Supporting Information

Kaasalainen et al. 10.1073/pnas.1200279109

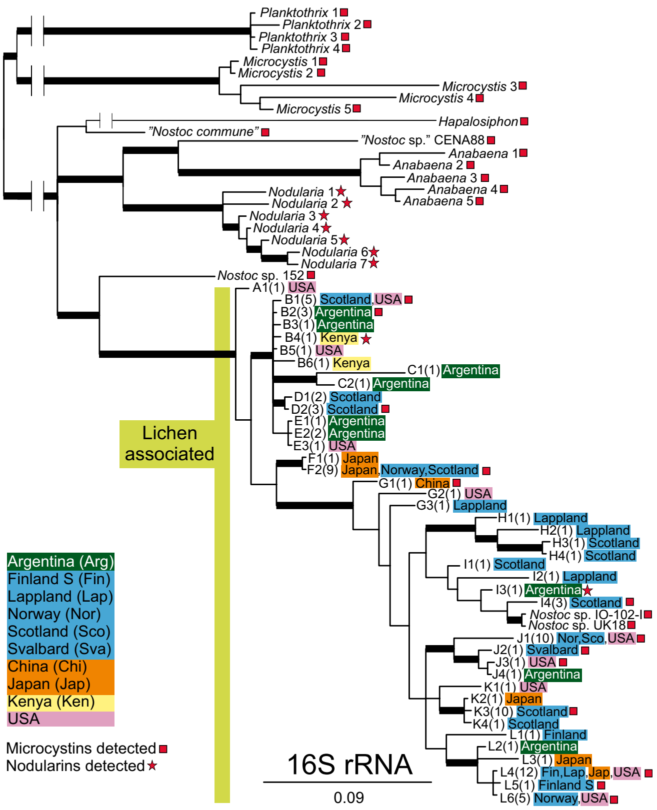

Fig. S1. Bayesian trees compiled from 16S rRNA. Thick branches have a posterior probability value of 0.95 or higher. The genotype codes (e.g., F1) are coupled with specimens in Table 2. The number of lichen specimens in which the genotype has been found is in parentheses. The regions with color coding are the collection sites of the specimens. Red boxes and stars show genotypes acquired from specimens that contained microcystins or nodularins.

Other Supporting Information Files

Table S1 (DOCX)
Table S2 (DOCX)
Table S3 (DOCX)