

# Dolichospermum uruguayense spec. nov., a planktonic cyanobacterium dominating the Lower Uruguay River, South America



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## Introduction

The Uruguay River is one of the largest rivers in South America (>1,800 km long, annual discharge 6230 m<sup>3</sup>s<sup>-1</sup>). It belongs to the La Plata Basin and its lower part flows between two countries, Argentina and Uruguay. The water quality and flow rate is affected by more than twenty hydropower dams, increasing urbanization and the expansion of agriculture. These effects, together with climate variations favour the proliferation of massive blooms of planktonic cyanobacteria. These cyanobacterial blooms usually contain several *Dolichospermum* morphospecies. Dominance of one of them, preliminarily determined as *D. cf. pseudocompactum*, was previously reported (Ferrari et al. 2011). Morphological characteristics of this morphospecies are similar to *D. pseudocompactum* (M. Watanabe 1996) Wacklin et al. 2009 in some points, but do not fully correspond with its description, neither with definitions of any *Dolichospermum* species described so far.

The main goal of this study was therefore a detailed polyphasic characterization of this *Dolichospermum* morphospecies, assessment of its phylogenetic relationships to other *Dolichospermum* spp. and clarification of its taxonomic status.



Fig. 1. A map of the Lower Uruguay River. The sampling site Fray Bentos is indicated by a red circle.

## Material & Methods

- 1) Isolation** of a clonal strain of *Dolichospermum* sp. from the Lower Uruguay River (Fray Bentos) using the capillary technique (Zapomělová et al. 2007).
- 2) Morphological evaluation**
  - a) of the original *Dolichospermum* sp. population in the natural sample.
  - b) of the isolated clonal strain under culture conditions.
- 3) Sequencing of the 16 S rRNA gene, phylogenetic analyses** (Maximum Likelihood – ML, Maximum Parsimony – MP, Neighbor Joining – NJ).

## Results - Phylogeny

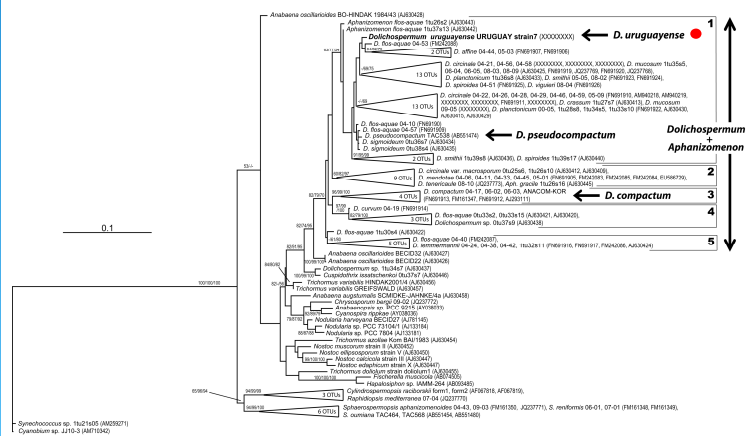


Fig. 3. Maximum Likelihood (ML) tree based on 16S rRNA gene sequences (1410 bp). The studied *Dolichospermum uruguayense* strain is in bold and indicated by a red circle. Phylogenetic affiliations of morphologically similar species *D. pseudocompactum* and *D. compactum* are indicated by arrows. Bootstrap values are written in a following order: ML/MP/NJ.

## Results - Morphology

Table 1. Morphometric parameters of the studied *Dolichospermum* strain, its original population in the environmental sample in comparison with morphology of the same *Dolichospermum* species observed by Ferrari et al. (2011). The order of the data is as follows: (minimum) 25% quartile-mean-75% quartile (maximum).

	Original natural population (November 2010)	Isolated strain (measured in May 2012)	Morphology observed by Ferrari et al. (2011) in the Uruguay River in 2009
Vegetative cells	Length (4.7)7.0-8.1-9.8(12.0)	(5.4)8.9-9.5-10.8(12.3)	6.0-8.0
	Width (7.1)8.1-8.6-9.0(9.7)	(7.1)8.2-8.6-9.0(11.1)	7.6-8.3
	Length:width ratio (0.5)0.8-1.0-1.1(1.5)	(0.6)1.0-1.1-1.2(1.4)	
Heterocytes	Length n.o.	(8.8)9.8-10.6-11.3(13.3)	9.0-12.0
	Width n.o.	(8.1)9.3-10.2-10.7(11.7)	9.0-12.0
	Length:width ratio n.o.	(1.0)1.0-1.1-1.1(1.2)	
Akinetes	Length n.o.	n.o.	22.3-25.0
	Width n.o.	n.o.	10.0-12.6
	Length:width ratio n.o.	n.o.	
Diameter of trichome coiling	(19.6)28.4-29.6-30.8(41.2)	(22.8)26.7-28.0-30.1(33.0)	27.0-30.0

Table 2. Matrix showing P-distances (%), based on the 16S rRNA gene sequences (1270 bp). All positions containing alignment gaps were only eliminated in pairwise sequence comparison.

	1	2	3	4	5	6	7	8
1 <i>D. uruguayense</i> strain 7								
2 <i>D. pseudocompactum</i> TAC 538	97.3							
3 <i>D. compactum</i> 04-17	97.2	97.7						
4 <i>D. compactum</i> 06-02	97.2	97.7	100.0					
5 <i>D. compactum</i> 06-03	97.2	97.7	100.0	100.0				
6 <i>D. compactum</i> ANACOM-KOR	97.2	97.7	100.0	100.0	100.0			
7 <i>D. ros-aquae</i> 04-53	98.0	98.1	98.3	98.3	98.3	98.3		
8 <i>D. affine</i> 04-44	98.0	98.7	98.4	98.4	98.4	98.4	98.9	
9 <i>D. affine</i> 05-03	97.6	98.6	98.3	98.3	98.3	98.3	98.8	99.8

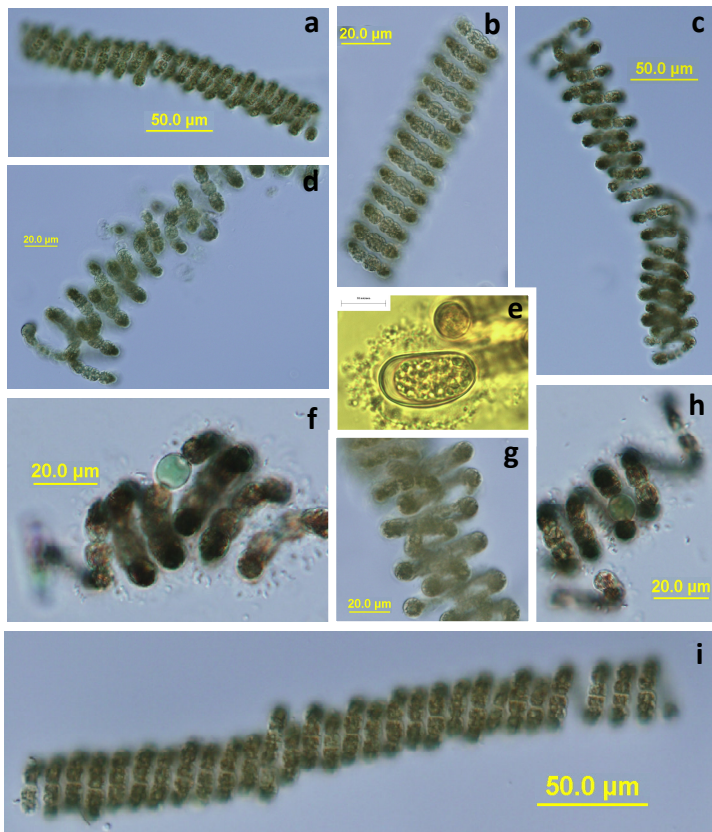


Fig. 2. The studied *Dolichospermum* morphospecies under natural conditions (a-e, g, i) and in culture (f, h).

## Discussion

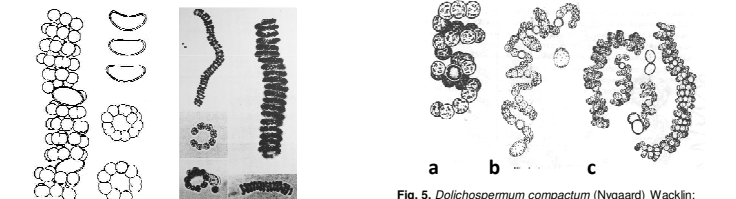


Fig. 4. A type species of *D. pseudocompactum* (M. Watanabe) Wacklin from Lake Teganawa, September 1989 (modified from Watanabe 1996).

### *D. pseudocompactum* (M. Watanabe) Wacklin

- original description (Watanabe 1996):
- Vegetative cells: 5.5–6.8 µm
- Heterocytes: 5.5–7.5 µm
- Akinetes – length: 16.8–21.3 µm
- width: 7.5–11.3 µm
- length:width ratio: 1.8–2.6

### *D. compactum* (Nygaard) Wacklin

- original description (Nygaard 1949):
- Vegetative cells: 5.5 µm
- Heterocytes: 5.5–7.5 µm
- Akinetes – length: 11.0–12.5 µm
- width: 8.0–10.4 µm
- length:width ratio: 1.2–1.4

## Conclusion

We propose a new species, *Dolichospermum uruguayense* spec. nov. The studied strain differed morphologically from all similar species described so far. This difference was also reflected at the genetic level, as this strain did not tightly cluster with any *Dolichospermum* strains whose sequences were available from Genbank.

**Description:** Coiled trichomes of varying length, diameter of coiling (19.6) 28.4–29.5–30.8 (41.2) µm, solitary or in couples, one filament twisted inside another (Fig. 2, c, d, g), more-or-less constricted at the cell-walls. Terminal cells with aerotopes, spherical or barrel-shaped, compressed during division, (7.1) 8.1–8.6–8.9 (9.7) µm wide. Heterocytes only intercalary, solitary, spherical, (8.1) 9.3–10.2–10.7 (11.7) µm wide. Akinetes kidney-shaped, 22.3–25.0 µm long and 10.0–12.6 µm wide, distant from heterocytes, very rare both in the natural population and under culture conditions. Planktonic.

**Automorphic characteristics:** Compactness of trichome coiling in combination with the dimensions of vegetative cells and akinete shape.

**Etymology:** The name of the species is derived from the Uruguay River, South America, from where the type population was described. The type strain will be deposited in two official culture collections.

## Literature

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