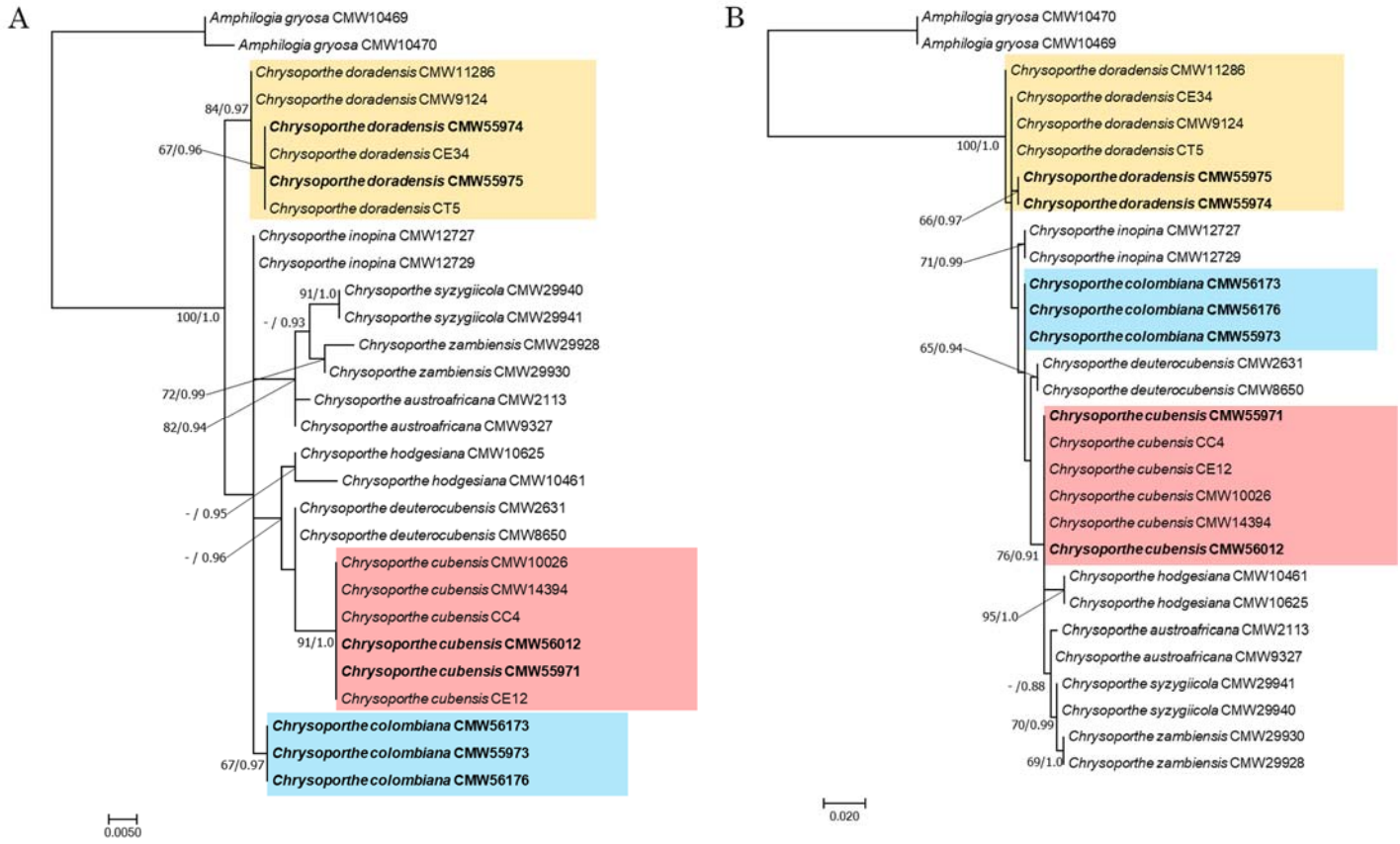


Supplementary Table 1 — Parameters used in phylogenetic analyses

| Parameter | ITS | <i>TUB1</i> | <i>TUB2</i> | <i>TUB1</i> + <i>TUB2</i> | Combined |
|--------------------|------|-------------|-------------|--|--|
| No. of taxa | 29 | 29 | 29 | 29 | 29 |
| No. of characters | 492 | 423 | 355 | 778 | 1270 |
| ML | | | | | |
| Substitution model | TPM3 | TPM3uf+G | TPM1uf+G | TrN+I | TPM3uf+I+G |
| Pinvar | N/A | N/A | N/A | 0.72 | 0.47 |
| Gamma shape | N/A | 0.15 | 0.31 | N/A | 0.40 |
| BI | | | | | |
| Substitution model | TPM3 | TPM3uf+G | TPM1uf+G | TPM3uf+G for <i>TUB1</i> TPM1uf+G for <i>TUB2</i> | TPM3 for ITS TPM3uf+G for <i>TUB1</i> TPM1uf+G for <i>TUB2</i> |

N/A: not applicable



Supplementary Figure 1 — Phylogenetic tree based on ML analysis of a sequence dataset of beta-tubulin 1 (**A**) and beta-tubulin 2 (**B**) regions of *Chrysoporthe* species. Bootstrap values > 65% for ML and >0.85 for BI PP are shown as ML/BI PP.