ARIANE GUIMARÃES

PAPEL DO IMPACTO DO CLIMA NA DISTRIBUIÇÃO DE CIANOBACTÉRIAS EM AMBIENTES AQUÁTICOS NEOTROPICAIS DE ÁGUA DOCE

Anápolis
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Tese de doutorado apresentado ao Programa de Pós-Graduação Stricto Sensu em Recursos Naturais do Cerrado, da Universidade Estadual de Goiás para obtenção do título de Doutora em Recursos Naturais do Cerrado.

Orientador: **Prof. Dr. Daniel Paiva Silva**

Anápolis
2021

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Título: PAPEL DO IMPACTO DO CLIMA NA DISTRIBUIÇÃO DE CIANOBACTÉRIAS EM AMBIENTES AQUÁTICOS NEOTROPICAIS DE ÁGUA DOCE

TIPO

(X) Tese ( ) Dissertação
Curso/Programa: Recursos Naturais do Cerrado - RENAC
Concorda com a liberação documento [X] SIM [ ] NÃO[1]

Anapólis, 04 de outubro de 2021.

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Guimarães, Ariane
PAPEL DO IMPACTO DO CLIMA NA DISTRIBUIÇÃO DE CIANOBACTÉRIAS EM AMBIENTES AQUÁTICOS NEOTROPICAIS DE ÁGUA DOCE / Ariane Guimarães; orientador Daniel Paiva Silva. -- , 2021.123 p.

Tese (Doutorado - Programa de Pós-Graduação Doutorado em Recursos Naturais do Cerrado(RENAC)) -- Câmpus Central - Sede: Anápolis - CET, Universidade Estadual de Goiás, 2021.

1. Cianobactéria. 2. CyanoHABs. 3. Modelos de nicho ecológico. 4. Mudança climática. 5. Fitoplâncton. 6. Ecossistemas de água doce. I. Paiva Silva, Daniel , orient. II. Título.

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Tese defendida no Programa de Pós-Graduação *Stricto Sensu* em Recursos Naturais do Cerrado da Universidade Estadual de Goiás, para a obtenção do grau de doutora, aprovada em 31 de Maio de 2021, pela Banca Examinadora constituída pelos seguintes professores:

Prof. Dr. Daniel Paiva Silva
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Universidade Federal de Goiás

Prof. Dra. Geiziane Tessarolo
Universidade Estadual de Goiás

Prof. Dr. Aloysio da Silva Ferrão Filho
Fundação FIOCRUZ

Para Maria, meu maior amor.

AGRADECIMENTOS

Nada mais justo que começar os agradecimentos pela Família. Família é árvore e existem diferentes tipos de famílias. Família grande, família pequena, Família com pai, mãe e filhos, família com pai e filhos, família com mãe e filhos, família com dois pais e duas mães, família em que os avós são pais, família de sangue, família de coração e a minha família que é um pouco de tudo. Agradeço a minha mãe, Maria, que carregou sozinha a maior de todas as responsabilidades e sempre colocou a minha felicidade em primeiro lugar. Mãe, você sempre será o maior exemplo de amor que algum dia conheci na vida. Agradeço por garantir a mim uma boa formação educacional. Agradeço ao meu marido Diego, que pensou junto comigo no nosso futuro e não me deixou desistir (Hoje estamos colhendo os frutos do nosso empenho! Esta vitória é sua também!!!). Agradeço ao meu sogro (Waldir) por sempre se interessar pelo meu mundo de cientista. Agradeço a minha tia, Olívia (que também foi mãe), e a minha madrinha, Elaine Vieira, por sempre estarem ao meu lado desde a pré-escola.

Não menos importante, eu também agradeço às minhas duas outras famílias, a de Anápolis (Meu padrinho, madrinha, Dênia, Isadora, Nicolas, Pedro, Manuela, David, Wasney) e à de Goiânia (Msc. Gabriella Caetano, Jabson, Msc. Ana Paula Teixeira) obrigada por todo o carinho, compreensão, acolhimento, amor e paciência. Obrigada madrinha por fazer o rabanete da Cida, obrigada padrinho pelo colo, obrigada Dênia pelos cultos. Agradeço novamente à minha família de Goiânia por ter me acolhido em um dos momentos mais difíceis e desafiadores. Obrigada Gaby por fazer o melhor escondindinho de carne seca e Ana por me encher de amor com chocolate quente. Especialmente, do fundinho do meu coração, quero dizer que amo vocês.

Agradeço aos amigos que são família também: à Waltelice Dourado Rodrigues, por me apresentar o mundo da leitura e o dicionário. Agradeço à minha irmã de coração Msc. Susana Sardinha Beker, que sempre esteve comigo e foi parte da minha família durante a minha estadia em Goiânia. Aos amigos que fizeram parte dessa caminhada sempre me ajudando e incentivando, em especial ao Pablo Henrique (meu tesouro), Hellen Basílio (meu presente), Esther Leão (fotográfa e amiga), Cristielly Luísa, Criatura, Isabel Oliveira, Mariane Vargas, Dra. Thâmara (capricorniana, você é a parte boa da meta-análise) e Nicolle Monteiro. Vocês são os melhores! Agradeço ao Antônio Galli (*in memorian*), Glória Galli (*in memorian),* Magda Galli, Margareth Galli por sempre estarem ao meu lado desde o ínicio da minha formação acadêmica (desde o fundamental).

Agradeço a Lúcia Lopes (minha educadora inspiração) por estar comigo nessa caminhada (O Toninho teria muito orgulho!).

Agradeço a todos os meus parceiros de jornada, Debora Bezerra (farmacêutica nerd e grande amiga), Ruan Faquim (amigo modelo), Wesley Fonseca (químico sensação...que me socorre nos momentos de bipolaridade), Patrícia (minha parceira de lamúrias), Kárita Boavent, Pedro Borges, Guilherme Rissate, Edgar Lima (ursinho da estatística), Facundo Alvarez pelo apoio e companhia agradável.

Ao Prof. Daniel Paiva Silva (meu orientador) e ao Prof. Guilherme Malafaia (orientador da graduação, mestrado e incentivador no doutorado) agradeço imensamente pela persistência, dedicação, profissionalismo, pelos puxões de orelha, pelas tentativas incansáveis de me fazer refletir e por se preocuparem com o meu bem-estar. Sem vocês não teria chegado até aqui! Muito obrigada! Caro Daniel, a minha dívida contigo é imensurável. Mais que um orientador, você foi amigo e resolveu me acolher quando eu mesma duvidava do meu potencial. Obrigada pelo acolhimento, pela compreensão, pelas conversas (e por dividir as melhores histórias na mesa do refeitório), por aceitar o meu jeito acelerado e o excesso de energia e por devolver a minha autoconfiança. Eu espero algum dia poder retribuir todo o bem que me fez.

Ao Programa de Pós-graduação em Recursos Naturais do Cerrado, ao Instituto Federal Goiano – Campus Urutaí e a Universidade Estadual de Goiás, por toda a estrutura. Aos colegas, funcionários e professores do RENAC. Em especial a Arminda Campos, ex-secretária do PPG, por estar sempre tão disposta a ajudar. À FAPEG e à Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES) pela concessão da bolsa de doutorado. Agradeço a todos os meus parceiros de jornada do Laboratório COBIMA, em especial ao João Pedro Justiniano, Letícia Rabelo, Wanderson Teles, Lucas Saavedra, Thaís Souza, Luíza Fulgêncio pelo apoio e companhia agradável.

Agradeço ao meu médico ortopedista Dr. Rogério José e a Dra. Marayza Pires (minha fisioterapeuta e instrutora de pilates) por não medirem esforços para controlar os efeitos da minha lesão por esforço repetitivo no pulso direito. Também agradeço ao médico Dr. Walter Costa por me ajudar a suportar a endometriose e ter uma qualidade de vida melhor. E também a Dra. Naiara Félix (minha dermato) que foi terapeuta também. Por fim, agradeço também aos coautores e membros da banca de avaliação da tese, por disporem do seu tempo. A todas as pessoas que de forma direta ou indireta contribuíram para a realização deste trabalho, ***muito obrigada****!*

"Tente uma, duas, três vezes e se possível tente a quarta, a quinta e quantas vezes for necessário. Só não desista nas primeiras tentativas, a persistência é amiga da conquista. Se você quer chegar aonde a maioria não chega, faça o que a maioria não faz".

Bill Gates

SUMÁRIO

RESUMO

Os ambientes de água doce neotropicais estão entre os ecossistemas de maior produtividade e fornecem vários produtos e serviços ecológicos para a humanidade. Nos ambientes aquáticos de água doce neotropicais, as mudanças climáticas são uma ameaça à segurança hídrica global, e os períodos hidrológicos extremos, como precipitação extrema ou seca extrema, sem dúvida, reestruturarão as cadeias alimentares, gerando novas comunidades compostas por novas combinações de espécies. Em corpos de água doce, os eventos extremos nas mudanças climáticas podem intensificar o florescimento de cianobactérias tóxicas (CyanoHABs). Em geral, as distribuições geográficas das cianobactérias são pouco conhecidas e apresentam inúmeras lacunas de informação (déficit Wallacean) muitas vezes relacionadas à falta de esforços de coleta. Nesta tese os dados disponíveis sobre a distribuição geográfica das espécies de cianobactérias em ambientes de água doce estão longe de estar completos e têm vieses geográficos óbvios. Muitos dos registros de cianobactérias em ambientes aquáticos não eram acessíveis, o que pode ter reduzido a capacidade de avaliar a distribuição das espécies. Os resultados aqui apresentados podem fornecer informações relevantes sobre as lacunas de amostragem em regiões que precisam de mais pesquisas para melhorar os dados de distribuição sobre a ocorrência dessas espécies e apoiar as práticas de monitoramento dessas espécies. De modo geral, nossos mapas apresentam dados disponíveis sobre as áreas com adequabilidade para cianobactérias tóxicas e o nosso esforço amostral foi investido na América do Sul. No capítulo 1, apresentamos um artigo de divulgação científica, contendo informações e conceitos científicos sobre as cianobactérias e seus florescimentos. No capítulo 2, descrevemos o número de publicações coletadas na literatura científica que documentaram a ocorrência de florações de cianobactérias ao longo dos anos, bem como as ordens responsáveis e os registros dos estados brasileiros onde ocorreram. Além disso, usamos os dados de ocorrência obtidos nesta investigação cienciométrica para estimar áreas climaticamente adequadas para a ocorrência de eventos de floração cianobacteriana. No capítulo 3, usamos ferramentas de modelagem de nicho ecológico a partir de registros de ocorrência coletados em bancos de dados disponíveis para prever as áreas suscetíveis na América do Sul para o cenário presente e futuro do Filo Cyanobacteria representado por: *Microcystis aeruginosa* (Kützing) Kützing 1846, *Planktothrix agardhii* (Gomont) Anagnostidis & Komárek 1988 e *Raphidiopsis raciborskii* (Woloszynska) Aguilera, Berrendero Gómez, Kastovsky, Echenique e Salerno 2018. Consideramos três métodos de modelagem diferentes: Modelo Linear Generalizado (GLM); Modelo Gaussiano (GAU) e Entropia Máxima (MXS). Nos resultados, as distribuições para o cenário atual foram consistentes com as distribuições conhecidas e, para o cenário futuro, identificamos novas áreas de pesquisa. Concluímos que as espécies modeladas respondem às mudanças ambientais atuais e futuras e que o Filo devem ocorrer em áreas que atualmente não são detectadas em nossa análise ENM.

Palavras-chave: Cianobactéria, CyanoHABs, Modelos de nicho ecológico; Mudança climática; Fitoplâncton; Ecossistemas de água doce.

ABSTRACT

Neotropical freshwater environments are among the most productive ecosystems and provide many ecological products and services to humanity. In neotropical freshwater aquatic environments, climate change is a threat to global water security, and extreme hydrological periods such as extreme precipitation or extreme drought will undoubtedly restructure food chains, generating new communities composed of new combinations of species. In freshwater bodies, extreme events in climate change can intensify the bloom of toxic cyanobacteria (CyanoHABs). In general, the geographic distributions of cyanobacteria are poorly known and present numerous information gaps (Wallacean deficit) often related to the lack of collection efforts. In this thesis the available data on the geographic distribution of cyanobacterial species in freshwater environments are far from complete and have obvious geographic biases. Many of the records of cyanobacteria in aquatic environments were not accessible, which may have reduced the ability to assess species distribution. The results presented here can provide relevant information about sampling gaps in regions that need further research to improve distribution data on the occurrence of these species and support monitoring practices for these species. In general, our maps present available data on the areas with suitability for toxic cyanobacteria and our sampling effort was invested in South America. In chapter 1, we present a scientific dissemination article, containing information and scientific concepts about cyanobacteria and their blossoms. In chapter 2, we describe the number of publications collected in the scientific literature that documented the occurrence of cyanobacterial blooms over the years, as well as the responsible orders and the records of the Brazilian states where they occurred. In addition, we used the occurrence data obtained in this scientometric investigation to estimate climatically suitable areas for the occurrence of cyanobacterial flowering events. In chapter 3, we use ecological niche modeling tools from occurrence records collected from available databases to predict the susceptible areas in South America for the present and future scenario of the Phylum Cyanobacteria represented by: *Microcystis aeruginosa* (Kützing) Kützing 1846, *Planktothrix agardhii* (Gomont) Anagnostidis & Komárek 1988 and *Raphidiopsis raciborskii* (Woloszynska) Aguilera, Berrendero Gómez, Kastovsky, Echenique and Salerno 2018. We consider three different modeling methods: Generalized Linear Model (GLM); Gaussian Model (GAU) and Maximum Entropy (MXS). In the results, the distributions for the current scenario were consistent with the known distributions and, for the future scenario, we identified new areas of research. We conclude that the modeled species respond to current and future environmental changes and that the Phylum must occur in areas that are currently not detected in our ENM analysis.

Keywords: Cyanobacteria, CyanoHABs; Ecological niche models; Climate change; Phytoplankton; Freshwater ecosystems

INTRODUÇÃO

Os ambientes de água doce neotropicais incluem a América Central, as ilhas do Caribe e quase toda a América do Sul (ANTONELLI; SANMARTÍN, 2011). Estão entre os ecossistemas de maior produtividade (LEE; GARCIA-ULLOA; KOH, 2011) e fornecem vários produtos e serviços ecológicos para a humanidade (LAURANCE; SAYER; CASSMAN, 2014). Nos ambientes aquáticos neotropicais de água doce, as mudanças climáticas são uma ameaça à segurança hídrica global (CHIA et al., 2018). Os períodos hidrológicos extremos (BORTOLINI; TRAIN; RODRIGUES, 2016), como a precipitação extrema (STOCKWELL et al., 2020) ou seca extrema (CROSSETTI et al. , 2019) irão, sem dúvida, reestruturar as cadeias alimentares (WELLS et al., 2020), gerando novas comunidades compostas por novas combinações de espécies (PADISÁK; NASELLI-FLORES, 2021). Em corpos de água doce, os eventos extremos na mudança do clima pode aumentar a sensibilidade à invasão das assembléias fitoplanctônicas (NASELLI-FLORES; PADISÁK, 2016; RIBEIRO; DUARTE; CROSSETTI, 2018).

As cianobactérias fazem parte das assembléias fitoplanctônicas, que por sua vez, formam um grupo extremamente diverso de organismos (BORTOLINI et al., 2014). São espécies que estão distribuídas em ambientes pelágicos de lagos de água doce, rios, reservatórios, ambientes marinhos, bem como em superfícies iluminadas de rochas e solos (SVIRČEV et al., 2019). Morfologicamente as cianobactérias podem ser unicelulares, coloniais e filamentosas multicelulares, (KOMÁREK et al., 2014). Embora sejam semelhantes estruturalmente às bactérias e funcionalmente às algas (uma vez que realizam a fotossíntese utilizando a clorofila-a (pigmento fotossintético também das algas e plantas), possuem estruturas que lhes diferenciam destes organismos, tais como a bainha mucilaginosa, os vacúolos gasosos, os pigmentos acessórios, os acinetos, os heterocitos (PADISÁK; VASAS; BORICS, 2016).

As cianobactérias podem produzir substâncias como o metilisoborneol (MIB) e a geosmina, que conferem gosto e odor de terra à água (WATSON, 2003). Além disso, as cianobactérias podem produzir florações (CyanoHABs). Diz-se, normalmente, que há florações quando o número total de células de cianobactérias passa a ser maior que a média normalmente encontrada naquele corpo d’água (HUISMAN et al., 2018), sendo que o tipo de substância produzida em uma floração varia amplamente entre as diferentes cepas da mesma espécie, já que as florações de cianobactérias geralmente consistem em misturas de cepas tóxicas e não tóxicas (KURMAYER et al., 2004). Essas toxinas, em contato com o ser humano – através, por exemplo, da ingestão da água ou de peixes contaminados (ZANCHETT; OLIVEIRA-FILHO, 2013) podem provocar danos no fígado e sintomas como diarréia, inflamações, problemas no cérebro e coceiras na pele (MANTZOUKI et al., 2018). Dentre os metabólitos com propriedades tóxicas produzidos, entre os mais conhecidos estão hepatotoxinas (microcistinas e nodularina), neurotoxinas (anatoxinas, saxitoxinas e o aminoácido β-metilamino-L-alanina - BMAA), citotoxinas (cilindrospermopsinas), dermatotoxinas (aplysiatoxins e lyngbyatoxins) e lipopolissacarídeos extracelulares irritantes para a pele (BURATTI et al., 2017).

Outra questão de grande preocupação é que a floração limita a transferência da produção primária para níveis tróficos mais elevados na cadeia alimentar (ULLAH et al., 2018) e compromete a capacidade do zooplâncton de pastar cianobactérias coloniais e filamentosas (FERRÃO-FILHO et al., 2019). Alguns metabólitos secundários produzidos pelas cianobactérias podem ser tóxicos para o zooplâncton. No entanto, determinadas espécies de zooplâncton desenvolveram adaptações à baixa qualidade nutricional das cianobactérias ou apresentam tolerância contra as cianotoxinas (SADLER; VON ELERT, 2014). Ainda, organismos planctônicos que se alimentam de cianobactérias, como *Daphnia*, são alvo de toxinas, ocorrendo frequentemente o aumento da taxa de mortalidade, redução da fecundidade, taxa de alimentação, paralisia, alterações comportamentais e bioquímicas (OMIDI; ESTERHUIZEN-LONDT; PFLUGMACHER, 2018), o que afeta a aptidão das populações de herbívoros (FERRÃO-FILHO; KOZLOWSKY-SUZUKI, 2011).

Considerando que as cianobactérias têm sido uma preocupação mundial por serem capazes de produzir diversos metabólitos com atividade biológica, o conhecimento sobre o padrão de distribuição de cianobactérias neotropicais é indispensável, porém ainda é inconsistente e fragmentado. Algumas espécies de cianobactérias são amplamente distribuídas, mas a maior parte do grupo ocorre em ambientes restritos. Portanto, algumas espécies apresentam ampla distribuição em diferentes regiões do mundo, mas sempre ocorrem em um dado tipo de ambiente, refletindo suas preferências ecológicas e adaptações a determinados habitats. Usualmente, as informações sobre as ocorrências de cianobactérias não são aleatoriamente distribuídas no espaço geográfico. Em geral, as distribuições geográficas dessas espécies apresentam inúmeras lacunas de informação (déficit Wallaceano) frequentemente relacionadas com a falta de esforços de coleta (WHITTAKER et al., 2005).

Ainda que o conhecimento das distribuições espaciais e temporais de espécies de cianobactérias no ambiente em escalas local, regional e continental seja limitado (NASELLI-FLORES; PADISÁK, 2016), é possível realizar estimativas para suprir a falta de informação sobre a distribuição dessas espécies com base no seu nicho ecológico. Nesta perspectiva, a determinação do padrão de distribuição de cianobactérias de ambientes continentais neotropicais pode demandar novas ferramentas para avaliação de impacto e propostas para conservação dos ambientes aquáticos neotropicais. Portanto, ao responder o padrão de distribuição de espécies de cianobácterias neotropicais de ambientes continentais pretende-se ainda entender se de fato essas espécies estão em todo local diante das suas altas taxas de dispersão ou se apresentam padrões claros de distribuição determinados pelo nicho ecológico das espécies.

No ***Capítulo 1,*** apresentamos um artigo de divulgação científica, onde disponibilizamos informações e conceitos sobre cianobactérias e suas florações para o público leigo e que desconhece ou pouco sabe sobre a temática. No ***Capítulo 2***, considerando que a ocorrência de florações de cianobactérias tóxicas é um problema recorrente em vários reservatórios de água doce em muitos países e que esses eventos tornem a água potável imprópria para consumo humano, há um grande interesse em desenvolver a capacidade de prever a ocorrência de florações de cianobactérias em ambientes de água doce. Assim, descrevemos o número de publicações coletadas na literatura científica que documentaram a ocorrência de florações de cianobactérias ao longo dos anos, bem como as ordens responsáveis e os registros dos estados brasileiros onde ocorreram. Além disso, usamos os dados de ocorrência obtidos nesta investigação cienciométrica para estimar áreas climaticamente adequadas para a ocorrência de eventos de floração de cianobactérias. No ***Capítulo 3,*** usamos ferramentas de modelo de nicho ecológico a partir de registros de ocorrência coletados em bancos de dados disponíveis para prever as áreas suscetíveis para o cenário presente e futuro do Filo Cianobactéria em ambientes de água doce Neotropicais. As espécies foram representadas por: *Microcystis aeruginosa* (Kützing) Kützing 1846, *Planktothrix agardhii* (Gomont) Anagnostidis & Komárek 1988 e *Raphidiopsis raciborskii* (Woloszynska) Aguilera, Berrendero Gómez, Kastovsky, Echenique e Salerno 2018.

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CAPÍTULO 1[1]

Por que a água está verde?

Figura 1. Ilustração de uma Floração de cianobactérias na Represa Billings, São Paulo, Brasil. Fonte: Guimarães, A.

Em janeiro de 2021, pelo segundo verão consecutivo, a água que chegava nas torneiras dos moradores do Rio de Janeiro voltou a apresentar gosto e cheiro de terra. Os cientistas afirmam que um organismo de forma de vida simples conhecido por formar “tapetes verdes” em lagos e oceanos, chamado de cianobactéria é o grande vilão. Imagine uma bactéria que não possue um núcleo e, que surgiu há aproximadamente 3,5 bilhões de anos (HUISMAN et al., 2018). A cianobactéria pode até ser uma bactéria, mas é capaz de produzir seu próprio alimento e ser encontrada no solo, em desertos, córregos, lagos, lagoas, rios, reservatórios, geleiras e ainda ocorrer em união com fungos.

As cianobactérias na evolução da vida em nosso planeta, foram as responsáveis pelo aparecimento do oxigênio em nossa atmosfera, liberado através da fotossíntese. O processo da fotossíntese é a forma como todas as plantas do mundo se alimentam, e aquele ipê amarelo na esquina da sua casa continua crescendo. Outra contribuição das

[1] O artigo de divulgação será publicado em forma de jornal no site do Centro de Educação Ambiental da Secretaria de Meio Ambiente e Recursos Hídricos do munícipio de Ipameri-GO. O texto também será divulgado no grupo da página do facebook (Cyanobactéria Brasil).

cianobactérias é o surgimento das plantas, já que os cloroplastos, através dos quais as plantas sintetizam seu próprio alimento, são cianobactérias que se tornaram parte das células vegetais. Mas, as cianobactérias também podem ser organismos tóxicos aos seres vivos (RAI; RAI, 2018), e apesar de serem organismos essenciais, as cianobactérias geralmente se multiplicam e crescem quando a água está quente, parada e rica em nutrientes (“esses nutrientes funcionam como “fertilizantes"). O crescimento industrial e urbano desordenado, o lançamento de esgotos sem tratamento (TAVARES; UZÊDA; DOS SANTOS PIRES, 2019), a construção de hidrelétricas, o desmatamento, a agropecuária, as queimadas, a erosão dos solos são responsáveis pelo aumento de nutrientes (LAURANCE; SAYER; CASSMAN, 2014). Logo, as cianobactérias ocorrem com maior frequência em locais onde os ambientes são eutrofizados, ou seja, em ambientes ricos em nutrientes.

As cianobactérias formam florações. As florações são aglomerados espessos e verdes nas margens dos rios e reservatórios e quando ocorrem, uma espuma pode flutuar na superfície da água (SCHULIEN et al., 2017). Um grande problema é que a floração produz substâncias como o metilisoborneol (MIB) e a geosmina, que conferem gosto e odor de terra à água (WATSON, 2003), afetando de forma negativa a qualidade da água e exigindo processos mais caros de tratamento para tornar a água própria para o nosso consumo (GENUÁRIO et al., 2016). As cianobactérias também liberam toxinas nocivas. Estas toxinas, podem ser perigosas para humanos e animais. Quando as toxinas estão em contato com o ser humano, pela ingestão da água ou de peixes contaminados (ZANCHETT; OLIVEIRA-FILHO, 2013), podem provocar danos no fígado e sintomas como diarréia, inflamações, problemas no cérebro (MANTZOUKI et al., 2018).

Além disto, a floração é um sério problema para as estações de tratamento de água, pois pode causar o entupimento e a perda dos filtros. No Brasil, há registros de florações tóxicas em reservatórios de água, açudes, rios, lagos e lagoas de todas as cinco regiões do país (GUIMARÃES et al., 2020), se em alguns estados ou mesmo municípios não ocorreram até o momento relato de floração de cianobactérias, pode ser o reflexo da falta de estudos e não uma melhor qualidade da água naquele local. Nas lagoas da Barra da Tijuca, Jacarepaguá (Rio de Janeiro), no rio Amazonas no Brasil (VIEIRA et al., 2003, 2005), no lago Dianchi na China (SHENG et al., 2012) no lago Erie nos EUA/Canadá (SCAVIA et al., 2019) e em reservatórios de abastecimento de água potável como em Cingapura (TORTAJADA; WONG, 2018) e países do continente africano, são alguns exemplos que mostram onde as florações de cianobactérias já são relatadas à várias décadas. As florações de cianobactérias tóxicas existem há milhões de anos. A mortalidade em massa pré-histórica envolvendo cervos, cavalos, elefantes, auroques e leões das cavernas nos lagos do Pleistoceno e Eoceno (BRAUN; PFEIFFER, 2002), uma seca severa há, aproximadamente, 4.000 anos atrás em áreas úmidas na ilha de Maurício (que coincidiu com a mortalidade em massa de milhares de dodôs e tartarugas gigantes) (DE BOER et al., 2015) e a perda de tropas do general Zhu Ge-Ling por envenenamento durante a travessia de um rio na dinastia Han da China, cerca de 1.000 anos atrás (CHORUS; BARTRAM, 1999) foram atribuídos às cianobactérias tóxicas e seus efeitos. Outros casos envolvendo toxinas ocorreram em Caruaru (Pernambuco), Itaparica e na África. Em Caruaru, no ano de 1996, ocorreu um surto de insuficiência hepática ocorrido em pacientes renais crônicos submetidos a hemodiálise onde 76 pessoas vieram a óbito (AZEVEDO et al., 2002). Em Itaparica no ano de 1993, 88 mortes foram confirmadas por gastroenterite causadas por espécies do gênero *Microcystis*.

Mesmo com o conhecimento de que as cianobactérias causam problemas, infelizmente, nos últimos anos em diversos locais do Brasil e do mundo, temos notado um aumento expressivo de florações com a presença de toxinas e com substâncias causadoras de gosto e odor. Para auxiliar na prevenção da formação de florações tóxicas, a sociedade pode se organizar para defender e melhorar a qualidade das águas dos lagos, rios e outras fontes, de forma a garantir água boa e em quantidade suficiente para o consumo humano. Em cada região do País acontecem ações programadas por grupos de pessoas que participam dos chamados Planos de Bacias Hidrográficas.

Essas ações representam o Governo e a Comunidade afetada. É através desse plano de recursos hídricos de uma bacia hidrográfica que as ações podem se transformar em realidade. Mas é preciso saber que é necessário dinheiro para realizar ações tão importantes, como: a construção de redes de coleta e tratamento de esgotos, reflorestamentos de margens de rios e de fontes de água, ou mesmo a análise da qualidade da água. Esses recursos financeiros devem ser fornecidos pelas prefeituras, governos estaduais, governo federal e pelas parcerias dos governos com empresas privadas (parcerias público-privadas). Você acha que a responsabilidade de proteger o meio ambiente é dever apenas instituições públicas e privadas? Claro que não. Somos todos responsáveis por preservar o planeta e tudo depende de grandes e pequenas ações. Até a conservação de uma pequena nascente de água ou o recolhimento e envio correto do lixo da sua residência são atitudes que contribuem para a qualidade da água que abastece a nossa casa. Coletar e tratar os lixos e esgotos são ações esperadas tanto das pessoas como dos que administram os serviços públicos e privados. Todos nós temos o direito e dever de manter e defender o meio ambiente.

Comece usando apenas as quantidades recomendadas de fertilizantes em gramados e plantas, faça a manutenção adequada dos sistemas sépticos domésticos e mantenha uma proteção de vegetação natural ao redor de lagoas, lagos e nascentes para filtrar a água que entra. Também é muito importante diminuir o desperdíco com a água em nosso dia a dia. É necessário que você compreenda que a água é um recurso que tem fim, e que pode se esgotar e gostaríamos de contar com a sua colaboração.

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CAPÍTULO 2[2]

Biota Neotropica 20(2): e20190756, 2020
www.scielo.br/bn

biotaneotropica
ISSN 1676-0611 (online edition)
Article

Using distribution models to estimate blooms of phytosanitary cyanobacteria in Brazil

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GUIMARÃES, A., SILVA, P. H., CARNEIRO, F. M., SILVA D. P. **Using distribution models to estimate blooms of phytosanitary cyanobacteria in Brazil**. Biota Neotropica. 20(2): e20190756. http://dx.doi.org/10.1590/1676-0611-BN-2019-0756

Abstract: The multiple uses of aquatic ecosystems by humankind and the continuous interference of their activities have contributed to the emergence of potentially toxic cyanobacteria blooms. Here, we firstly created a database of occurrences of cyanobacteria blooms in Brazil through a systematic review of the scientific literature available in online platforms (e.g. Web of Science, Capes Thesis Catalogue). Secondly, we carried out ecological niche models with occurrence data obtained from these studies to predict climatically suitable areas for blooms. We select 21 bioclimatic variables input environmental data. We used five modeling methods for the current climate scenario: (1) Maxent; (2) Support Vector Machines; (3) Random Forest; (4) Maximum Likelihood e (5) Gaussian. We found that the number of publications about bloom events was higher in 2009 with a decline in the years 2012, 2013 and 2017. Furthermore, the years with the higher records of blooms in freshwater environments were 2005, 2011 e 2014. These events occurring mainly in public supply reservoirs and are mostly of the genera *Microcystis* Lemmermann, 1907, *Dolichospermum* (Ralfs ex Bornet & Flahault) P.Wacklin, L.Hoffmann & J.Komárek, 2009 and *Raphidiopsis* F.E.Fritsch & F.Rich, 1929. Modeling the potential distribution of blooms, we found sampling gaps that should be targeting for future researches, especially in the Amazon biome. Overall, the models did not predict highly suitable areas in the /north of Brazil, while other regions were relatively well distributed with a higher number of occurrence records in the Southeast region.
Keywords: freshwater ecosystems, species distribution models, bloom occurrence, cyanobacteria.

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[2] Artigo publicado. GUIMARÃES, A., SILVA, P. H., CARNEIRO, F. M., SILVA D. P. **Using distribution models to estimate blooms of phytosanitary cyanobacteria in Brazil**. Biota Neotropica. 20(2): e20190756. http://dx.doi.org/10.1590/16760611-BN-2019-0756.

Usando modelos de distribuição para estimar florações de cianobactérias fitossanitárias no Brasil

Resumo: Os múltiplos usos dos ecossistemas aquáticos pela humanidade e a contínua interferência das suas atividades têm contribuído para o surgimento de florações de cianobactérias potencialmente tóxicas. Aqui, primeiramente criamos um banco de dados de ocorrências de floração de cianobactérias no Brasil por meio de uma revisão sistemática da literatura científica disponível em plataformas on-line (por exemplo, Web of Science, Catálogo de Teses da Capes). Em segundo lugar, realizamos modelos de nicho ecológico com dados de ocorrência obtidos a partir desses estudos para prever áreas climaticamente adequadas para as florações. Selecionamos 21 variáveis bioclimáticas como dados ambientais de entrada. Usamos cinco métodos de modelagem diferentes para no cenário climático atual: (1) Maxent; (2) Support Vector Machines; (3) Random Forest; (4) Maximum Likelihood e (5) Gaussian. Encontramos que o número de publicações sobre eventos de floração foi maior em 2009 com um declínio nos anos de 2012, 2013 e 2017. Além disso, os anos com os registros mais altos de florescimento em ambientes de água doce foram 2005, 2011 e 2014. Esses eventos ocorrem principalmente em reservatórios de abastecimento público e são na sua maioria dos gêneros *Microcystis* Lemmermann, 1907, Dolichospermum (Ralfs ex Bornet & Flahault) P.Wacklin, L.Hoffmann & J.Komárek, 2009 *e Raphidiopsis* F.E.Fritsch & F.Rich, 1929. Modelando a distribuição potencial das florações, encontramos lacunas de amostragem que devem ser direcionadas para futuras pesquisas, especialmente no bioma Amazônia. Em geral, os modelos não previram áreas altamente adequadas no norte do Brasil, enquanto outras regiões estavam relativamente bem distribuídas com um número maior de registros de ocorrência na região Sudeste.

Palavras-chave: ecossistema de água doce; modelos de distribuição de espécie; ocorrência de floração; cyanobacteria.

Introduction

Freshwater ecosystems sustain much of Earth's biodiversity, providing multiple products and ecological services to humankind (LAURANCE; SAYER; CASSMAN, 2014). However, these ecosystems are suffering from several kinds of human pressures, such as changes in use and land cover (HUISMAN et al., 2018). Inadequate use of natural resources, as well as the different process of overexploitation, pollution, eutrophication, dam construction and silting, has intensified over recent decades (HANNAH et al., 2013), causing negative impacts on the environment and the health of human populations (GREEN et al., 2015). Specifically, the broad degradation has generated a loss of species and habitats, threatening several biological communities of rivers, lakes and flood plains (VITULE et al., 2017).

Overgrowth of algae, especially cyanobacteria, is one of the problems in aquatic environments (Walls et al., 2018). Results from the interaction of physical, chemical and biotic factors (Behrenfeld & Boss, 2017), which is marked mainly by increased cyanobacterial density broadly geographically distributed, and that respond rapidly to environmental changes in aquatic environments (PADISÁK; VASAS; BORICS, 2016), such as light intensity, CO_2 accessibility, high pH and low N:P ratio (GENUÁRIO et al., 2016). The growth of harmful cyanobacteria in high densities, known as water-blooms or blooms (PAERL; OTTEN, 2013), produces a variety of cyanotoxins (KOSTEN et al., 2012) that may cause liver, digestive and neurological diseases when ingested by birds or mammals (MANTZOUKI et al., 2018). Furthermore, they directly affect water quality, producing taste and odor, increased turbidity, decreased submerged aquatic vegetation (MEREL et al., 2013), decreasing, and promoting the death of fish and benthic invertebrates (JOSUÉ et al., 2018). The problems tend to increase with the abundance, frequency, and extent of blooms (O'NEIL et al., 2012). Thus, it is of great importance to know what determines the occurrence of these events in aquatic environments (GLIBERT et al., 2008).

Patterns that determine the spatial and temporal distributions of these organisms are environmental characteristics (HERNÁNDEZ-FARIÑAS et al., 2014), biological interactions and dispersal capacity of the species (SOBERÓN, 2007; SOBERÓN; PETERSON, 2005). These species act as "refined sensors of environmental properties" because they respond quickly to variations in the availability of environmental resources (MEKONNEN; HOEKSTRA, 2018). However, lack of knowledge about the global distribution and abundance of cyanobacteria restricts our ability to understand the mechanisms that determine its distribution (FLOMBAUM et al., 2013). In general, geographic distributions are poorly known and have numerous information gaps (MOREIRA; VASCONCELOS; ANTUNES, 2013). The Wallacean shortfall refers to inadequate knowledge about the species' geographic distribution (HORTAL et al., 2015; WHITTAKER et al., 2005b) and is a constraint particularly important to improve understanding about cyanobacterial blooms events (HORTAL et al., 2015). The predominance of studies close to traditional research centers (NEWBOLD, 2010) or uneven spatial distribution of infrastructure (OLIVEIRA et al., 2016) may also generate a geographic bias about known cyanobacterial bloom events (SASTRE; LOBO, 2009).

To reduce the Wallacean shortfall it is necessary to find the potential geographic gaps of these organisms and fill them in. In this context, scientometrics studies can contribute significantly to a general analysis of the patterns found. This research method allows us to measure the available data on species geographic distribution and to assess existing citations (CARNEIRO; NABOUT; BINI, 2008), revealing trends and gaps in scientific production (DEBACKERE et al., 2002). Additionally, scientometric analyzes can identify gaps in Cyanobacterial geographic distribution, helping to formulate new hypotheses about the mechanisms that determine these distributions. Thereby, it is possible to use Ecological Niche Models (hereafter ENMs) to fill these gaps (JENSEN; MOUSING; RICHARDSON, 2017). ENMs are statistical procedures that use species occurrence records to estimate suitable areas through environmental similarity between different sites (PETERSON, 2017).These models assume the premise that species' ecological niche is fully known and never changes over time, being completely dependent on the amount observed and the distribution pattern of the occurrence records (PETERSON, 2011). Therefore, it is possible to estimate new environmentally similar areas for species to occur. These models are widely used to (i) define potential distributions (FLOMBAUM et al., 2013); (ii) indicate suitable areas for future sampling (JENSEN; MOUSING; RICHARDSON, 2017); (iii) test biogeographic and evolutionary hypotheses (SILVA et al., 2014); (iv) suggest the establishment of conservation units (LOYOLA et al., 2008; NÓBREGA; DE MARCO, 2011); and (v) determine how species respond to climate change (BARTON et al., 2016; OLIVEIRA; CASSEMIRO; ESTADUAL, 2015).

Assuming that the occurrence of toxic cyanobacterial blooms is a recurring problem in several freshwater reservoirs in many tropical countries and that these events make drinking water unfit for human consumption (MOWE et al., 2015), there is a strong interest in developing an ability to predict the occurrence of cyanobacterial blooms in freshwater environments. A major obstacle in attempting to reduce cyanobacterial growth events in freshwater ecosystems is a consequence of the lack of reliable data on the distribution of these species. From this perspective, we describe the number of publications collected in the scientific literature that documented the occurrence of cyanobacterial blooms over the years, as well as the responsible orders and the records of the Brazilian states where they occurred. Also, we used the occurrence data obtained in this scientometric investigation to estimate climatically suitable areas for the occurrence of cyanobacterial bloom events. For us, the pattern of the wide distribution of flowering events reflects the arrangement of their corresponding habitats, and the occurrence of these species is restricted to environments that correspond to specific adaptations of the species. As cyanobacterial bloom events are more common in lentic environments (e.g., reservoirs), we hypothesize that locations with higher intensity of use (e.g.: higher population density) and greater damming of rivers (e.g. reservoirs) will exhibit a higher frequency of blooms.

Material and methods

Database of blooms events in freshwater environments

We created our database of cyanobacteria blooms occurrences in Brazil through a systematic review of the scientific literature available in the platforms Web of Science (WoS, http://apps.isiknowledge.com) maintained by Clarivate Analytics and Capes Thesis Catalogue (http://catalogodeteses.capes.gov.br), using the code of search: [("bloom*") AND ("Brasil" OR "Brazil")

AND ("cyanobacteria" OR "cyanophyceae")] and "florações" (in Portuguese). The WoS database has the advantage of providing data on publications over a broad time, presenting detailed and accurate scientific articles data, and is widely used in systematic review articles (FALAGAS et al., 2007). The Capes Thesis Catalogue stores many dissertations and thesis published in Brazil, facilitating the compilation of blooms events that occurred in the Brazilian territory.

In both databases, we searched for articles and reviews that contained the search terms in the title, abstract and/or keywords (access date: May 22th, 2018). We established two criteria to select the occurrence records in the scientific articles: (1) cyanobacteria blooms classified according to the distribution of cells and individuals in the water column (accumulation of high concentrations of chlorophyll-a in the first centimeters of the water surface; accumulation of high concentrations of chlorophyll-a in water depth; and when the cells are dispersed in the water column); and (2) blooms according to the density of chlorophyll-a (minimum concentration of 10 µg/L^{-1} of chlorophyll-a; and minimum density of 20.000 cells/mL of cyanobacteria) (DE LEÓN; CHALAR, 2003). In our search, we obtained 208 scientific articles in the WoS database, selected 98 studies after reading the abstracts and included 47 in our study. At the Capes Thesis Bank, we found 385 records. However, not all records were made available for reading. Thus, according to the established criteria, we were able to include only 18 studies in our database. We also included 10 studies cited in the bibliographic review of Freitas et al., (2012), in which they present a synthesis of blooms events in Brazil. Finally, we added two other scientific studies found in two Brazilian repositories (Universidade Nacional de Brasília e Universidade Federal de Goiás). Of the 77 papers found in the scientific literature, five papers were of the same area and the same species or were located in marine water environments, therefore they were not included.

Scientometric analysis

We compiled a list of 72 scientific studies that mention cyanobacterial blooms in freshwater environments in Brazil. The species names were updated following information from the On-line Database of Cyanobacterial Genera (CyanoDB.cz, http://www.cyanodb.cz/) (Komárek et al. 2014). We classified the occurrence records according to the distribution of the taxa at the collection sites. We corrected possible georeferencing errors considering several quality criteria (latitude and longitude exchange; occurrence records outside of the freshwater environments; and duplicate records) (GIOVANNI et al., 2012). When the latitude and longitude were incorrect, but there was information about the sampling and collecting site, we used Google Earth to get surrogate information. Each event record in a given location was considered as a sample. Bloom events that occurred in distinct months were considered as different records. To estimate the sampling effort in Brazil, we counted the number of bloom events in 1-degree cells.

Then, we elaborated on a map demonstrating the total number of bloom events distributed in Brazil. Also, we produced bar charts evidencing the number of blooms events and the number of scientific studies published per year. To identify whether there is a relation between the number of blooms and the number of scientific studies, we performed a simple linear regression analysis between those variables. We verified the residues normality and used a transformation (log+1) to meet that basic premise based on the protocol for data exploitation provided by (ZUUR; IENO; ELPHICK, 2010). To identify if there was a relationship between the number of flowering in freshwater environments and the population density, we performed a simple regression analysis between the variables using the premise mentioned above. For this, we consider the population density per municipality and the year for each point where the flowering event occurred. For the collection of the population estimation data, we consider the information provided by the IBGE (https://cidades.ibge.gov.br/). We combined the same geographic coordinates, and then our N which was 90 points, resulted in 59 records of reports of bloom in freshwater environments.

Environmental variables

To produce the ENMs, we used the environmental variables obtained from WorldClim 1.4 (http://worldclim.org/current; Hijmans et al., 2005) and WorldClim 2.0 databases (http://worldclim.org/version2; Fick and Hijmans, 2017). We select all 19 bioclimatic variables from WorldClim 1.4, average altitude and solar radiation from WorldClim 2.0 as input environmental data. These variables have a spatial resolution of 5 arc-minutes (≈10 km of cell size). We considered the variables already reported in other studies. For example, the temperature variable is often considered the most important determinant of growth and metabolism in freshwater algae, including cyanobacteria, due in part to the fact that many of the enzymatic reactions involved in photosynthesis and respiration are temperature dependent. Solar radiation is justified because it is an essential resource for photosynthesis since these organisms are autotrophic (WALLS et al., 2018). We used altitude as a variable because it is highly related to weather variables (TEITTINEN et al., 2017). Finally, we chose the precipitation variable, in the rainy season the highest nutrient transport takes place for the aquatic ecosystems, being observed the increase in the density of cyanobacteria. Furthermore, climate variations can modify from the community structure in freshwater ecosystems. For instance, the cyanobacteria presence may be strongly influenced by physical factors, such as the local climate conditions (KARADŽIĆ et al., 2013). The extreme precipitation in a reservoir cause increased nutrients concentration and, then, altered the composition of the phytoplankton community by cyanobacteria, evidencing the first bloom events after the suppression of other species (SIMIĆ; DORDEVIĆ; MILOŠEVIĆ, 2017).

To reduce the multicollinearity of the data, we performed the Principal Component Analysis (PCA) (PEARSON, 1901). This method calculates the mean of all variables and subtracts from the individual values. Then, the resulting values are divided by the standard deviation of each variable (z transformation). Thus, the cells of all variables range from -1 to 1, with zero mean. Thereby, we produced 21 orthogonal principal components (independent) and selected the first seven, which accounted for 96.4% of the variation of the original dataset (Table 1). This method allows the variables to have the same importance in the ENM predictions (DORMANN et al., 2012). Consequently, it also avoids the overfitting of the models, which can result in unreliable predictions (DE MARCO; NÓBREGA, 2018).

Table 1 Summary of the Principal Component Analysis performed from 21 environmental variables used in the Ecological Niche Modeling. Principal Component axes (PC) were selected until the cumulative explanation proportion reached 95% or more of the total variation of the original matrix. Loadings of PCs for each variable are presented, as well as PC's eigenvalues, the proportion of explained variance of each PC, and accumulated proportion of explained variance.

Variables	PC1	PC2	PC3	PC4	PC5	PC6	PC7
Annual Mean Temperature (bio1)	-0.266	-0.240	-0.063	-0.015	-0.044	0.078	0.056
Mean Diurnal Range (bio2)	0.197	-0.206	0.026	0.456	-0.045	-0.052	0.539
Isothermality (bio3)	-0.225	0.018	0.370	0.030	0.064	0.263	0.382
Temperature Seasonality (bio4)	0.233	-0.053	-0.384	0.120	0.135	-0.130	0.107
Max Temperature of Warmest Month (bio5)	-0.157	-0.355	-0.262	0.112	0.038	-0.060	0.170
Min Temperature of Coldest Month (bio6)	-0.296	-0.111	0.049	-0.155	-0.001	0.104	0.016
Temperature Annual Range (bio7)	0.244	-0.138	-0.264	0.279	0.031	-0.175	0.152
Mean Temperature of Wettest Quarter (bio8)	-0.211	-0.290	-0.136	0.122	-0.107	0.157	0.037
Mean Temperature of Driest Quarter (bio9)	-0.270	-0.167	0.012	-0.117	0.078	-0.004	0.130
Mean Temperature Warmest Quarter (bio10)	-0.204	-0.304	-0.258	0.028	0.034	0.021	0.019
Mean Temperature of Coldest Quarter (bio11)	-0.286	-0.171	0.072	-0.057	-0.069	0.099	0.081
Annual Precipitation (bio12)	-0.268	0.190	-0.017	0.215	0.028	-0.183	0.034

Precipitation of Wettest Month (bio13)	-0.268	0.076	0.122	0.217	-0.014	-0.391	0.154
Precipitation of Driest Month (bio14)	-0.153	0.325	-0.233	0.188	0.147	0.307	0.088
Precipitation Seasonality (bio15)	0.057	-0.278	0.404	0.190	-0.056	-0.192	0.139
Precipitation of Wettest Quarter (bio16)	-0.269	0.087	0.116	0.212	-0.030	-0.395	0.105
Precipitation of Driest Quarter (bio17)	-0.163	0.324	-0.229	0.190	0.156	0.273	0.077
Precipitation of Warmest Quarter (bio18)	-0.165	0.174	-0.093	0.437	-0.539	0.162	0.270
Precipitation of Coldest Quarter (bio19)	-0.207	0.187	-0.016	0.035	0.583	-0.309	0.131
Radiation solar	0.047	-0.309	0.116	0.281	0.506	0.329	0.545
Altitude	0.178	0.091	0.399	0.335	0.105	0.217	0.123
Proportion explain by each PC %	0.490	0.205	0.115	0.062	0.038	0.034	0.020
Accumulated Proportion Explained by the PCs	0.490	0.695	0.811	0.872	0.910	0.944	0.964

Modeling procedures

We performed the ENMs only for orders of cyanobacteria that had a minimum of 10 occurrence points. For Phylum Cyanobacteria, we compiled a total of 109 occurrence records, where 47 belonged to Chroococcales, 44 to Nostocalles, 12 to Oscillatoriales and 6 to Synechoccales. We also included a general model for Cyanophyta to represent the order Synechoccales in our study. To ensure independence in the dataset used to fit and evaluate the performance of the models, we chose to use geographic partitions in a grid format, similar to a checkerboard (MUSCARELLA et al., 2014). This partition subdivides the study area equally and in a spatially independent manner, alternating between training (to perform the model) and testing (to evaluate the model). We used five ENM algorithms to model the distribution of bloom events: (1) Maximum Entropy (MXE) (PHILLIPS; ANDERSON; SCHAPIRE, 2006); (2) Support Vector Machine (SVM) (GUO; KELLY; GRAHAM, 2005); (3) Random Forest (RDF) (BREIMAN, 2001); (4) Maximum Likelihood (MLK) (ROYLE et al., 2012) e Gaussian (GAU) (GOLDING; PURSE, 2016a).

The MXE algorithm is a technique of machine-learning that estimates the nearest probability distribution of the uniform distribution under constraint whose expected values for each variable are in agreement with empirical values observed in the occurrence records (PHILLIPS; ANDERSON; SCHAPIRE, 2006). This technique constrains the possibilities of adjusting linear or quadratic functions, reducing the complexity of the models and producing better predictions in certain situations (PHILLIPS et al., 2017; PHILLIPS; DUDÍK; SCHAPIRE, 2004). The SVM algorithm is a set of methods of supervised learning belonging to the family of generalized linear classifiers. This algorithm reduces the probability of misclassifying in patterns not observed by the distribution of data probabilities (RANGEL; LOYOLA, 2012). SVM creates hyperplanes to differentiate the occurrence records from absence sets (GUO; KELLY; GRAHAM, 2005). The RDF algorithm produces accurate predictions that do not overload data, fitting the models based on decision trees that use a subset of random predictors (BREIMAN, 2001). The MLK algorithm predicts the species occurrence probability in a given location by estimating a distribution of occurrence probability based on observed environmental conditions (ROYLE et al., 2012). The GAU algorithm predicts the species occurrence probability based on adjustments made by Bayesian inference (GOLDING; PURSE, 2016a).

We used a method to create pseudo-absence to meet some algorithms' requirements. Here, we used bioclimatic envelopes similar to the BioClim algorithm (BOOTH et al., 2014). This procedure constraints the occurrence points of the taxa in the geographical space using a bioclimatic envelope (LOBO; TOGNELLI, 2011; VANDERWAL et al., 2009). Then, the external area is considered as not suitable for the occurrence of species. In this area, pseudo-absences are created in a ratio of 1:1. We used a threshold that maximizes the sum of the sensitivity and specificity obtained from the Receiver Operating Characteristic (ROC) curve. This method is given by the graphical representation of True Positive Rate and True Negative Rate in several threshold settings. We measured the performance of the ENM algorithms by True Skill Statistics (TSS; Allouche et al., 2006). TSS is a threshold-dependent metric and ranges from -1 to 1. Predicted distributions with negative values and close to zero are not considered better than random models. 'Acceptable' projections for potential species distributions generally reach TSS values close to 0.5. 'Good' projections reach TSS values close to 0.7, while 'excellent' projections reach close to 0.9.

We represented the final distributions using consensus maps to reduce the uncertainties associated with each algorithm (ARAÚJO; NEW, 2007). We made the consensus maps using the average of the models that presented TSS values above the average. The idea of the consensus models considers that different errors may affect the final result (e.g. sensitivity of the models, lack of true absences). For this reason, it has been argued in the literature that the use of consensus maps as final distribution models may reduce the number of errors (DINIZ FILHO et al., 2010).

Results

Scientometric analysis

We found 72 scientific studies in the literature that mention the occurrence of bloom events in freshwater environments in Brazil. We detected that the orders Chroococcales, Nostocales, Oscillatoriales, and Synechococcales were the most reported. Species of the orders Chrococcales and Nostocales, represented by the genera *Microcytis*, *Raphidiopsis*, and *Dolichospermum* (old *Anabaena)*, occurred mainly in the states of São Paulo, Paraná, Rio Grande do Sul and Minas Gerais (Fig. 1). There were differences in the number of records distributed among Brazilian states. In some states we obtained a large number of blooms, while there were no records at all for others. The highest numbers of blooms found in the literature were obtained in the states of São Paulo, Minas Gerais, Pernambuco, and Rio Grande do Norte. On the other hand, we found the smallest amounts of bloom registered in the literature in the Amazon hydrographic basin. Mainly, bloom events were reported in sites of high human concentrations and with public supply reservoirs: Acarape do Meio Reservoir (Ceará), Armando Ribeiro Gonçalves Reservoir and Cruzeta Reservoir (Rio Grande do Norte), Carpina Reservoir (Pernambuco), Billings and Guarapiranga Reservoir (São Paulo), Utinga Reservoir (Belém do Pará) and Juturnaíba Reservoir (Rio de Janeiro).

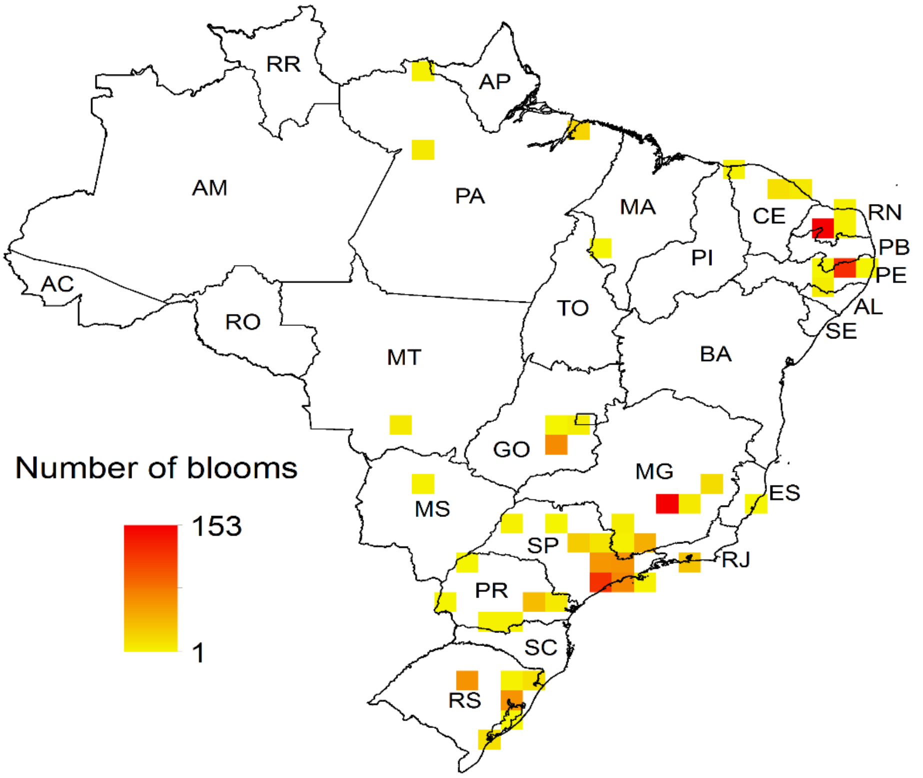

Fig. 1 The number of events registered in the literature in freshwater environments. Each cell has a spatial resolution of 1 decimal degree. The number of bloom events was counted in each cell considering the entire time series for all occurrence records (evaluating the temporal consistency of the blooms). All records are of freshwater environments. The maximum value for each cell is 153 bloom events. Note: the initials for the twenty-six states and Federal District (in Portuguese, Distrito Federal) are, respectively: Acre-AC; Alagoas-AL; Amapá-AP; Amazonas-AM; Bahia-BA; Ceará-CE; Distrito Federal-DF; Espírito Santo- ES; Goiás-GO; Maranhão- MA; Mato Grosso- MT; Mato Grosso do Sul- MS; Minas Gerais-MG; Pará-PA; Paraíba- PB; Paraná- PR; Pernambuco- PE; Piauí- PI; Roraima- RR; Rondônia- RO; Rio de Janeiro-RJ; Rio Grande do Norte- RN; Rio Grande do Sul-RS; Santa Catarina-SC; São Paulo-SP; Sergipe-SE; Tocantins-TO.

We observed the first bloom events in 1982 (n = 2) and the highest number of bloom records in 2010 (n = 89) (Fig. 2A). On the other hand, the year with the highest number of studies reporting blooms are 2009 (n = 9), 2005 and 2014 (n = 6), with the first study published in 1994 (n = 1) (Fig. 2B). We found no relationship between the number of blooms and the number the scientific studies (F = 3.231; R^2 = 0.076; p = 0.083). However, we must point out that since our database is composed of scientific studies and is not based on random sampling and probably does not have the same number of repetitions in each region, the sampling effort is an important factor in the frequency of occurrence of bloom. Thus, although the statistical relation has not been observed, it is difficult to consider that there is no relation between a number of blooms events and the numbers of scientific studies. We observed a relationship between the number of blooms in freshwater environments and population density (R^2 adjusted = 0.35; p = <0.001). Furthermore, we observed that the years with the relationship number of blooms are not necessarily the years with the relationship numbers of studies.

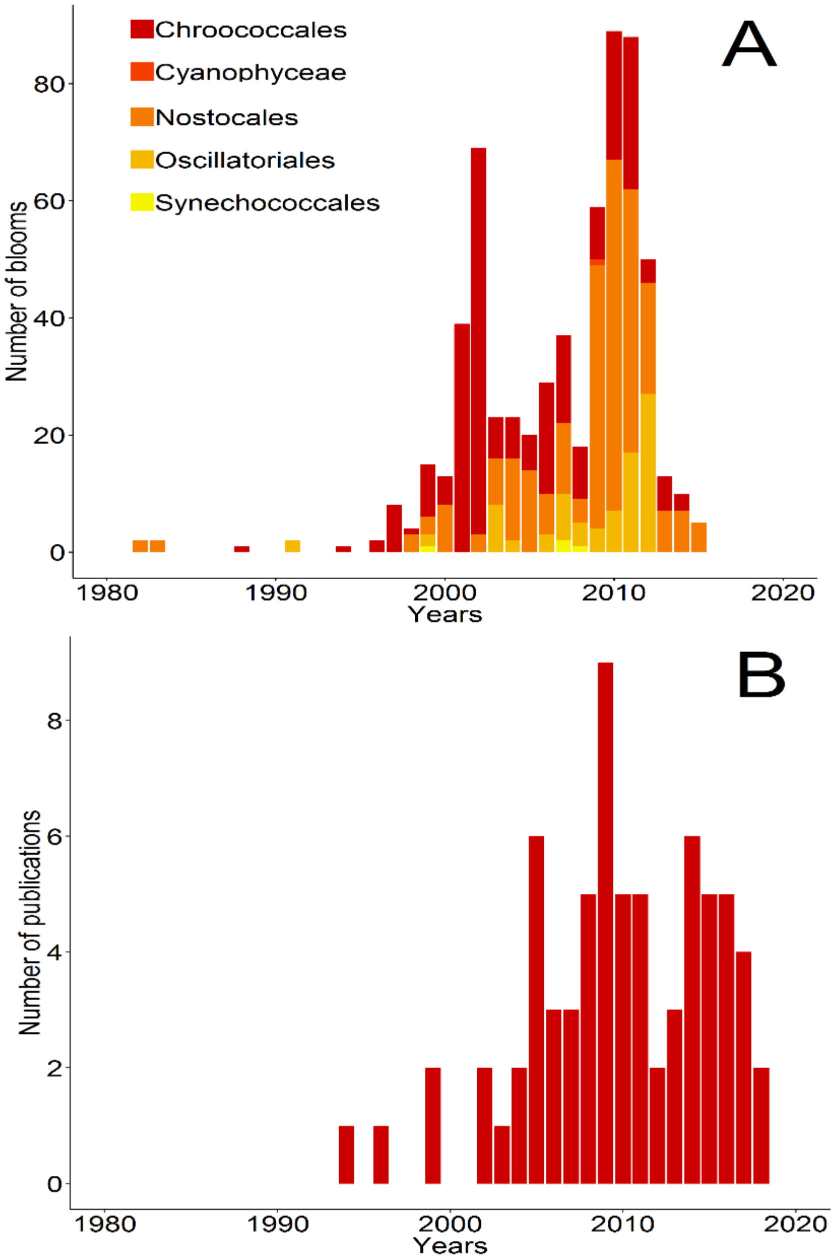

Fig. 2 The number of occurrence records and number of publications (scientific studies) over the years. (A) The total number of cyanobacterial blooms per year in freshwater ecosystems in Brazil. (B) The number of scientific studies reporting blooming events in the Brazilian territory per year.

Cyanobacteria potential distributions

In general, TSS values obtained for the modeled taxa were considered acceptable (greater than 0.5) or excellent (greater than 0.7). TSS values for phylum Cyanobacteria (0.856) and the order Chrococcales (0.882) were the highest. For the orders Nostocales (0.743) and Oscilatoriales (0.657) the values indicate models with good adjustment (Table 2).

Table 2 TSS values for the evaluation of the distribution models of the Phylum Cyanobacteria and of the orders Chroococcales, Nostocales and Oscillatoriales in different algorithms and for the ensemble map.

			TSS			
Taxonomic group	GAU	MLK	MXS	RDF	SVM	Ensemble
Phylum Cyanobacteria	0.769	0.595	0.828	0.725	0.798	0.856
OrderChroococcales	0.799	0.417	0.646	0.819	0.750	0.882
Order Nostocales	0.690	0.192	0.590	0.799	0.668	0.743
Order Oscillatoriales	0.343	0.271	0.586	0.486	0.243	0.657

While the Phylum Cyanobacteria, the orders Chroococcales and Nostocales obtained wide potential distributions range among the Northeast, South, Southeast and Midwest regions, the order Oscillatoriales presented a restricted distribution between Northeast and Southeast regions (Fig. 3). Altogether, no model designed suitable areas in the Northern region, so that the distribution of the taxa was mainly concentrated in Southeastern Brazil. The prediction for the phylum Cyanobacteria showed that 52.5% of the Brazilian territory has highly suitable area for the occurrence of blooming events. The orders Chroococcales, Nostocalles and Oscillatoriales showed high suitability in 55.5%, 49.9% and 17.3% of the Brazilian territory.

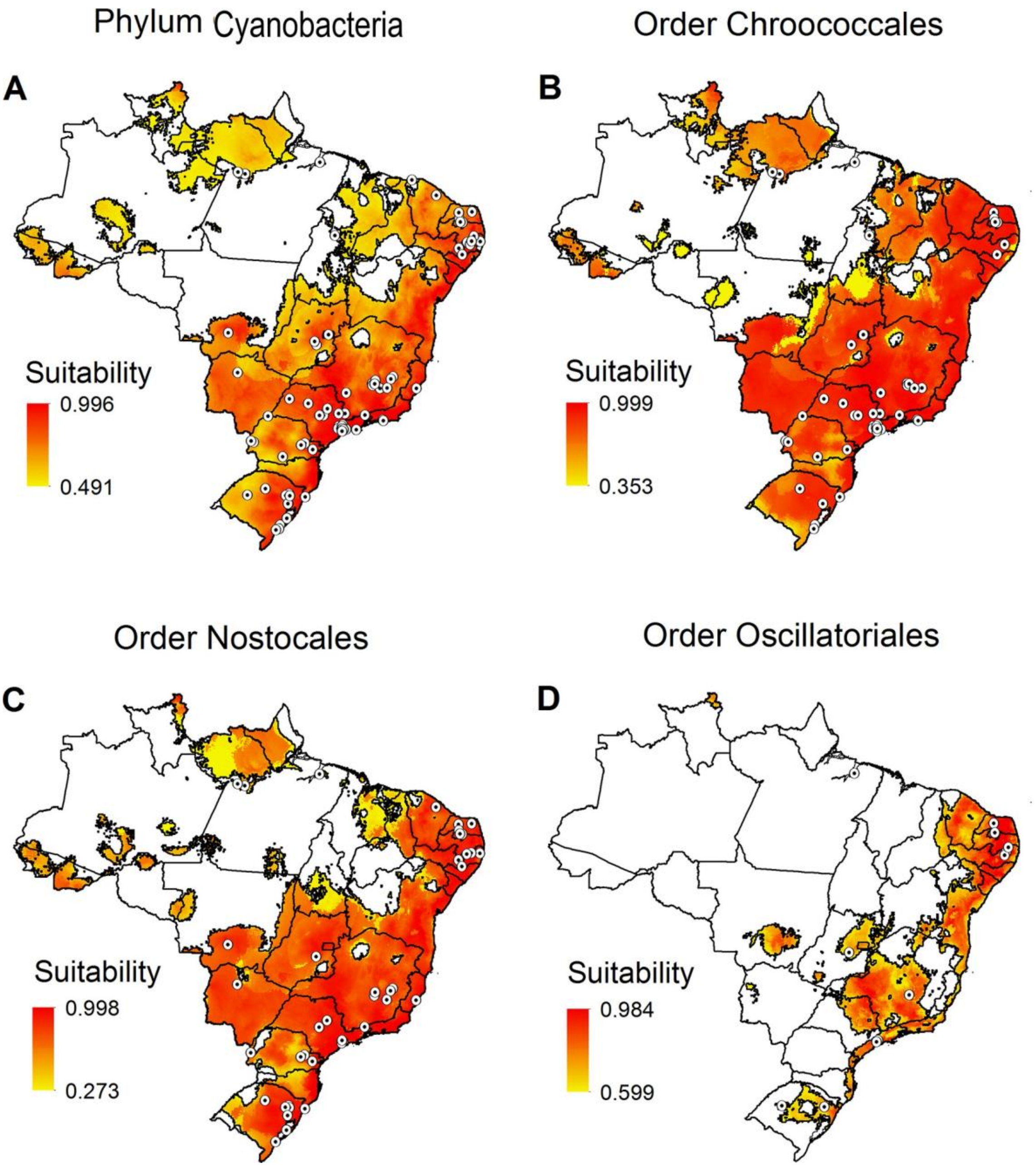

Fig. 3 Potential distributions for the groups of modeled Cyanobacterial in the Brazilian territory. (A) Phylum Cyanobacteria; (B) order Chrococcales; (C) order Nostocales; and (D) Order Oscillatoriales. The most suitable areas are represented colors closer to red, while the less suitable regions have colors closer to yellow. The dark line spatially delimits the threshold obtained from the values that maximized the sum of the sensitivity and specificity of the models, selecting only areas of high suitability.

Discussion

We observed that the number of publications on blooming events was higher in 2009, showing a decline in 2012, 2013 and 2017. However, the blooms have been reported in publications with data since

1982. Our results indicate the higher number of freshwater blooms in 2005, 2011 and 2014, and the vast majority of these records occurred in public supply reservoirs. We observed a relationship between the number of blooms in freshwater environments and population density (R^2 adjusted = 0.35; $p = <0.001$). Furthermore, we observed that the years with the relationship number of blooms are not necessarily the years with the relationship numbers of studies. For instance, 2009 presented the highest number of scientific studies and a median number of bloom events. Then, we also observed that species of potentially toxic genera, such as *Microcystis*, *Raphidiopsis*, and *Dolichospermum* have a wide geographic distribution.

The increase in publications during the years 2005, 2009 and 2014 indicates an increase in the number of researchers in this field of study, as well as its scientific and technological progress, considering that the number of publications is one of the most used measures to quantify the scientific production (DEBACKERE et al., 2002). Between the years of 2010 and 2018, the publications did not exceed the number of five studies, demonstrating a small number of scientific studies mentioning the bloom occurrences. The lack of studies on the occurrence of cyanobacterial bloom events, as well as the concentration of records sampled in large cities and close to researches centers, were the main observed biases. The amount of published research over the years may indicate gaps to be filled in later studies since cyanobacteria are potentially toxin-producing organisms lethal to aquatic biota and humans. Our findings indicate that the occurrences are located where there is a greater human population density and in public supply reservoirs with historic of persistent blooms. What may justify the greatest number of events recorded in supply reservoirs is the existence of criteria related to the growth of cyanobacteria that are set out in the Ministry of Health Ordinance Nº. 2.914, dated December 12, 2011, and which, in turn, revoked the Ministry of Health Ordinance Nº. 518 of March 25, 2004. The federal law evidences the need to monitor cyanobacteria in all sources of public supply, thus contributing to the largest number of publications in supply reservoirs.

Since bloom events occur mainly in large urban centers favors the accumulation of pollutants and the accelerated growth of the phytoplankton community, causing a considerable increase in biomass (BEHRENFELD; BOSS, 2018). This biomass has negative consequences on the efficiency and cost of water treatment, which can generate a loss of the resources destined to the public supply due to the economic unviability related to the water treatment (LORENZI et al., 2018). The blooms were mostly of the genus *Microcystis*, which in turn provide great shading for the other phytoplankton species, hindering their development, reducing the competition rate and eventually reducing the richness and diversity of organisms (CIRES et al., 2013). Also, morphological adaptations and the presence of gas vesicles allow buoyancy (VAN GREMBERGHE et al., 2011) and access to active photosynthetic radiation that facilitates its success in aquatic ecosystems (PADISÁK, 1997). Yet, the dense mucilage in cyanobacteria (REYNOLDS, 2007) ensures the increase in tolerance to high luminous intensities due to the acclimation by an increase in the production of photoprotective pigments (PAERL; OTTEN, 2013). In contrast, species of the genus *Cylindrospermopsis* can to adapt to low luminous intensity, being able to coexist with 'floating' genera, such as *Dolichospermum* and *Microcystis*, forming blooms in greater depths (PAERL; HUISMAN, 2008). Also, the genera *Cylindrospermopsis* presents success in dispersal attributed, in large part, to its ability to tolerate journeys along with river courses (MOREIRA; FATHALLI; VASCONCELOS, 2015; RICK; NOEL; RICK, 2007). In the genera *Dolichospermum* and *Microcystis*, the wind is an important dispersing agent for phytoplankton (CHRISOSTOMOU et al., 2009), as well as the animals that can also transport their vegetative forms on their body surface (PADISÁK; VASAS; BORICS, 2016). Cyanobacteria occur at environmentally suitable sites, where adequate dispersion rates are paramount for tracking changes in environmental conditions between localities (HEINO; VIRKKALA; TOIVONEN, 2009). Cyanobacterial dominance is associated with high temperatures, and the close relationship between temperature and the dominance in water bodies is evident (COTTINGHAM et al., 2015).

The use of ENMs can estimate environmentally suitable areas where the knowledge about cyanobacterial geographic distribution is incomplete (SILVA et al., 2013); guiding future field surveys (JENSEN; MOUSING; RICHARDSON, 2017). In an attempt to reduce the lack of knowledge about the geographic distribution of cyanobacteria responsible for bloom events, also known as Wallacean shortfall (CARDOSO et al., 2011; WHITTAKER et al., 2005b), the data compilation from specialized literature, becomes an effective tool to mitigate such a problem. However, it is necessary not only to record the collection biases but also to identify the priority areas for inventories to overcome this problem (SOUSA-BAENA; GARCIA; PETERSON, 2014).

Our ensemble distribution maps revealed that the northern portion of Brazil does not have high suitability for bloom events, being that the blooms are distributed in greater number of occurrences in the Southeast region. This result is the same for all four models. The suitability observed in this region may be a reflection of the lack of information about bloom events due to the low human concentration. Another explanation for the low occurrence in the North is that in these environments there is still a large proportion of the rivers preserved and not converted into reservoirs. Lentic environments are more amenable to flowering than lotic. Also, these species that were more reported are more successful in reservoirs (KOMÁREK et al., 2014). Incomplete data of geographic distribution are common in biological datasets from tropical regions (BALLESTEROS-MEJIA et al., 2013; KAMINO et al., 2012; SOBERÓN, 2007); with the Amazon region being generally sub-sampled (FREITAS et al., 2012). The distribution data are overlapped to regions with high human density (LETTERS; JAN, 2013) and the spatial patterns that we observed reflect the activities of the Brazilian researchers in reservoirs that show the historical persistence of blooms (LORENZI et al., 2018). Sampling bias is quite common for several biological groups and can have a strong effect on ENMs results (KRAMER-SCHADT et al., 2013).

Although the sampling bias demonstrated here is one of the main reasons that may explain the fragmentary distributional patterns we observed, less appreciated factors may also explain this pattern, such as: (1) material sampled extensively in a given area, causing an accumulation of many data to be processed (HORTAL et al., 2015); (2) Financial and/or human insufficient resources for the identification and curation of species (FONTAINE; PERRARD; BOUCHET, 2012); and (3) social and logistical variables (e.g., accessibility, number of inhabitants of a region, economy) (WHITTAKER et al., 2005b). Even more subjective factors, such as the researcher's preference for certain organisms or regions, may leave incomplete the distribution and occurrence scenarios for cyanobacteria (FICETOLA et al., 2014).

Our results indicate that the available data on the geographic distribution for cyanobacterial blooms in freshwater environments are far from complete and have obvious geographical biases. However, it is much more comprehensive than the information available in the literature, as also reported in Freitas et al. (2012). We are aware that many of the cyanobacterial bloom events in water environments were not accessible, which may have reduced our ability to assess bloom events in Brazil. In our study, we mapped the available biological data about cyanobacteria responsible for the bloom events and the sample effort invested in the Brazilian territory. Our results can provide useful information on current sampling gaps that need further research to improve distribution data on the occurrence of bloom events in public supply reservoirs and support the monitoring practices of these events.

Monitoring practices and risk assessments in water bodies include a proactive approach, encompassing inspection and monitoring programs with specific preventive actions (HUISMAN et al., 2018). However, although the enrichment of freshwater environments by nutrients is considered a major problem of pollution worldwide (GLIBERT et al., 2008), it is also one of the most important factors contributing to the increase in the number of bloom events (GLIBERT et al., 2008). In Brazil, eutrophication is still on the rise because of the increasing human population in many regions, which increases energy demands, increases the use of nitrogen fertilizers (N) and phosphorus (P) for agriculture, and increases the production of meat and animal waste. Nevertheless, we have noticed that the monitoring programs developed in Brazil are divided into four types of policies: prevention, restoration, improvement and no action (CARON et al., 2010). In other countries (e.g. the United States of America), advances are being made to detect bloom events and, in some cases, predict the occurrence and potentially reduce impacts. The rapid detection ability of phytosanitary cyanobacteria has progressed greatly from classical microscopic methods for detection involving specific molecules and genomes, which can be detected with a fluorescent signal (reviewed by Sellner et al., 2003). In addition, uses of remote images, packets and arrays that can detect and provide real-time information about species, as well as physical and chemical parameters have been enhanced (LOPES et al., 2016; MISHRA; MISHRA, 2014; STUMPF; TYLER, 1988). In Brazil, such advances and techniques are still far from being widely used, which may underestimating the actual bloom's occurrence in the country, affecting the data available on bloom events (SELLNER; DOUCETTE; KIRKPATRICK, 2003).

Thus, we hope that this study will stimulate new cyanobacterial samplings and increase efforts to understand and predict algal blooms to reduce its occurrence or impacts in the future. The most effective way is to reduce the entry of nutrients into aquatic environments since blooms are a widespread problem affecting estuaries, coasts and freshwaters around the world with effects on ecosystems, human health, and economies.

Conclusions

Using a scientometric analysis and ENMs, we demonstrate that many of the bloom events of phytosanitary cyanobacteria reported in the Brazilian literature are of the toxic genera *Microcystis*, *Raphidiopsis*, and *Dolichospermum.* These genera are broadly distributed in Brazil and respond quickly to current environmental changes and should certainly occur in areas that were not currently detected in our scientometric and ENMs analyzes. Thus, we believe that there are still several sampling gaps to be filled to effectively unravel the geographic distribution of cyanobacterial that cause blooms in freshwater environments and, consequently, diminish the effect of the Wallacean shortfall in this group. For instance, the northern portion of Brazil, which still has low suitability for bloom events compared to the occurrences in other Brazilian regions with a large concentration of human centers and population, needs to be better sampled, especially, in large urban centers. The cyanobacteria overgrowth has been highlighted because of possible problems in aquatic ecosystems, and by ecological and sanitary interest.

Acknowledgements

We would like to thank the editor and several anonymous reviewers who provided important suggestions to previous versions of this manuscript. AG thanks FAPEG-CAPES (Fundação de Amparo à Pesquisa do Estado de Goiás - Coordenação de Aperfeiçoamento de Pessoal de Nível Superior) for her Ph.D. scholarship and the graduate program in Recursos Naturais do Cerrado from UEG for the financial support for the publication of this study.

Author Contributions

a) Substantial contribution to the design and design of the work;

Ariane Guimarães, Fernanda Melo Carneiro, Pablo Henrique, Daniel Paiva Silva;

b) Contribution to data acquisition

Ariane Guimarães, Fernanda Melo Carneiro

c) Contribution in the analysis and interpretation of data

Pablo Henrique, Daniel Paiva Silva, Ariane Guimarães

d) Contribution in the writing of the work

Ariane Guimarães

e) Contribution in critical review adding intellectual content

Daniel Paiva Silva

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CAPÍTULO 3[3]

Role of the climate in the distribution of toxic cyanobacteria in Neotropical freshwater aquatic environments

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Abstract: Neotropical freshwater environments are among the most productive ecosystems and provide many ecological products and services to humanity. In neotropical freshwater aquatic environments, climate change is a threat to global water security, and extreme hydrological periods such as extreme precipitation or extreme drought will undoubtedly restructure food chains, generating new communities composed of new combinations of species. In freshwater bodies, extreme events in climate change can intensify the bloom of toxic cyanobacteria (CyanoHABs). Modeling the distribution potential of Cyanobacteria in freshwater environments can serve as a new tool for impact assessment and conservation proposals for Neotropical aquatic environments. We used ecological niche tools (ENMs) from occurrence records collected from available databases to predict the susceptible areas for the present and future scenario of the cyanobacteria phylum (*Microcystis aeruginosa* (Kützing) Kützing, *Raphidiopsis raciborskii* (Woloszynska) Aguilera, Berrendero Gómez, Kastovsky, Echenique and Salerno 2018, and *Planktothrix agardhii* (Gomont) Anagnostidis & Komárek 1988). We considered three different modeling methods: generalized linear models (GLM), Gaussian model (GAU), and maximum entropy (MXS). In the results of the ENMs, the distributions for the current scenario were consistent with the known distributions, and, for the future scenario, we identified new areas of research. We concluded that the modeled species respond to current and future environmental changes and should occur in the regions where the species are currently not detected in our ENM analyses.

[3] O manuscrito foi submetido ao Jornal Limnologica (2020: 2.093 © Clarivate Analytics Journal Citation Reports 2021).
A Limnologica publica artigos revisados por pares abordando aspectos biológicos, físicos e químicos de ecossistemas de água doce e habitats adjacentes.

Keywords: CyanoHabs; Ecological Niche Model; Freshwater ecosystems; Microcystis aeruginosa; Planktothrix agardhii Raphidiopsis raciborskii; Toxins.

1. Introduction

The proliferation and persistence of toxic cyanobacteria (CyanoHABs) in freshwater ecosystems have increased significantly lately (WELLS et al., 2020). Additionally, in scenarios of temperature increases, the flowering of cyanobacteria is stimulated, with the abundance peaks of many (but not all) cyanobacteria species occurring at relatively high temperatures, often above 25°C (HUISMAN et al., 2018). Therefore, climate change is a strong catalyst for expanding cyanoHABs proliferation (PAERL; HUISMAN, 2009). In the future, climate change (CC) will undoubtedly restructure food chains, generating new communities made up of new species combinations (PADISÁK; NASELLI-FLORES, 2021). CC concerns events related to climate or meteorology (KASPRZAK et al., 2017) as extreme hydrological periods (BORTOLINI; TRAIN; RODRIGUES, 2016), extreme precipitation (STOCKWELL et al., 2020), or severe drought (CROSSETTI et al., 2019).

In freshwater bodies, abrupt changes are related to the composition of phytoplankton but without dramatic changes in the number of species or community composition, although such extreme events may increase sensitivity to the invasion of phytoplankton assemblages (CROSSETTI et al., 2019; PADISÁK; VASAS; BORICS, 2016). CC raises the temperature, consequently the water evaporation, and decreases the dilution of nutrient inputs in rivers and lakes (CHARLTON et al., 2018). The increase in water temperature can especially favor the blooming of cyanobacteria, which can negatively impact the functioning and services of the ecosystem. Therefore, climate change is a strong catalyst for expanding cyanoHABs proliferation (CONLEY et al., 2009).

The cyanoHABs are characterized by the formation of thick clusters on the margins of water bodies (MILLER et al., 2017) and loss of water clarity that suppresses macrophyte growth and impacts invertebrate fish and habitats (PAERL; OTTEN, 2013). CyanoHABs are often formed by both toxin producers and non-producer cyanobacteria species. Independently of the kind of strain, compounds like geosmin (GSM) and 2-metilisoborneol (2-MIB) produced and conferred unpleasant taste and odor to the water (WATSON, 2003). Furthermore, these organisms produce a variety of cyanotoxins that cause liver, digestive and neurological diseases in humans (AZEVEDO et al., 2002) and animals (FERRÃO-FILHO; KOZLOWSKY-SUZUKI, 2011), besides compromising the quality of the water supply and increase their treatment costs (GENUÁRIO et al., 2016). These potential results of cyanobacterial growth also imply increased surveillance responsibilities to authorities responsible for producing water consumed by humans (HAMILTON et al., 2013). Therefore, there is an urgent need to identify suitable areas for cyanobacteria species to reduce water quality problems.

A significant obstacle in reducing the cyanobacterial growth in freshwater ecosystems is, to some extent, a consequence of the lack of reliable data on the distribution of those species at the geographical space, called the Wallacean shortfall (HORTAL et al., 2015). This gap may constrain a profound understanding of the actual distribution of potentially toxic cyanobacteria (OLIVEIRA et al., 2016). In general, the geographic distributions of these species are poorly known and present numerous information gaps (Wallacean deficit) often related to the lack of collection efforts. (WHITTAKER et al., 2005).

The distribution of a species is represented by the intersection of environmental conditions suitable for its survival (A), fundamental biological interactions to maintain their main ecological functions (B), and the ability to disperse to occupy the regions suitable for its persistence over time (M). Based on this, it is possible to assume that the areas where the set of environmental conditions and ecological functions are preserved represent the fundamental niche of a species, but mobility will define precisely the realized niche of the species. For cyanobacteria, the accessible region is very extensive, with practically no geographical limitation for their occurrence. Still, they necessarily need some dispersal agent (e.g., river, air, animals, man) and travel conditions that meet the transport tolerance of the species (PADISÁK; VASAS; BORICS, 2016). Therefore, given the lack of restriction for dispersion, it is possible to conclude that the effect of mobility is very low or even non-existent and, therefore, the set of environmental conditions can be very representative for the geographic distribution of these organisms (Figure. 1).

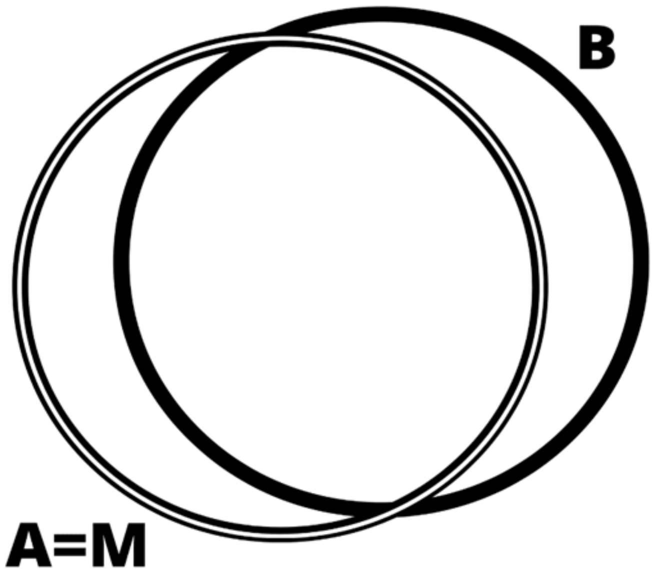


Figure 1. Diagram of BAM according to SOBERÓN (2007). It represents the biotic (B), abiotic (A), and mobility (M) conditions related to the life of a cyanobacterium. (M) concerns areas that are physically accessible, (A) represents the entire region with environmental conditions (abiotic factors) favorable to the establishment, survival, and reproduction of individuals who are established by the fundamental niche. (B) represents the geographic space where the species can occur, given the restrictions imposed by biotic interactions. (M) represents the entire region accessible to the species according to its dispersal capacity.

The classic concept of ecological niche established by Hutchinson (1957) (HUTCHINSON, 1957) is defined as an n-dimensional space of physical and biological requirements that would allow the survival and reproduction of a species and, at the same time, limit its abundance and distribution. However, this concept has changed over time to establish a more robust view of what defines the presence or absence of a species in a given location. One of the elements that most contributed to a concise explanation of the actual distribution of a species is the mobility, very well-argued from the BAM diagram (biotic, abiotic, and mobility) (SOBERÓN, 2007; SOBERÓN; PETERSON, 2005). The concept of niche in this work was thought of in the view of Grinnell (GRINNELL, 1917), where the Grinnellian niche is defined by abiotic or scenopoetic environmental variables and large-scale environmental conditions (SOBERÓN, 2007). It fits best to larger scales, where distribution areas are typically defined. When it comes to the large-scale distribution of species, the Grinnelian niche components are the most significant explanatory/predictive power (ARAÚJO; GUISAN, 2006).

Ecological niche models (ENMs) relate species occurrence records to a set of environmental predictors to determine suitable environments for cyanobacterial survival (GUISAN; EDWARDS; HASTIE, 2002). In ENMs, it is assumed that the ecological niche of the species is fully known and is conserved over time, being dependent on the pattern of distribution of occurrence records (PETERSON, 2011). Based on this, we can estimate environmentally suitable areas for the occurrence of a particular species (PETERSON, 2017). These models are widely used to (i) define potential distributions (FLOMBAUM et al., 2013); (ii) indicate suitable areas for further sampling efforts (JENSEN; MOUSING; RICHARDSON, 2017); (iii) estimate suitable areas for the occurrence of cyanobacterial bloom events (GUIMARÃES et al., 2020), for example.

In this study, our goal was to test the hypothesis that climate change will influence the size of areas suitable for cyanobacterial species when incorporated into niche models. Assuming that CC is responsible for broader geographic distributions of cyanobacteria species, with changing rain patterns (e.g., higher frequency of high-intensity rain events and more extended drought periods), cyanobacteria may expand geographically due to more extended and more stable stratification periods. Also, the higher expected frequency of extreme rain events would lead to the enrichment of nutrients and, consequently, a competitive advantage for cyanobacteria. Thus, we would observe changes in the size of the potential distribution for the future.

2 Material and Methods

2.1 Target species

We applied this approach in three cyanobacteria, *Microcystis aeruginosa* (Kützing) Kützing (order Chroococcales), *Planktothrix agardhii* (Gomont) Anagnostidis & Komárek 1988 (order Oscillatoriales) and *Raphidiopsis raciborskii* (Woloszynska) Aguilera, Berrendero Gómez, Kastovsky, Echenique, and Salerno 2018 (order Nostocales). The cyanobacterium *M. aeruginosa* (order Chroococcales) produces the toxin Microcystin-LR and is an uncomfortable species, as it forms large blooms on the water surface and predominantly dominates the ecosystem through the formation of colonies in temperate and tropical water bodies worldwide (HUISMAN et al., 2018). Such blooms create a shading that hinders the development of other species, reducing competition and decreasing diversity (MONCHAMP et al., 2018). The morphological adaptations and presence of aerotypes (gas vesicles) allow for buoyancy (MOREIRA; VASCONCELOS; ANTUNES, 2013), and access to photosynthetic radiation of this species facilitates its success in freshwater ecosystems (HARKE et al., 2016a). These species cause a wide range of toxic effects that can cause severe liver damage, alter the redox system and cause cellular inflammation after acute or severe exposure (HARKE et al., 2016b) and damage to other tissues in mammals (JACOBY et al., 2000). Such substances are also responsible for the deaths of various birds, mammals, including sheep, dogs, and cattle (HANNON et al., 2010). Further, microcystins can be harmful to aquatic animals (FERRÃO-FILHO; KOZLOWSKY-SUZUKI, 2011).

The cyanobacterium *P. agardhii* is a filamentous species that also produces microcystin and occurs in eutrophic shallow lakes. (PADISÁK; VASAS; BORICS, 2016). Blooms of *M. aeruginosa* and *P. agardhii* are a significant problem in countries with inadequate water treatment, as microcystin production causes several severe toxic effects to the liver and other mammalian tissues (MATSUDA et al., 2006). The cyanobacterium *R. raciborskii* is an invasive, very toxic species that forms blooms and affects water quality and public health by producing different types of toxins such as cylindrospermopsin and saxitoxin (PONIEDZIAŁEK; RZYMSKI; KOKOCIŃSKI, 2012). Such toxins affect multiple organs and tissues in mammals and inhibit protein synthesis in animals and plants. Saxitoxin is also one of the most potent paralyzing toxins (PST) found in freshwater ecosystems. (BURFORD et al., 2016). There are reports that drinking water contaminated with saxitoxins (STX) by humans infected with the Zika Virus results in fetal malformation and more severe microcephaly cases (PEDROSA et al., 2020).

2.2 Occurrence records

To estimate suitable areas in neotropical environments in South America, we used occurrence records (Figure 3A) of three widely distributed cyanobacterial species. We carried out the search on a global scale in the Global Biological Information Facility (GBIF; http://www.gbif.org) on June 15th, 2020. We obtained 789 records for *R. raciborskii*, 8.207 records for *P. agardhii*, and 1.089 records for *M. aeruginosa*. Overall, we fixed possible tradeoffs between longitude and latitude, removed records that did not contain geographic coordinates and duplicates. We did not consider occurrences in marine environments. Together, we obtained 69 records for *R. raciborskii*, 1,352 records for *P. agardhii*, and 330 records for *M. aeruginosa*. We chose to use occurrence records on a global scale, as the cyanobacteria species are globally distributed, and therefore, using data only for Brazil would leave the model incomplete. In such conditions, we would not be capturing the complete realized niche of the species, biasing the model.

We also include cyanobacteria in our database blooms occurrences in Brazil through a systematic review of the scientific literature available in the platforms Web of Science (WoS, http://apps.isiknowledge.com) maintained by Clarivate Analytics using the code of search: [(“bloom*”) AND (“Brasil” OR “Brazil”) AND (“cyanobacteria” OR “cyanophyceae”)]. We searched both databases for articles and reviews that contained the search terms in the title, abstract, or keywords (access date: on June 15th, 2020). In our search, we obtained 208 scientific articles in the WoS database, selected 98 studies after reading the abstracts, and included 47 in our study.

2.3 Environmental variables

We selected environmental variables that maximized the set of primary conditions to understand the ecological niche of cyanobacteria. We used the environmental variables taken from WorldClim Version 1.4 (HIJMANS et al., 2005), considering the resolution of 10 arc-min (~ 18.5 km at the Equator) (Figure 3B). We chose this resolution because cyanobacteria are species with high rates of dispersion. Thus, larger cells could show a more significant effect of climate on the distribution of the species.

We selected 19 bioclimatic variables, and for future models, we considered the climate variables available for the 17 Global Atmosphere-Ocean Circulation Models (AOGCMs): ACCESS1-0, BCC-CSM1-1, CCSM4, CNRMCM5, GFDL124 CM3, GISS-E2-R, HadGEM2-AO, HadGEM2-CC, HadGEM2-ES, INMCM4, IPSL-CM5A125 LR, MIROC-ESM-CHEM, MIROC-ESM, MIROC5, MPI-ESM-LR, MRICGCM3, NorESM1- 126 M. The representative carbon pathway scenario that we used was carbon concentration ("Representative Carbon Pathway" - RCP) 8.5, which corresponds to the most pessimistic scenario, in which it forecasts warming of approximately 4˚ C throughout the 21st century (IPCC, 2013; Chou *et al.*, 2014).

Once climate variables are correlated with local aquatic variables, such variables can be considered for the large-scale representation of the aquatic processes (ALVAREZ et al., 2020). Climate variations in large geographical scales can modify community structures in freshwater ecosystems (DOMISCH; AMATULLI; JETZ, 2015). For example, extreme precipitation contributes to increased nutrient concentration and biomass, and abundance values of the cyanobacterial community (SIMIĆ; DORDEVIĆ; MILOŠEVIĆ, 2017). The temperature variable directly influences competition between phytoplankton species, potentially intensifying cyanobacterial proliferation (MESQUITA et al., 2019). The direct effects are related to its growth, which affects the metabolic processes related to photosynthesis and biosynthesis (MOSS, 2011). Other effects can be observed, such as stratifying the water column and reducing and increasing vertical mixing sediment nutrient flow (JÖHNK et al., 2008).

We standardized the variables to have their mean zero and their variances |1|. Next, we performed principal component analysis (PCA) to reduce the number of predictor variables and produce new orthogonal principal components (PCs) to be used as new environmental variables to predict the distribution in the species (Figure 3B). The selected orthogonal components accounted for 95% of the gross climate variation before the PCA analysis. For each scenario, we used the 19 bioclimatic variables of each scenario, which were later standardized. We then projected the PCA linear coefficients of the current scenario in each of the future scenarios to ensure future scenarios on the current scenario. Finally, we performed a PCA for each of the 17 scenarios and selected the main orthogonal components responsible for 95% of the original raw climate variation.

2.4 Modeling procedures and model evaluation

The algorithms we used in this predictive modeling are classified into three categories according to their model fit method: (i) based only on actual presences, (ii) presences and background, and (iii) presences and absences. Here, we use algorithms belonging to the three groups to avoid mistaken adjustments conditioned by the range of species distribution or the number of occurrence records. The entire modeling procedure was performed in R software version 4.0.3, using the ENMTML Package (ANDRADE; VELAZCO; DE MARCO JÚNIOR, 2020). We chose to use a checkerboard partition to guarantee independence between the data set used (MUSCARELLA et al., 2014) and used a method to create pseudo-absence to meet some algorithms requirements (Figure 3D). Here, we used bioclimatic envelopes similar to the BioClim algorithm (BOOTH et al., 2014). This procedure constraints the occurrence points of the taxa in the geographical space using a bioclimatic envelope (LOBO; TOGNELLI, 2011; VANDERWAL et al., 2009). Then, the external area is considered unsuitable for the occurrence of species. In this area, pseudo-absences are created in a ratio of 1:1.

We considered three different modeling methods for distribution modeling: Generalized Linear Model (GLM); (GUISAN; EDWARDS; HASTIE, 2002), Gaussian Model (GAU; (VANHATALO; VENERANTA; HUDD, 2012) and the Entropia Máxima (MAX) (PHILLIPS; ANDERSON; SCHAPIRE, 2006; PHILLIPS; DUDÍK, 2008). The GLM algorithm is a statistical method. MAX is a machine learning method, while the

GAU method predicts the probability of occurrence of a species based on Bayesian inference adjustments (GOLDING; PURSE, 2016).

We focused the evaluation metrics on three components of the confusion matrix: true positives, false positives, and false negatives. In particular, we sought to maximize true positives and minimize false positives and false negatives relative to true positives. The Jaccard metric (the metric is based on how well predictions match observations based only on observed presences) measures the similarity between predictions and observations. A value of 1 indicates that the forecasts perfectly match the observations without any false positives or false negatives, while a value of 0 indicates that none of the forecasts corresponded to the observation. The lower the similarity value, the greater the number of false positives and false negatives concerning the number of true ones (LEROY et al., 2018). The predictions are assumed as acceptable to reach values close to 0.7, while “excellent” projections reach values closer to 0.9.

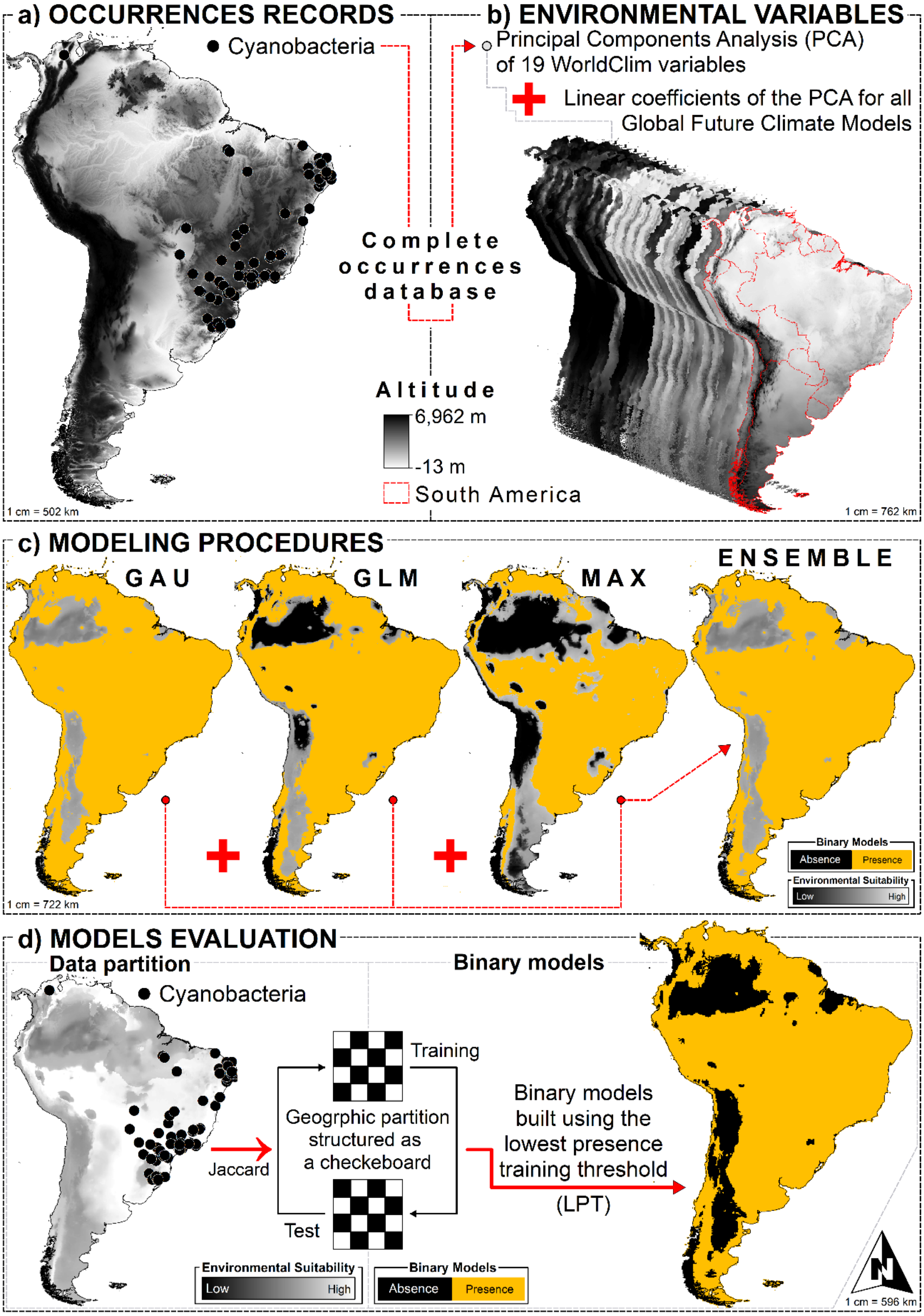


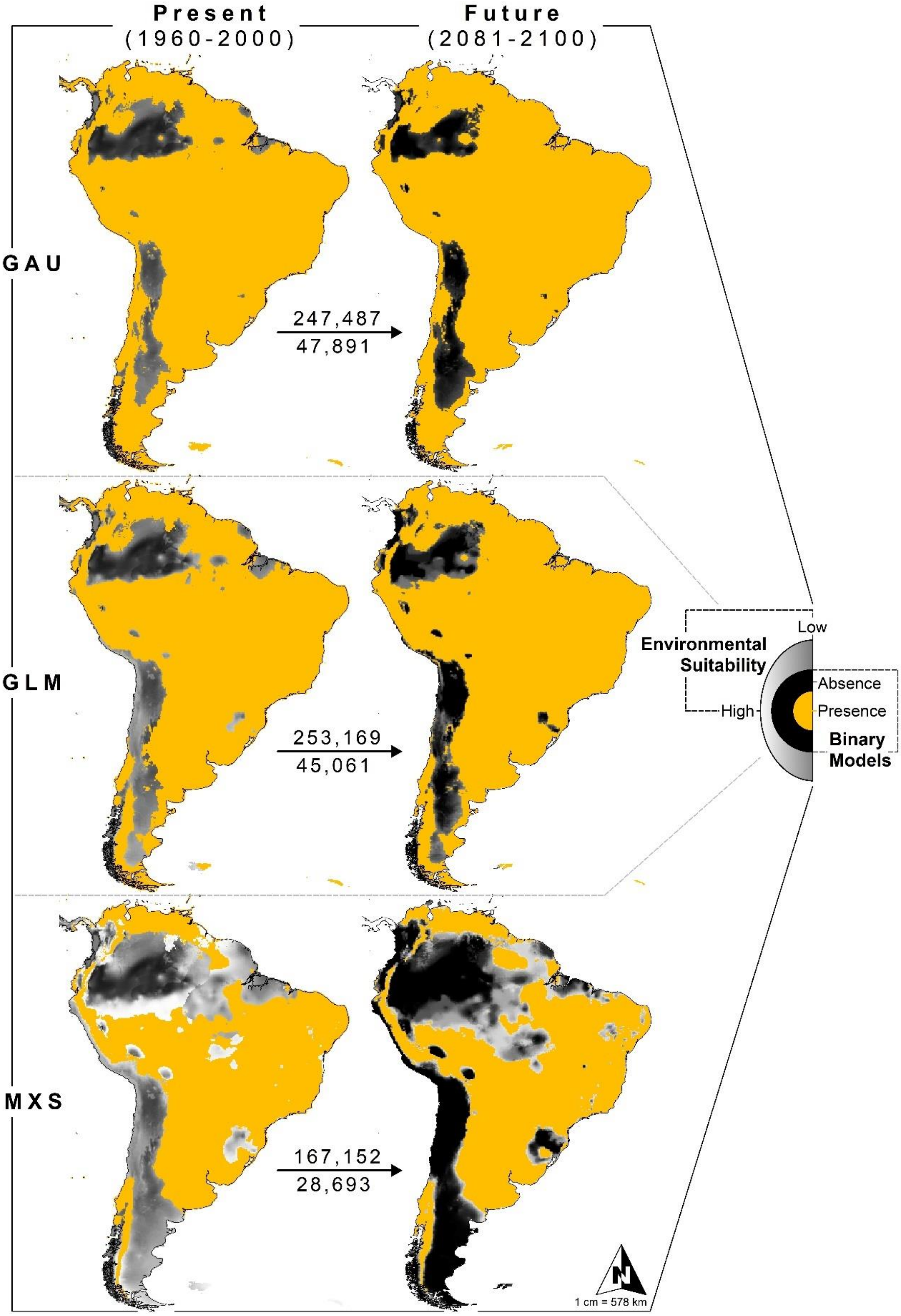
Figure 3. Flowchart depicting the cyanobacteria distribution modeling procedures showing the four main steps required to model the potential species distribution: occurrence records A; Environmental variables B- Modeling procedures C; Evaluation of model D. The flowchart summarizes the procedures performed for the modeling of cyanobacteria. The processes that were used were used to make the models in the present and future scenarios.

2.5 Ensemble

To ensure a high quality of the models, we represent the final distributions using consensus maps to reduce the uncertainties associated with each algorithm (ARAÚJO; NEW, 2007). We made the consensus maps using the mean of the models that presented Jaccard values above the mean. The mean was 0.945, which means that the GLM method was not used in the *ensemble*. The idea of consensus models considers that different errors can affect the final result (e.g., the sensitivity of models, lack of true absences). For this reason, it has been argued in the literature that the use of consensus maps as final distribution models can reduce the number of errors (DINIZ-FILHO et al., 2010). This method produces ecological niche models from the most accurate algorithms, resulting in potentially more realistic predictions.

3 Results

The predicted potential distribution for the group (Phylum Cyanobacteria) of cyanobacteria was not similar in the climate scenarios considered (present and future scenarios). We observed differences in the size of the potential distribution for the group when using the different algorithms to model (Figure 4). We observed that the areas with suitability for the group in the MXS method scenarios were smaller than the other algorithms used. The evaluation values of the models obtained by the Jaccard method were MSX (0.988), GAU (0.984), GLM (0.861), *Ensemble* (0.991). Such values were high and indicated models with excellent fit.



2257

2258 **Figure 4.** Ecological niche modeling was used to estimate the potential distributions for
2259 two cyanobacteria and, consequently, for monitoring. These models represent three
2260 modeling methods [Generalized Linear Model (GLM), Gaussian (GAU), and Maximum
2261 Entropy (MAX)] for potentially toxic cyanobacteria (*R. raciborskii* and *M. aeruginosa*).

Analyzing the projection of suitable areas for the present and future scenarios (Figure 3A and 3B), we observe that for South America, there is a broad geographic distribution of suitable areas, which corresponds to an area of 17,840,000 km^2 with suitability for the occurrence of toxic cyanobacteria. In Argentina, Bolivia, Paraguay, Uruguay, and practically all Brazilian regions, there was high suitability for the occurrence of the group of toxic cyanobacteria in both projected scenarios. We also observed that for the current scenario (14,385,469 km2), the suitability was lower in the northern portion of Brazil, comprising the Amazon Basin. Nonetheless, in the projection for the future scenario (15,088,370 km2) (Figure 3B), we observed an increase in suitable areas, with an increase of 702,901km2 of areas with suitability for the occurrence of cyanobacteria.

Furthermore, from the current scenario to the future (Figure 3C), we observed an increase in favorable areas, especially in the northern South American region, with advances in aquatic environments within the Amazon Basin. Also, a loss of areas with suitability in the lower region of Chile. In general, there was an increase of suitable regions in climate change projections. Furthermore, when we looked at the maximum adequacy values, our modeling results indicated concern.

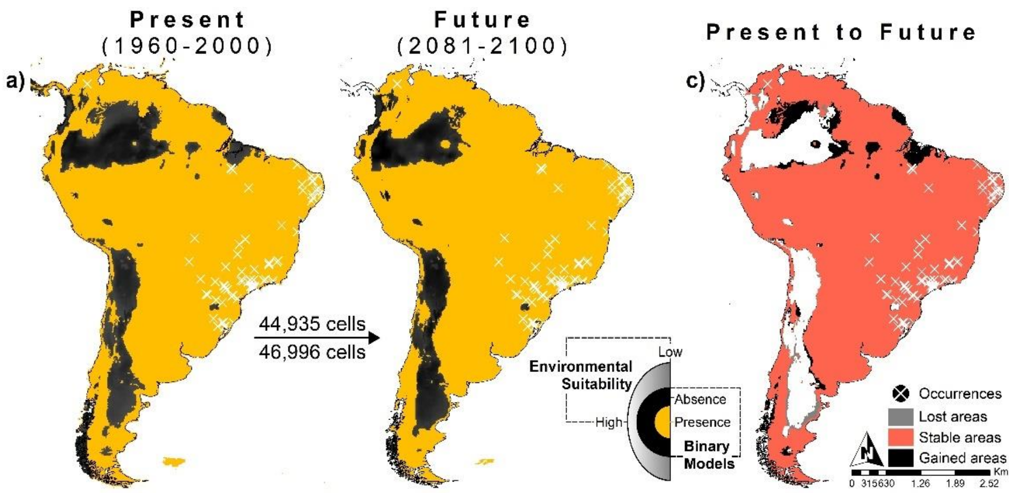


Figure 5. Ecological niche modeling used to estimate the potential distributions for cyanobacteria. These models represent three modeling methods [Generalized Linear Model (GLM), Gaussian (GAU), and Maximum Entropy (MAX)] for potentially toxic cyanobacteria.

4 Discussion

Here, we showed the current and future potential distribution of a group of cyanobacteria. Estimating the potential distribution of species is one of the main objectives of macroecology, especially when sampling biases can affect knowledge about how the environment and variables affect this distribution. Our niche models predicted potential distribution areas for cyanobacterial species based on their environmental requirements. We chose to make a single model joining the occurrences of the three species because cyanobacteria have similar environmental preferences, so there would be no significant differences if we made models for each species individually. Therefore, to reveal the potential distribution and area suitability of cyanobacteria, we consider that the distribution patterns of these organisms depend on environmental filters (PADISÁK; VASAS; BORICS, 2016).

Although the prediction that changes in climate will contribute to the increase in temperature and precipitation patterns, the evidence that the higher temperature will favor the occurrence of cyanobacterial blooming and the impact of altered rain patterns is largely under-researched and, therefore, even less understood (REICHWALDT; GHADOUANI, 2012). Overall, we can expect the two extremes, greater frequency of storms and prolonged droughts. The frequency of extreme rain events will change precipitation limits, and heavy rains will occur more frequently (CHANGING; OF, 2003). However, total precipitation is forecasted to change slowly (GROISMAN et al., 2005). Consequently, changes in rainfall patterns will lead to favorable conditions for the growth of cyanobacteria due to a more significant entry of nutrients into water bodies during heavy rains (BUDAI; CLEMENT, 2007), combined with potentially longer periods of high evaporation and stratification (BOUVY et al., 2003). Such conditions can contribute to intensifying the eutrophication process and prolonged periods of heating without mixing the water column (CHARLTON et al., 2018). Primarily, precipitation episodes produce changes in physicochemical conditions (e.g., temperature, nutrients, light, conductivity). These changes, in turn, depend on the particularities of the precipitation event, the hydrology of the basin, the use of the soil in the catchment area, and the trophic state of the aquatic system (NÕGES et al., 2011). In the absence of nutrient limitations, higher concentrations of nutrients in eutrophic systems lead to higher biomass loading and production capacities, which favors the occurrence of potentially toxic cyanobacterial biomass due to its greater affinity for nutrients compared to other phytoplankton (HUISMAN et al., 2018).

On the other hand, the frequent occurrence of heavy rain events can also lead to a temporary halt in the proliferation of cyanobacteria due to discharge and de-stratification, and significant storm events have a long-term adverse effect on cyanobacteria proliferation (XIAO et al., 2017). We notice that cyanobacteria are sensitive to temperature, and it is known that environmental variables play a role at the beginning of the formation of the resulting colonies de *M. aeruginosa* (HUISMAN et al., 2018).

The lack of suitability observed in some regions may reflect incomplete data from regional distribution or concentration in high human density centers (WHITTAKER et al., 2005b). This problem is quite common for many groups and can seriously affect the ENM results (KRAMER-SCHADT et al., 2013). Thus, the estimated occurrence of the species of cyanobacteria produced may not yet fully reflect the distribution capacity in Brazilian freshwater environments. Our results show that the most significant concern areas are distributed in locations with high human density and public supply reservoirs.

The lack of suitability observed in some regions may reflect incomplete regional distribution or concentration data in areas high-populated by humans. Thus, the estimated occurrence of the cyanobacteria may not yet fully reflect the distribution capacity in América of Sul freshwater environments.

Problems of cyanobacteria growth in freshwater environments for man arise due to direct contact during their recreational time in contaminated water bodies, through poor treatment of drinking water reservoirs, by bioaccumulation of microcystins and other cyanotoxins in biological matrices, or through the consumption of irrigated vegetables and contaminated fish (as a result of these risks, maximum daily intake of 0.04 μg kg^{-1} body weight of microcystin-LR (MC-LR) from fish and other food products is recommended) (CHIA et al., 2021). Cyanobacterial toxins can also enter the human body by inhalation or absorption through the skin (ZANCHETT; OLIVEIRA-FILHO, 2013). In Brazil, two intoxication events in human beings caused by cyanobacteria are described. In 1988, an epidemiological correlation was found between cyanobacterial blooms in the Itaparica Reservoir (Bahia, Brazil) and the death of 88 people and 2000 people had gastroenteritis symptoms due to intoxication (TEIXEIRA et al., 1993). In 1996, microcystin, a toxin released by *M. aeruginosa*in in the water supply from the Caruaru Hemodialysis Center in Pernambuco, Brazil, was confirmed. Out of 116 intoxicated people, 76 patients died after treatment at this institution (AZEVEDO et al., 2002).

Overall, compared to the current scenario, we observed that the distributions of the two species were similar. Our consensus distribution maps revealed that species are distributed in more significant numbers of occurrences in the Southeast region and smaller proportions in the northern region of the country, comprising the Amazon basin. Our findings indicate that areas of suitability for the current scenario are higher human density, and the supply reservoirs have persistent blooming histories. Regarding the future scenario, our projection results indicate an increase in the areas with the potential distribution of the two species.

Therefore, the monitoring of toxic cyanobacteria and cyanotoxins is essential to identify potential risk sites. Usually, monitoring programs collect samples in the field and analyze them in the laboratory, requiring both time, sophisticated equipment, and specialized staff, limiting the collection points and frequency. Consequently, conventional monitoring programs are limited to providing a generic assessment of the ecological quality of the studied sites and are insufficient for providing monitored bloom development warning systems throughout the monitored water body (HUNTER et al., 2010). It is well known that the rapid detection capability of potentially toxic cyanobacteria can be accomplished through the ability to detect both remote images and packages and arrays that can detect and provide real-time information (STUMPF et al., 2016). In countries such as the United States, rapid advances are being made to detect events and, in some cases, to predict their occurrence and potentially reduce their impacts (SELLNER; DOUCETTE; KIRKPATRICK, 2003). In Brazil, such advances and techniques are still far from being widespread, which may underestimate the current occurrence rates of bloom events in the country, affecting the availability of event data.

In an attempt to reduce ignorance about the geographical distribution of potentially toxic cyanobacteria, also known as a Wallacean deficit (WHITTAKER et al., 2005b), it is necessary not only to record collection biases but also to identify priority areas to overcome this problem (SOUSA-BAENA; GARCIA; PETERSON, 2014). Given this, we also propose the use of suitable habitat extension maps (concern areas maps). This approach is practical for monitoring planning because it combines readily available data from databases for many species in regions with insufficient data (LIST et al., 2010). Thus, we hope that this work will stimulate further sampling of the potential distribution of cyanobacteria and increased efforts to understand and predict their blooms, reducing their occurrence and impacts.

The suitable areas that we observe for the species are distributed in the central-southeast portion of South America. For most species with distribution in low latitudes (temperate climate), the temperature is considered the main barrier for expanding to latitudes. Considering the occurrence data of *R. raciborskii* at low temperatures, its occurrence is possible at temperatures below 12º C. This winter survival ensures that it reestablishes a population when conditions become favorable again, which allows the species to expand and thrive in new environments (DOKULIL, 2016). This ensures a competitive advantage, allowing them to colonize waters in temperate or cooler regions of the globe. (VÁRKONYI et al., 2000). To ensure the successful dispersal of cyanobacteria, traveling along river courses has been the most evident form of dispersal, as the risk of desiccation can be controlled. The successful dispersal of *R. raciborskii* is primarily attributed to its ability to tolerate travel in river courses. (PADISÁK, 1997).

For *M. aeruginosa,* which forms colonies surrounded by mucilage, colony formation is essential for its success in freshwater ecosystems. (BULLERJAHN et al., 2016). The wind is a crucial dispersing agent (CHRISOSTOMOU et al., 2009) and animals that can also carry their vegetative forms on the body surface (PADISÁK; VASAS; BORICS, 2016). Environmental variables play a role in the early formation of your colonies and influence the size and morphology of the resulting colonies (XIAO et al., 2017). The species *P. agardhii* is a widespread cyanobacterium that changes in time scale from days to weeks due to changes in cloudiness or wind-induced sediment resuspension in shallow and turbid lakes. Changes in light conditions affect microcystin production, and thus *P. agardhii* is more toxic during periods of sunny weather when recreational activities in lakes are more attractive. (TONK et al., 2005).

5 Conclusions

Our results indicate that the available data on the geographic distribution of cyanobacterial species in freshwater environments is far from complete and has obvious geographic biases. We know that many of the records of cyanobacteria in aquatic environments were not accessible, which may have reduced our ability to assess species distribution. In our study, we mapped the available data on toxic cyanobacteria, and our sampling effort was invested on a world scale and our models for the neotropical environments of South America. Our results can provide relevant information about sampling gaps in regions that need more research to improve distribution data on the occurrence of these species and support monitoring and management practices for these species.

The toxic species are widely distributed, respond rapidly to current environmental changes, and should undoubtedly occur in areas not detected in our ENMs analysis. We know that cyanobacteria multiply in the environment and can be concentrated in certain lakes and reservoirs by wind action. The formation and dispersion of blooms can change in days or even hours, making it difficult to assess the associated hazards. Then, planning a monitoring program should consider the objective to be achieved and the characteristics of the evaluated water body. Furthermore, monitoring programs may also include identifying susceptible areas and information and education for the population. Our monitoring planning approach, which combines data available from the database, can stimulate new sampling methods of the potential distribution of cyanobacteria and reduce the impacts of toxins in the supply areas.

6 Acknowledgments

AG thanks FAPEG-CAPES (Research Support Foundation of the State of Goiás - Coordination for the Improvement of Higher Education Personnel) for her Ph.D. DPS was supported by the CNPq research productivity fellowship (304494/2019-4).

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CONCLUSÕES GERAIS

No geral, as distribuições geográficas das cianobactérias são pouco conhecidas e apresentam inúmeras lacunas de informação (déficit Wallaceano) frequentemente relacionadas com a falta de esforços de coleta. Na tese, os registros disponíveis sobre a distribuição geográfica das espécies de cianobactérias em ambientes de água doce estão longe de estar completos. Sabemos que muitos dos registros de cianobactérias em ambientes aquáticos não eram acessíveis, o que pode ter reduzido a capacidade de avaliar a distribuição potencial das espécies de cianobactérias. Nós, demonstramos que muitos dos eventos de floração de cianobactérias fitossanitárias relatados na literatura brasileira são dos gêneros tóxicos Microcystis, Raphidiopsis e Dolichospermum. Esses gêneros estão amplamente distribuídos no Brasil e respondem rapidamente às mudanças ambientais atuais e certamente devem ocorrer em áreas que não foram detectadas atualmente em nossas análises cienciométricas e ENMs.

Aqui, os dados disponíveis sobre as cianobactérias tóxicas e o esforço amostral foi investido em escala mundial. Para produzirmos os modelos para a América do Sul, optamos por usar registros de ocorrência em escala global, pois as espécies de cianobactérias estão globalmente distribuídas e, portanto, usar dados apenas para o Brasil deixaria o modelo incompleto. Nessas condições, não estaríamos capturando todo o nicho realizado da espécie, enviesando o modelo. Na América do Sul existem evidências que destacam um grande esforço amostral na região da Mata Atlântica, enquanto na região da Floresta Amazônica poucas regiões são de fato amostradas. A porção norte do Brasil, que ainda apresenta baixa aptidão para eventos de floração em comparação com as ocorrências em outras regiões brasileiras com grande concentração de centros urbanos e população, precisa ser amostrada com maior precisão. De fato, os resultados aqui apresentados podem fornecer informações relevantes sobre as lacunas de amostragem em regiões que precisam de mais pesquisas para melhorar os dados de distribuição sobre a ocorrência dessas espécies e apoiar as práticas de monitoramento dessas espécies. O estudo é inovador, pois na literatura especializada não há nenhum trabalho publicado envolvendo a modelagem de nicho e cianobactérias em ambientes de água doce Neotropical. Dessa forma, o estudo poderá fornecer embasamento teórico para futuras medidas de monitoramento, podendo esta abordagem ser aplicada não somente na região neotropical, mas em qualquer outra área de estudo.