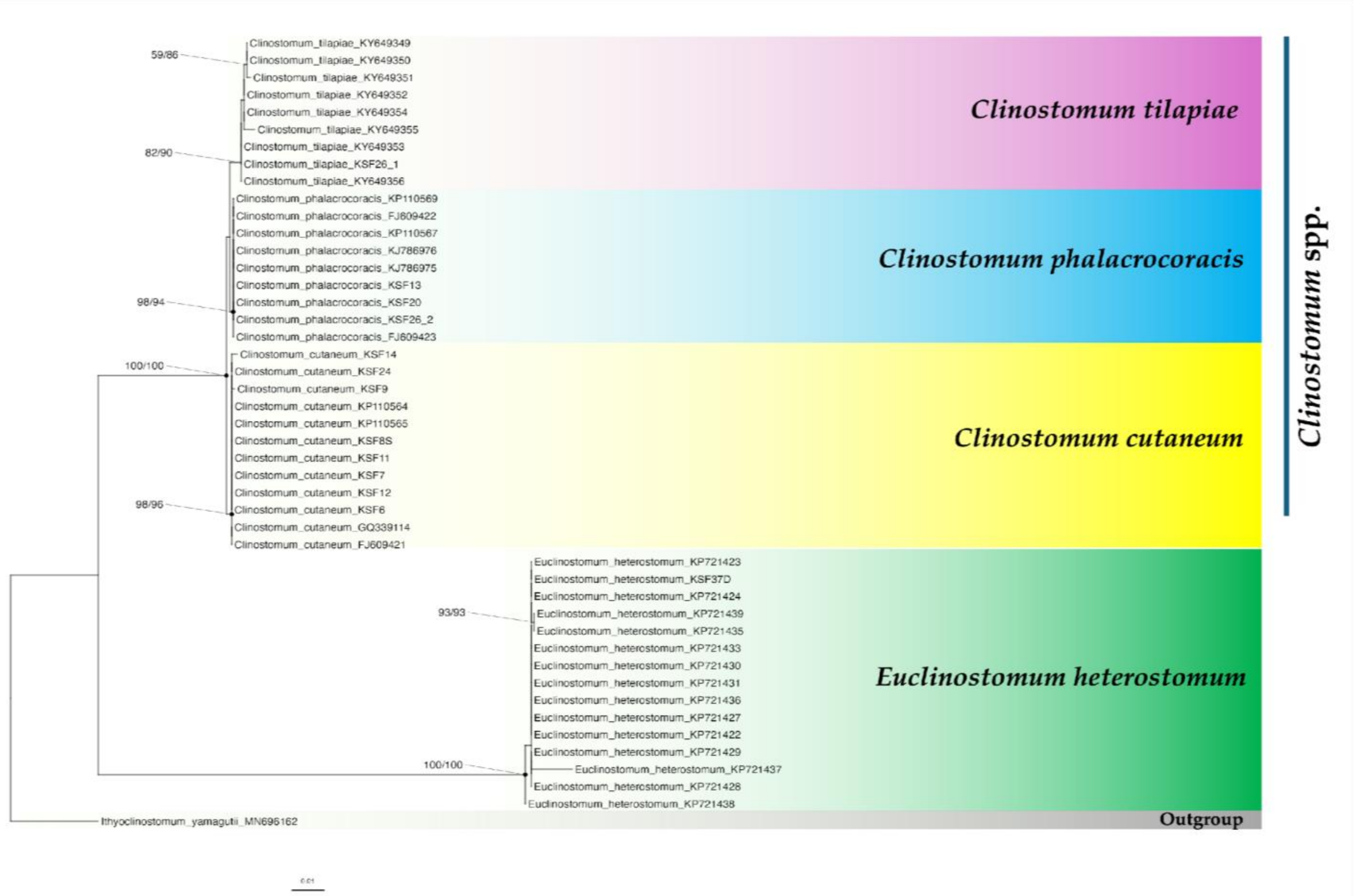

Supplementary Figure 1. Phylogeny based on maximum likelihood method using ITS1-5.8S-ITS2 rDNA generated using Geneious Prime 2025.0 (https://www.geneious.com). Node support values include SH-aLRT and UFBoot (1000 Ultrafast bootstraps). Black dots indicate strong support (SH-aLRT > 80, UBoost > 95) across analyses. The scale bar represents the number of expected substitutions per site.