







Figure 1. Maximum-likelihood phylogenetic analyses by internal transcribed spacer (ITS) sequence alignment for the endophytic fungi from *Tupista chinensis* Baker belonging to Apiosporaceae (A); Aspergillaceae (B); Chaetomiaceae (C); Cladosporiaceae (D); Coniochaetaceae (E); Didymellaceae (F); Entolomataceae (G); Glomerellaceae (H); Hypoxylaceae (I); Leptosphaeriaceae (J); Mortierellaceae (K); Nectriaceae (L); Peniophoraceae (M); Periconiaceae (N); Phaeosphaeriaceae (O); Pleosporaceae (P); Rhytismataceae (Q); Sporidiobolaceae (R); Sporocadaceae (S); Stachybotryaceae (T); Trichocomaceae (U); Trichosphaeriaceae (V); Valsaceae (W); Xylariaceae (X) and incertae sedis (Y).