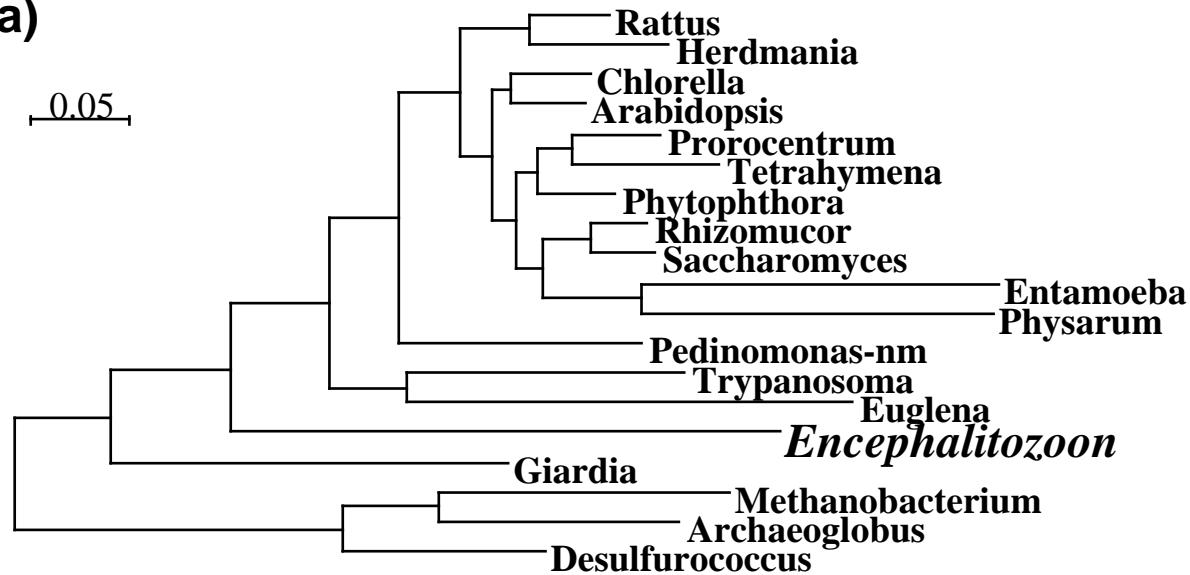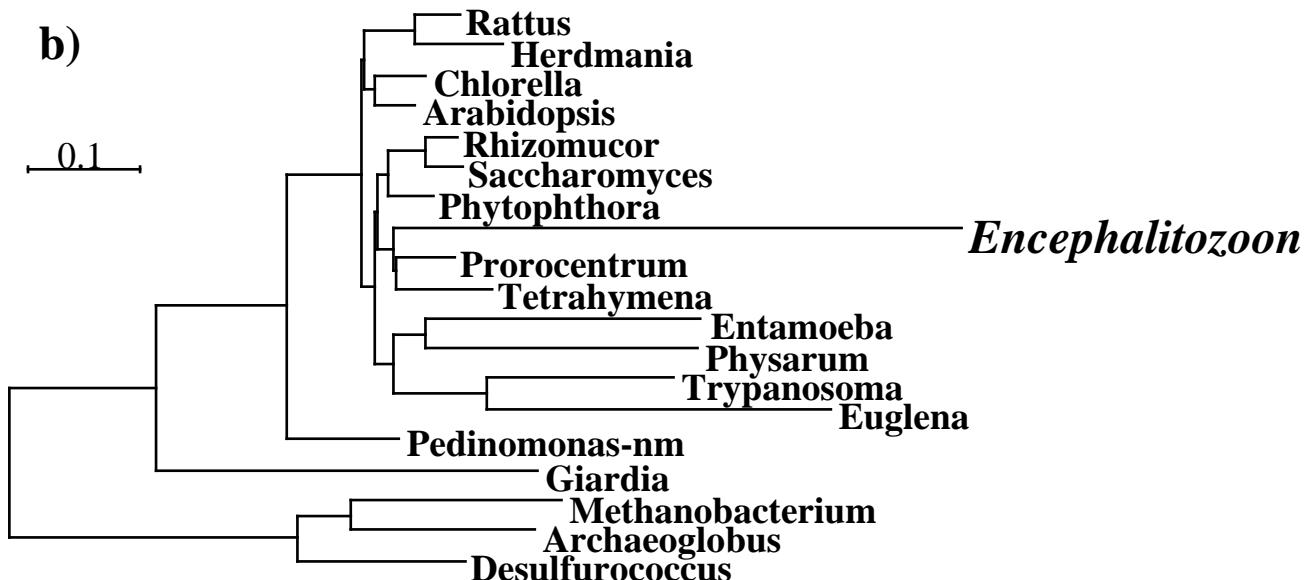Figure 5. Phylogenetic relationships between 16 eukaryotic and 3 archaeal LSU rRNA sequences inferred by the fastDNAml method (a) and the BASEML method (b) rooted between eukaryotic and archaeal sequences. Horizontal branches are drawn proportionally to inferred evolutionary distances (see scales). Species names and sequence accession numbers: *Rattus norvegicus*, X01069; *Herdmania momus*, X53538; *Chlorella ellipsoidea*, D17810; *Arabidposis thaliana*, X52320; *Rhizomucor racemosus*, M26190; *Saccharomyces cerevisiae*, J01355; *Phytophtora megasperma*, X75631; *Encephalitozoon cuniculi*, this work; *Prorocentrum micans*, X16108; *Tetrahymena thermophila*, X54512; *Entamoeba histolytica*, X65163; *Physarum polycephalum*, V01159; *Trypanosoma brucei*, X14553; *Euglena gracilis*, X53361; nucleomorph of *Pedinomonas minutissima*, U58510; *Giardia ardeae*, X58290; *Methanobacterium thermoautotrophicum*, X15364; *Archaeoglobus fulgidus*, M64487; *Desulfurococcus mobilis*, X05480. To accelerate computation of b), the following well established groupings were fixed: (*Rhizomucor, Saccharomyces*); (*Trypanosoma, Euglena*); (*Rattus, Herdmania*); (*Chlorella, Arabidopsis*); (*Methanobacterium, Archaeoglobus*), *Desulfurococcus*.