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Utility of 16S-23S ITS sequence and secondary structure for recognition of intrageneric and intergeneric limits within cyanobacterial taxa: *Leptolyngbya corticola* sp. nov. (Pseudanabaenaceae, Cyanobacteria)

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With 56 figures and 4 tables

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Abstract: An unusual species of *Leptolyngbya* was isolated from tree bark by Marie Takačová in 1983. Originally it was considered to be a *Lyngbya* species, but since revision of the Oscillatoriales (Anagnostidis & Komárek 1988), it has resided in the Culture Collection of the Czech Academy of Sciences under the tentative designation *Leptolyngbya foveolarum* TAKACOVA 1983/4. We have studied the morphology, ultrastructure and 16S ribosomal RNA gene sequence data for this strain and have found it to be unique among all previously described species. Analysis of 16S rRNA gene sequence data for many *Leptolyngbya* taxa indicates close affinity with *L. boryana, L. tenerrima* and *L. angustata*, which is consistent with the morphological similarity we have seen among the three taxa. The 16S-23S ITS regions of 19 strains in the polyphyletic taxon *Leptolyngbya* were sequenced and folded, and the structure and sequence of these ITS regions were highly congruent with phylogeny determined from 16S rRNA gene sequence data. This agreement provides a straightforward way of recognizing intrageneric and possibly intergeneric taxonomic diversity. This taxon has distinct 16S-23S ITS sequences which, together with the morphological autapomorphies it possesses, are sufficient to clearly differentiate it from the three sister taxa sequenced thus far. For this strain, we propose the name *L. corticola*.

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