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ABSTRACT

With the aim of explaining the variations in microcystin (MC) concentrations during cyanobacterial blooms, we studied several Microcystis aeruginosa populations blooming in different freshwater ecosystems located in the same geographical area. As assessed by real-time PCR, it appeared that the potentially MC-producing cells (mcyB+) were predominant (70 to 100%) in all of these M. aeruginosa populations, with the exception of one population in which non-MC-producing cells always dominated. Apart from the population in the Grangent Reservoir, we found that the proportions of potentially MC-producing and non-MC-producing cells varied little over time, which was consistent with the fact that according to a previous study of the same populations, the intergenic transcribed spacer (ITS) genotype composition did not change (38). In the Grangent Reservoir, the MC-RR variant was the dominant microcystin variant throughout the bloom season, despite changes in the ITS composition and in the proportions of mcyB+ cells. Finally, the variations in total MC concentrations (0.3 to 15 µg liter−1) and in the MC cellular quotas (0.01 to 3.4 pg cell−1) were high both between and within sites, and no correlation was found between the MC concentrations and the proportion of mcyB+ cells. All of these findings demonstrate that very different results can be found for the proportions of potentially MC-producing and non-MC-producing cells and MC concentrations, even in M. aeruginosa populations living in more or less connected ecosystems, demonstrating the importance of the effect of very local environmental conditions on these parameters and also the difficulty of predicting the potential toxicity of Microcystis blooms.

INTRODUCTION

Microcystins (MCs) are the most common cyanotoxins and have been involved in several animal and human poisoning episodes (8). These hepatotoxic cyclic heptapeptides are synthesized by a multifunctional enzyme complex (10, 40), and the discovery of the gene cluster encoding this complex has made it possible in recent years to develop molecular tools for studying the relative proportions of MC-producing and non-MC-producing cells in natural cyanobacterial populations. Potentially MC-producing and non-MC-producing cells can coexist in these populations, but the factors and processes governing the dynamics of these subpopulations remain unclear. Some recent papers on the Microcystis genus have shown that the proportions of potentially MC-producing cells can differ considerably from lake to lake. For example, in Lake Wannsee, Germany, this proportion was between 0 and 40% (28), as it was in Lake Oneida, United States (18), and in Lake Mikata, Japan (48). In contrast, large variations over time (6 to 93%) of potentially MC-producing cells were found in the Grangent Reservoir, France (4). Major variations (30 to 80%) were also found in a natural French population of Planktothrix agardhii (3), and the variations in the proportions of potentially MC-producing cells reflected those of the MC concentrations. However, only 54% of the variation in MC concentrations could be explained by changes in the proportion of MC-producing cells, suggesting that a considerable part of the MC concentrations was also due to variations in MC cell quotas. These findings suggest that the toxic risks during cyanobacterial proliferations are due to variations in both the proportion of MC-producing cells and the production of MC by the toxic cells.
Numerous papers have already investigated the impact of various biotic and abiotic environmental factors on microcystin production by toxic cells. These studies demonstrate that MC production can be influenced by temperature (35), light (46), nutrients such as nitrogen and phosphorus (12, 32), pH (39), iron (42), xenobiotics (17, 34, 45), and predators (22, 23, 47). Despite inconsistent results, the production of microcystins by the cells does seem to be linked to their growth rate (11, 31, 33), which is itself affected by environmental conditions. On the other hand, several studies of variations in the proportions of MC-producing cells have demonstrated the potential influence of nutrient concentrations (9, 48) and light and temperature (5), and two papers (3, 5) have suggested that there is a negative correlation between the proportions of MC-producing cells and the abundance of cyanobacterial cells. These findings are consistent with the data of Kardinaal and Visser (26), showing that in Dutch lakes there is a negative relationship between the densities of cyanobacterial cells and the mean MC concentration in the cells.

In an overall attempt to explain the variations of toxicity during cyanobacterial blooms, we studied the spatiotemporal variations in MC concentrations and in the proportions of MC-producing and non-MC-producing cells in several Microcystis aeruginosa populations blooming in different freshwater ecosystems located in the same geographical area. The point of this study was to analyze these variations in terms of the characteristics of these ecosystems and the population dynamics of the M. aeruginosa populations. In addition, these data were compared to the variations in the intergenic transcribed spacer (ITS) composition of the same populations recently reported by Sabart et al. (38). The proportion of potentially MC-producing cells was estimated by a real-time quantitative PCR approach, the change in threshold cycle (Ct) method recently developed by Briand et al. for Planktothrix (2) and Microcystis (4) and targeting the mcyB (mcyA for Planktothrix) and phycocyanin (PC) genes.

MATERIALS AND METHODS

Study sites, sampling, and counting of cyanobacterial abundances.
The study was conducted in 2006 at six sampling stations located in the catchment area of the river Loire in central France (Fig. 1). Four of the stations were located in the river Loire itself: one in the Grangent Reservoir (45°27N, 4°15E; area of 0.08 km², depth of 6 m, and volume of 13.6 million m³), one in the Villereyt Reservoir (45°55’N, 4°02’E; area of 7.12 km², depth of 34 m, and volume of 130 million m³) located 70 km downstream of Grangent, and another two located in the fluvial section between these two reservoirs (Cuzieu, 45°36’N, 4°14’E; and Feurs, 45°44’N, 4°12’E). In addition, two small ponds (Place Pond, 45°43’N, 4°14’E, area of 0.08 km², depth of 2.5 m, and volume of 0.13 x 10⁶ m³; and Sables Pond, 45°43’N, 4°14’E, area of 0.1 km², depth of 1.4 m, and volume of 0.145 x 10⁶ m³) dedicated to fish production and located close to the river (3 km) were also studied. Microcystis was the only MC-producing genus that was present at our study sites during our sampling period. Further biotic and abiotic parameters for these sites are given in Table 1.

The study sites were sampled twice a month between June and September 2006. Water samples (20 liters) were collected using an electric pump equipped with a 20-µm-pore mesh (29), from a depth of 0.5 m below the surface at all stations. For the Grangent Reservoir, the 0- to 10-m surface water layer was sampled in order to obtain a greater concentration of cyanobacteria for subsequent analysis. The Microcystis colonies obtained were then resuspended in 1 ml of distilled water and kept at –20°C until analyzed. The abundance of Microcystis cells in the samples was estimated by microscopical cell counts. One milliliter of each sample was fixed with 1% glutaraldehyde, and then the colonial structure of Microcystis was rapidly disrupted (<1 min) by ultrasonication (at 20 kHz) (36). Microcystis cells were counted in triplicate using a Thoma hemocytometer.

Microcystin analysis.
The intracellular microcystins were extracted twice by sonication in 75% methanol (MeOH). The lysate was centrifuged to remove cell debris, and the supernatant was filtered through a 0.2-µm-pore syringe filter to remove any remaining smaller particulates. The samples were evaporated using a concentrator (Concentratrator 5301; Eppendorf, Hamburg Germany), and the extracts obtained were dissolved in 100 µl 20% MeOH. Microcystin concentrations were determined by the protein phosphatase 2A (PP2A) inhibition bioassay developed by Rivasseau et al. (37). This assay is based on the degradation of paranitropheophosphylphosphate (pNPP;
colorless) into paranitrophenol (pNP; yellow) by the PP2A. This reaction is inhibited by microcystins. The activity of the PP2A was determined by measuring the color produced as a result of the formation of pNP from the substrate pNPP. The assay was carried out in triplicate in a 96-well microtiter plate. Controls (in which sample was replaced by MeOH), blanks (in which there was no sample), and sample blanks (in which all components were present except the enzyme) were also included in the assays. Methanolic samples of MC were diluted in 100 µl buffer B (40 mM Tris-HCl, 34 mM MgCl₂, 4 mM EDTA, 4 mM dithiothreitol, pH 8.3). 50 µl of buffer B containing 27 µM/ml PP2A, and 0.5 mg ml⁻¹ bovine serum albumin, and 50 µl of buffer B containing 28 mM pNPP was added to initiate the enzymatic reaction. After incubation for 60 min at 37°C, the absorbance was measured at 405 nm on a MultiSkän Ascent microplate-reader (Thermo, Vantaa, Finland). The toxin concentrations were calculated from a standard MC-LR calibration curve. The cellular quotas were expressed in picogram equivalents of MC-LR per cell, and the microcystin concentrations were expressed in microgram equivalents of MC-LR per liter of lake water.

In order to obtain further insight into the proportions of the specific congeners of microcystin present, selected samples were also analyzed by high-pressure liquid chromatography (HPLC)-mass spectrometry (MS). Liquid chromatography (LC)-MS measurements were performed using a micrOTOF electrospray ionization-time-of-flight (ESI-TOF) mass spectrometer (Bruker Daltonik GmbH, Bremen, Germany) coupled to an HPLC system (Agilent Technologies, Waghaeusel-Wiesental, Germany) controlled by HyStar chromatography software (Bruker Daltonik GmbH). A mobile-phase system consisting of water (A) and acetonitrile (B) (each containing 0.1% formic acid) was used, and separation was performed with an RP-18 column (100 by 2.1 mm, 3.5-µm particle size; Agilent Zorbax Eclipse Plus) and the following gradient: 0 to 2 min, 98% A; 2 to 12 min, 98% to 2% A (linear); and 12 to 13 min, 2% to 98% A.

Data sets were acquired in positive electrospray (ESI) mode in a scan range from 50 to 1,500 m/z at a sampling rate of 2 Hz. Sodium formate solution was used for the calibration and injected at the beginning of each chromatographic run by infusion (Harvard Apparatus; flow rate, 220 µl/h). Quality control samples (MC-LR) and blank runs were interspersed between the samples under investigation.

The LC-MS data were smoothed before automatic peak integration on extracted ion chromatograms (EICs) created at a 10-mDa mass accuracy, using internal routines constructed using DataAnalysis software (Bruker Daltonik GmbH). Chromatographic trace definitions were based on the measured masses of MC-LR, MC-RR, MC-YR, and MC-LY. The microcystin concentrations in the samples were quantified on the basis of standard curves. The linearity of the TOF detector was suitable for the range of toxin concentrations in samples. The relative proportion of each of the MC congeners was calculated as a ratio of the MC pool (defined as the sum of the four congeners measured).

**Chemicals.**

All reagents were of HPLC-MS grade (>99.9%) or analytical grade. Methanol was purchased from Sigma-Aldrich (Saint Quentin Fallavier, France), and acetonitrile and water were obtained from Rhiedel de Hahn (Chromasolv LC-MS grade; Sigma-Aldrich, Saint Quentin Fallavier, France). pNPP, dithiothreitol, and bovine serum albumin were purchased from Sigma-Aldrich (Saint Quentin Fallavier, France). The four microcystin standards MC-LR, MC-RR, MC-YR, and MC-LY were purchased from Alexis Biochemicals (Enzo Life Sciences, Lausanne, Switzerland). PP2A purified from human red blood cells was obtained from Upstate (Millipore Corporation, Billerica, MA).

**DNA extraction and multiplex real-time PCR.**

The potential of MC-producing cells was determined by real-time PCR analysis. DNA was extracted using the DNeasy plant minikit (Qiagen), as described previously by Sabart et al. [38]. Two target genes were used: the intergenic spacer region within the phycocyanin (PC) operon, and the mcyB region. The primers and probes used for the PC operon and mcyB genes (listed in Table 2) have been described previously [4, 28].

Amplification by real-time PCR was carried out using an MX3005P thermal cycler (Stratagene, Netherlands). All of the reactions were performed in 20-µl volumes in 96-well plates. The multiplex reaction mixture contained 10 µl of 2× Quantitec probe PCR kit mix (Qiagen), a 300 nM (300 fmol µl⁻¹) concentration of each primer, a 100 nM concentration of the TaqMan probe for PC gene amplification, and a 900 nM concentration of each primer, a 250 nM concentration of the TaqMan probe for mcyB, and 2 µl of template containing various amounts of genomic DNA. The mixture was then filled to 20 µl with sterile Millipore water. Each sample was prepared in triplicate. Negative controls without DNA were included for each PCR run. For each run of samples, serial dilutions containing 1.1 × 10⁻¹, 1.1 × 10⁻², 1.1 × 10⁻³, 1.1 × 10⁻⁴, and 1.1 × 10⁻⁵ ng of the genomic DNA µl⁻¹ were prepared from the DNA extract of an MC-producing M. aeruginosa strain to serve as external standards for the real-time PCR. The temperature cycle consisted of an initial preheating step of 15 min at 95°C, followed by 40 cycles each consisting of 30 s at 95°C (denaturing), 1 min at 60°C (annealing), and 30 s at 72°C (extension). For data analysis, the fluorescence threshold of all of the samples was set manually to 132 (relative
Population dynamics, microcystin concentrations, and proportions of MC-producing cells in the M. aeruginosa population of the Grangent Reservoir.

As previously reported in the paper by Sabart et al. (38), in 2006 the peak of M. aeruginosa cells in the Grangent Reservoir was reached on 24 July (8.05 x 10^7 cells liter^-1). After that, a marked decrease was found from 7 August to 4 September, reaching values of about 1.9 x 10^7 cells liter^-1. Finally, the last sampling date (18 September) was marked by an increase in the cell concentration (about 3.9 x 10^7 cells liter^-1) (Fig. 2a).

The pattern of MC concentration (estimated after extracting the MC from the cells) was similar overall to that of the concentration of Microcystis cells (Fig. 2a). The only exception was observed on 7 August, when there was a decrease in the cell abundance of M. aeruginosa but an increase in the MC concentration. There was no significant change over time in the relative proportions of each MC variant (Fig. 2b). MC-RR was always the dominant variant (73 to 88%), the second most abundant being MC-LR, which accounted for 9 to 20% of the total MC. The other two variants (MC-YR and MC-LY) were always detected in low concentrations and accounted for less than 10% of the total MC.

The proportions of MC-producing cells assessed by real-time PCR ranged from 95% to 66% during the study period (Fig. 2c). The highest value was found at the first sampling date, just before the abundance of M. aeruginosa cells peaked. After an initial dip, this proportion subsequently remained stable at around 80% until the beginning of September, just before falling to the lowest proportion, which was recorded on 18 September. Finally, the MC cellular quotas (Fig. 2c) appeared to be very stable throughout the study, except on 7 August, when the cellular quota reached a value six times higher than that at other times (repeated-measures ANOVA, Tukey's post hoc test; P < 0.0001). With regard to the relative proportion of MC-producing cells, we also calculated the cellular quotas taking only toxic cells into account. These quotas were multiplied by 1.26 (± 0.15)-fold on average compared to the cellular quotas calculated for all Microcystis cells present. These MC cellular quotas were significantly correlated with the changes in MC concentrations (Spearman's $r^2 = 0.78$; $P = 0.033$), but no correlation with Microcystis cells densities or with the proportion of MC-producing cells was detected.

**RESULTS**

**Population dynamics, microcystin concentrations, and proportions of MC-producing cells in the M. aeruginosa population of the Grangent Reservoir.**

The two fluvial M. aeruginosa populations contained lower cell concentrations than that in the Grangent Reservoir (Fig. 3a and b), with no significant difference being found between them (Spearman's $r^2 = 0.89$; $P = 0.017$). The maximum cell densities (about 5.7 x 10^6 cells liter^-1) were found on 8 August. The cell concentrations of the Microcystis population in the Villereau Reservoir were higher than those in the Grangent Reservoir (comprising between 9 x 10^6 and 2.3 x 10^7 cells liter^-1), and the pattern of change was very different,
with cell concentrations in the Villerest population increasing throughout the summer to peak on 4 September (Fig. 3c).

In the Loire River (Cuzieu and Feurs), the MC concentrations displayed a similar pattern (Pearson's $r^2 = 0.74; P = 0.027$), with maximum values of 10.1 and 10.8 µg liter$^{-1}$ recorded for Cuzieu and Feurs, respectively (Fig. 3a and b). Moreover, the changes in these MC concentrations were synchronous with those of the *Microcystis* cell concentrations, as previously found in the Grangent Reservoir, but MC concentrations in the river were up to four times higher than those in the Grangent Reservoir. In the Villerest Reservoir (Fig. 3c), the MC concentrations were in the same range as those in the Loire River. As at Cuzieu and Feurs, there was a positive correlation (Pearson's $r^2 = 0.7; P = 0.039$) between the temporal variations in MC concentrations and *Microcystis* cell concentrations.

The proportions of potentially MC-producing cells in the *M. aeruginosa* samples from the Loire River and from the Villerest Reservoir ranged from 70 to 100% and did not display any significant fluctuation over the sampling period (Fig. 3d to f).

Finally, the MC cellular quotas appeared to be much higher in samples from the Loire River than in those from the Villerest Reservoir (Fig. 3d to f) or Grangent Reservoir (Fig. 2c). The variations in these MC cellular quotas were similar at the two river sampling sites at Cuzieu and Feurs (Spearman's $r^2 = 1; P = 0.03$), with the highest values recorded at the first sampling date and a subsequent progressive decline until the last sampling date (Fig. 3d and e). In the Villerest Reservoir, there was no significant change in the MC cellular quotas over the sampling period (Fig. 3f). Where possible (i.e., when the relative proportion of MC-producing genotypes was known), we also calculated the MC cellular quotas, taking into account only the toxic cells. As previously observed for the Grangent Reservoir, these quotas were multiplied by 1.25 ($\pm 0.13$)-fold on average compared to the cellular quotas calculated for all of the *Microcystis* cells.

**Population dynamics, microcystin concentrations, and proportions of MC-producing cells in the *M. aeruginosa* population of the Sable and Place Ponds.**

*M. aeruginosa* cell abundances in these ponds (Fig. 4 a and b) were in the same range as those of the Villerest Reservoir ($1.1 \times 10^6$ to $4.3 \times 10^8$ cells liter$^{-1}$). These two ponds displayed two very different patterns with regard to the proportion of MC-producing cells present. In the Sable Pond, the *M. aeruginosa* population was dominated by non MC-producing cells throughout the study (9.2 to 27.6%, with a mean value of 17.8%) (Fig. 4a). On the other hand, the proportion of potentially MC-producing cells was very high in the Place Pond and was characterized by little temporal variation (75.5 to 82%) (Fig. 4b).

**DISCUSSION**

This study is the first one to estimate changes in both MC concentrations and the proportions of MC-producing cells during a bloom season, on the basis of measurements of several *M. aeruginosa* populations located in the same geographical area but living in separate but connected freshwater ecosystems. Our results show that large variations can be found in both the MC concentrations and the proportions of potentially MC-producing cells, depending on the ecosystem and also depending on time.

**Comparison of the changes in potentially MC-producing cells in the different ecosystems.**

It is interesting to look at the variations in the proportions of potentially MC-producing cells in the *M. aeruginosa* population of the Grangent Reservoir alongside the dynamics of the *M. aeruginosa* population and the temporal variations in the ITS composition of this population, which were investigated in the same samples by Sabart and colleagues (38). In the present study, the development of the proliferation (in July) was associated with a decrease in the proportion of MC-producing cells and in ITS genotypic diversity, with the dominance of just a few genotypes (38). The same concomitant evolution was found in the Grangent Reservoir in 2007 by Briand et al. (4). In their study, there was a more marked decline in the proportion of MC-producing cells (from 93% to 14%), while the ITS genotypic composition was dominated by three genotypes when the *M. aeruginosa* population reached its peak. The magnitude of the blooms and the pattern of their development over the course of the summer were quite different in these 2 years (with lower cellular abundances in 2007), as were the environmental conditions (a hot and dry summer in 2006 versus a wet summer in 2007). Despite these differences in the overall patterns of the ecosystem, the patterns of change in the genotypic composition of the *M. aeruginosa* population were similar, which suggests that potential toxicity confers a competitive advantage in the early stages of a bloom.
The postbloom study that we carried out in 2006 allowed us to analyze the evolution of an M. aeruginosa population under changing environmental conditions (cooler weather, destratification of the water column, and changes in the hydrological regime [38]). Indeed, dramatic changes in the genotypic composition occurred 2 weeks after the decrease in biomass (21 August), whereas the change in the proportion of toxic cells occurred only in mid-September and was concomitant with a significant drop in water level that caused disruption of the ecosystem. The results obtained during this interesting period showed that changes in the ITS composition of the population were not always associated with changes in the proportions of potentially MC-producing cells, suggesting that characteristics other than the ability to produce MC are selected for during bloom events. From this study and that of Briand et al. (4), it looks as though toxic cells tend to dominate in M. aeruginosa populations when cyanobacteria do not dominate the phytoplankton community (e.g., at the onset of the bloom, as illustrated by the results from July 2006 and May 2007, and also when the bloom resumes, as illustrated by those from August 2006 just before the cyanobacteria peaked).

At the sampling points located downstream of the Grangent Reservoir (Cuzieu, Feurs, and Villerest), we did not find any significant changes in the proportion of MC-producing cells, which was high throughout the study. This is an interesting finding given that the same dominant ITS genotype was also found throughout the study at these sites (38). This dominant genotype selected under fluvial conditions was probably an MC-producing genotype. Finally, the two ponds, which are connected in winter, displayed very different proportions of MC-producing cells (18 versus 78%), which is consistent with the contrasting ITS genotype compositions of these two M. aeruginosa populations (38). No major variations in the proportions of MC-producing cells were found in the M. aeruginosa populations in these two ecosystems, in agreement with the fact that no dramatic change was found in their ITS genotypic compositions (38). All of these findings demonstrate that it is local environmental conditions rather than global processes, such as climate, that seem to have a major impact on the potential toxicity of M. aeruginosa populations. Indeed, despite the fact that all of the populations studied here were exposed to the same overall climatic conditions due to their being located in the same area, variable proportions of toxic cells were found in these populations associated with contrasting patterns in the evolution of these proportions. Moreover, when our results are compared with all of the data available on the proportions of toxic cells in cyanobacterial populations (Table 3), it emerged that it was not possible to establish any link between the different descriptors of the ecosystems (e.g., trophic status, surface, etc.) and the proportions of MC-producing cells in the cyanobacterial populations, which confirms the importance of local conditions and probably the complexity of interactions occurring between toxic and nontoxic cells in the populations. These findings seem to contradict the hypothesis of Davis et al. (9), who propose that global changes, and climate warming in particular, could be leading to the dominance of toxic cells during cyanobacterial blooms.

### Relationship between variations in MC production, proportions of mcyB+ cells, and cell abundances of Microcystis.

In the Grangent Reservoir, the proportions of the MC variants barely changed over time, as previously reported in other lakes (15, 16), and the major MC variant was always MC-RR, whereas MC-LR has been reported to be the dominant MC variant in most Microcystis blooms (2, 13, 43, 44). Previous studies have demonstrated the influence of various environmental factors, such as light, water temperature (1, 35), and also amino acid availability (41), on the MC composition of cyanobacterial populations. However, considering the lack of change in the MC variant composition in the Grangent Reservoir during this study and the fact that the M. aeruginosa population was exposed to major variations in the water temperature or availability of light during the study period (38), it seems to be unlikely that these factors have any impact on MC composition in the Grangent Reservoir. Fastner et al. (16) suggested that the lack of change in MC variant composition during cyanobacterial blooms could result from the absence of any change in the genotype composition of the cyanobacterial population, but our findings do not corroborate this hypothesis, because we detected major changes in the ITS composition of the Grangent population of M. aeruginosa during the summer of 2006 (38), suggesting that environmental determinism was involved in the MC variant composition.

The concentrations of MCs were in a range of the same order as those reported in the literature for Microcystis blooms (3, 6, 13, 18, 19, 26), and they were frequently above the WHO advisory level for drinking water of 1 μg liter⁻¹ equivalent of MC-LR. Overall, in both the reservoirs and the fluvial sites, the MC concentrations in the water parallel the changes in Microcystis abundance, but not those in the proportion of potentially MC-producing cells. Our findings are inconsistent with previous results (20, 27), which found that changes in MC concentrations were predominantly a result of changes in the proportion of MC-producing cells. In contrast to these studies, our results indicate that measurement of the mcy gene with real-time PCR is not an appropriate way to predict MC concentrations in freshwater ecosystems. The lack of correlation between MC concentrations in the water and the proportion of the mcyB⁺ cells could be due to the presence of an incomplete mcy operon, leading to an overestimation of the proportion of MC-producing genotypes, as previously suggested by Hotto et al. (18).
Our MC cellular quotas were generally higher than those found in experimental studies performed using isolated strains (21, 33, 46), but they were usually in the same range as those found in cyanobacterial populations in other lakes (3, 7, 14). These high values could be due to an overestimation generated by the fact that non-colony-forming M. aeruginosa cells may have been taken into account in the MC analysis but not in the cell count (48). Despite this possible overestimation, the highest MC cellular quotas were found at the beginning of the sampling period at the three sampling sites located downstream of Grangent and generally when Microcystis cell abundance was low (for example, after the biomass peak in Grangent, when the bloom was starting in Villerest or at the two fluvial sites). In the same way, high MC cellular quotas preceding blooms of Planktothrix and Microcystis have been reported in Dutch lakes (24, 25), suggesting that high concentrations of MC in the early stages of a bloom could enhance growth efficiency or could act as a grazing deterrent. We can also assume that high cellular quotas during the early stages of the bloom are due to the recruitment of highly toxic cells, since high MC contents have been found in the benthic colonies in the Grangent Reservoir (30).

In conclusion, we found major variations in space and time in the proportion of potentially MC-producing cells in different M. aeruginosa populations living in interconnected freshwater ecosystems located in the same geographical area. We also show that the relative selection of the MC-producing and non-MC-producing genotypes occurs at the scale of each ecosystem and probably depends on many local environmental factors and processes. The variations in the proportion of potentially microcystin-producing genotypes did not explain those of the MC concentrations. Finally, the fact that the highest MC cellular quotas were observed at low Microcystis cell abundances at each site suggests that toxic cells have an advantage under suboptimal conditions for growth. These findings are of particular interest with regard to the ecological role of microcystin, which could be implicated in sustaining Microcystis under adverse conditions or fluctuating environments.

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FOOTNOTES

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