

Biodiversity of cyanobacteria in Tunisian freshwater reservoirs: occurrence and potent toxicity – a review

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ABSTRACT

In spite of the great environmental and sanitary importance of cyanobacteria, their biodiversity is little known in Tunisia. In this work, a review was carried out, based on literature data, of potentially toxic cyanobacteria occurrence in Tunisia. *Microcystis*, one of the most widely distributed toxic bloom-forming cyanobacteria genera, was represented by *Microcystis wesenbergii*, found only in Lebna water reservoir, and *Microcystis aeruginosa* recorded in different water bodies. The invasive potentially toxic cyanobacterium *Cylindrospermopsis raciborskii*, reported for the first time in Tunisia in October 2004, was observed in the semi-arid to arid areas. The harmful genus *Planktothrix* was represented in Tunisian freshwater by the green-pigmented species *P. agardhii*. The filamentous cyanobacteria dominance is increasingly reported in Tunisia in eutrophic water bodies. This dominance increases especially during the summer–autumn period. Recently, potentially toxic cyanobacteria blooms have been reported in some reservoirs in the north east of the country. These blooms were generated by the potentially toxic Chroococcale *Microcystis aeruginosa*. Harmful cyanobacteria tend to spatio-temporal expansion in the Tunisian inland waters. The toxicological potential evaluated by several methods showed that none of the Tunisian strains were proved to be cylindrospermopsin nor saxitoxin producers. However, the majority of *Microcystis* were able to synthesize microcystin.

Key words | cyanobacteria, cyanotoxins, genetic variability, Tunisian freshwaters

INTRODUCTION

Cyanobacteria are a major group of prokaryotes that occur throughout the world (WHO 1998). They are the Earth's oldest known oxygen-producing organisms, with fossil remains dating back 3500 million years (Schopf 2000). Through their photosynthetic activity, they were largely responsible for the modern-day oxygen-enriched atmosphere, and subsequent evolution of our planet's higher plant and animal life (Schopf 2000; Whitton & Potts 2000). Cyanobacteria have many unique features among phytoplankton, such as buoyancy and nitrogen fixation, and the production of a wide variety of bioactive compounds. Several species of cyanobacteria form blooms that are frequently toxic, and thus pose a health risk for humans and animals (Sivonen & Jones 1999). They can produce toxic secondary metabolites

including hepatotoxins that have carcinogenic potential, neurotoxins and lipopolysaccharide endotoxins (Carmichael & Falconer 1993; Codd 2000; Carmichael 2001). The tragic deaths of 70 of 131 patients exposed to the hepatotoxins microcystins (MC) through renal dialysis in Brazil are the only well known substantiated human fatalities due to cyanotoxins (Jochimsen *et al.* 1998). Nevertheless, some illnesses reported previously were life-threatening (Ressom *et al.* 1994), such as the poisoning of 138 children and 10 adults due to hepatotoxin cylindrospermopsin (CYN) in Palm Island (Australia) (Hawkins *et al.* 1985).

While cyanobacterial harmful algal blooms have been reported in the scientific literature for more than 130 years (Francis 1878), in recent decades, the incidence and intensity

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of these blooms, as well as economic loss associated with these events, has increased in both fresh and marine waters (Chorus & Bartram 1999; Carmichael 2001; Hoagland et al. 2002; Teneva et al. 2005; Hudnell 2008; Heisler et al. 2008; Paerl 2008; Paul 2008; Paerl & Huisman 2008). The most common cyanobacterial genera known for their potential ability to produce toxins include *Anabaena*, *Aphanizomenon*, *Cylindrospermopsis*, *Lyngbya*, *Microcystis*, *Nodularia*, *Nostoc* and *Planktothrix*. However, the number of identified toxic cyanobacteria is still increasing as a result of new detections (Sivonen 1998; Aboal & Puig 2005; Humpage et al. 2012). In fact, Ballot et al. (2005) reported that the hepatotoxin MC-YR and the neurotoxin anatoxin-a were produced, in a monocyanobacterial strain of *Arthrospira fusiformis*, isolated from Lake Sonachi (Kenya). It is important to note that the cyanobacterium *Arthrospira* (*Spirulina*), having a long history of use as food for humans (Vonshak 1997), is used as a nutritive supplement for its beneficial effects, including detoxication, increased energy, weight loss and therapeutic applications (Ciferri 1983; Belay 1997; Mei Li & Zao Qi 1997). *Limnothrix*, a commonly occurring cyanobacterial genus, was recently shown to produce a novel toxin 'Limnothrix' (Torres-Ariño & Mora-Heredia 2010; Bernard et al. 2011).

The dominance of cyanobacteria in aquatic ecosystems, in different geographical locations, with considerable variability in terms of size, morphology, salinity and hydrologic conditions, indicates that climate change can help synergistically with anthropogenic nutrient enrichment on the growth of these micro-organisms across the globe (Paerl & Paul 2012). Several studies reported that freshwater cyanobacteria blooms are typically associated with eutrophic and poorly flushed waters (Paerl 1988; Carmichael 1995; Lee et al. 2000; Albay et al. 2003). Kosten et al. (2012) conducted monitoring in 143 lakes of different trophic situations, localized according to the latitudinal gradient from north of Europe to South America. They found that the percentage contribution of cyanobacteria in total phytoplankton biomass increases significantly with temperature. These authors noted also that the rise in temperature can reduce the levels of nutrient uptake that cause the initiation and maintenance of blooms. Recent studies in laboratory scale as well as field observations have clearly demonstrated that the combination of anthropogenic inputs of nutrients,

rising temperatures, increased stratification and elevated atmospheric CO₂ concentrations, favored the dominance of cyanobacteria in a wide range of aquatic ecosystems (Paerl & Paul 2012). The warm Mediterranean climate favors the occurrence and extended duration of the cyanobacterial blooms in eutrophic freshwaters, which may start in spring and persist until December, or in hypertrophic lakes, may even be continuous throughout the year (Moustaka-Gouni et al. 2007). Although toxic and non-toxic strains usually co-exist in a water body, distinguishing toxic strains from non-toxic strains is impossible under a microscope. Therefore, many studies have focused on the discriminative detection of toxin-producing strains (Baker et al. 2001; Via-Ordorika et al. 2004; Ouahid et al. 2005). Researchers have already described the MC-producing mechanism on the genetic level (Dittmann et al. 1997; Tillett et al. 2000). MC are produced by the enzyme complex MC synthetase encoded in the *mcy* gene cluster, which code for both non-ribosomal peptide synthetases (PSs) and polyketide synthases (PKSs) (Dittmann et al. 2001). *Microcystis mcy* genes are organized in a cluster of two operons. One operon contains PS genes (*mcyA*, *mcyB*, *mcyC*), responsible for the incorporation and activation of the amino acid [MDha-Ala-X-MAsp-Z] constituents of MC. The second operon includes one PKS gene (*mcyD*), two hybrid genes corresponding to PS and PKS (*mcyE* and *mcyG*), and additional genes (Nishizawa et al. 2000). *McyD*, *-G* and *-E* genes code for the Adda group synthesis. The association of glutamic acid with the Adda group and its activation are encoded by the *mcyE* gene (Sivonen & Börner 2008). Kellmann & Neilan (2007) have proposed the saxitoxin (STX) biosynthesis pathway. The *sxt* gene clusters within each organism all contain a core set of genes putatively responsible for the biosynthesis of STX. The production cylindrospermopsin (CYN) implicates enzymes coded by the PS and the PKS genes. Schembri et al. (2001) described a novel amidinotransferase (AMT) gene within the genomic region encoding PS and PKS. Fergusson & Saint (2003) developed a multiplex-polymerase chain reaction (PCR) test to amplify PS and PKS determinants associated with CYN production and to distinguish *Cylindrospermopsis raciborskii* strains from other CYN-producing cyanobacteria. The discovery of these genes will allow the rapid and accurate detection of harmful paralytic shellfish poisoning (PSP)-producing species in water (Kellmann et al. 2008).

TUNISIAN CONTEXT

Tunisia is a Mediterranean country located in the northeastern extremity of Africa. With Sicily, it defines both eastern and western basins of the Mediterranean. It covers an area of 164,150 km². Being under the disruptive climatic influence of the temperate region in the north and the Saharan region in the south, Tunisia is characterized by relative aridity on the major part of its territory. Indeed, two-thirds of the country receives rainfall amounts between 50 and 350 mm/year (Ben Boubaker *et al.* 2003). To this aridity is added the variability of the Mediterranean climate, with erratic and unpredictable periods of drought and violent floods, to make water an often limited resource and distributed unequally in time and space (Benzarti 2003). Bergaoui & Louati (2010) showed the temperature increase with an inflow reduction even for relatively wet hydrological years. Tunisia's hydric potential, mainly formed by surface water, is very modest. It was estimated at 4,630 thousand million m³. It is the lowest value of the Maghreb countries (Ben Boubaker *et al.* 2003). In fact, the important evaporation which is the cause of the climatic water balance to be in deficit, and the reduced size of the catchment areas make Tunisia one of the Mediterranean countries less endowed with hydraulic resources. The water resource volume available per capita is 450 m³/year against 556 m³/year in Morocco, 776 m³/year in Syria and 2,200 m³/year in Turkey (Cherif 2003).

Tunisia's freshwater resources are under increasing stress from a growing population and an expanding economy. In addition, almost all of the country's freshwater resources have been fully allocated, while the water quality of these resources has declined due to increased pollution caused by industry, urbanization and agriculture. The reservoirs have become progressively more enriched during recent decades. The importance and current extent of eutrophication in Tunisian water bodies has been highlighted in previous studies, showing that these ecosystems present an increasing productivity stimulated continually by fertilizing contributions owing to the important anthropisation and the drier climate (Mouelhi 2000; Turki 2002; Fathalli *et al.* 2006; El Herry *et al.* 2008a). Eutrophication is generally indicated by high values of nutrients, accumulation of metabolic

products (e.g., hydrogen sulfide in deep waters), discoloration or turbidity of water (resulting in low or poor light penetration), deterioration in the taste of water, depletion of dissolved oxygen and an enhanced occurrence of toxic cyanobacterial bloom-forming species (Dauta & Feuillade 1995). However, in spite of its great environmental and sanitary importance, the biodiversity of cyanobacteria is little known in Tunisia as a consequence of a small number of publications. In fact, the first reference to Tunisian freshwater toxic cyanobacteria was published only in 2006 (Ben Rejeb Jenhani *et al.* 2006).

In this review, we report the available information on the presence of potentially toxic cyanobacteria in Tunisian water storage reservoirs that have already been subject of limnological studies.

OCCURRENCE OF POTENTIALLY TOXIC CYANOBACTERIA IN TUNISIAN FRESHWATER

Data were obtained from scientific articles, reports, theses and communications at congresses. The water bodies are located in the four most important Tunisian hydrological basins (Figure 1, Table 1).

Investigations conducted in Tunisian reservoirs revealed the presence of 55 species of cyanobacteria belonging mainly to filamentous strains. In fact, these species are represented by 34 Oscillatoriales, 16 Chroococcales, three Nostocales and two Pleurocapsales. Some of them have been described in the literature as potentially toxic (Table 2). The identification of the majority raw cyanobacterial samples was performed using UTERMÖHL technique based on classic inverted microscopy. However, some of them are confirmed by molecular biology tools using isolated and cultured strains (El Herry *et al.* 2008a; 2008b; Fathalli *et al.* 2010, 2011a, 2011b). In fact, molecular taxonomy proved necessary in order to avoid confusion between morphologically similar species.

Microcystis, one of the most widely distributed toxic bloom-forming cyanobacteria genera, was observed in 58% of studied Tunisian reservoirs. It was represented by *Microcystis wesenbergii*, found only in the Lebna dam, and *Microcystis aeruginosa* recorded in different water bodies from different geographic situations across the country (Figure 2) (El

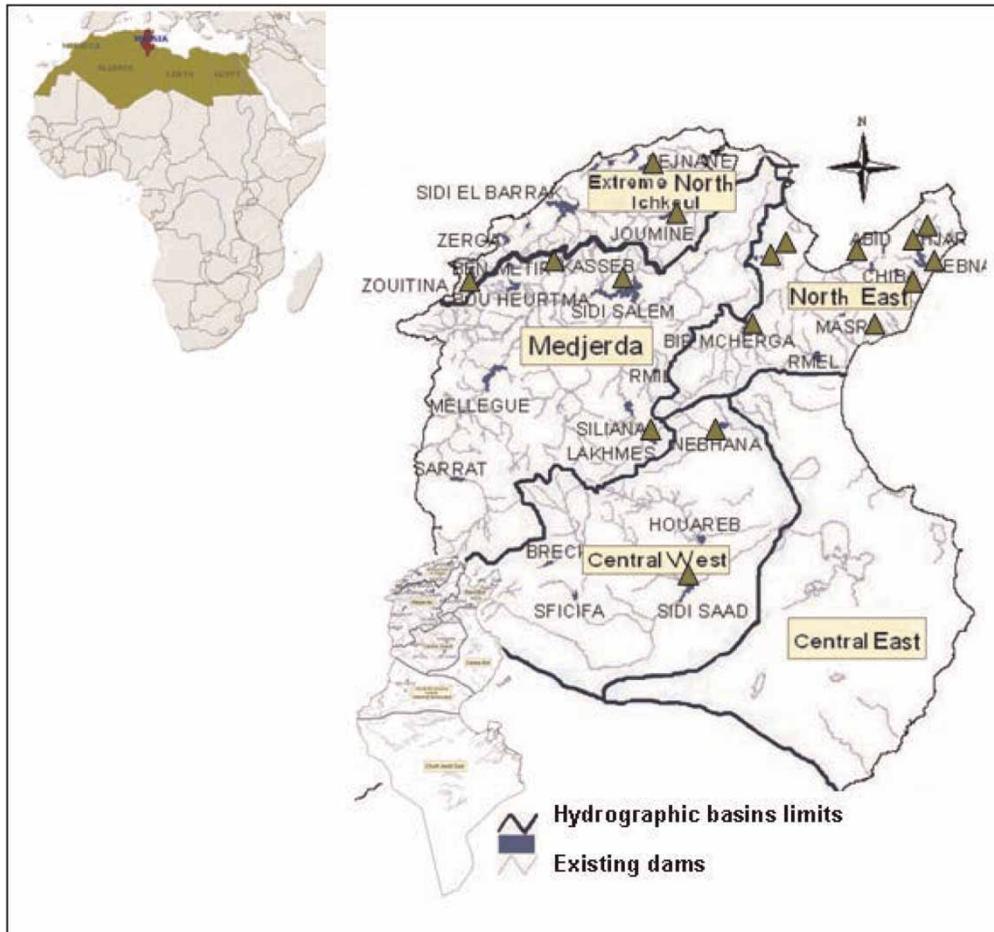


Figure 1 | Tunisian hydrological basins and the location of major dams (Ben Mammou and Louati 2007).

Herry et al. 2008a; Fathalli et al., 2011a; Sellami et al. 2012). This latter species was the most incriminated cyanobacterium in incidents of human and animal poisoning over the world by production of the hepatotoxins MC that present over 70 natural structural variants, and are potent and specific inhibitors of protein phosphatases (Chorus & Bartram 1999; Codd et al. 2005). Based on morphological criteria, 10 species have been distinguished in Europe, the other side of the Mediterranean: *Microcystis aeruginosa*, *M. viridis*, *M. wesenbergii*, *M. novacekii*, *M. ichthyoblabe*, *M. flos-aquae*, *M. natans*, *M. firma*, *M. smithii* and *M. botrys* (Komárek & Anagnostidis 1999). In North African freshwater bodies, four species are found: *Microcystis aeruginosa*, *M. wesenbergii*, *M. ichthyoblabe* and *M. novacekii* (Abdel-Rahman et al. 1993; Oudra et al. 2001; Oudra et al. 2002; Nasri et al. 2004; Ben Rejeb Jenhani et al. 2006; El Herry et al. 2009).

The invasive potentially toxic freshwater cyanobacterium *Cylindrospermopsis raciborskii*, which was firstly recorded in tropical to subtropical climate regions, was reported for the first time in Tunisia in October 2004 (Fathalli et al. 2010). It was observed in freshwater Bir M'cherga reservoir as pale blue-green, straight trichomes without mucilaginous sheaths, bearing terminal drop-shaped heterocysts with pointed ends. Coiled trichomes were never observed in Tunisian freshwater. This species was observed, later, in Nebhana and Sidi Saâd reservoirs, located in the center of the country (Fathalli et al., 2011a). These reservoirs are characterized by relatively high trophic levels (Fathalli et al. 2010; Sellami et al. 2010, 2012) and their environmental conditions seemed to be favorable for the species appearance. Fathalli et al. (2010) showed that the *Cylindrospermopsis* density was correlated positively with

Table 1 | Characteristics and uses of some water bodies in Tunisia

Dams	Geographic coordinates	Impoundment	Main supply	catchment area (Km ²)	Volume (10 ⁶ m ³)	Area (Ha)	Min-max or means			Uses
							T (°C)	NO ₃ ⁻ (mg/l)	PO ₄ ³⁻ (mg/l)	
S	N37° 10' 42" E09° 28' 25"	1994	Séjnène river	376	138	790	18.56	2.25 – 5.,88	-	Drinking water; irrigation; fish farming
J	N36° 59' 23" E09° 36' 59"	1983	Joumine river	418	130	660	19.3	2.52 – 5.34	0.01 – 0.29	
H	N36° 52' E11° 02'	1996	El Hjar river	61	5	254	12.3–28.8	7.05	0.031	Irrigation
B	N 36° 43' 16" E 10° 37' 57"	1959	Bezirk river	84	6.5	102	13.2–31.2	3.02–8.24	0.00–0.08	
MI	N 36° 49' 27" N10° 59' 26"	1965	Mlaabi river	35	3.7		13.2–29.4	0.42–4.23	0.00–0.09	
Ch	N 36° 41' 52" E 10° 46' 17"	1963	Chiba river	63	6.9	66	12.3–28.3	1.35–6.86	0.00–0.08	
M	N 36° 31' 50" E 10° 29' 08"	1968	Masri river	53	6.9	66	12.1–30	2.35–9.60	0.00–0.07	Drinking water; irrigation
BMt	N 36° 43' 10" E 08° 44' 10"	1953	El lil river	103	57.6	310.6	-	-	-	Drinking water irrigation; fish farming
K	N 36° 45' 30" E 09° 00' 50"	1968	Kasseb river	101	81	437	21,4	2,22	0,02	Drinking water irrigation; fish farming electric energy
SSM	N36° 35' 27" E 09° 23' 51"	1981	Medjerda river	18,000	555	4,300	10.2 – 27.4	0.12 – 2.88	0.001 – 0.056	
GG	N 36° 44' E 09° 58' 50"	1968	Kasseb reservoir Medjerda/Cap Bon channel	-	3	40	12.5–29.5	0.35–5.96	0.005–0.042	Drinking water
Mo	N 36° 44' E 09° 58' 50"	1982	Kasseb reservoir Medjerda/Cap Bon channel	-	15	150	12.5–29.5	0.22–6.35	0.00–0.035	
L	N36° 44' 01" E10° 55' 08"	1986	Lebna river	189	30.2	650	19,7	0.72	0.09	Irrigation; fish farming
LK	N 35° 59' 58" E 09° 28' 31"	1966	Lakhmess river	127	8	102	-	-	-	
BM	N36° 30' 36" E10° 00' 38"	1971	Méliane river	1,260	209	2,000	20.3	1.69	0.16	
N	N36° 03' 34" E09° 52' 34"	1965	Nebhana river	855	87.2	532	22.04	2.34	0.09	
SS	N35° 25' 31" E09° 41' 50"	1981	Zeroud river	8,950	53	110	8.7 – 29	0.04 – 0.43	0.03	

S: Séjnène; J: Joumine ; H: Hjar; L: Lebna; B: Bezirk ; M: Masri; MI: Mlaabi; Ch: Chiba; BMt: Beni Mtir; K: Kasseb; SSM: Sidi Salem; GG: Gdir el golla; Mo: Mornaguia; LK: Lakhmess; BM: Bir M'cherga; NB: Nebhana; SS: Sidi Saâ.

temperature, transparency and salinity. In fact, the occurrence of *C. raciborskii* was recorded in summer when the temperature values were higher than 20 °C. This confirms previous observations (Padisák 1997; Briand et al. 2002) showing that a water temperature ranging between 22 and

23.5 °C is a key factor for the germination of akinetes. The presence of this species during this period was also supported by the decrease of nitrate values (Fathalli et al. 2010). The same result was found by Briand et al. (2002), who observed a low nitrate concentration during the

Table 2 | Inventory cyanobacteria species in Tunisian reservoirs

Order	Species	S	J	H	L	B	M	MI	Ch	BMt	K	SSM	GG	Mo	LK	BM	NB	SS
Chroococcales	<i>Aphanothece c.v. brevis</i>											X						
	<i>Merismopedia glauca</i>	X	X	X	X	X	X	X	X					X				
	<i>Merismopedia elegans</i>										X	X		X				
	<i>Merismopedia miniata</i>											X						
	<i>Merismopedia sp.</i>															X		
	<i>Microcytis aeruginasa</i>	X●	X●	X●	X●						X		X		X	X●	X●	X
	<i>Microcytis wesenbergii</i>				X●													
	<i>Chroococcus sp.</i>			X	X	X	X	X	X							X	X	X
	<i>Chroococcus minutus</i>												X					
	<i>Chroococcus turgidus</i>					X												
	<i>Aphanothece sp.</i>												X					
	<i>Aphanocapsa muscicola</i>												X					
	<i>Snowella sp.</i>					X												
	<i>Snowella atomus</i>					X												
	<i>Synechococcus elongatus</i>											X				X		
	<i>Synechocystis aqualis</i>					X												
Nostocales	<i>Anabaena sp.</i>			X	X			X				X						X
	<i>Aphanizomenon sp.</i>															X		
	<i>Cylindrospermopsis raciborskii</i>															X●	X●	X●
Oscillatoriales	<i>Borzia trilocularis</i>				X			X			X							
	<i>Limnothrix sp.</i>															X●		
	<i>Limnothrix redekei</i>																	X●
	<i>Leptolyngbya sp.</i>																X●	
	<i>Lyngbya sp.</i>										X	X				X		
	<i>Lyngbya limnetica</i>												X	X				
	<i>Lyngbya rubida</i>										X							
	<i>Oscillatoria acutissima</i>													X				
	<i>Oscillatoria amphibia</i>													X				
	<i>Oscillatoria articulata</i>	X	X															
	<i>Oscillatoria chlorina</i>	X			X			X				X	X	X		X		
	<i>Oscillatoria geminata</i>											X						
	<i>Oscillatoria homogenea</i>	X	X								X					X	X	X
	<i>Oscillatoria lacustris</i>										X	X				X		X
	<i>Oscillatoria limnetica</i>	X	X		X													
	<i>Oscillatoria planctonica</i>	X		X	X		X	X				X				X		X
	<i>Oscillatoria pseudogeminata</i>										X					X		
	<i>Oscillatoria simplissima</i>				X													
	<i>Oscillatoria splendida</i>												X	X				
<i>Oscillatoria spp.</i>	X	X	X	X	X	X	X	X	X		X	X		X	X	X		
<i>Oscillatoria tenuis</i>				X●							X	X			X			
<i>Phormidium cf. incrustatum</i>											X			X				

(continued)

Table 2 | continued

Order	Species	S	J	H	L	B	M	MI	Ch	BMT	K	SSM	GG	Mo	LK	BM	NB	SS
	<i>Phormidium frigidum</i>													X				
	<i>Phormidium luridum</i>												X	X				
	<i>Phormidium olivascens</i>												X	X				
	<i>Phormidium rezii</i>												X	X				
	<i>Phormidium</i> sp.	X			X						X		X	X				
	<i>Phormidium tenue</i>												X	X				
	<i>Planktolyngbya subtilis</i>													X				X
	<i>Planktothrix agardhii</i>		●													●	●	X
	<i>Planktothrix mougeotii</i>															●	●	X
	<i>Pseudanabaena catenata</i>				X	X		X			X	X	X	X		X		X
	<i>Pseudanabaena constricta</i>	X			X						X	X	X	X		X		X
	<i>Romaria</i> sp.																	X
Pleurocapsales	<i>Hydrococcus</i> sp.																	
	<i>Hydrococcus rivularis</i>				X						X							

x: species identified by the classical method of inverted microscopy; ●: species confirmed by the molecular biology tools.

S: Sejhène; J: Joumine; H: Hjar; L: Lebna; B: Bezirk; M: Masri; MI: Mlaabir; Ch: Chloa; BMT: Beni Mtir; K: Kasseb; SSM: Sidi Salem; GG: Gdir el golla; Mo: Mornaguia; LK: Lakmess; BM: Bir M'cherga; NB: Nebhana; SS: Sidi Saâd. List established from following references (Ben Rejeb Jenhani et al. 2006; Fathalli et al. 2006; INSTM 2006; Romdhane et al. 2006; El Herry et al. 2008a; Fathalli et al. 2011a; Fathalli 2012; Sellami et al. 2012).

summer proliferation. Chorus & Bartram (1999) reported that the lack of nitrate was considered to be the main reason for the proliferation of heterocystic species, such as *C. raciborskii*.

Hepatotoxin-producing strains of *C. raciborskii* have been found in Europe, Australia, Asia and Africa (Hawkins et al. 1997; Saker et al. 1999, 2003; Li et al. 2001; Fastner et al. 2003; Bernard et al. 2003; Mohamed 2007), while neurotoxin-producing strains have been reported in Brazil, where it produced PSP toxin (Lagos et al. 1999). Incidents where *C. raciborskii* has been suspected to cause human sickness (Bourke et al. 1983; Hawkins et al. 1985) and cattle mortality (Saker et al. 1999) have been restricted to Australia. This toxic effect is now known to be due to the alkaloid CYN (Terao et al. 1994).

In Africa, the occurrence of *C. raciborskii* has also been recorded in Algeria, Egypt, Uganda, Senegal and South Africa (Bouaïcha & Nasri 2004; Mohamed 2007; Haande et al. 2008; Janse van Vuuren & Kriel 2008). From all these strains, only the Egyptian one was reported as hepatotoxic by the mouse bioassay (Mohamed 2007). *C. raciborskii* has been observed in other Mediterranean countries, including Spain, France, Italy, Greece and Israel (Romo & Miracle 1994; Bernard et al. 2003; Vardaka et al. 2005; Moustaka-Gouni et al. 2007; Messineo et al. 2010; Alster et al. 2010).

Planktothrix, considered to be an important genus of harmful cyanobacteria since it is one of the most frequent MC producers (Kurmayer et al. 2005), was represented in Tunisian freshwater by the green-pigmented species *P. agardhii*. This genus may contain a higher concentration of MC per cell than *Microcystis*. So, the risk level is uppermost when *Planktothrix* is dominant (Codd et al. 2005). The species *P. agardhii* was recorded at four different reservoirs (Joumine, Bir m'cherga, Nebhana and Sidi Saâd). Fathalli (2012) reports that, from 1 year to another, there is a considerable development increase of the species. Indeed the average density, in Bir M'cherga dam, changes from 0.017×10^6 filaments/l in 2005 to 0.5×10^6 filaments/l in 2006. Moreover, the same author notes a very high density of *P. agardhii* at the beginning of 2007 reaching 6.69×10^6 filaments/l. The species *P. agardhii* has generally presented a relatively homogeneous vertical distribution. It is endowed with dispersed development ecostrategy (Chorus & Bartram 1999). Despite its preference for warm waters (Berger &

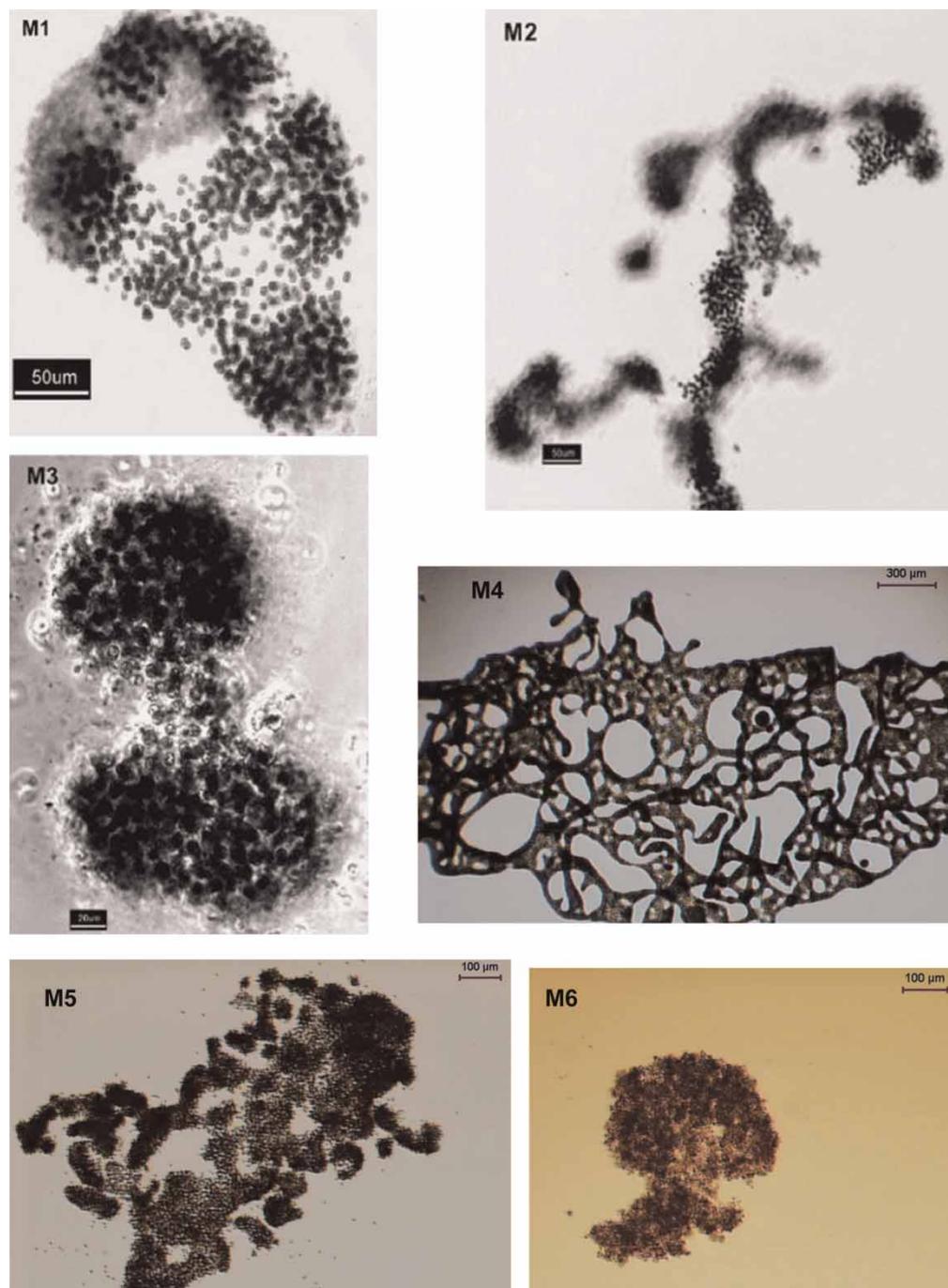


Figure 2 | Toxic strains of *Microcystis* observed in Tunisian freshwater (El Herry et al. 2008a; Fathalli 2012). M1, M2: *M. aeruginosa* occurred in Lebna reservoir; M3: *M. wesenbergii* occurred in Lebna reservoir; Micro-NB-01: *M. aeruginosa* isolated from Nabhena reservoir; Micro-JM-02: *M. aeruginosa* isolated from Joumine reservoir; Micro-HJ-02: *M. aeruginosa* isolated from Hjar reservoir.

Sweers 1988), this species can occur in high densities throughout the year thanks to its tolerance for low temperatures and low light intensities (Dokulil & Teubner 2000;

Scheffer, 1998). Thus, a competitive advantage is expressed in taxa that tolerate low light intensities, i.e., *Planktothrix*, *Cylindrospermopsis raciborskii* and *Limnothrix*, which

thrive better than the species susceptible to loss of light, i.e., *Anabaena* spp. and *Aphanizomenon* spp. (Reynolds et al. 2002). In fact, an assemblage of these three filamentous cyanobacteria (Figure 3) (*Planktothrix agardhii*, *Cylindrospermopsis raciborskii* and *Limnothrix* sp.) was reported in the freshwater Bir M'cherga dam (Fathalli 2012).

The filamentous cyanobacteria dominance is increasingly reported in Tunisia in eutrophic water bodies such as Sidi Saâd (Sellami et al. 2012) and Bir M'cherga dams (Fathalli et al. 2010). This dominance increases especially during the summer–autumn period. Indeed, Fathalli (2012) showed the persistence of high cyanobacteria density in freshwater Bir M'cherga reservoir throughout the year. Upper densities of 6.14×10^6 and 9.58×10^6 individuals

per liter were recorded during July 2005 and 2006, respectively. Recently, potentially toxic cyanobacteria blooms have been reported in some reservoirs in the north (Hjar and Lebna dams). These blooms were generated by the potentially toxic Chroococcale *Microcystis aeruginosa* (Ben Rejeb Jenhani et al. 2010). Oudra et al. (2001), Sabour et al. (2002), Nasri et al. (2004, 2008) and Douma et al. (2010) showed that in Morocco and in Algeria, a neighboring country with close climatic conditions, natural cyanobacterial blooms containing MC were dominated by the genus *Microcystis*. Thus, harmful cyanobacteria tend to spatio-temporal expansion in the Tunisian inland waters. They are consequently considered as precursors of freshwater-quality degradation.

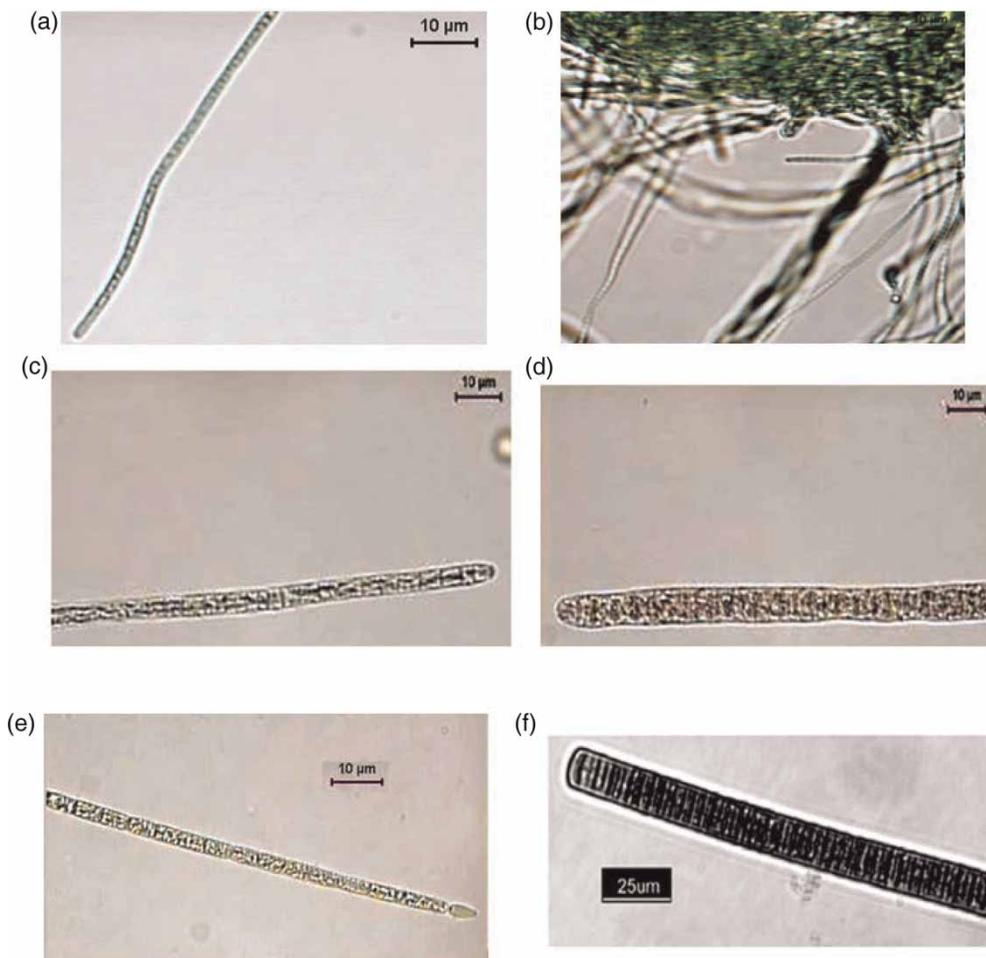


Figure 3 | Some filamentous cyanobacteria strains observed in Tunisian freshwater (El Herry et al. 2008a; Fathalli 2012). (a): *Limnothrix* sp. isolated from Bir M'cherga reservoir; (b): *Leptolyngbya* sp. isolated from Nabhena reservoir; (c): *Planktothrix agardhii* isolated from Bir M'cherga reservoir; (d): *P. agardhii* isolated from Joumine reservoir; (e): *Cylindrospermopsis raciborskii* isolated from Bir M'cherga reservoir; (f): *Oscillatoria tenuis* occurred in Lebna reservoir.

OCCURRENCE OF CYANOBACTERIAL TOXINS IN TUNISIAN FRESHWATER

While the occurrence of cyanotoxins was reported worldwide since the beginning of the last century (Sivonen & Jones 1999), in Tunisian freshwater, their presence has been confirmed only in 2003, from Hjar Reservoir in the Cap Bon region, North-East of the country, using high performance liquid chromatography coupled to a diode array detector and tandem mass spectrometry technique that revealed three variants of the hepatotoxins MC: MC-LR, MC-RR, MC-YR (El Herry et al. 2007). The cyanotoxicity monitoring of the Tunisian freshwater was performed mainly using the protein phosphatase (PP2A) inhibition assay (Table 3). Ben Rejeb Jenhani et al. (2006) demonstrated that, compared to other untreated water, those of Hjar, Mlaabi and Lebna dams are distinguished by their higher levels of toxins, often observed in the particulate fraction. The same authors report that the maxima observed in these water bodies have coincided with a relatively massive development of *Oscillatoria* and *Pseudoanabaena* genera in the Hjar dam and the species *Oscillatoria chlorina* in Mlaabi freshwater. El Herry et al. (2008a) noted that toxin concentrations reached a value of 5.57 µg MC-LR equivalent per liter in the Lebna reservoir suggesting that the three morphospecies of *Microcystis* and the filamentous species *O. tenuis* that occurred in this dam are potentially toxigenic. In this water body two variants of MC (MC-LR and MC-YR), were

Table 3 | Extreme values of cyanotoxins concentrations in Tunisian freshwaters (using PP2A inhibition assay)

	Total cyanotoxins (µg MC-LR equivalent L ⁻¹)	References
Ghdir el Golla	0.001–0.028	Ben Rejeb Jenhani et al. (2006)
Mornaguia	0–0.024	
Sejnene	0.001–0.837	
Joumine	0.001–0.168	
Hjar	0.023–7.455	
Bezirk	0.011–0.500	
Masri	0.032–0.752	
Mlaabi	0.010–1.040	
Chiba	0.003–0.495	
Kasseb	0–0.034	Fathalli et al. (2006)
Lebna	0.021–5.485	El Herry et al. (2008a)
Bir M'cherga	0.002–0.931	Fathalli et al. (2010)

identified. This finding is certainly consistent with prior studies from Mediterranean countries, which have shown that MC-LR is the major toxin in cyanobacterial blooms from France (Vezie et al. 1998), and Morocco (Oudra et al. 2002) and frequently co-occurs with MC-YR and/or MC-RR in Morocco (Oudra et al. 2001), in Algeria (Nasri et al. 2004; 2008), and in Turkey (Albay et al. 2005). The cyanotoxins concentrations detected in the three above-mentioned dams, used mainly for irrigation, was higher than the guideline value for MC-LR (1 µg L⁻¹) established by the WHO (1998) for drinking water. However, they remain lower than those found in Algeria (Nasri et al. 2004) and in Morocco (Oudra et al. 2001), where the MC concentrations were estimated to be 29,163 µg MC-LR equivalent L⁻¹ and >500 µg MC-LR equivalent L⁻¹. Saqrane & Oudra (2009) reported that cyanotoxicity impact on both aquatic and terrestrial crop plants irrigated by water containing these toxins has become more and more available. This fact is gaining importance since plants could in a direct or indirect manner contribute to cyanotoxin transfer through the trophic network, and thus constitutes a potent health risk source. The use of this contaminated irrigation water can also have an economic impact which appears as a reduction in the germination rate of seeds, and alteration of the quality and the productivity of crop plants (Silva & Vasconcelos 2010).

The Tunisian freshwaters studied were classified according to three levels of toxicity: <0.1 µg MC-LR equivalent L⁻¹, 0.1–1 µg MC-LR equivalent L⁻¹ and >1 µg MC-LR equivalent L⁻¹. All Tunisian reservoirs used for drinking water production have been characterized by toxicity values less than 1 µg MC-LR equivalent L⁻¹ (Ben Rejeb Jenhani et al. 2006). The highest values of toxicity were recorded at dams situated in the north-east hydrologic basin characterized by high anthropogenic activity. In fact, this region which represents 8.5% of the whole area of Tunisia, concentrates paradoxically 45% of urban population, 49% of industrial employment, 36% of tourism capacity and 30% of irrigable surface (Cherif 2003).

GENOMIC POTENTIALITY OF CYANOTOXINS SYNTHESIS

The cyanotoxins have been reported in almost the whole regions where cyanobacteria were studied, thus making the cyanotoxicose a public health problem of global

concern. Cyanobacterial toxins are usually classified according to their mode of action, into hepatotoxins (MC, nodularins and cylindrospermopsins), neurotoxins such as the STXs, and dermatotoxins which is characterized by their lipopolysaccharide nature (Chorus & Bartram 1999). The toxic and non-toxic character of the same species may vary between different strains (Carmichael 1992). Recent development of techniques in biotechnology has enabled the development of new methods of molecular detection of cyanobacteria and their toxins. Detection methods based on PCR amplification of DNA of Cyanobacteria are interesting because of their potential selectivity with respect to genes involved in the biosynthesis of toxins, their sensitivity and timeliness (Ouellette & Wilhelm 2003). In Tunisia, few studies have been conducted on the biodiversity of cyanobacteria and their molecular characterizations (Table 4). El Herry et al. (2008a) showed the expression of the NMT domain of the MC synthetase genes *mcyA*, *-B* and *-C* in the genome of three morphospecies of *Microcystis* and the filamentous species *Oscillatoria tenuis* collected from the natural samples of Lebna reservoir. The authors indicated that these cyanobacterial species were responsible for MC production in this dam. They confirmed this result through the detection of MC-LR and MC-YR, in the cyanobacterial sample containing the three morphospecies of *Microcystis* and the filamentous species *O. tenuis*, via LC/MS/MS technique. Fathalli et al. (2011a) evaluated, also by molecular biology tools, the toxicological potential of 27 cyanobacterial strains isolated from seven reservoirs located in the north and center of Tunisia and belonged mainly to *Microcystis aeruginosa*, *Cylindrospermopsis raciborskii* and *Planktothrix agardhii* species. This study showed that none of the isolated strains carried segments of the gene cluster responsible for the production of cylindrospermopsin and STX, while the majority of *Microcystis* isolates were able to synthesize MC, since they presented the six characteristic segments of the MC synthetase *mcy* cluster (*mcyA*, *-B*, *-C*, *-D*, *-E* and *-G*). This was further confirmed by MALDI-TOF analysis that showed the presence of eight MC variants, including MC-LR. *Microcystis* strains isolated from Lebna (Micro-LB-01) and Bir M'cherga (Micro-BM-02) reservoirs did not produce any kind of MC. In fact, these strains showed the absence of either the gene *mcyA* or *mcyA*, *-C*, *-D* and *-E*. In another study, Fathalli et al. (2011b) assessed the

toxicity of four *C. raciborskii* strains isolated from the Bir M'cherga Tunisian reservoir. They concluded that all the isolated strains were not producing cylindrospermopsin, STX or MC. This result was further confirmed by HPLC and MALDI-TOF analyses. However, these authors reported for the first time in *C. raciborskii* the presence of *mcy A* and *mcy E*, two segments of the MC synthetase *mcy* cluster in the strain Cyl-BM-07. The strain *C. raciborskii* (MG) that was confirmed not producing cylindrospermopsin present only the PKS gene (Fathalli et al. 2010). Schembri et al. (2001) confirmed that both the PS and the PKS genes were associated with the ability to produce cylindrospermopsins.

PHYLOGENY

As previously reported in the literature, the research performed on the phylogeny of Tunisian cyanobacteria strains confirmed that the 16S rRNA, which is commonly used to distinguish broad phylogenetic relationships among cyanobacteria because of availability of many sequences of this gene for different species of cyanobacteria, may not fully discriminate closely related species even when they are morphologically distinct. In fact, the phylogenetic tree based on 16S rDNA sequences showed that three morphospecies of *Microcystis*, isolated from Lebna reservoir and assigned to *Microcystis aeruginosa* and *Microcystis wesenbergii*, are indistinguishable from each other, from the reference strain PCC 7806 and from many other known *Microcystis* species and, therefore, this tree did not necessarily correlate to the distinctions between morphospecies (El Herry et al. 2008b). To elucidate the phylogenetic relationships of these strains, El Herry et al. (2008b) used the PCR amplification and restriction fragment length polymorphism (RFLP) analysis of the 16S-23S rRNA spacer region (ITS) of these three morphospecies of *Microcystis*, that provided a similar pattern type for the whole strains. However, it was shown that this region is a good tool to discriminate bacteria strains at the species level and interspecific (Jensen et al. 1993; Neilan 1995). Phylogenetic study based on ITS sequences of *Microcystis aeruginosa* strains isolated from five Tunisian waters bodies with several other morphospecies listed in the NCBI database, revealed the existence of two clusters. The first one was formed by most of the Tunisian isolates that were

Table 4 | Toxicity assessment of cyanobacteria in Tunisian freshwater

Cyanobacteria	Origins	Samples	Tested genes number ^a	Expressed genes (PCR+ sequencing)	Toxins	Methods	references
<i>Oscillatoria</i> spp. + <i>Pseudoanabaena</i> spp.	Hjar	natural			MC-LR, MC-RR, MC-YR	HPLC/MS/MS	El Herry <i>et al.</i> (2007)
<i>Microcystis aeruginosa</i>	Lebna	natural	3	<i>mcyA</i> , -B and -C	MC	PP2A	El Herry <i>et al.</i> (2008b)
<i>Microcystis aeruginosa</i>	Lebna	Culture	11	<i>mcyB</i> , -C, -D, -E and -G	No toxins	MALDI-TOFMS	Fathalli <i>et al.</i> (2011a), Fathalli (2012)
<i>Microcystis aeruginosa</i>	Bir M'cherga	Culture	11	<i>mcy B</i> and -G	No toxins	MALDI-TOFMS	Fathalli <i>et al.</i> (2011a), Fathalli, (2012)
<i>Microcystis aeruginosa</i>	Hjar	Culture	11	<i>mcyA</i> , -B, -C, -D, -E and -G	MC-LR, MC-FR, MC-RR MC-WR, Demethyl-MC-LR	MALDI-TOFMS	Fathalli <i>et al.</i> (2011a), Fathalli (2012)
<i>Microcystis aeruginosa</i>	Nebhana	Culture	11	<i>mcyA</i> , -B, -C, -D, -E and -G	MC-LR, MC-YR	MALDI-TOFMS	Fathalli <i>et al.</i> (2011a), Fathalli (2012)
<i>Microcystis aeruginosa</i>	Joumine	Culture	11	<i>mcyA</i> , -B, -C, -D, -E and -G	MC-LR, MC-YR, Demethyl-MC-LR, Demethyl-MC-YR	MALDI-TOFMS	Fathalli <i>et al.</i> (2011a), Fathalli (2012)
<i>Microcystis aeruginosa</i>	Séjnène	Culture	11	<i>mcyA</i> , -B, -C, -D, -E and -G	MC-LR, MC-RR, MC-YR, Demethyl-MC-LR, Demethyl-MC-RR, Demethyl-MC-YR	MALDI-TOFMS	Fathalli <i>et al.</i> (2011a), Fathalli (2012)
<i>Microcystis wesenbergii</i> .	Lebna	Natural	3	<i>mcyA</i> , -B and -C	MC	PP2A	El Herry <i>et al.</i> (2008b)
<i>Oscillatoria tenuis</i>	Lebna	Natural	3	<i>mcyA</i> , -B and -C	MC	PP2A	El Herry <i>et al.</i> (2008a)
<i>Planktothrix agardhii</i>	Joumine	Culture	11	<i>mcyA</i>	No toxins	MALDI-TOFMS	Fathalli <i>et al.</i> (2011a), Fathalli (2012)
<i>Leptolyngbya</i> sp.	Nebhana	Culture	11	<i>mcyA</i>	No toxins	MALDI-TOFMS	Fathalli <i>et al.</i> (2011a), Fathalli (2012)
<i>Cylindrospermopsis raciborskii</i>	Bir M'cherga	Culture	11	PKS (MG strain) <i>mcyA</i> and <i>mcyE</i> (CYL-BM-07 strain)	No toxins	Elisa , HPLC MALDI-TOFMS	Fathalli <i>et al.</i> (2010, 2011b); Fathalli (2012)

^aNumber of genes tested; 3: *mcyA*, -B and -C (NMT domain of the MC synthetase gene)

11: *mcyA*, -B, -C, -D, -E, -G (MC synthetase gene cluster); AMT (hepatotoxins); GAMT, PS, PKS (cylindrospermopsin synthase); sxt1 (STXs).

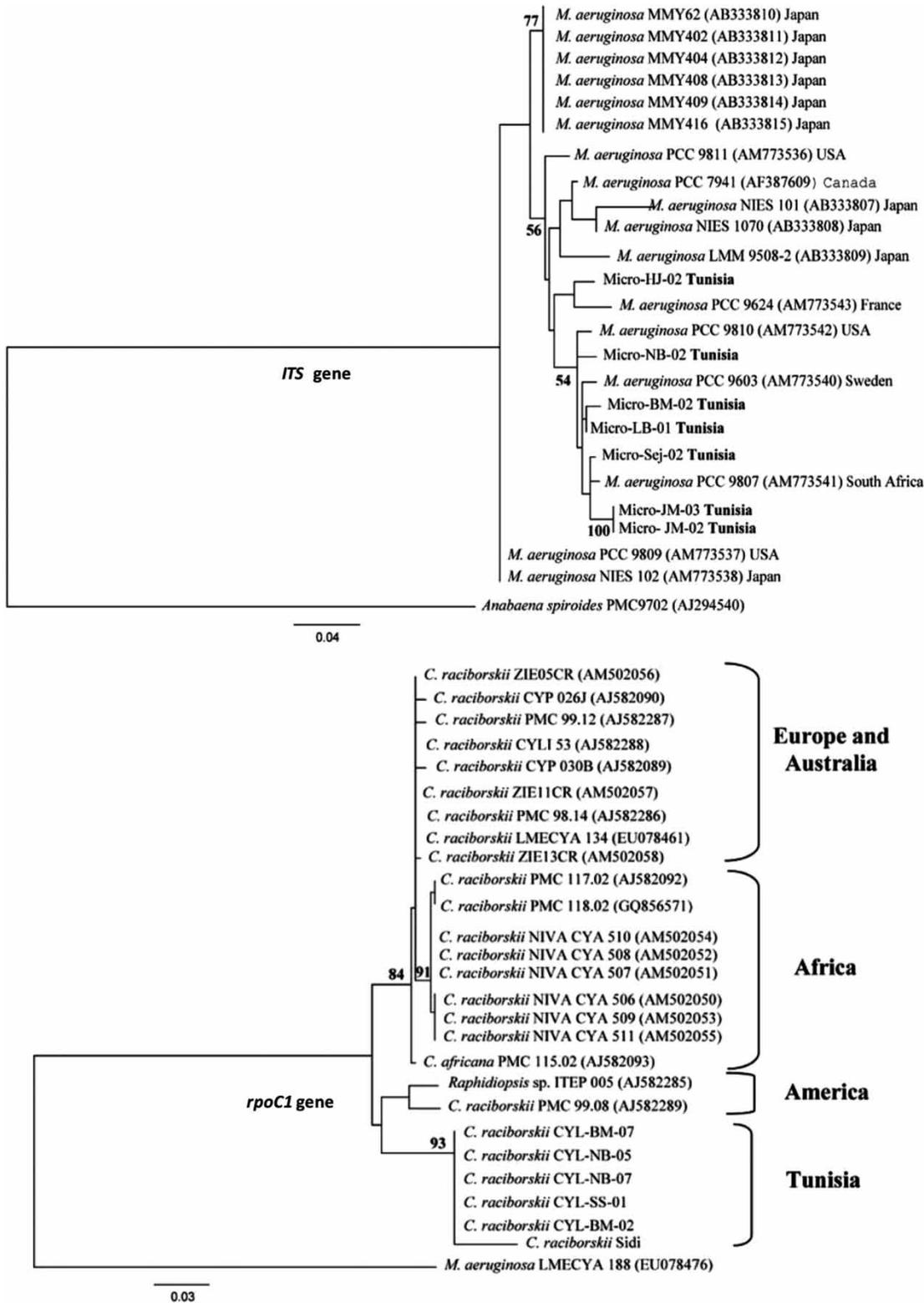


Figure 4 | Neighbour-joining phylogenetic trees based on ITS gene for *Microcystis aeruginosa* species and based on *rpoC1* gene for *Cylindrospermopsis raciborskii* species. Bootstrap values are placed at each branch point (Fathalli et al. 2011a).

highly similar to *M. aeruginosa* from the continents of Africa, Europe and America. The second one was composed of one toxic *Microcystis* strain that also clustered with European strains (Fathalli et al. 2011a). None of the Tunisian *M. aeruginosa* strains were similar to those found in Asia. No clustering was observed between the toxic and non-toxic *Microcystis* strains; although a well defined sub-group was formed by two non-toxic Tunisian *Microcystis* strains (Figure 4) (Fathalli et al. 2011a). Otsuka et al. (1999) reported that the same cluster included all the *Microcystis novacekii* and *M. ichthyoblabe* strains and most *M. aeruginosa* strains. These authors also noted that MC-synthesizing and non-producing genotypes were closely related. Tillett et al. (2001) confirmed that the analysis of the ITS region was not helpful in distinguishing between MC-producing and non-producing.

Tunisian isolates of *C. raciborskii* were highly similar to each other and they formed a distinct cluster based on *rpoC1* sequences, which was separate from other African strains collected in Senegal and Uganda. In fact, the phylogenetic tree based on *rpoC1* sequences separated our species from American, African and European/Australian clusters (Figure 4) (Fathalli et al. 2011a). The *rpoC1* gene was reported to be more discriminatory at the species level than the 16S rRNA, for this species (Wilson et al. 2000). This different clustering of the African strains demonstrates that the population structure in this continent is somewhat heterogeneous, supporting the uniqueness of the Tunisian isolates relative to *C. raciborskii* strains from other geographical locations (Fathalli et al. 2011b). Moreira et al. (2011) showed, based on a concatenated fragment of 2.9 Kb encompassing the four genetic markers 16S rRNA, ITS longer spacer, ITS shorter spacer and *rpoC1* sequences, that the Tunisian *C. raciborskii* strains were clustered with the American strain. In fact, this study revealed that the *C. raciborskii* strains grouped in to three well-supported distinct clusters: (i) European, (ii) African (Tunisian)/American (Brazilian) and (iii) Asian/Australian. This method provided a better phylogeographical distinction of the strains, with higher statistical significance than if considering the information of each gene alone. In fact, several authors attribute the recent dispersion of *C. raciborskii* to migration of water birds, like gulls, that carry these organisms in their intestinal tract or even owing to the importation of items from tropical countries that bring resistant cyanobacterial

cells that can later grow when suitable conditions are found (Manti et al. 2005; Vasconcelos 2006).

CONCLUSION

In Tunisia, the increase in cyanobacterial occurrence, observed in some water bodies, poses a potential risk to the environment and public health. *Microcystis*, one of the most widely distributed toxic bloom-forming cyanobacteria genera, was represented mainly by *Microcystis aeruginosa* recorded in different water bodies. The invasive potentially toxic cyanobacterium *Cylindrospermopsis raciborskii* was observed in the semi-arid to arid areas. The harmful genus *Planktothrix* was represented in Tunisian freshwater by the green-pigmented specie *P. agardhii*. The filamentous cyanobacteria dominance is increasingly reported in Tunisia in eutrophic water bodies. These cyanobacteria which synthesize secondary metabolites responsible for the deterioration of water quality and their uses did not form real blooms at all prospected water bodies, except for el Hjar and Lebna reservoirs. Thus, the question remains, 'How long will these environments still be safe?' knowing that neighboring countries (Morocco and Algeria) currently are faced with the complexity of this phenomenon.

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