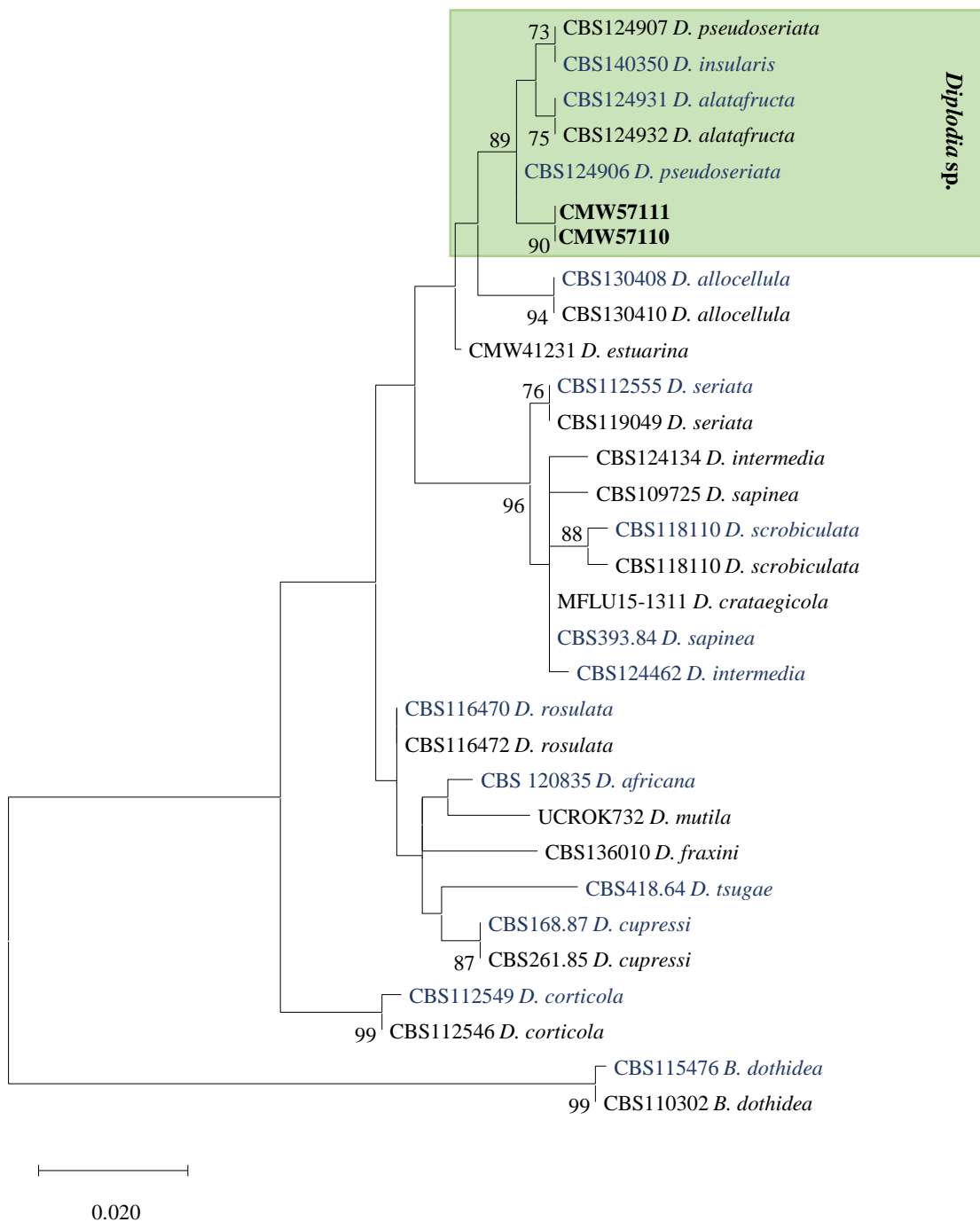
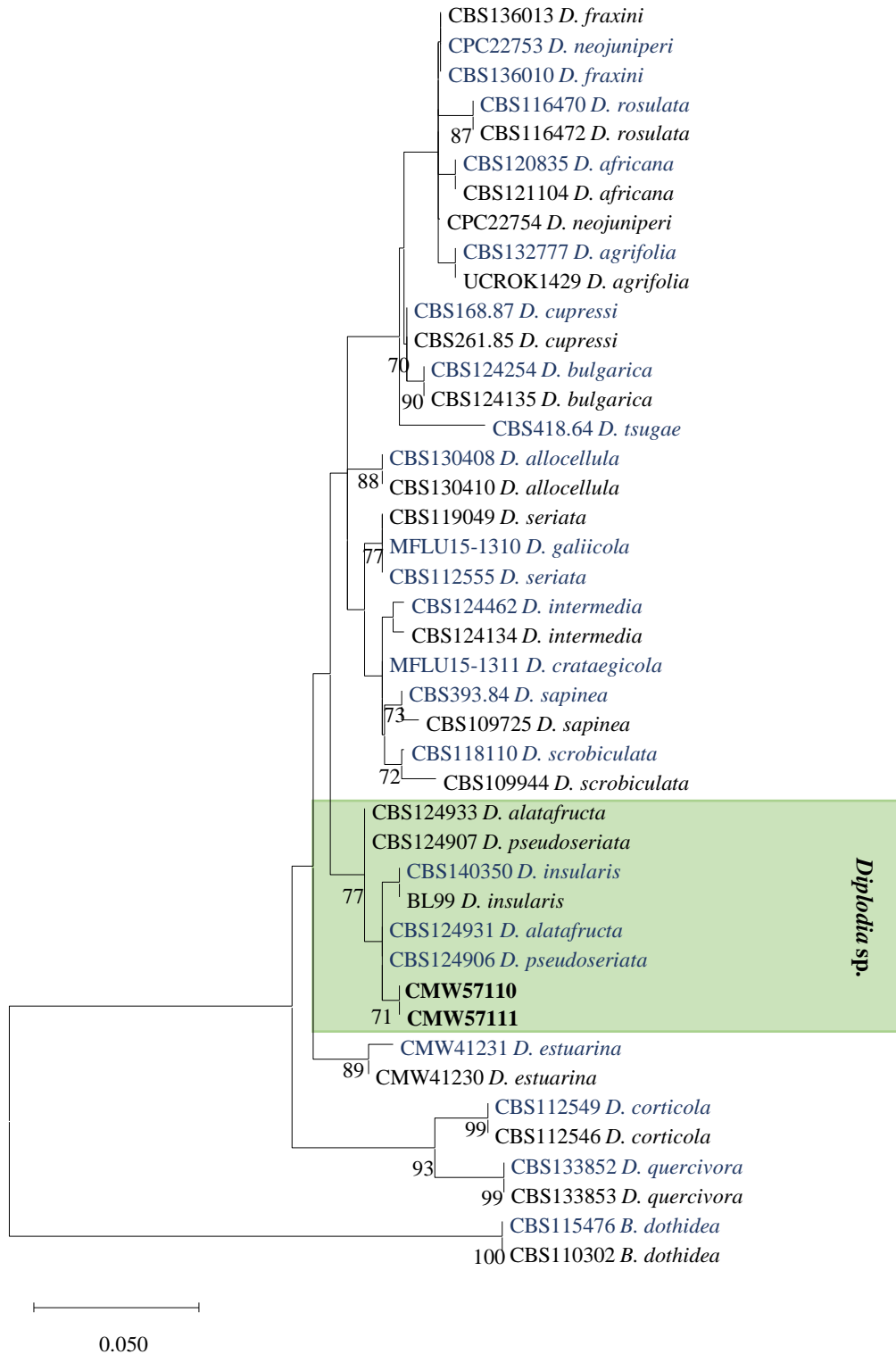


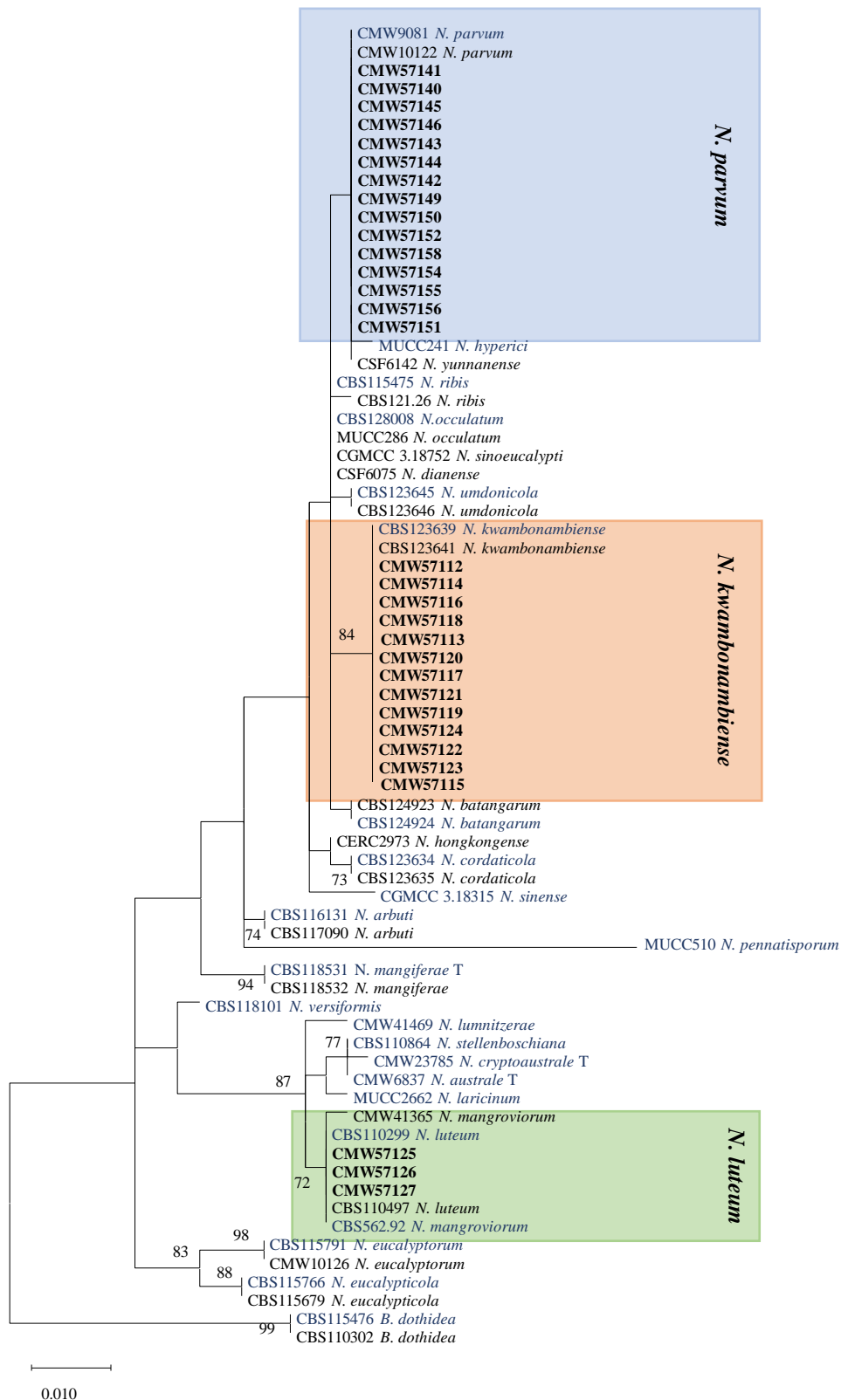
Online Resource 2a Maximum Likelihood (ML) tree of the genus *Diplodia* produced with from ITS sequences of the genus *Diplodia* showing the phylogenetic placement of two *Diplodia* isolates collected in this study. Bootstrap values above 70% are given at the nodes. Isolates sequenced in this study appear in bold and type species are in blue. The tree was rooted to *Botryosphaeria dothidea* (CBS115476 and CBS110302)



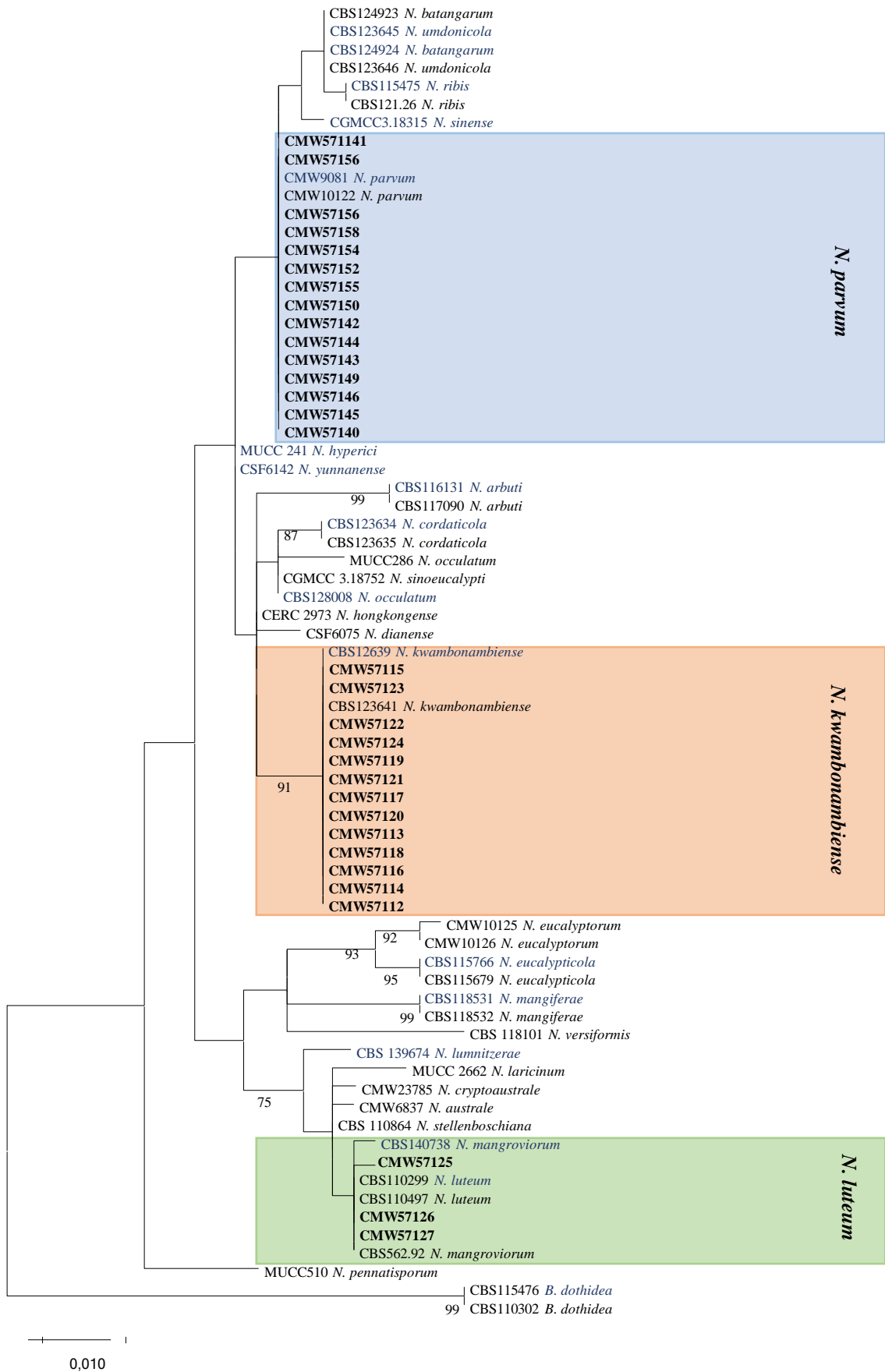
Online Resource 2b Maximum Likelihood (ML) tree of the genus *Diplodia* produced with from a combined *tub2* sequences of the genus *Diplodia* showing the phylogenetic placement of two *D.* isolates collected in this study. Bootstrap values above 70% are given at the nodes. Isolates sequenced in this study appear in bold and type species are in blue. The tree was rooted to *Botryosphaeria dothidea* (CBS115476 and CBS110302)



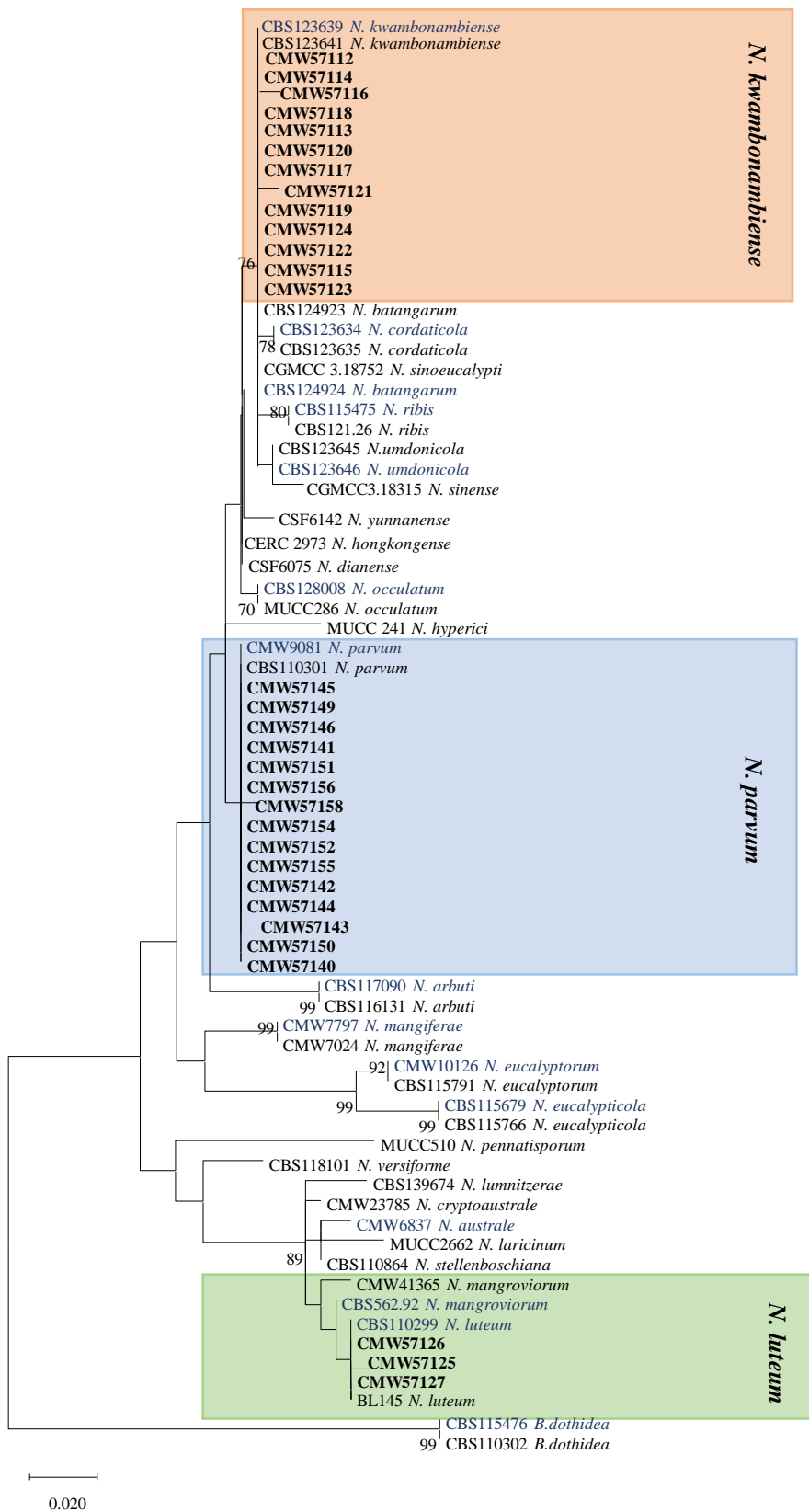
Online Resource 2c Maximum Likelihood (ML) tree of the genus *Diplodia* produced with from *tef-1α* sequences of the genus *Diplodia* showing the phylogenetic placement of two *Diplodia* isolates collected in this study. Bootstrap values above 70% are given at the nodes. Isolates sequenced in this study appear in bold and type species are in blue. The tree was rooted to *Botryosphaeria dothidea* (CBS115476 and CBS110302)



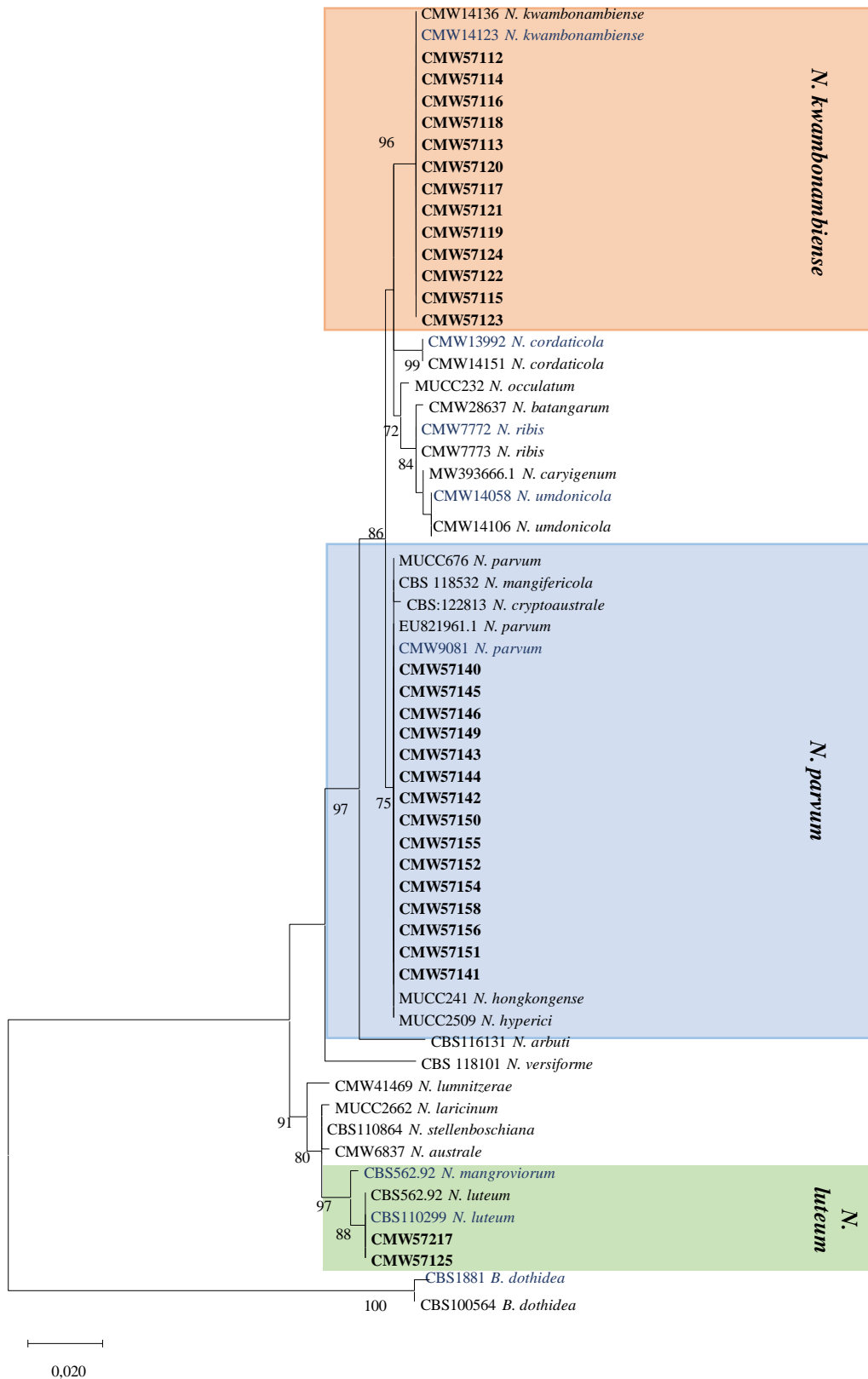
Online Resource 3a Maximum Likelihood (ML) tree of the genus *Neofusicoccum* produced with sequence data of ITS showing the phylogenetic placement of 30 isolates collected in this study. Bootstrap values above 70% are given at the nodes. Isolates sequenced in this study appear in bold and type species are in blue. The tree is rooted to *Botryosphaeria dothidea* (CBS115476 and CBS110302)



Online Resource 3b Maximum Likelihood (ML) tree of the genus *Neofusicoccum* produced with a sequence data of *tub2* showing the phylogenetic placement of 30 isolates collected in this study. Bootstrap values above 70% are given at the nodes. Isolates sequenced in this study appear in bold and type species are in blue. The tree was rooted to *Botryosphaeria dothidea* (CBS115476 and CBS110302)



Online Resource 3c Maximum Likelihood (ML) tree of the genus *Neofusicoccum* produced with a sequence data of *tef-1a* showing the phylogenetic placement of 30 isolates collected in this study. Bootstrap values above 70% are given at the nodes. Isolates sequenced in this study appear in bold and type species are in blue. The tree was rooted to *Botryosphaeria dothidea* (CBS115476 and CBS110302)



Online Resource 3d Maximum Likelihood (ML) tree of the genus *Neofusicoccum* produced with a sequence data of *rpb2* showing the phylogenetic placement of 30 isolates collected in this study. Bootstrap values above 70% are given at the nodes. Isolates sequenced in this study appear in bold and type species are in blue. The tree was rooted to *Botryosphaeria dothidea* (CBS115476 and CBS110302)

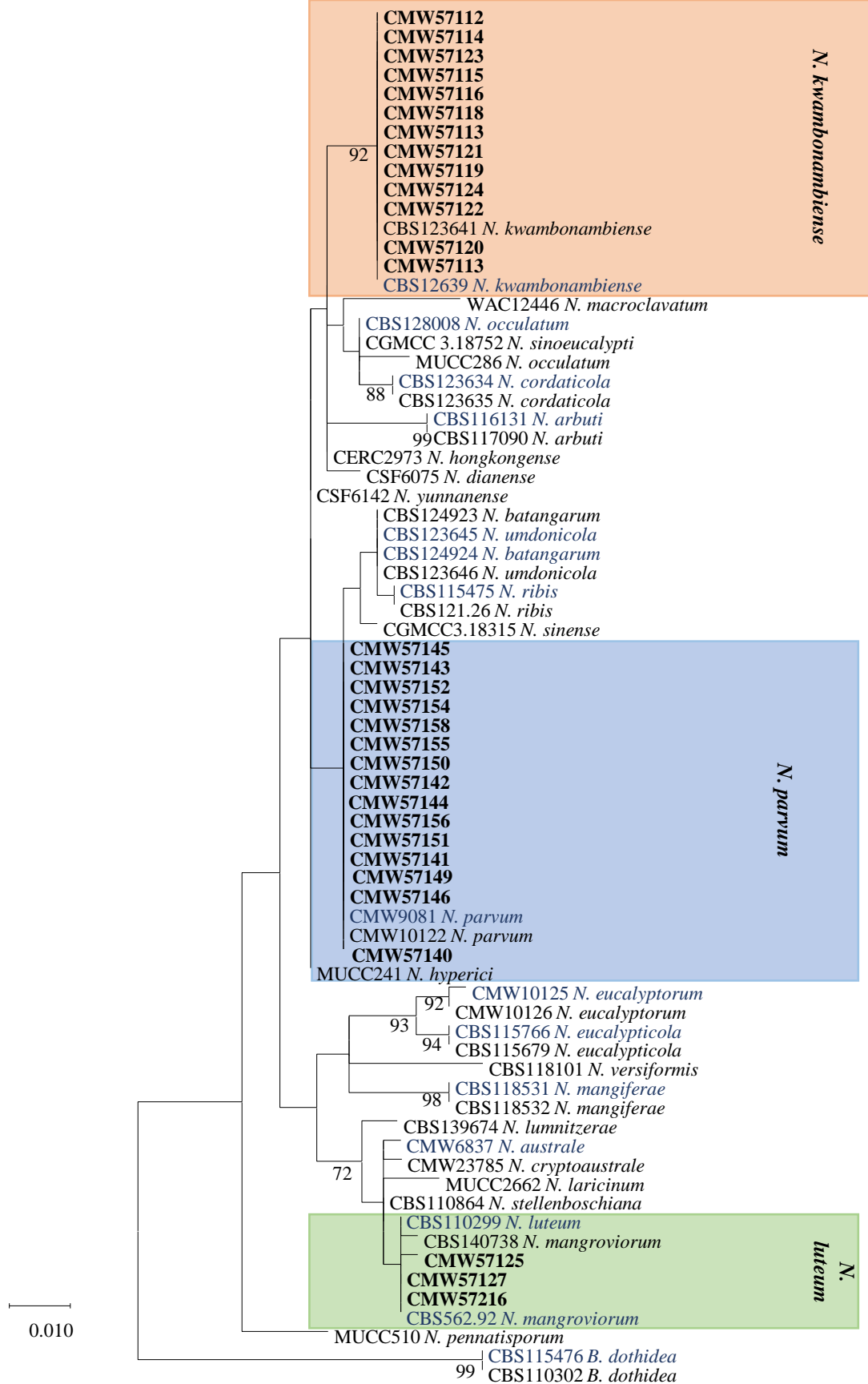
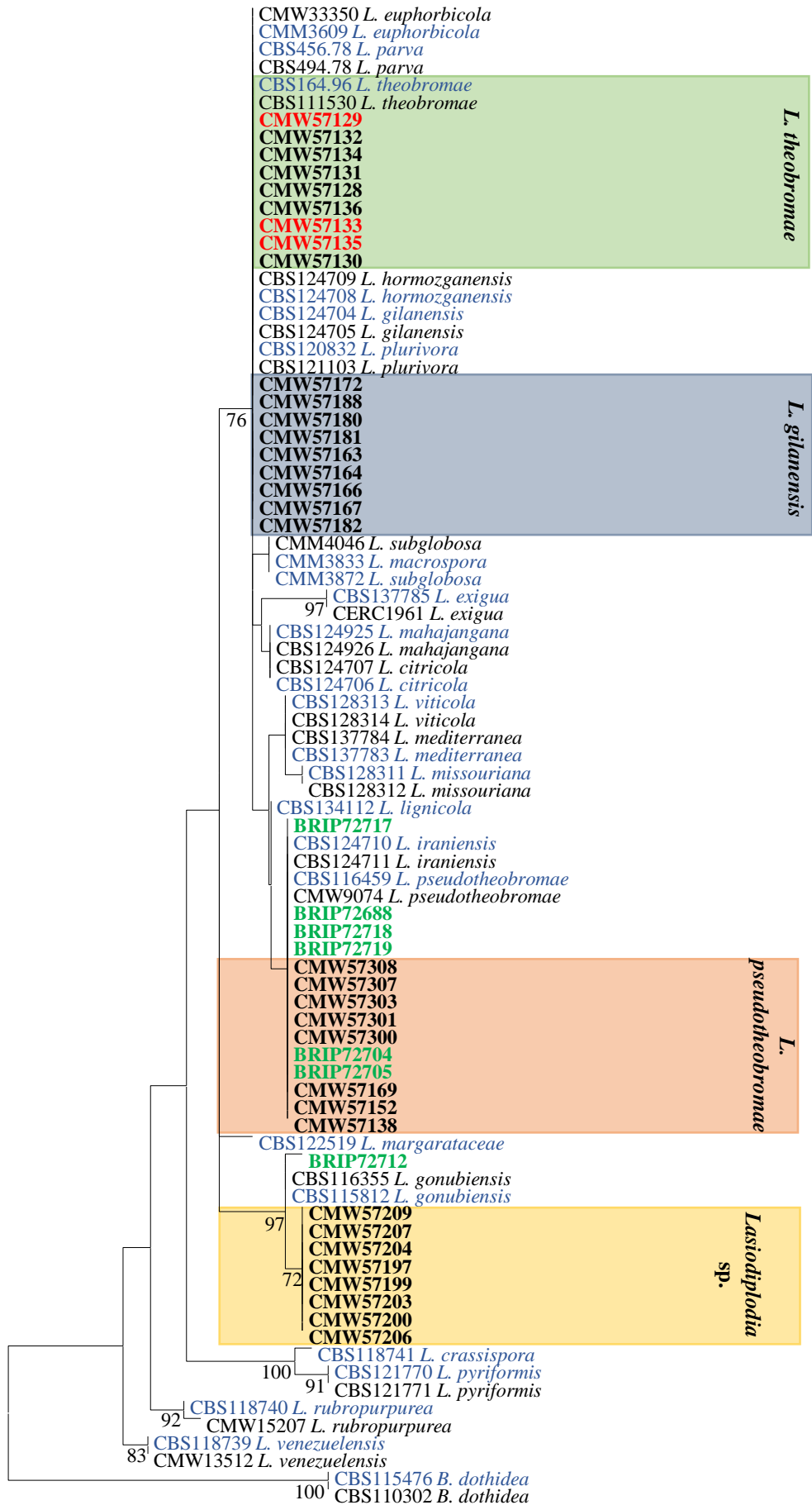
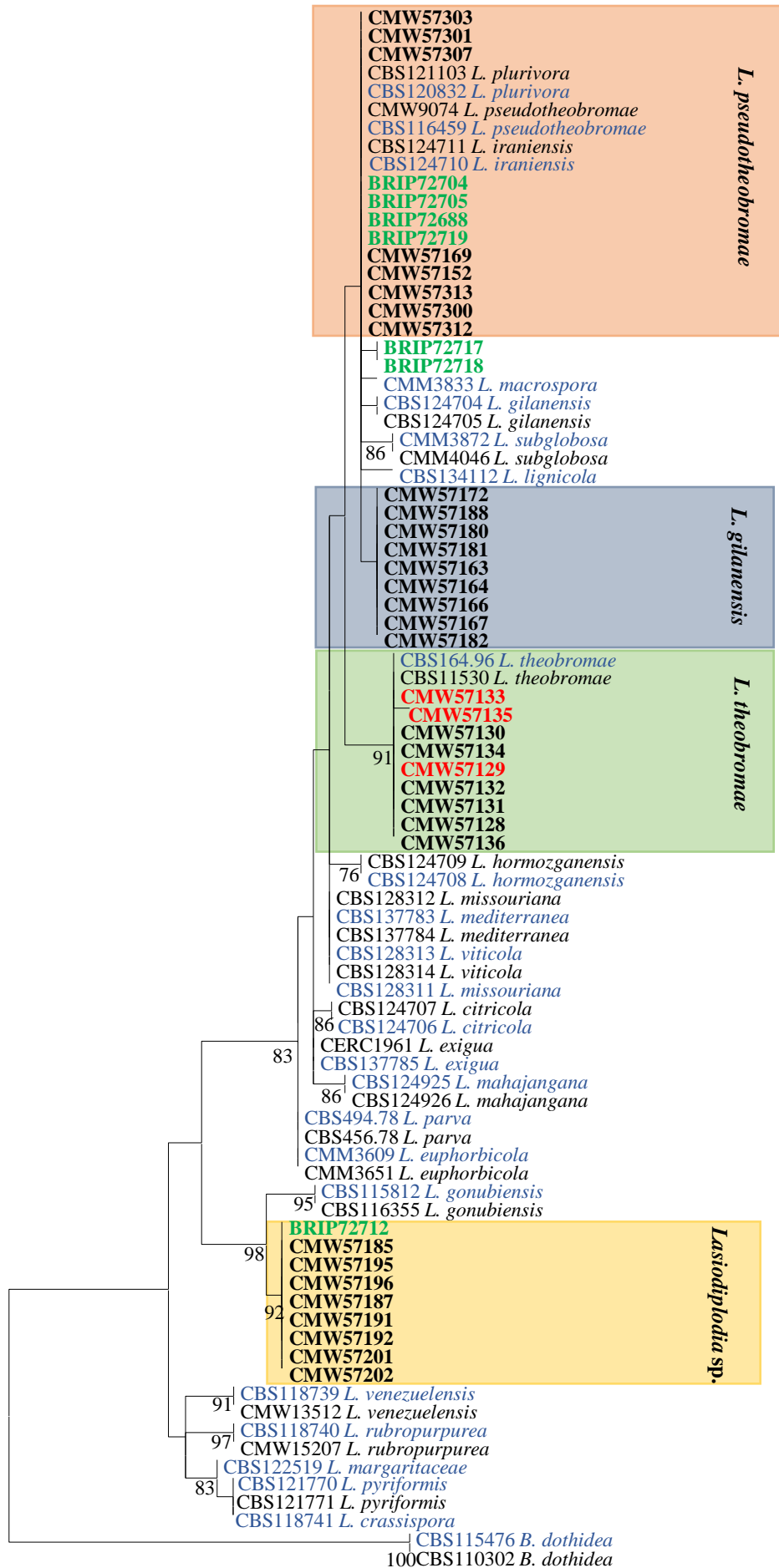


Fig 3 Maximum Likelihood (ML) tree of the genus *Neofusicoccum* produced with a combined sequence data of ITS, *tub2*, *rpb2* and *tef-1a* showing the phylogenetic placement of 30 isolates collected in this study. Bootstrap values above 70% are given at the nodes. Isolates sequenced in this study appear in bold and type species are in blue. The tree was rooted to *Botryosphaeria dothidea* (CBS115476 and CBS110302)

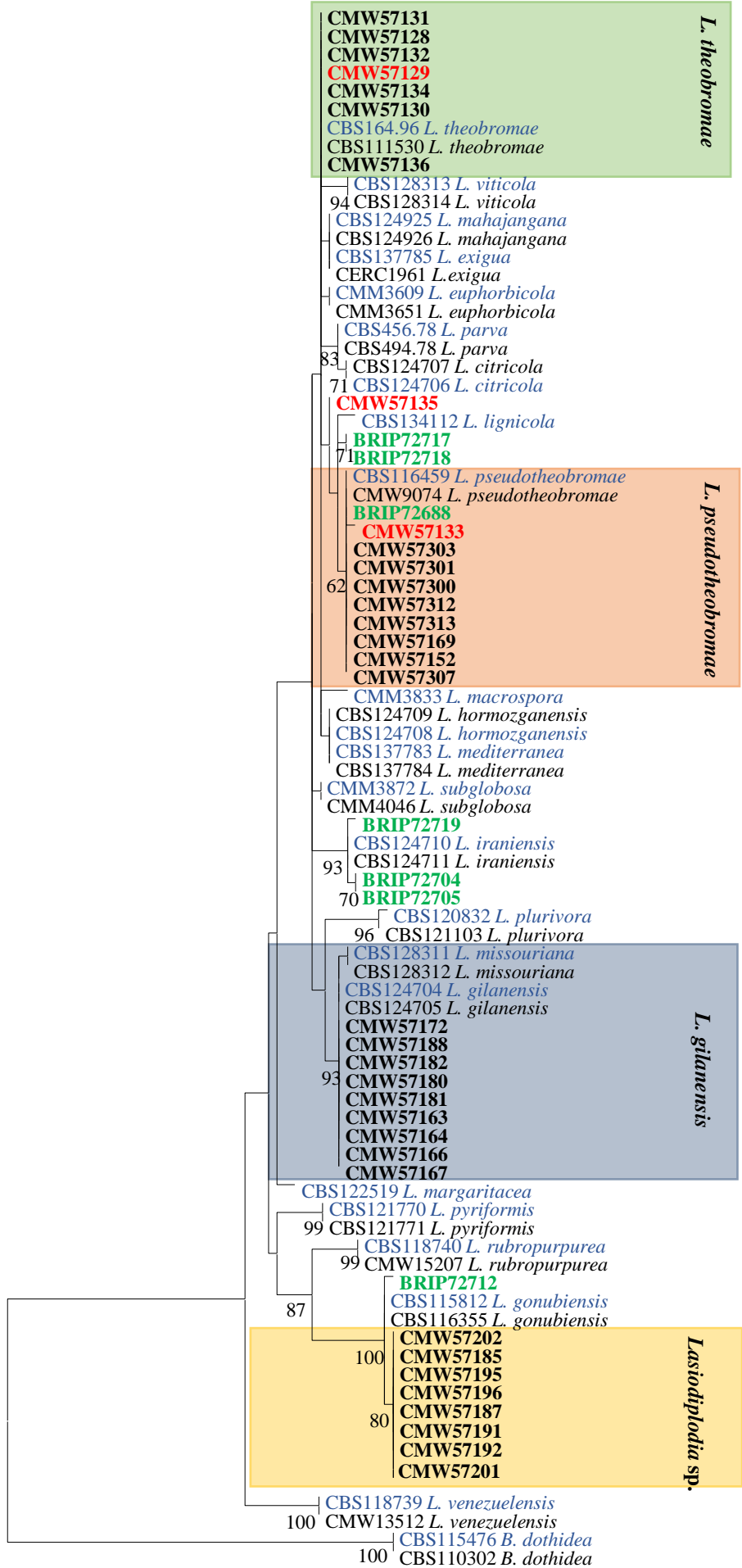


Online Resource 4a Maximum Likelihood (ML) tree of the genus *Lasiodiplodia* produced with a sequence data of ITS showing the phylogenetic placement of isolates collected in this study. Bootstrap values above 70% are given at the nodes. Isolates sequenced in this study appear in bold and type species are in blue. Potential hybrid isolates are given in red and isolates from Australia are in green. The tree was rooted to *Botryosphaeria dothidea* (CBS115476 and CBS110302)



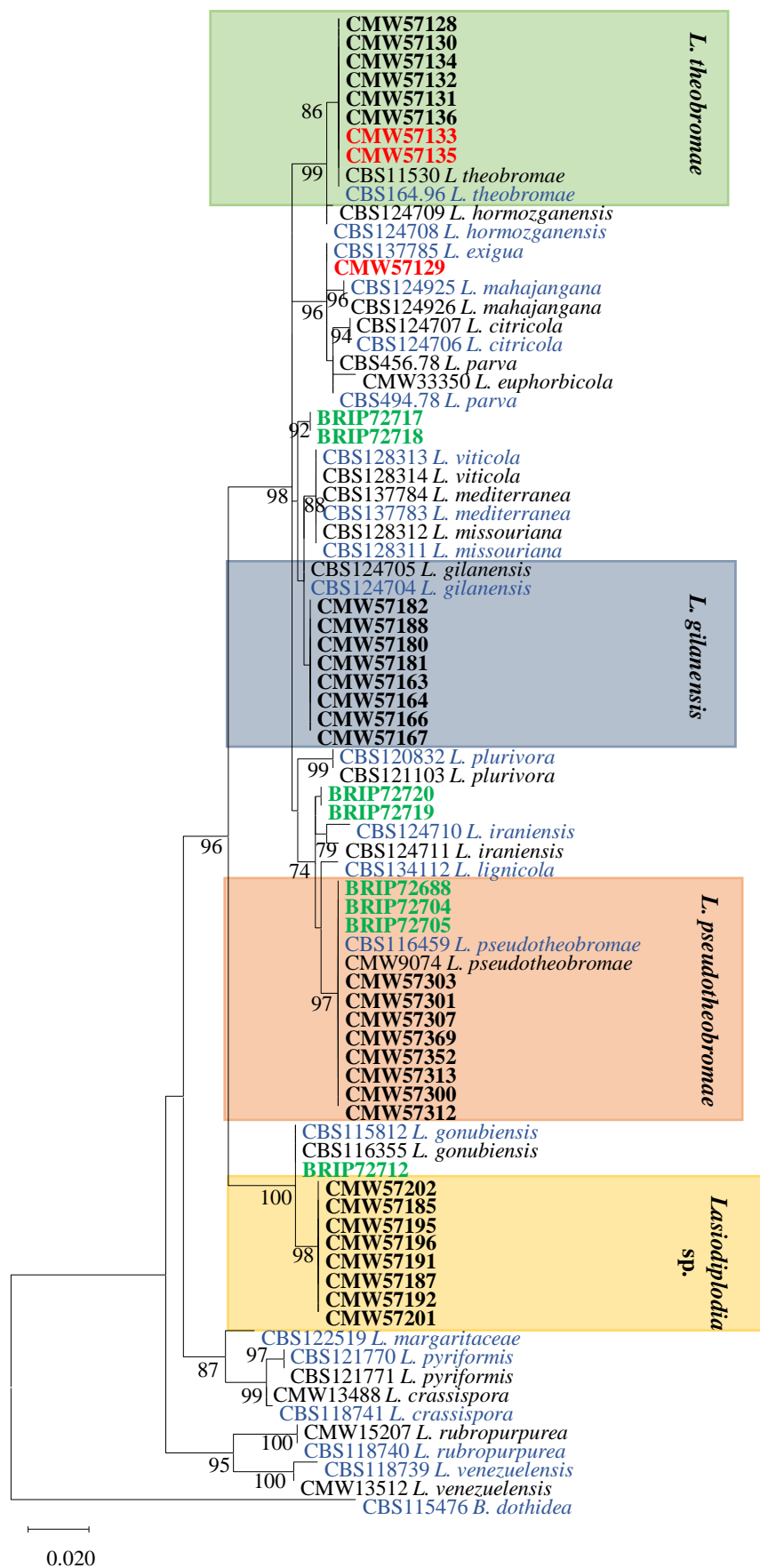
0.010

Online Resource 4b Maximum Likelihood (ML) tree of the genus *Lasiodiplodia* produced with a sequence data of *tub2* showing the phylogenetic placement of isolates collected in this study. Bootstrap values above 70% are given at the nodes. Isolates sequenced in this study appear in bold and type species are in blue. Potential hybrid isolates are given in red and isolates from Australia are in green. The tree was rooted to *Botryosphaeria dothidea* (CBS115476 and CBS110302)



0.050

Online Resource 4c Maximum Likelihood (ML) tree of the genus *Lasiodiplodia* produced with a sequence data of *tef-1a* showing the phylogenetic placement of isolates collected in this study. Bootstrap values above 70% are given at the nodes. Isolates sequenced in this study appear in bold and type species are in blue. Potential hybrid isolates are given in red and isolates from Australia are in green. The tree was rooted to *Botryosphaeria dothidea* (CBS115476 and CBS110302)



Online Resource 4d Maximum Likelihood (ML) tree of the genus *Lasiodiplodia* produced with a sequence data of *rpb2* showing the phylogenetic placement of isolates collected in this study. Bootstrap values above 70% are given at the nodes. Isolates sequenced in this study appear in bold and type species are in blue. Potential hybrid isolates are given in red and isolates from Australia are in green. The tree was rooted to *Botryosphaeria dothidea* (CBS115476 and CBS110302)

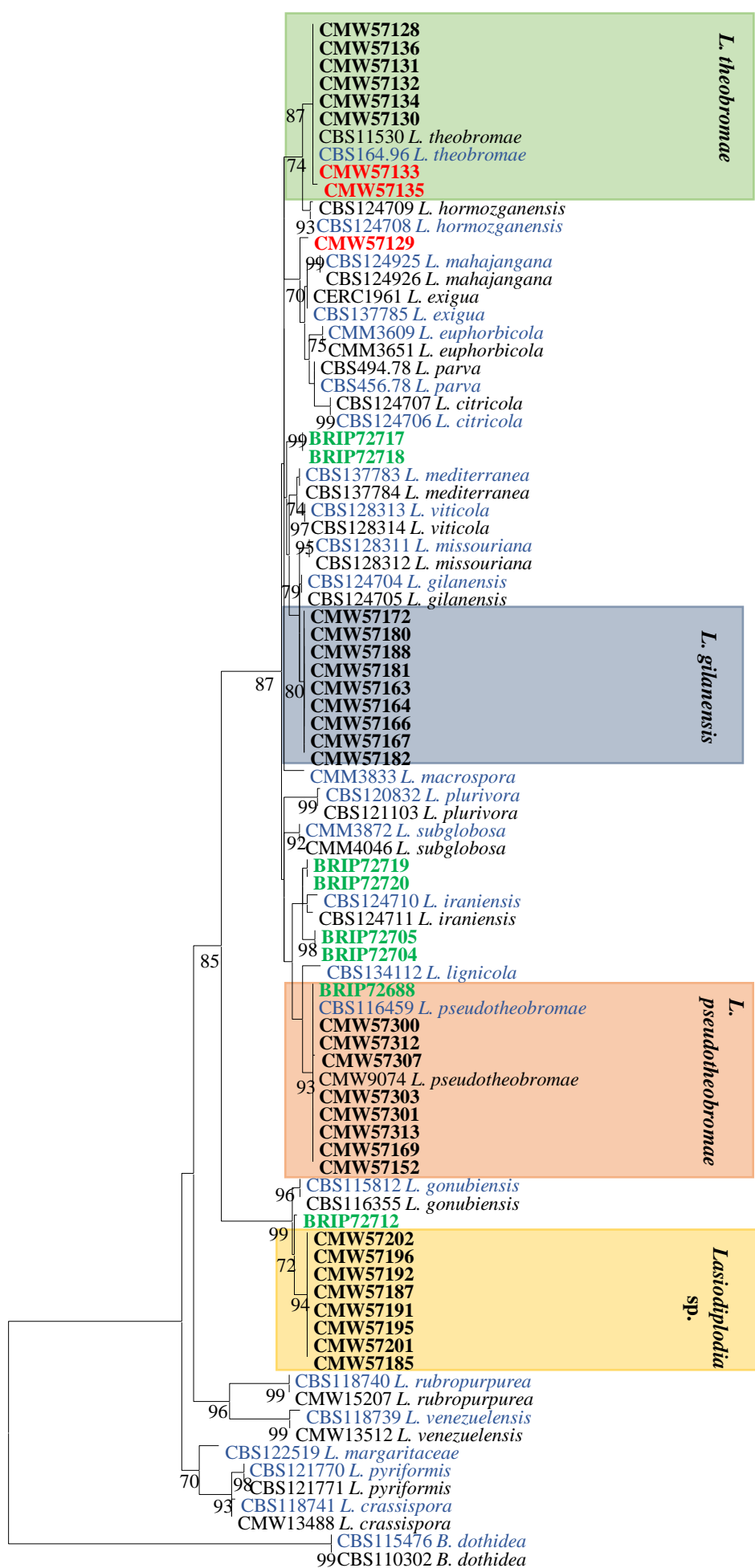


Fig 4 Maximum Likelihood (ML) tree of the genus *Lasiodiplodia* produced with a combined sequence data of *ITS*, *tub2*, *rpb2* and *tef-1a* showing the phylogenetic placement of isolates collected in this study. Bootstrap values above 70% are given at the nodes. Isolates sequenced in this study appear in bold and type species are in blue. Potential hybrid isolates are given in red and isolates from Australia are in green. The tree was rooted to *Botryosphaeria dothidea* (CBS115476 and CBS110302)