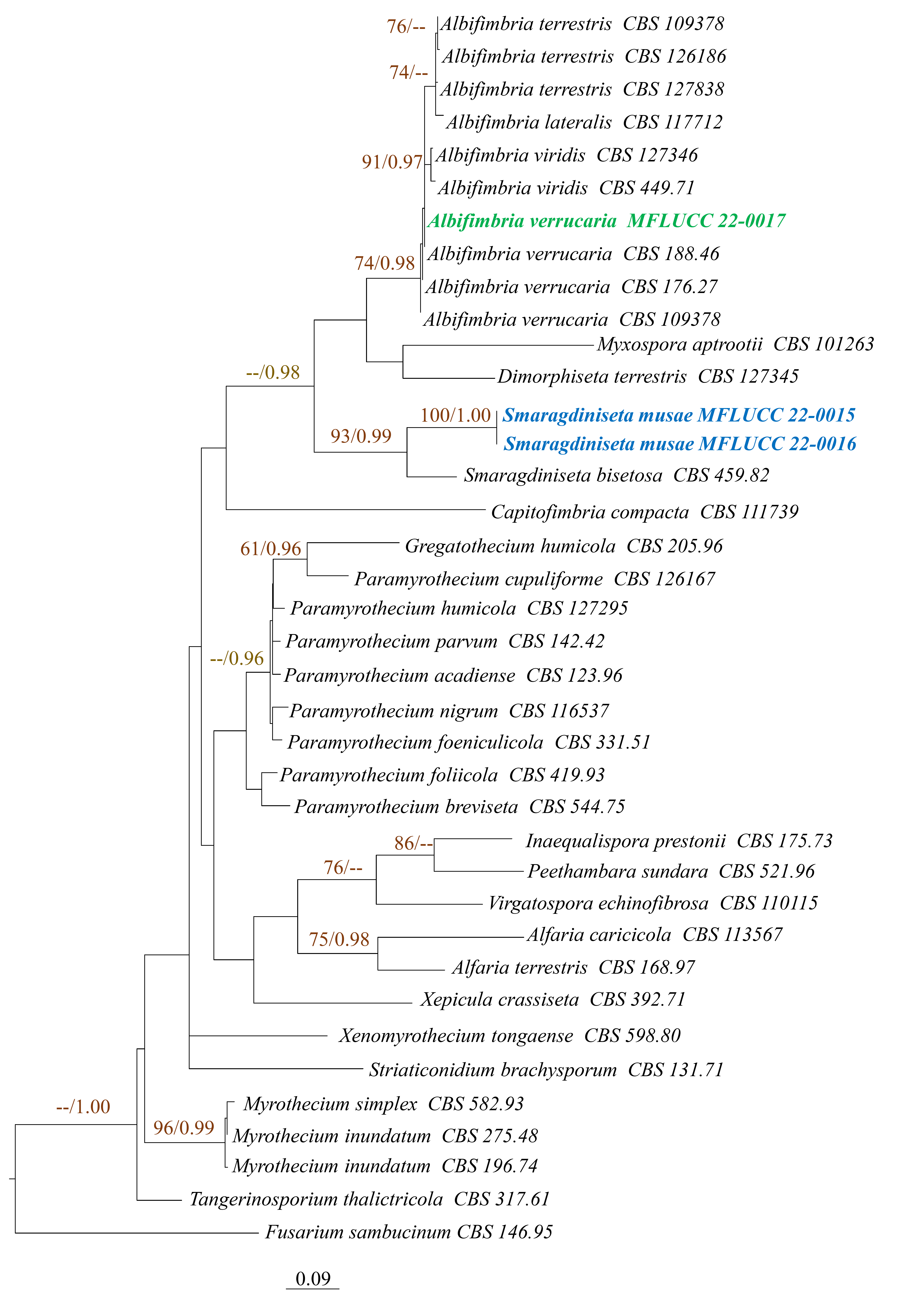
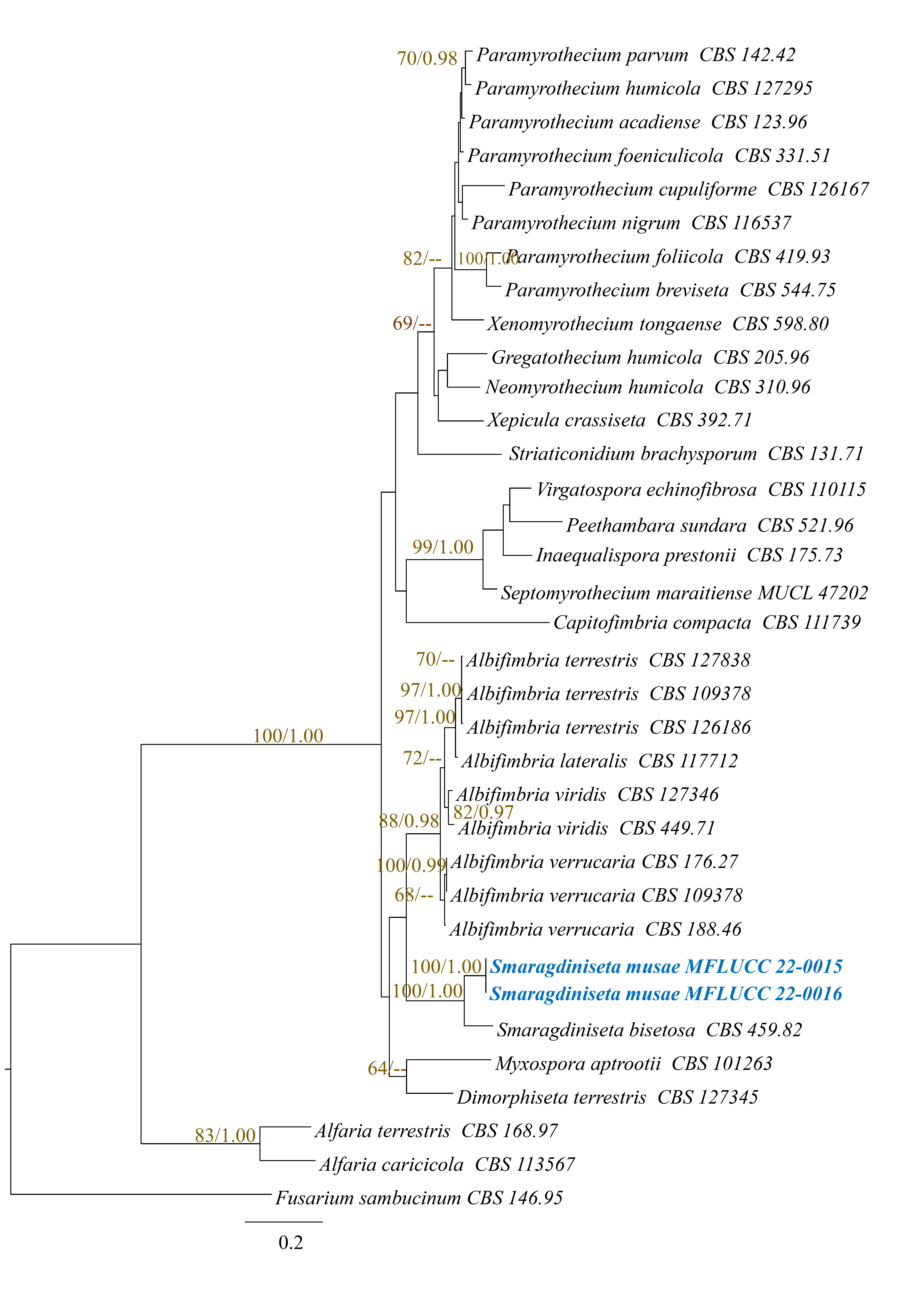


**Figure 1.** Maximum likelihood tree revealed by RAxML analyses of ITS sequence data of selected genera of Stachybotryaceae, showing the phylogenetic position of *Albifimbria verrucaria* (MFLUCC 22-0017) and*Smaragdiniseta musae* (MFLUCC 22-0015, MFLUCC 22-0016). ML bootstrap supports (≥60%) and Bayesian posterior probabilities (≥0.95 BYPP) are given above the nodes, respectively. The tree is rooted with *Fusarium sambucinum* (CBS146.95) (Nectriaceae). The scale bar represents the expected number of nucleotide substitutions per site.



**Figure 2.** Maximum likelihood tree revealed by RAxML analyses of tub2 sequence data of selected genera of Stachybotryaceae, showing the phylogenetic position of *Albifimbria verrucaria* (MFLUCC 22-0017) and*Smaragdiniseta musae* (MFLUCC 22-0015, MFLUCC 22-0016). ML bootstrap supports (≥60%) and Bayesian posterior probabilities (≥0.95 BYPP) are given above the nodes, respectively. The tree is rooted with *Fusarium sambucinum* (CBS146.95) (Nectriaceae). The scale bar represents the expected number of nucleotide substitutions per site.



**Figure 3.** Maximum likelihood tree revealed by RAxML analyses of rpb2 sequence data of selected genera of Stachybotryaceae, showing the phylogenetic position of *Albifimbria verrucaria* (MFLUCC 22-0017) and*Smaragdiniseta musae* (MFLUCC 22-0015, MFLUCC 22-0016). ML bootstrap supports (≥60%) and Bayesian posterior probabilities (≥0.95 BYPP) are given above the nodes, respectively. The tree is rooted with *Fusarium sambucinum* (CBS146.95) (Nectriaceae). The scale bar represents the expected number of nucleotide substitutions per site.