



Figure Legend. Phylogenetic tree of *Cryptococcus nemorosus*, *Cr. perniciosus* and related taxa, obtained by maximum parsimony analysis of the total ITS region (one of two equally parsimonious trees). *Tremella mesenterica* was included to root the tree. Percentage bootstrap values of 1000 replicates are given at each node (values under 50% are not shown). Sequences determined in this study have their accession numbers in boldface.