

Supplementary information

Supplementary Tables

Table S1 Comparison of percent similarity values based on the *rbcLX* gene sequences (657 bp) among selected taxa phylogenetically related to *Scytonema foetidum* sp. nov. (NUACC05 and NUACC06). The *S. foetidum* strains and its similarity values are shown in bold letter.

Strain	1	2	3	4	5
1 <i>Scytonema foetidum</i> NUACC05&NUACC06					
2 <i>Scytonema hofmanii</i> PC7110	93.0				
3 <i>Scytonema</i> sp. FM05-MK45	93.3	98.7			
4 <i>Scytonema hyalinum</i> HHT-U-KK4	85.7	86.0	86.5		
5 <i>Brasilonema</i> sp. 4 CR6-5A	86.0	84.7	85.2	92.7	

Table S2 Comparison of percent similarity values based on the *nifH* gene sequences (323 bp) among selected taxa phylogenetically related to *Scytonema foetidum* sp. nov. (NUACC05 and NUACC06). The *S. foetidum* strains and its similarity values are shown in bold letter.

Strain	1	2	3	4	5	6	7	8
1 <i>Scytonema foetidum</i> NUACC05&NUACC06								
2 <i>Scytonema hofmanii</i> PC7110	91.4							
3 <i>Scytonema</i> sp. NC-4B, DC-A &FGP-7A-1	88.4	92.6						
4 <i>Scytonema hofmanni</i> UTEX 2349	87.0	86.3	89.8					
5 <i>Ewamiania thermalis</i> TS0513	85.7	85.3	86.4	84.7				
6 <i>Scytonema</i> sp. FGP-7A-2	84.9	86.0	89.9	90.2	85.0			
7 <i>Nodularia sphaerocarpa</i> CCAP 1452	83.6	85.0	85.5	86.6	81.1	83.4		
8 <i>Brasilonema</i> sp. CENA360	82.7	82.7	85.1	83.4	90.2	85.0	80.8	

Supplementary Figure

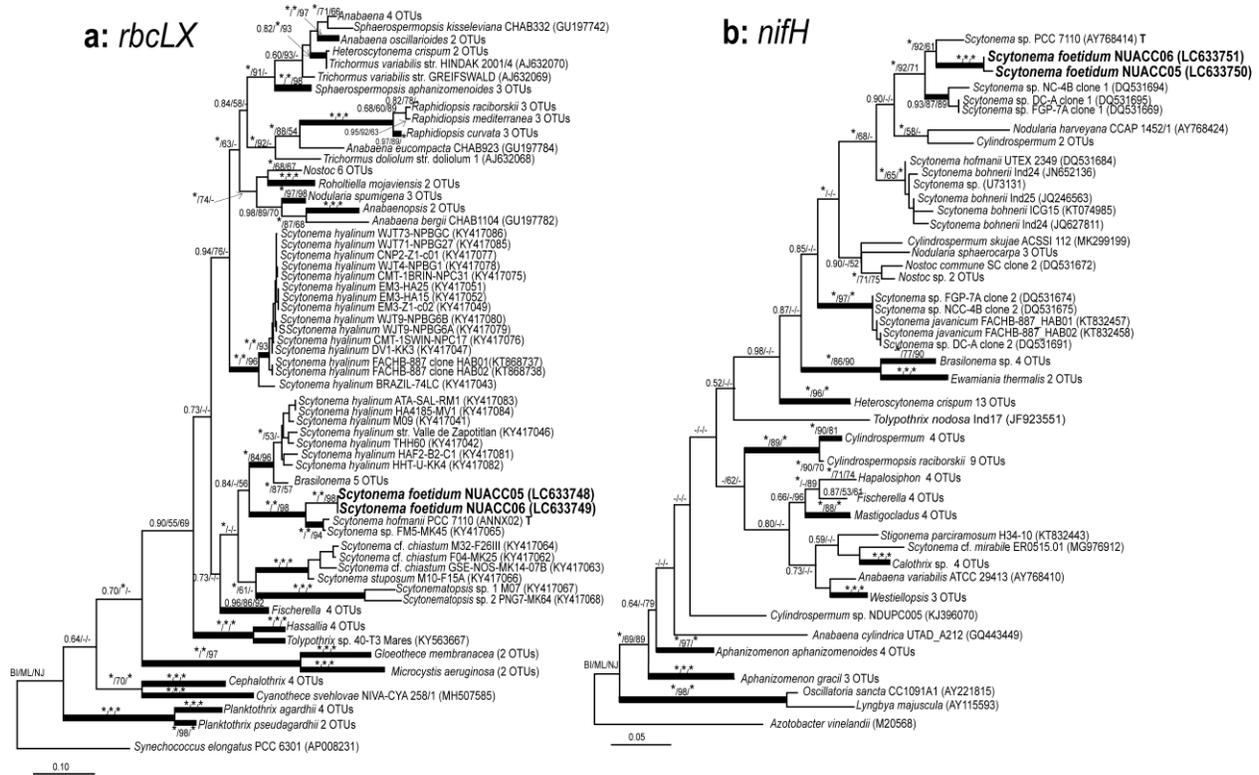


Fig. S1. Maximum likelihood trees based on the phylogenetic relationship of (a) *rbcLX* gene sequences (859 base pairs) and (b) *nifH* gene sequences (323 base pairs) of *Scytonema foetidum* strains and other cyanobacterial taxa. Studied *Scytonema foetidum* are in bold. *Synechococcus elongatus* PCC6301 was used as the outgroup for the *rbcLX* gene phylogenetic tree and *Azotobacter vinelandii* was used as the outgroup for the *nifH* gene phylogenetic tree. Numbers associated with nodes indicate support values including posterior probabilities from BI analysis and bootstrap supports from ML, and NJ analyses, respectively. Only posterior probabilities >0.50 and bootstrap supports > 50% are reported and the lower value is shown as a hyphen (-). (T) represents the type strain of the genus *Scytonema*. Asterisks at the nodes equal the 0.99–1.00 posterior probabilities or the 99–100% bootstrap support values. Bold horizontal lines show clades supported by at least 0.75 of BI posterior probabilities and 75% of ML and NJ bootstrap values. Scale bar indicates the number of nucleotide substitutions per site.

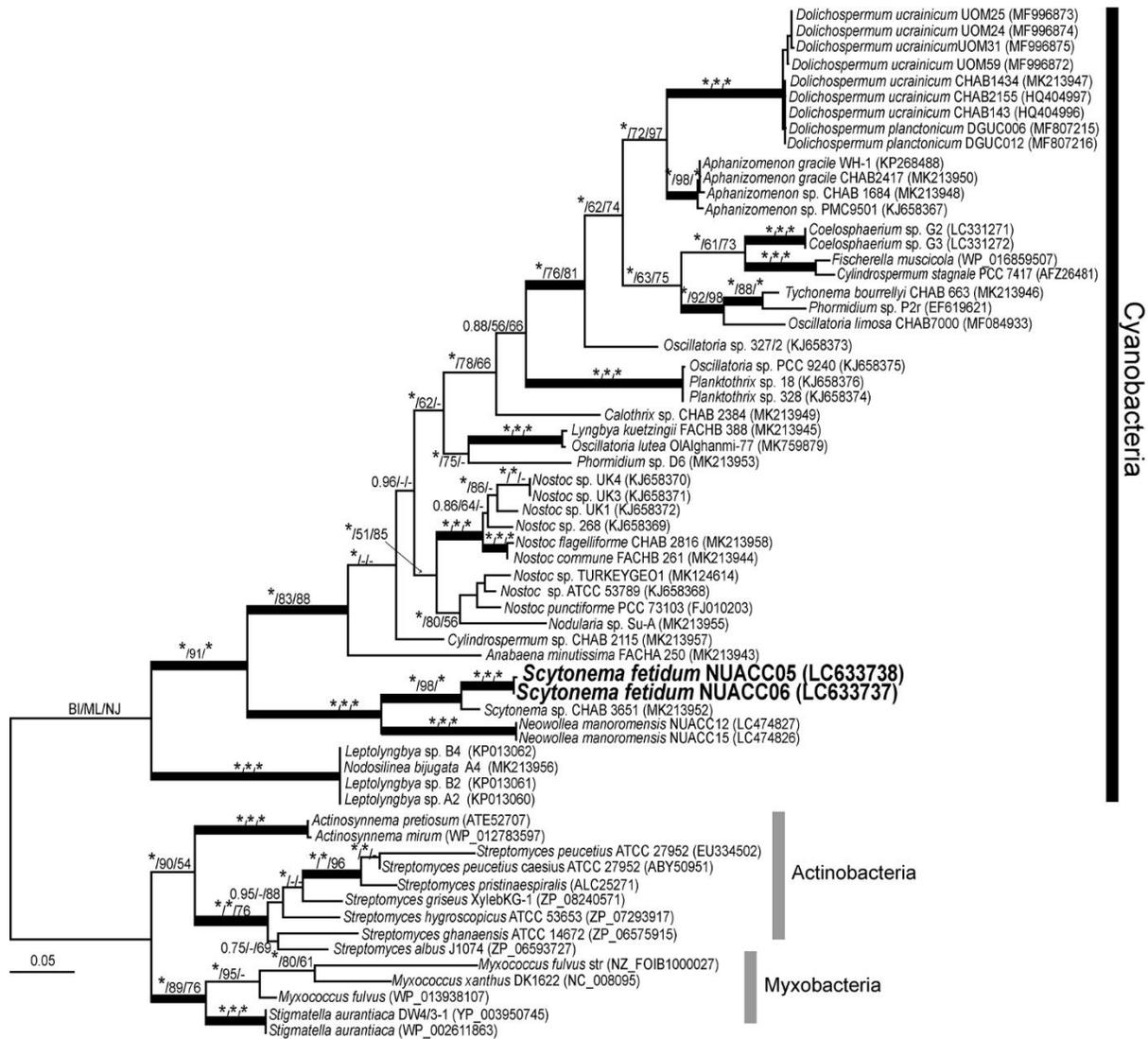


Fig. S2. Maximum likelihood tree based on the phylogenetic relationship of the geosmin synthase (*geoA*) gene sequences (885 base pairs) of *Scytonema foetidum* strains and 62 other cyanobacterial taxa. *Scytonema foetidum* strains studied in this work are exhibited by boldface letter. *Azotobacter vinelandii* was used as the outgroup. Numbers associated with nodes indicate support values including posterior probabilities from BI analysis and bootstrap supports from ML, and NJ analyses, respectively. Only posterior probabilities >0.50 and bootstrap supports >50% are reported and the lower value is shown as a hyphen (-). (T) represents the type strain of the genus *Scytonema*. Asterisks at the nodes equal 0.99–1.00 of posterior probabilities or the 99–100% of bootstrap support values. Bold horizontal lines show clades supported by at least 0.75 BI posterior probabilities and 75% of ML and NJ bootstrap values. Scale bar indicates the number of nucleotide substitutions per site.

