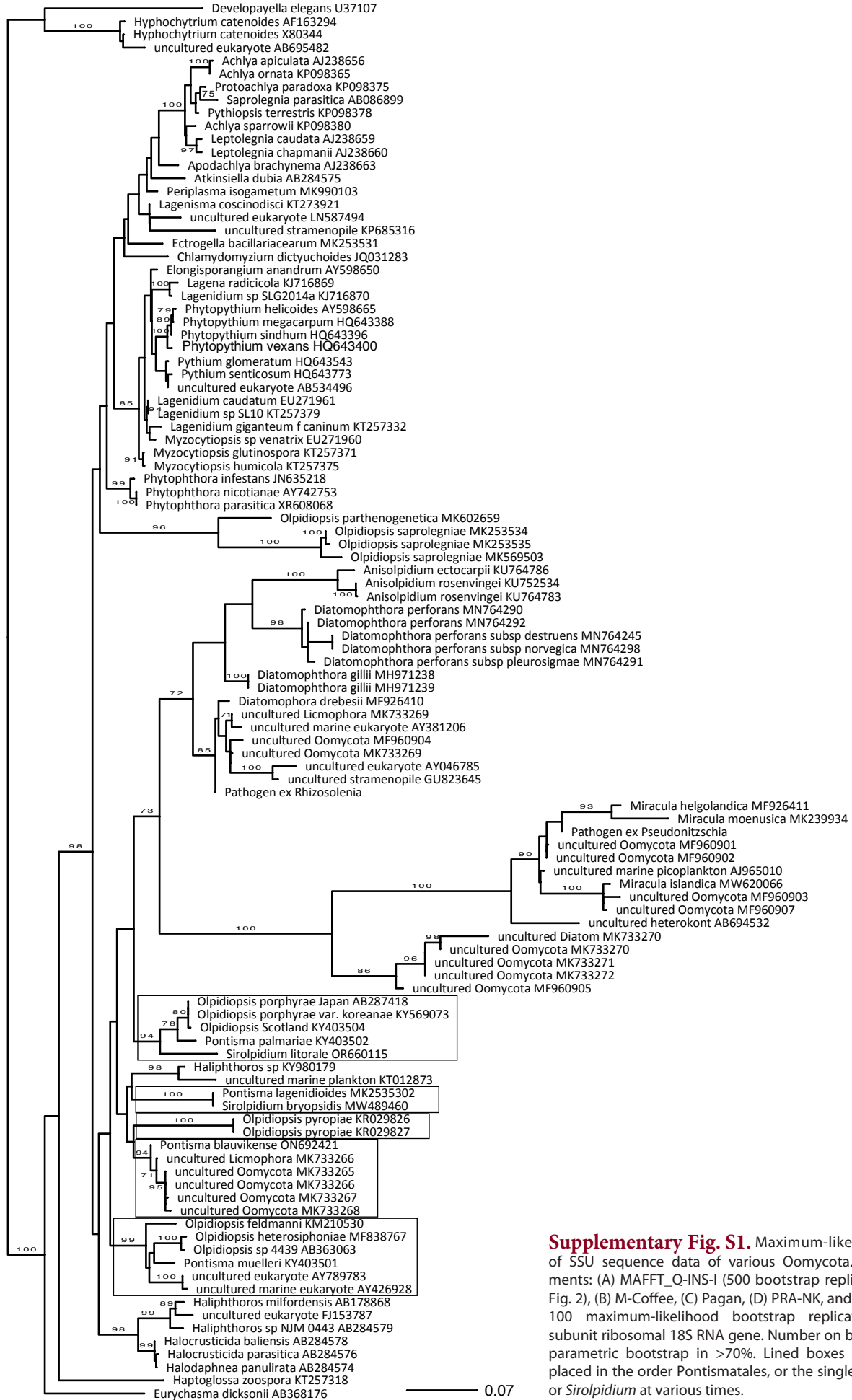
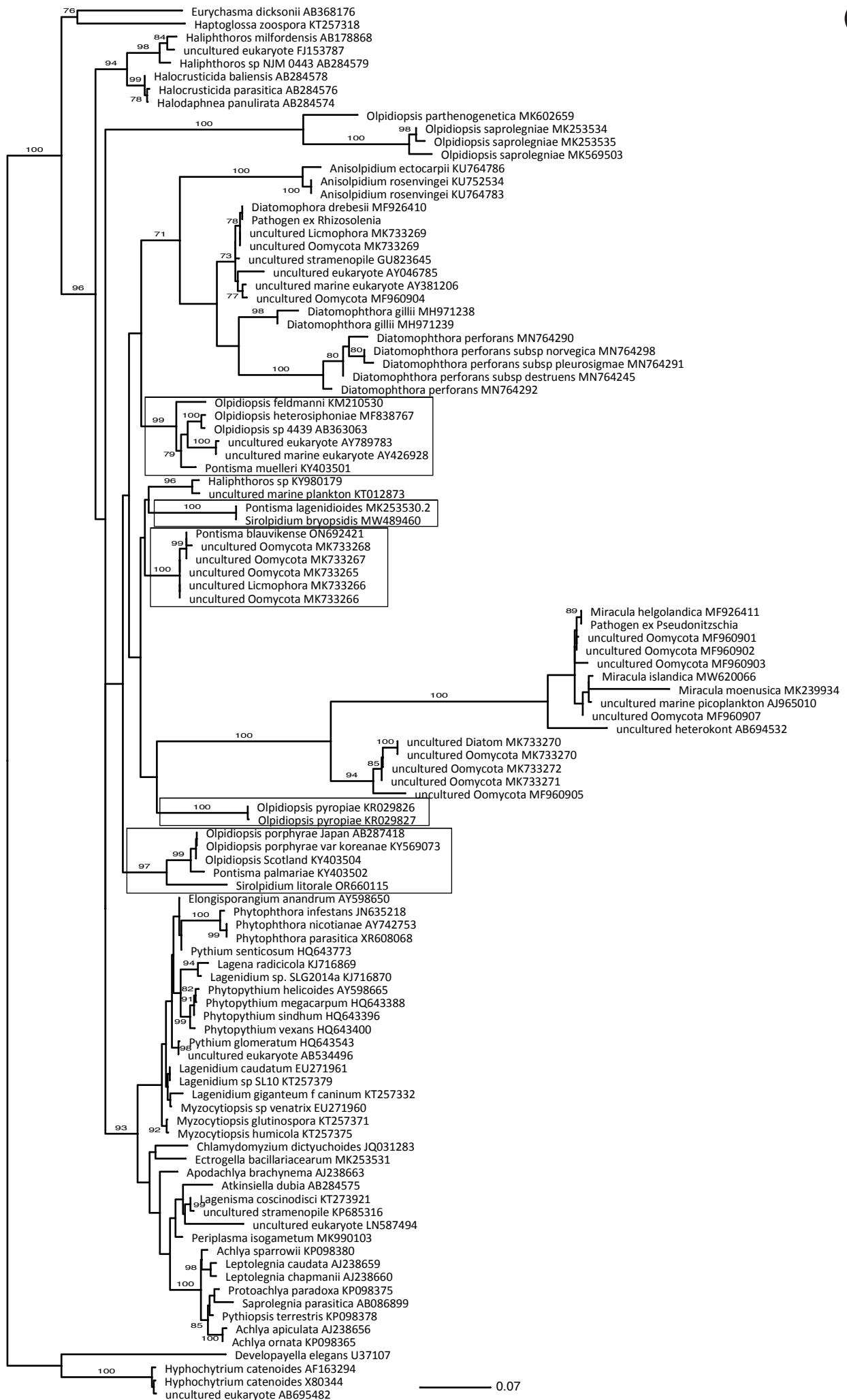
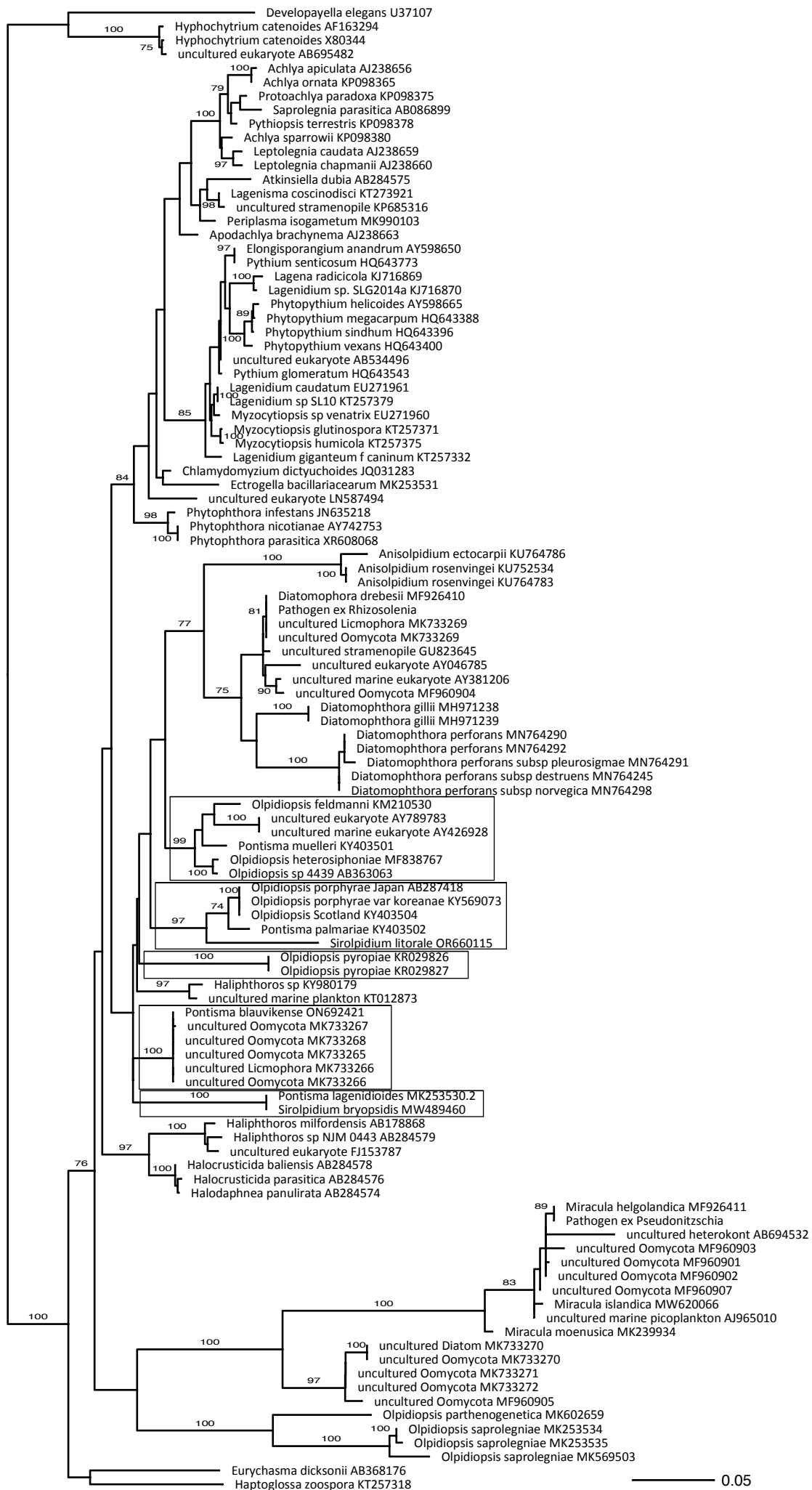


A



Supplementary Fig. S1. Maximum-likelihood topology of SSU sequence data of various Oomycota. Different alignments: (A) MAFFT_Q-INS-I (500 bootstrap replicates, cartoon in Fig. 2), (B) M-Coffee, (C) Pagan, (D) PRA-NK, and (E) SINA. All with 100 maximum-likelihood bootstrap replicates. SSU, small subunit ribosomal 18S RNA gene. Number on branches are non-parametric bootstrap in >70%. Lined boxes show specimens placed in the order Pontismatales, or the single genus *Pontisma* or *Sirolopidium* at various times.





D

