Fig. S4. Phylogenetic relationships amongst *Umbilicaria* species, based on a maximum likelihood analysis (IQ) of ITS1-5.8S-ITS2 and mtLSU. The reliability of each branch was tested by ML method. Numbers at tree nodes indicate bootstrap values of ML. Thicker branches indicate when the bootstrap value of ML is ≥ 70%. GenBank accession numbers are given in Table 1. Branch lengths represent the estimated number of substitutions per site assuming the respective models of substitution (Table 2).