The coevolution of mycoparasitic *Tremella* sensu lato species and their hosts

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The genus *Tremella* sensu lato is featured by mycoparasitic life style. They can parasitize a variety of species belonging to Basidiomycetes and Ascomycetes. *Tremella* species are delimitated mainly by the phylogenetic relationship because of the morphological characters are scarce. Whether hosts and their parasites speciate by cospeciation, or through host switching, is a key issue in host-parasite evolution. Understanding the evolutionary dynamics of parasitism of *Tremella* spp. and their hosts could provide evidence partly for the taxonomy of *Tremella* species. The phylogenies of *Tremella* spp. and hosts were generated based on the ITS and D1D2 sequences of 45 and 100 species, respectively. We investigated the congruence between parasites and hosts phylogenies using distance-based and event-cost based methods. Distance-based test supported an overall congruence between the phylogenies of *Tremella* spp. and their hosts. Reconciliation reconstructions determined host-switching (27-30) other than cospeciation (10-13) is a major impetus driving *Tremella* species diversity. The number of failure-to-diverge case (62) is also high and stable, independently of the cost regimes, which means that some *Tremella* species are able to parasitize closely related species to be generalists.