”, and absent analysis values are marked with “-”. Ex-type isolates are marked with “T”. Isolates sequenced in this study are highlighted in bold and shown in color. Two isolates of *Curviciadiella cigna* (CBS 109167 and CBS 109168) were used as outgroups.

Supplementary Figure S2. Phylogenetic tree of *Calonectria* species based on maximum likelihood (ML) analyses of the *tub2* gene sequences in this study. Bootstrap support value $\geq 70\%$ for ML and posterior probabilities values ≥ 0.95 for Bayesian inference (BI) analyses are presented above the branches as follows: ML/BI. Bootstrap values $< 70\%$ or probabilities values < 0.95 are marked with “*”, and absent analysis values are marked with “-”. Ex-type isolates are marked with “T”. Isolates sequenced in this study are highlighted in bold and shown in color. Two isolates of *Curviciadiella cigna* (CBS 109167 and CBS 109168) were used as outgroups.

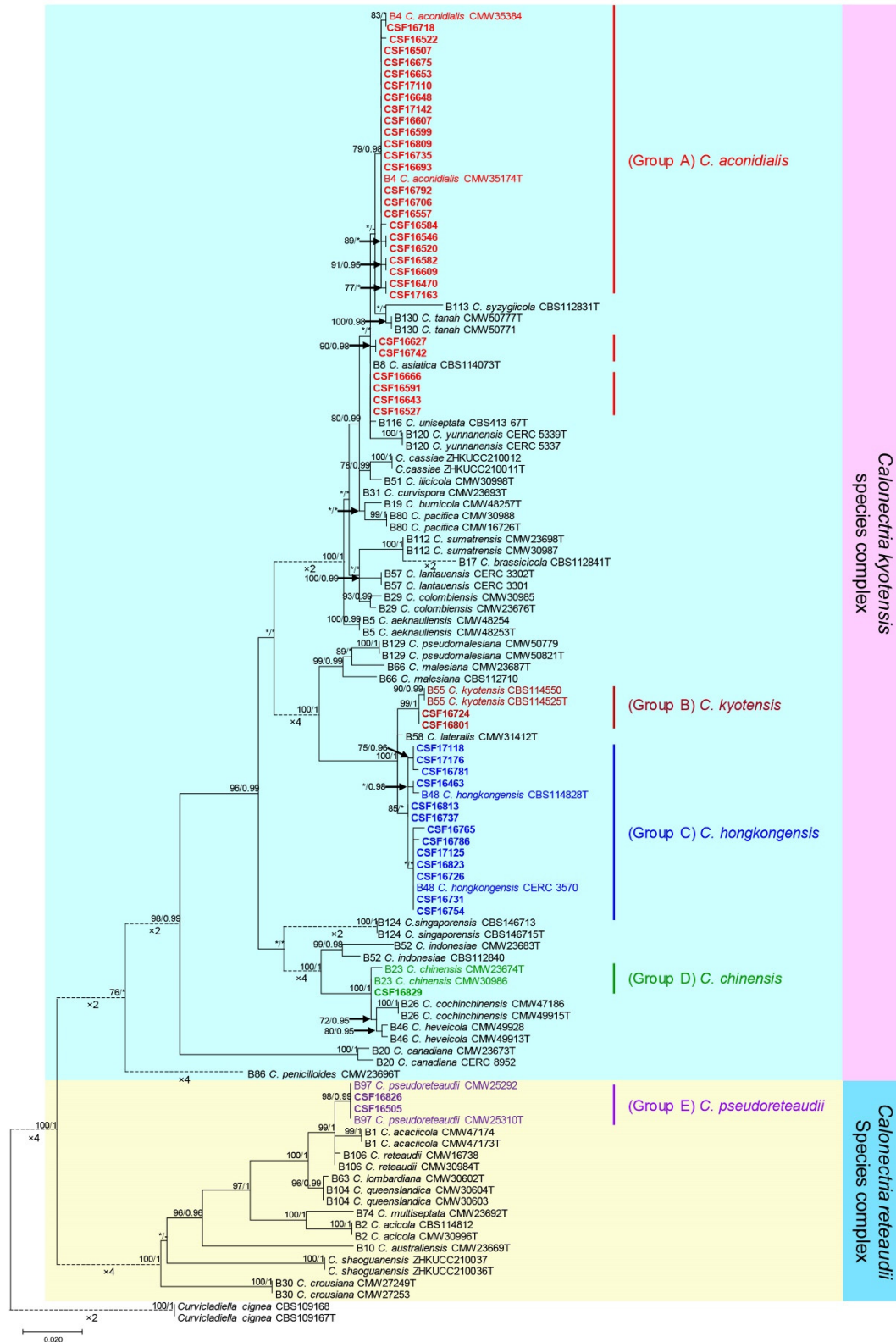
Supplementary Figure S3. Phylogenetic tree of *Calonectria* species based on maximum likelihood (ML) analyses of the *cmdA* gene sequences in this study. Bootstrap support value $\geq 70\%$ for ML and posterior probabilities values ≥ 0.95 for Bayesian inference (BI) analyses are presented above the branches as follows: ML/BI. Bootstrap values $< 70\%$ or probabilities values < 0.95 are marked with “*”, and absent analysis values are marked with “-”. Ex-type isolates are marked with “T”. Isolates sequenced in this study are highlighted in bold and shown in color. Two isolates of *Curviciadiella cigna* (CBS 109167 and CBS 109168) were used as outgroups.

Supplementary Figure S4. Phylogenetic tree of *Calonectria* species based on maximum likelihood (ML) analyses of the *his3* gene sequences in this study. Bootstrap support value $\geq 70\%$ for ML and posterior probabilities values ≥ 0.95 for Bayesian inference (BI) analyses are presented above the branches as follows: ML/BI. Bootstrap values $< 70\%$ or probabilities values < 0.95 are marked with “*”, and absent analysis values are marked with “-”. Ex-type isolates are marked with “T”. Isolates sequenced in this study are highlighted in bold and shown in color. Two isolates of *Curviciadiella cigna* (CBS 109167 and CBS 109168) were used as outgroups.

tef1

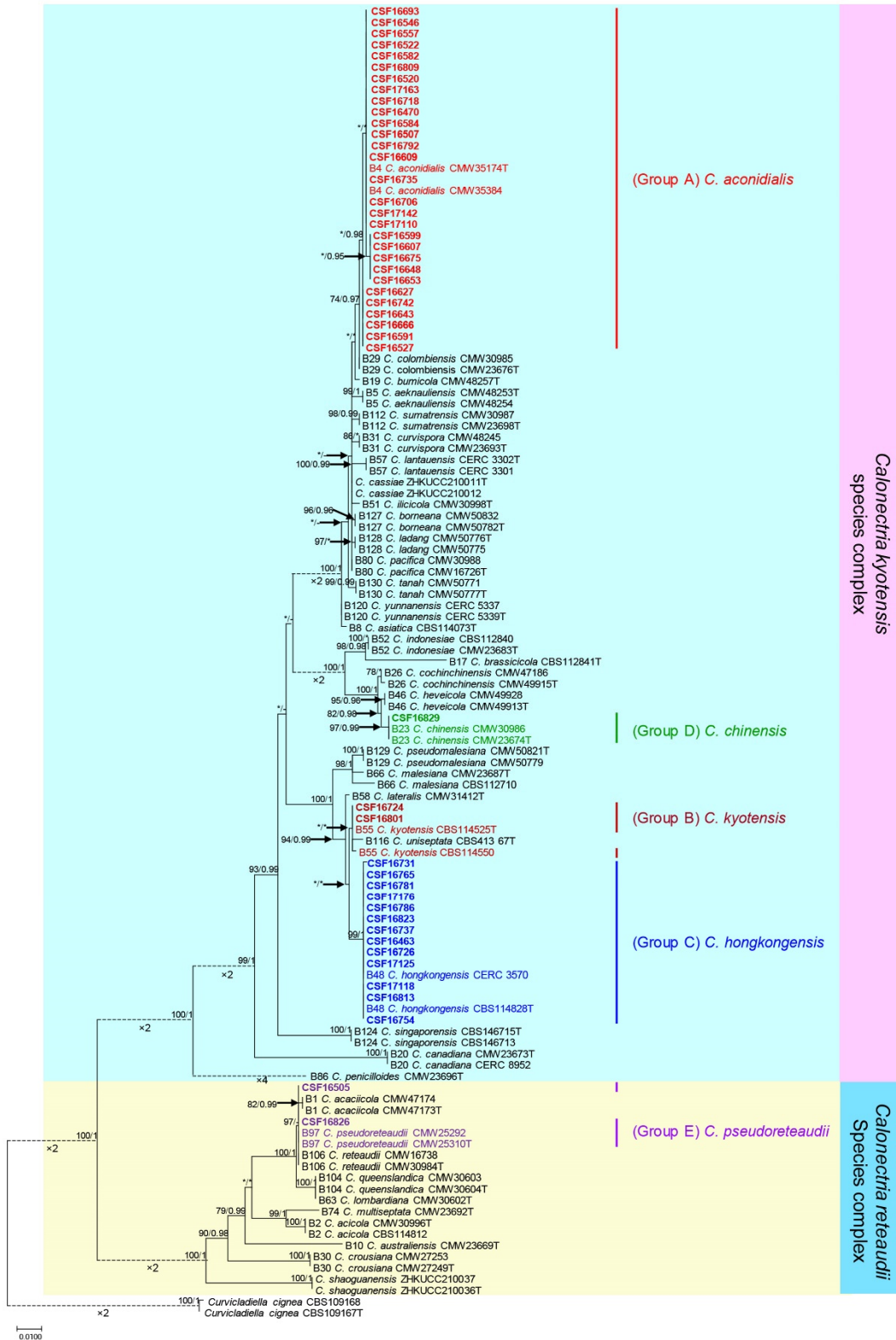


Supplementary Figure S1.



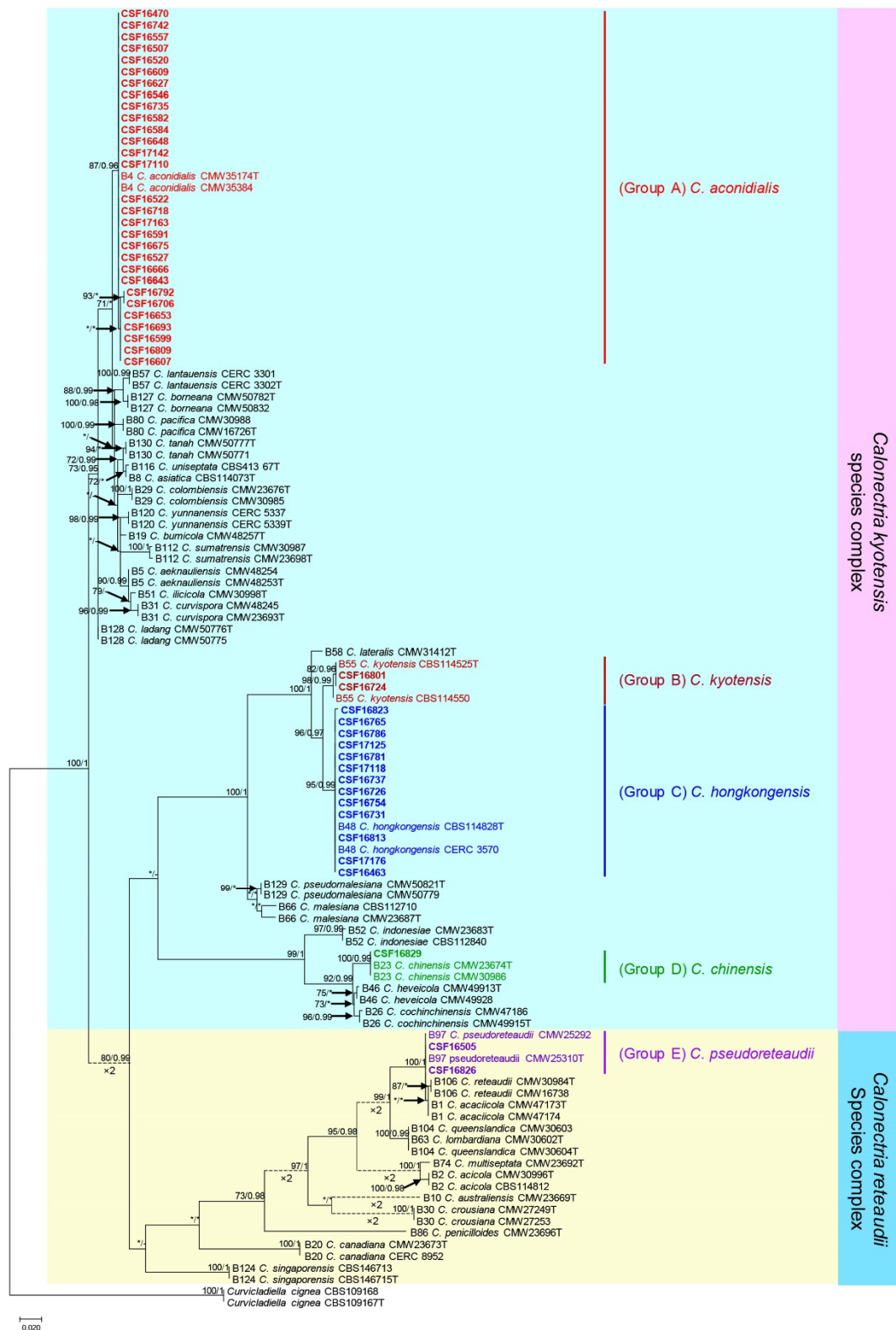
Supplementary Figure S2.

cmdA



Supplementary Figure S3.

his3



Supplementary Figure S4.