Lichen symbioses represent a major way of life among the Fungi. Almost one-fifth of all known fungal species are lichenized, and about 1500 species of lichens contain cyanobacterial photobionts, most of which belong to the genus *Nostoc*. Despite extensive studies, many basic aspects of their biology remain poorly known, especially cyanobiont diversity and specificity (1).

Cyanolichen specimens were collected from northern Europe, western North America, and central China. Epiphytic lichen communities in two old-growth forests in central Finland were studied in detail (tables S1 and S2). Lichens were identified, and free-living cyanobacteria were cultured from substrate samples. The small subunit (16S) of the ribosomal gene repeat and the tRNA<sup>Leu</sup> (UAA) intron sequences were used to resolve phylogenetic relationships, and the tRNA<sup>Leu</sup> intron sequences were used for identifying *Nostoc* strains (2).

Cyanobacterial 16S rDNA sequences were obtained from 16 species of cyanolichens. Additional sequences were acquired from cyanobacterial cultures and GenBank (table S1). A phylogenetic analysis of these sequences resulted in a consensus tree in which all *Nostoc* formed a monophyletic group with 100% support (Fig. 1). The *Nostoc* clade was divided into two subgroups; the first only included cyanobionts of epiphytic lichen species (*Nephroma* guild). Further subdivisions within this group did not correlate with the geographical origin or generic identity of the lichen specimens. The second subgroup (*Peltigera* guild) included cyanobionts of terrestrial lichens, free-living *Nostoc* strains, and a symbiotic *Nostoc* from the roots of a cycad (Fig. 1).

Most epiphytic cyanolichens in central Finland contained similar tRNA<sup>Leu</sup> intron genotypes (table S2). One intron genotype was found from all six sample plots, and it was shared extensively by four different species of *Nephroma* and *Parmelia*.* Two other intron genotypes differed from the most frequent intron genotype by only one base change each; these genotypes were found from several epiphytic lichens on different sample plots. These and a fourth Finnish intron genotype shared the same repeat motif in their P6b element (3). Four North American and two Chinese intron genotypes also had this repeat motif. As in Finland, all these sequences were obtained from epiphytic cyanolichens (table S2).

A different set of tRNA<sup>Leu</sup> intron genotypes was obtained from *Peltigera* thalli and cultured *Nostoc* strains (table S2). These sequences had a different repeat motif in the P6b element and could not be readily aligned with the sequences from epiphytic cyanolichens (3). Species of *Peltigera* are predominately terricolous, and when growing epiphytically, they are usually confined to mossy basal trunks. Two intron genotypes also had the same repeat motif in their P6b element (3). Four North American and two Chinese intron genotypes also had this repeat motif. As in Finland, all these sequences were obtained from epiphytic cyanolichens (table S2).

**Lichen Guilds Share Related Cyanobacterial Symbionts**

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A strict consensus tree showing phylogenetic relationships among symbiotic and free-living cyanobacteria based on 16S rDNA sequence data (table S1). Bootstrap support >50% is shown at nodes. All *Nostoc* strains form a monophyletic group. The cyanobionts of the *Nephroma* guild form a well-supported subgroup within the *Nostoc* clade. The cyanobionts of the *Peltigera* guild group together with free-living *Nostoc* strains. These groupings are congruent with data from tRNA<sup>Leu</sup> (UAA) intron sequences (table S2).

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**References and Notes**

2. Supporting material is available on Science Online.
6. We thank B. McCune, K. Sivonen, and P. Lindblad for cooperation and help. We are especially grateful to P. Paulsrud, who has pioneered the use of molecular methods in the study of lichenized cyanobacteria. Our research was supported by the Academy of Finland (project number 168 332).

**Supporting Online Material**

www.sciencemag.org/cgi/content/full/297/5580/357/DC1

Materials and Methods
Tables S1 and S2

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