Fig. 2. A maximum likelihood (ML) tree constructed from small subunit, internal transcribed spacer 1, 5.8S, and internal transcribed spacer 2 ribosomal DNA sequences. Numbers at each node are the ML (>50%, left) and Bayesian values (>0.95, right). Antarctic strains are in bold, and the type species of the genus *Micractinium* is highlighted with a star.