



Fig. 4.1. Phylogeny of the gomphoid-phalloid fungi. Tree topology is based on the Bayesian analyses with 2,000,000 generations of MCMC. GTR+G+I model was used for the nuc-LSU-rDNA, mt-SSU-rDNA, and each codon position for the remaining protein coding genes. Maximum parsimony analyses were conducted with 10000 random additions of heuristic search with TBR and Multrees option off, followed by 500 random addition of heuristic search with TBR and Multrees option on, starting with all the trees in memory from the first step. Numbers on branches are Bayesian posterior probability/maximum parsimony bootstrap values. The provisional taxon names are indicated with slash (/).