



Fig. S3. Phylogenetic relationships amongst *Umbilicaria* species, based on a maximum likelihood analysis (IQ) of ITS1-5.8S-ITS2. The reliability of each branch species was tested by ML method. Numbers at tree nodes indicate bootstrap values of ML. Thicker branches indicate when the bootstrap value of ML is $\geq 70\%$. 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).