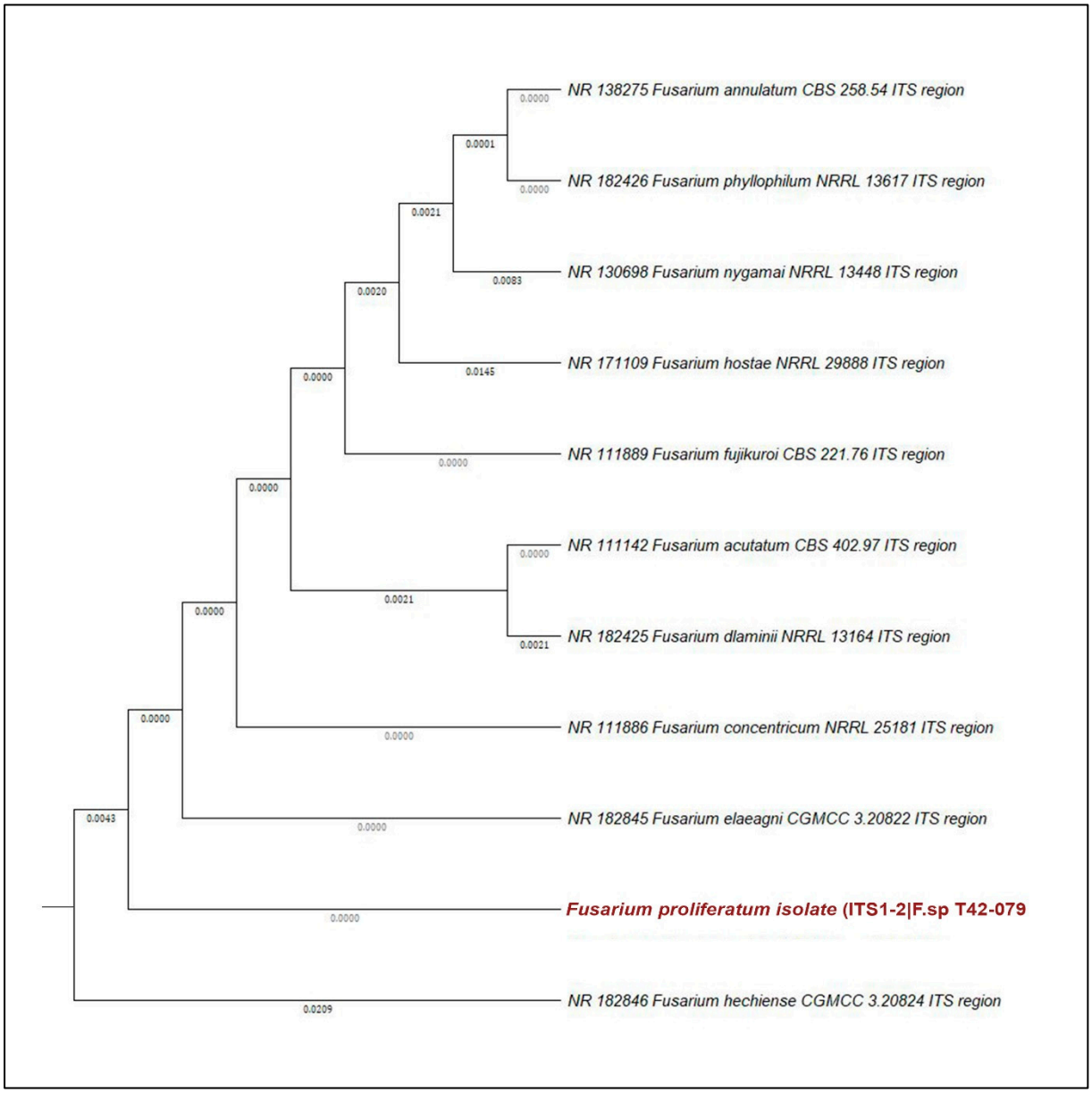


Figure S1. Phylogenetic tree constructed using the Maximum Likelihood (ML) method based on the ITS region sequences of *Fusarium* spp. The tree was generated with MEGA software, and the branch labels represent genetic distances (substitutions per site) between sequences. The isolate "*Fusarium proliferatum* isolate (ITS1-2|F.sp T42-079)" is highlighted in red and shows its evolutionary relationship with closely related *Fusarium* species. The sequences are labeled with GenBank accession numbers and species names.

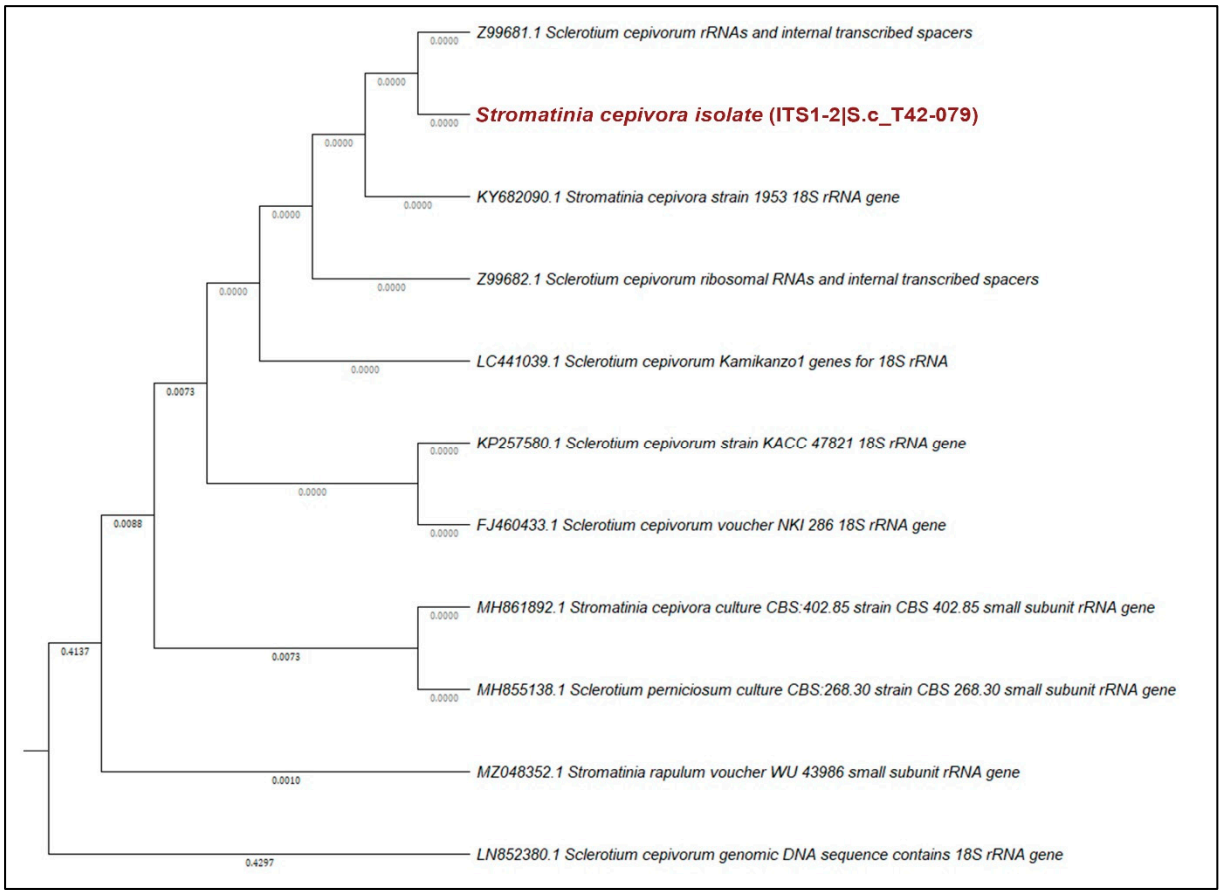


Figure S2. Phylogenetic tree constructed using the Maximum Likelihood (ML) method based on the ITS region sequences of *Stromatinia* spp. (*Sclerotium* spp.). The tree was generated with MEGA software, and the branch labels represent genetic distances (substitutions per site) between sequences. The isolate "*Stromatinia cepivora* isolate (ITS1-2|S.c T42-079)" is highlighted in red and shows its evolutionary relationship with closely related *Fusarium* species. The sequences are labeled with GenBank accession numbers and species names