



## Morphological and Molecular Characterization of *Brasilonema roberti-lamii* (Cyanophyceae, Nostocales, Scytonemataceae), from Central Mexico

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### Abstract

This paper is a contribution to the morphological and molecular characterization of the cyanobacterium *Brasilonema roberti-lamii* from populations found in Central Mexico. The general growth form and the morphological, morphometric and ecological characteristics of the populations studied clearly correspond to those described for *Brasilonema roberti-lamii* (basionym: *Tolypothrix roberti-lamii*) from the French Antilles. Based on molecular data from DNA sequencing of the 16S rRNA gene and the IGS of the *cpcB-cpcA* phycocyanin operon (*cpcBA*-IGS), we propose that the populations that we studied are closely related to those of other *Brasilonema* species, including *B. octagenarum* UFV-OR1, UFV-E1 and HA4187-MV1-p1F, *Brasilonema sennae* CENA 114, *B. tolantongensis*, *B. terrestre* CENA 116, *B. angustatum* HA4187-MV1-B2+p1F and HA4187-MV1-B2+p1H and *B. bromeliae* SPC951. Our findings support the transference of *Tolypothrix roberti-lamii*, which was made based exclusively on morphological criteria, to *Brasilonema*. The use of molecular analyses in addition to traditional morphological and ecological criteria, known as polyphasic approach, is a good alternative to describe taxa of cyanobacteria, mainly at the genus and species levels.

**Keywords:** *cpcBA*-IGS gene, Cyanobacteria, 16S rRNA gene, *Tolypothrix roberti-lamii*, polyphasic approach, systematics, taxonomy

### Introduction

The use of several criteria, in addition to the morphological, such as molecular, ultrastructural, etc. (known as the “polyphasic approach”) has been proven to be adequate for the recognition and characterization of different taxa of cyanobacteria. The term “polyphasic” has been used in this sense by several researches (Flechtner *et al.* 2002, González-Resendiz *et al.* 2013, Komárek 2010, Vaccarino & Johansen 2011, 2012). The results reported by several authors (Wilmotte & Golubic 1991, Komárek 2006, 2010) show a clear relationship between the morphology and the DNA sequences of different genes within cyanobacteria, mainly the 16S rRNA. Several traditional cyanobacterial genera in the classification proposed by Geitler (1932) have been supported by DNA sequencing. Some recently described cyanobacteria have been separated from traditional genera to establish new genera such as *Brasilonema* Fiore, Sant’Anna, Azevedo, Komárek, Kaštovský, Sulek & Lorenzi (2007: 794), *Coleofasciculus* Siegesmund, Johansen & Friedl in Siegesmund *et al.* (2008: 1575), *Geminocystis* Korelusová, Kaštovský & Komárek (2009: 933) or *Phormidesmis* Turicchia, Ventura, Komárková & Komárek (2009: 179). Some studies of extreme habitats have also led to the discovery of new genetically and morphologically well-defined genera, i.e. *Spirirestis* Flechtner & Johansen in Fletcher *et al.* (2002: 6) or *Rexia* Cassamata, Gomez & Johansen (2006: 23).

The sequencing of the 16S rRNA gene has been used as a standard genetic approach to delimitate cyanobacterial genera. However, There are cases where some morphological and ecological different species. show a high percentage of DNA similarity, whereas other populations with similar morphology appear in different clades when their 16S rRNA gene sequences are compared (the so-called “cryptic species”, Komárek 2005, 2006, 2010).

The genus *Brasilomena* was erected based on both its morphological characters and DNA sequences, analyzed from the 16S rRNA gene and the IGS of the *cpcB-cpcA* phycocyanin operon sequences. At present, nine species

**TABLE 2.** Similarity matrix (percentages) for 16 strains comparing partial sequences of the 16S rRNA gene. Strain access numbers: (1) GQ443308, (2) HQ847567, (3) EF150855, (4) HQ847562, (5) JN676147, (6) EF490447, (7) DQ486055, (8) EF117246, (9) AJ544085, (10) AJ544079, (11) AJ544084, (12) AJ544083, (13) AF334700, (14) AB075996, (15) AY069954, (16) AB093483.

	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1. <i>Brasilonema roberti-lamii</i>	99	99	99	98	97	97	97	96	94	94	95	95	93	93	93
2. <i>B. angustatum</i> HA4187-MV1		99	99	98	98	97	97	96	95	94	95	95	93	93	93
3. <i>B. octagenarum</i> UFV-OR1			100	99	98	97	97	96	95	94	95	95	93	93	93
4. <i>B. octagenarum</i> HA4186-MV1				99	98	97	97	96	95	94	95	95	93	93	93
5. <i>B. tolantongensis</i>					98	98	98	97	95	94	95	94	93	93	93
6. <i>B. terrestre</i> CENA116						97	97	97	95	94	95	94	93	93	93
7. <i>B. bromeliae</i> SPC951							99	96	95	94	95	94	93	92	92
8. <i>B. semae</i> CENA114								96	95	95	95	94	93	92	93
9. <i>Symphyonemopsis</i> VAPOR 1									95	94	94	94	93	93	93
10. <i>Mastigocladopsis repens</i> MORA										96	96	95	93	92	92
11. <i>Symphyonema</i> sp. 1517											99	97	93	92	92
12. <i>Symphyonema</i> sp. 1269-1												96	93	92	92
13. <i>Scytonema hyalinum</i>													93	92	91
14. <i>Scytonema hoffmannii</i> PCC7110														95	95
15. <i>Scytonema</i> sp. U-3-3															98
16. <i>Scytonema</i> sp. IAM M-262															100

## Conclusions

The taxonomy of Cyanobacteria has changed considerably in recent years. The incorporation of molecular techniques has been of great help to delimit and characterize genera and higher-level taxa, allowing to understand the diversification processes within cyanobacteria, which in turn has affected their classification. At the species level, however, the use of the 16S rRNA gene is not generally sufficient by itself for species delimitation because the similarity values are often high (above 98%) and phylogenetic analyses allow already the recognition of significant differences. Nevertheless, the interpretation of such differences requires the use of other criteria (such as morphological and ecological) to provide sufficient data for species delimitation. For this reason, the best approach available to date is the use of complementary criteria (polyphasic approach).

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