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Chapter

Picocyanobacteria in Surface Water Bodies

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Abstract

Cyanobacterial harmful algal blooms (CyanoHABs) in lentic, low tidal water bodies with high concentrations of easily assimilated nutrients have generated worldwide concern. However, CyanoHABs often formed from a variety of lesser-known taxa, such as nanocyanobacteria and picocyanobacteria, which are characterized as numerous and ubiquitous in diverse environments. Studies indicate that some taxa of picocyanobacteria can produce toxins. However, their identification through conventional methods is limited by their size and physiological plasticity, recently molecular methods have been chosen for more reliable results. This systematic review aims to summarize the results of original research articles on predominant picocyanobacteria in surface water bodies collected in indexed journal articles and gray literature. The methodology used consisted of searching for original publications in 3 specific databases and one general, using thesauri and free terms; the articles were filtered by previously defined inclusion and exclusion criteria. Thirty-four articles were selected and analyzed. The results show that the predominant picocyanobacteria in freshwater systems belong to the genus *Synechococcus*, reported in oligotrophic systems and capable of producing cyanotoxins. Likewise, from 2015 to 2019, the largest number of publications on this topic was obtained, mainly in countries such as China and the United States, which invest in research resources.

Keywords: cyanobacteria, cyanoHAB, freshwater, picocyanobacteria

1. Introduction

In recent years, the excessive growth of phytoplanktonic organisms in reservoirs, lagoons, and in general, in lentic, low-tide water bodies with a high concentration of phosphate and nitrogenous nutrients, which are easily assimilated, has generated worldwide concern [1, 2]. Physical factors such as temperature, solar radiation, wind, rain, water column stratification, water flow, or biological interactions with other organisms, among others, play an important role in the so-called cyanobacterial harmful blooms (CyanoHAB) [3, 4].

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CyanoHABs can be defined as events in which visually noticeable turbidity of the water occurs due to a rapid accumulation of cyanobacterial cells, often at the water surface, but sometimes deeper in the water column [3, 5]. These blooms have the potential to generate a variety of adverse effects due to their ability to produce toxins [6, 7] that, in turn, cause negative impacts on animals, including humans, aquatic ecosystems, the economy, drinking water supply, real property values, and recreational activities, including swimming and commercial and recreational fishing [8, 9].

CyanoHAB-forming cyanobacteria are often accompanied by a variety of lesser-known taxa that contribute greatly to the total cyanoHAB biomass, such as nanocyanobacteria and picocyanobacteria [10]; e.g., Vardaka et al. [11] have described blooms composed of multiple species.

Picocyanobacteria are bacteria that play a key role in primary production and dominate phytoplankton biomass in both oligotrophic and eutrophic waters [12, 13]. They are the smallest cell-sized, most numerous, and ubiquitous cyanobacteria in freshwater, marine, and even in environments with high salt concentrations [14]. Among the cyanobacteria are the so-called planktonic picocyanobacteria; microorganisms that are part of the smallest aquatic plankton and are often associated with various species [15]. In freshwater, the main representatives are the genera *Synechococcus*, *Cyanobium,* and *Synechocystis*, and in brackish water, *Synechococcus* and *Prochlorococcus* predominate [13, 16].

Although this group of microorganisms is ubiquitous and causes environmental concerns, it is still understudied [13]. Much research continues to use microscopy techniques that require long processing times and can produce erroneous results [17] since picocyanobacteria are difficult to observe and most of the time are found forming groups or present diverse biological forms ranging from single cells to microcolonies [18]; besides, their physiological or epigenetic plasticity means that cyanobacteria with the same genotype can appear very different due to the external factors to which they are influenced [19]. This is determined by the growth conditions, adaptations, and expansion of the cells in response to the stay in complex communities and fluctuating environments [20].

Recently, attempts have been made to study picocyanobacteria through molecular techniques by amplification and sequencing of the 16S rRNA gene or next-generation sequencing (NGS), which allows obtaining results quickly, with high sensitivity and high detection efficiency [21]. However, research aimed at describing picocyanobacteria present in surface waters is atomized, moreover, it is limited and there are no current review articles focused on this. Therefore, this study aims to summarize the results of original research articles on the predominant picocyanobacteria in surface water bodies collected from indexed journal articles and gray literature involving the molecular identification of picocyanobacteria. It also provides an understanding of the factors that influence the predominance of picocyanobacteria in these environments, such as trophic status and the method of molecular identification, as well as research trends and the countries that contribute most to this field of research.

2. Materials and methods

2.1 Data collection

This research was conducted as described in the PRISMA Declaration [22]. Thus, for the development of this study, a systematic literature search was carried out in

("Picocyanobacteria" AND lakes OR lagoons AND Freshwater)
("Picocyanobacteria" AND reservoirs OR dams AND freshwater)
("Picocyanobacteria" OR "smallest cyanobacteria" AND freshwater)
("Smallest Cyanobacteria" AND lakes OR lagoons AND freshwater)
("Picocyanobacteria" OR "smallest cyanobacteria" AND lagoons OR lakes AND freshwater)
("Small blue-green algaes" AND "freshwater" OR "sweet water")
("Small blue-green algaes" AND "lakes" OR "lagoons")
("Small blue-green algaes" AND "reservoirs" OR "dams")
("Smallest cyanobacteria" AND "reservoirs" OR "dams")
("Smallest cyanobacteria" AND "freshwater" OR "sweet water")
("Smallest cyanobacteria" AND "lagoons" OR "lakes")
("Picocyanobacteria" AND "reservoirs" OR "dams")

Table 1.
Searches applied for the selection of articles in the three databases used.

three bibliographic databases: Scopus, ScienceDirect, and Scielo, which articles are part of publications in indexed journals [23]; in addition, the Google Scholar search engine was used, focused and specialized in the search for scientific-academic content and bibliography that includes gray literature defined by Garousi et al. [24] as: "literature that is not formally published in sources such as books or journal articles". This allowed an exhaustive search, broadening the information to be analyzed.

Keywords were defined using free terms and the Agrovoc and DeCS thesauri to increase the sensitivity of the search: picocyanobacteria, freshwater, sweetwater, small cyanobacteria, reservoirs, dams, lakes, lagoons, and small blue-green algae. At the same time, Boolean operators (AND and OR) were used to logically connect concepts or groups of terms and to quickly broaden, specify, limit, and define the search (**Table 1**) see annex.

We then proceeded to eliminate duplicate articles using the free tool Zotero-5.0.93. Three investigators independently applied the inclusion and exclusion criteria presented in **Table 2** (see annex) to the resulting articles to avoid bias and ensure reproducibility of the selection.

2.2 Data analysis

The statistical program R Studio® (V 3.6.1) was used to perform the descriptive analysis of the collected data. A database was created using Microsoft Excel where

Inclusion criteria	Exclusion criteria
Original article in english	Brackish water bodies
Molecular identification of picocyanobacteria	Use of collection strains
Field collected sample	

Table 2.
Inclusion and exclusion criteria established and applied to each article for eligibility.

certain attributes of the research were recorded, such as year of publication, the country where the article was published, journal, picocyanobacteria species, water body, trophic state, and picocyanobacteria molecular identification method. Particularly, using this database, the relative and absolute frequencies of the number of publications of pico-cyanobacteria per year, the number of publications per country, and the number and species of picocyanobacteria most frequently found were determined, as well as some factors related to the prevalence of picocyanobacteria in surface water bodies.

The free software VOSviewer (V 1.6.14) was used to analyze the data on the frequencies of index and author keywords to determine the most frequent keywords researched in the articles included in the systematic review and thus identify trends in research on the topic.

3. Results

3.1 Search strategy and articles obtained

A total of 371 articles were obtained from the databases (Scopus: 251, ScienceDirect: 118, and Scielo: 2) and 57 articles from the Google Scholar search engine. A total of 243 duplicate articles were deleted, resulting in a total of 185 articles subject to eligibility. After applying the inclusion and exclusion criteria, 34 articles were filtered out (**Figure 1**) see annex.

3.2 Articles description

Table 3 shows the detailed information of each of the articles: year of publication, authors, journal in which it was published, the molecular method applied for the identification of picocyanobacteria, and type of water body where the research was carried out.
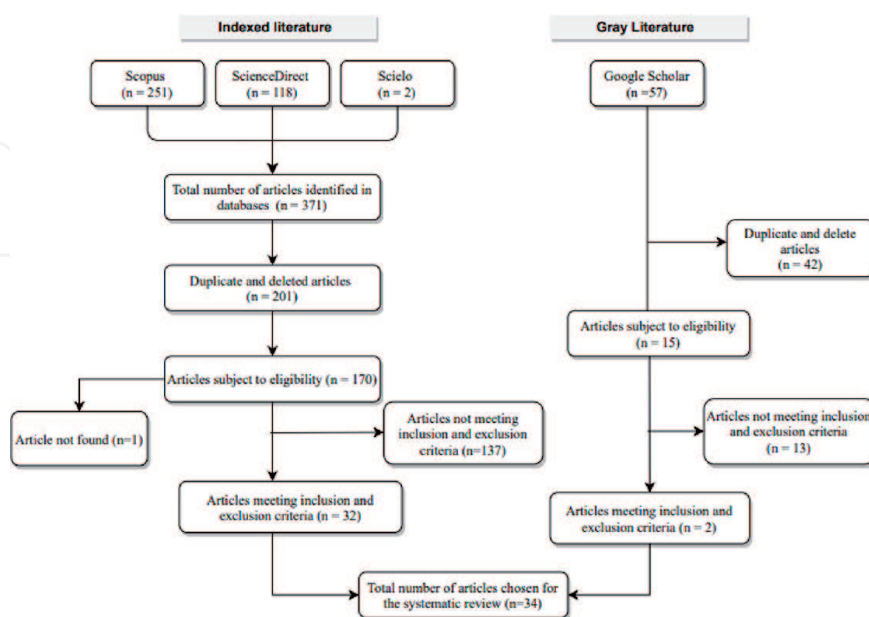

Figure 1.
Flowchart of the research search strategy. Source: own elaboration through the application diagrams.net.

N°	Article name	Year	Author(s)	Journal	Molecular identification method	Water body
1	Sedimentary DNA record of eukaryotic algal and cyanobacterial communities in a shallow Lake driven by human activities and climate change	2021	Hanxiao Zhang, Shouliang Huo, Kevin M. Yeager, Fengchang Wu	Science of The Total Environment	Amplification and Sequencing of the 16S rRNA Gene	Lake
2	Spatiotemporal variability of cyanobacterial community in a Brazilian oligomesotrophic reservoir: The picocyanobacterial dominance	2019	Ana María M. Batista, Alessandra Giani	Ecohydrology & Hydrobiology	Amplification and Sequencing of the 16S rRNA Gene	Reservoir
3	Insights into the evolution of picocyanobacteria and phycoerythrin genes (mpeBA and cpeBA)	2019	Patricia Sánchez Baracaldo, Giorgio Bianchini, Andrea Di Cesare, cristiana Callieri, Nathan A. M. Chrisma	Frontiers in Microbiology	DNA Extraction by PCR and Genome Sequencing	Lake
4	Metabarcoding reveals a more complex cyanobacterial community than morphological identification	2019	Xiao Chuang, LShouliang Huoa, Jingtian Zhanga, Chunzi Ma, Zhe Xiao, Hanxiao Zhang, Beidou Xi, Xinghui Xia	Ecological Indicators	DNA Extraction, Amplification, and Sequencing of the 16S rRNA Gene	Lake and Pond
5	High-throughput DNA sequencing reveals the dominance of pico- and other filamentous cyanobacteria in an urban freshwater Lake	2019	Li, H., Alsanea, A., Barber, M., Goel, R.	Science of the Total Environment	Sequencing of DNA by PCR	Lake
6	Seasonal succession and spatial distribution of bacterial community structure in a eutrophic freshwater Lake, Lake Taihu	2019	Zhu, C., Zhang, J., Nawaz, M.Z., Mahboob, S., Al-Ghanim, K.A., Khan, I.A., Lu, Z., Chen, T	Science of the Total Environment	Amplification and Sequencing of the 16S rRNA Gene	Lake

N°	Article name	Year	Author(s)	Journal	Molecular identification method	Water body
7	Seasonal succession and spatial distribution of bacterial community structure in a eutrophic freshwater Lake, Lake Taihu	2018	Zhu, C., Zhang, J., Nawaz, M.Z., Mahboob, S., Al-Ghanim, K.A., Khan, I.A., Lu, Z., Chen, T	Science of the Total Environment	Amplification and Sequencing of the 16S rRNA Gene	Lake
8	Ecological and genomic features of two widespread freshwater picocyanobacteria	2018	Cabello-Yeves, P.J., Picazo, A., Camacho, A., Callieri, C., Rosselli, R., Roda-Garcia, J.J., Coutinho, F.H., Rodriguez-Valera, F.	Environmental Microbiology	Sequencing of DNA by PCR	Reservoir
9	Planktonic cyanobacteria from a tropical reservoir of Southeastern Brazil: A picocyanobacteria rich community and new approaches for its characterization	2018	Marcele Laux, Vera Regina Werner, Ricardo A. Vialle, José Miguel Ortega, Alessandra Giani	Nova Hedwigia	Amplification of DNA by PCR	Reservoir
10	Novel *Synechococcus* genomes reconstructed from freshwater reservoirs	2017	Cabello-Yeves, P.J., Haro-Moreno, J.M., Martin-Cuadrado, A.-B., Ghai, R., Picazo, A., Camacho, A., Rodriguez-Valera, F.	Frontiers in Microbiology	Amplification and Sequencing of the 16S rRNA Gene	Reservoir
11	Metagenomic analysis in Lake Onego (Russia) *Synechococcus* cyanobacteria	2017	Vasileva, A., Skopina, M., Averina, S., Gavrilova, O., Ivanikova, N., Pinevich, A	Journal of Great Lakes Research	Amplification and Sequencing of the 16S rRNA Gene	Lake
12	Phenotypic plasticity in freshwater picocyanobacteria	2017	Huber, P., Diovisalvi, N., Ferraro, M., Metz, S., Lagomarsino, L., Llames, M.E., Royo-Llonch, M., Bustingorry, J., Escaray, R.	Environmental Microbiology	Amplification and Sequencing of the 16S rRNA Gene	Lake

N°	Article name	Year	Author(s)	Journal	Molecular identification method	Water body
13	Microbial community structure and interannual change in the last epishelf lake ecosystem in the north polar region	2017	Taller, M., Vincent, W.F., Lionard, M., Hamilton, A.K., Lovejoy, C	Frontiers in Marine Science	Amplification and Sequencing of the 16S rRNA Gene	Lake
14	*Synechococcus* diversity along a trophic gradient in the Osterseen Lake District, Bavaria	2016	Ruber, J., Bauer, F.R., Millard, A.D., Raeder, U., Geist, J., Zwirglmaier, K	Microbiology (United Kingdom)	Amplification and Sequencing of the 16S rRNA Gene	Lake
15	CO2 alters picophytoplankton community structure in freshwater ecosystems	2016	Shi, X., Li, S., Wang, X., Liu, M., Kong, F.	Fundamental and Applied Limnology	DNA Sequencing of 18S RNA Genes	Lake
16	Community analysis of picocyanobacteria in an oligotrophic lake by cloning 16S rRNA gene and 16S rRNA gene amplicon sequencing	2015	Fujimoto,N., Mizuno, K., Yokoyama, T., Ohnishi, A., Suzuki, M., Watanabe, S., Komatsu, K., Sakata, Y., Kishida, N., Akiba, M., Matsukura, S.	Journal of General and Applied Microbiology	Amplification and Sequencing of the 16S rRNA Gene	Lake
17	Diversity of Lake Ladoga (Russia) bacterial plankton inferred from 16S rRNA gene pyrosequencing: An emphasis on picocyanobacteria	2015	Skopina, M., Pershina, E., Andronov, E., Vasileva, A., Averina, S., Gavrilova, O., Ivanikova, N., Pinevich, A.	Journal of Great Lakes Research	Amplification and Sequencing of the 16S rRNA Gene	Lake
18	Genetic diversity of picocyanobacteria in Tibetan lakes: Assessing the endemic and universal distributions	2014	Huang, S., Liu, Y., Hu, A., Liu, X., Chen, F., Yao, T., Jiao, N.	Applied and Environmental Microbiology	Amplification and Sequencing of the 16S and 23S rRNA Genes	Lake
19	Free-living and particle-associated bacterioplankton in large rivers of the Mississippi River basin demonstrate biogeographic patterns	2014	Colin R. Jackson, Justin J. Millar, Jason T. Payne, Clifford A. Ochs	Applied and Environmental Microbiology	DNA Extraction, Amplification, and Sequencing of the 16S rRNA Gene	River

N°	Article name	Year	Author(s)	Journal	Molecular identification method	Water body
20	Detection and expression of genes for phosphorus metabolism in picocyanobacteria from the Laurentian Great Lakes	2013	Kutovaya, O.A., McKay, R.M.L., Bullerjahn, G.S.	Journal of Great Lakes Research	Sequencing of DNA by PCR	Lake
21	Seasonal and Spatial Diversity of Picocyanobacteria Community in the Great Mazurian Lakes Derived from DGGE Analyses of 16S rDNA and cpcBA-IGS Markers	2013	Jasser, I., Królicka, A., Jakubiec, K., Chróst, RJ	Journal of Microbiology and Biotechnology	DGGE analysis of molecular markers derived from the 16S–23S internal transcribed spacer (ITS) of the ribosomal operon.	Lake
22	Picocyanobacterial community structure and space–time dynamics in the subalpine Lake Maggiore (N. Italy)	2012	Callieri, C., Caravati, E., Corno, G., Bertoni, R.	Journal of Limnology	Amplification and Sequencing of the 16S and 23S rRNA Genes	Lake
23	Genome sequences of siphoviruses infecting marine *Synechococcus* unveil a diverse cyanophage group and extensive phage-host genetic exchanges	2012	Sijun Huang, Kui Wang, Nianzhi Jiao, Feng Chen	Environmental Microbiology	Amplification and Sequencing of the 16S rRNA Gene	Bay
24	Vertical and longitudinal distribution patterns of different bacterioplankton populations in a canyon-shaped, deep prealpine lake	2011	Salcher, M.M., Pernthaler, J., Frater, N., Posch, T.	Limnology and Oceanography	Amplification and Sequencing of the 16S rRNA Gene	Lake
25	East Tibetan lakes harbor novel clusters of picocyanobacteria as inferred from the 16S–23S rRNA internal transcribed spacer sequences	2010	Wu, Q.L., Xing, P., Liu, W.-T.	Microbial Ecology	Fragment Polymorphism Analysis of 16S–23S rRNA Internal Transcribed Spacer (ITS) PCR Amplicon	Lake
26	Photosynthetic picoplankton dynamics in Lake Tahoe: Temporal and spatial niche partitioning among prokaryotic and eukaryotic cells	2009	Winder, M.	Journal of Plankton Research	Phycoerythrin (PE) and Chlorophyll (Chl) Fluorescence by Cytogram	Lake

N°	Article name	Year	Author(s)	Journal	Molecular identification method	Water body
27	High ratio of bacteriochlorophyll biosynthesis genes to chlorophyll biosynthesis genes in bacteria of humic lakes	2009	Eiler, A., Beier, S., Säwström, C., Karlsson, J., Bertilsson, S.	Applied and Environmental Microbiology	Sequencing of DNA by PCR	Lake
28	Lake superior supports novel clusters of cyanobacterial picoplankton	2007	Ivanikova, N.V., Popels, L.C., McKay, R.M.L., Bullerjahn, G.S.	Applied and Environmental Microbiology	Sequencing of 16S rRNA Gene and cpcBA Phycocyanin Operon Intergenic Spacer (IGS) Sequences	Lake
29	Photosynthetic characteristics and diversity of freshwater Synechococcus at two depths during different mixing conditions in a deep oligotrophic lake	2007	Callieri, C., Corno, G., Caravati, E., Galafassi, S., Bottinelli, M., Bertoni, R.	Journal of Limnology	Amplification and Sequencing of the 16S rRNA Gene	Lake
30	Abundance and diversity of picocyanobacteria in High Arctic lakes and fjords	2006	Patrick Van Hove, Warwick F. Vincent, Pierre E. Galand, Annick Wilmotte	Algological studies	DNA Extraction, Amplification, and Sequencing of the 16S rRNA Gene	Lake
31	Rapid establishment of clonal isolates of freshwater autotrophic picoplankton by single-cell and single-colony sorting	2003	Crosbie, N.D., Pöckl, M., Weisse, T.	Journal of Microbiological Methods	Direct Sequencing of the 16S rRNA Gene and cpcBA-IGS Region	Lake
32	Dispersal and phylogenetic diversity of nonmarine picocyanobacteria, inferred from 16S rRNA gene and cpcBA-intergenic spacer sequence analyses	2003	Crosbie, N.D., Pöckl, M., Weisse, T.	Applied and Environmental Microbiology	Amplification and Sequencing of the 16S rRNA Gene	Lake
33	Identification of cultured and uncultured picocyanobacteria from a mesotrophic freshwater lake based on the partial sequences of 16S rDNA	2001	Toshiya Katano Manabu Fukui Yasunori Watanabe	Limnology	Amplification and Sequencing of the 16S rRNA Gene	Lake

| N°	Article name	Year	Author(s)	Journal	Molecular identification method	Water body
34	Systematics and ecology of chlorophyte picoplankton in German Inland waters along a nutrient gradient	2001	Dominik Hepperle., Lothar Krienitz	International Review of Hydrobiology	Amplification of DNA by PCR	Lake

Table 3.
Summary of the results of each article selected for the research.

The number of publications per year ranged from 2001 to 2021. Of the 34 articles analyzed, it was found that 2019 was the year with the highest number of publications recorded on the subject, followed by 2017, which had five and four publications, respectively (**Table 3**) see annex. This is evidence that research on picocyanobacteria has increased in recent years.

In addition, **Figure 2** (see annex) shows the countries with the greatest number of research projects developed for the study and identification of picocyanobacteria in the environments described above. Thus, the country where the institute or center where the research was carried out is located was identified. It is important to clarify that these countries corresponded to the sampling sites.

The countries with the highest number of research studies were China (7), United States (6), and United Kingdom (3). The countries with at least two publications were: Brazil, Canada, Spain, Italy, Japan, and Russia. Germany, Argentina, Switzerland, Sweden, Austria, and Poland had only one publication.

Figure 3 (see annex) shows the picocyanobacteria identified in the articles analyzed, showing that *Synechococcus* was the predominant genus in surface water bodies, with a frequency of 24 articles, followed by *Cyanobium* with a frequency of 4 articles.
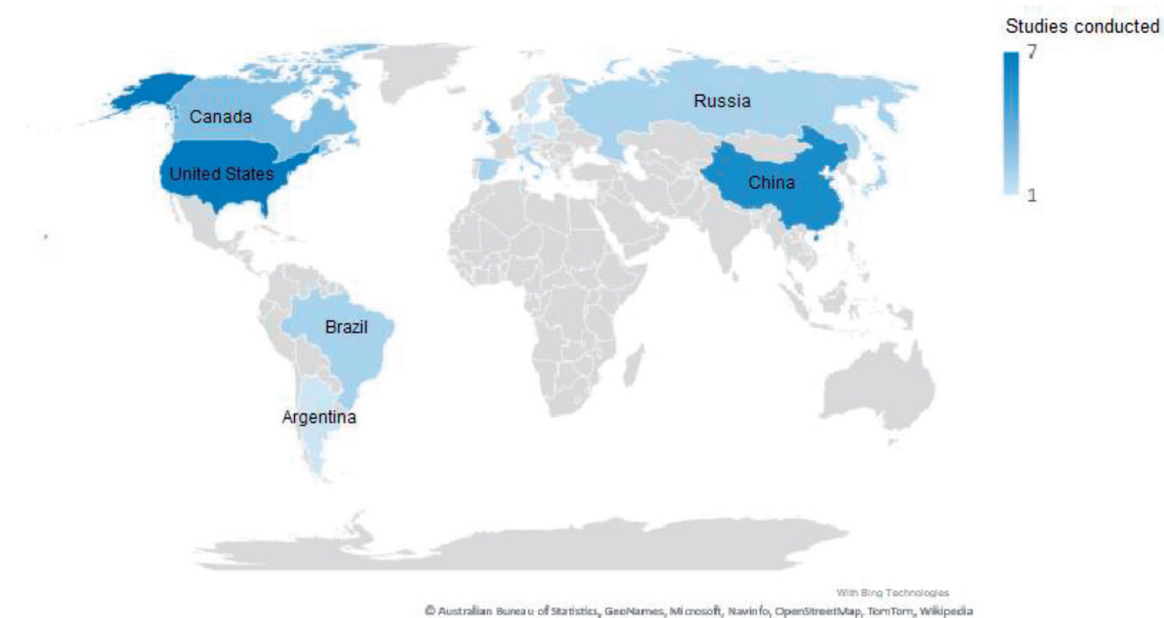
Figure 2.
Countries where research studies on picocyanobacteria molecularly identified in surface waters have been carried out.Source: own elaboration through the software program Microsoft Excel.
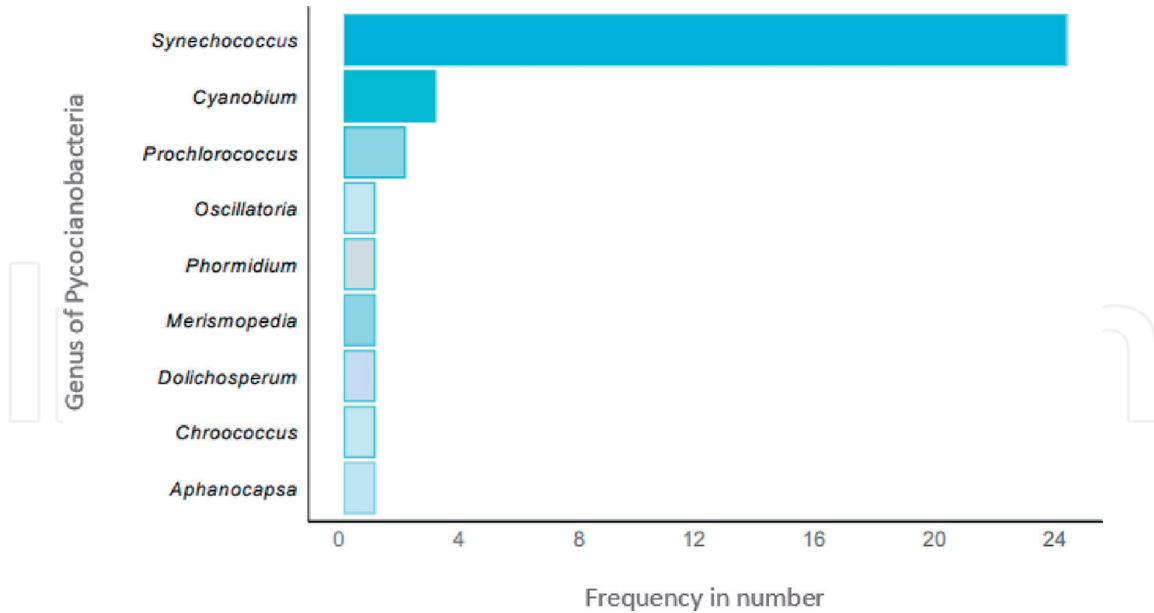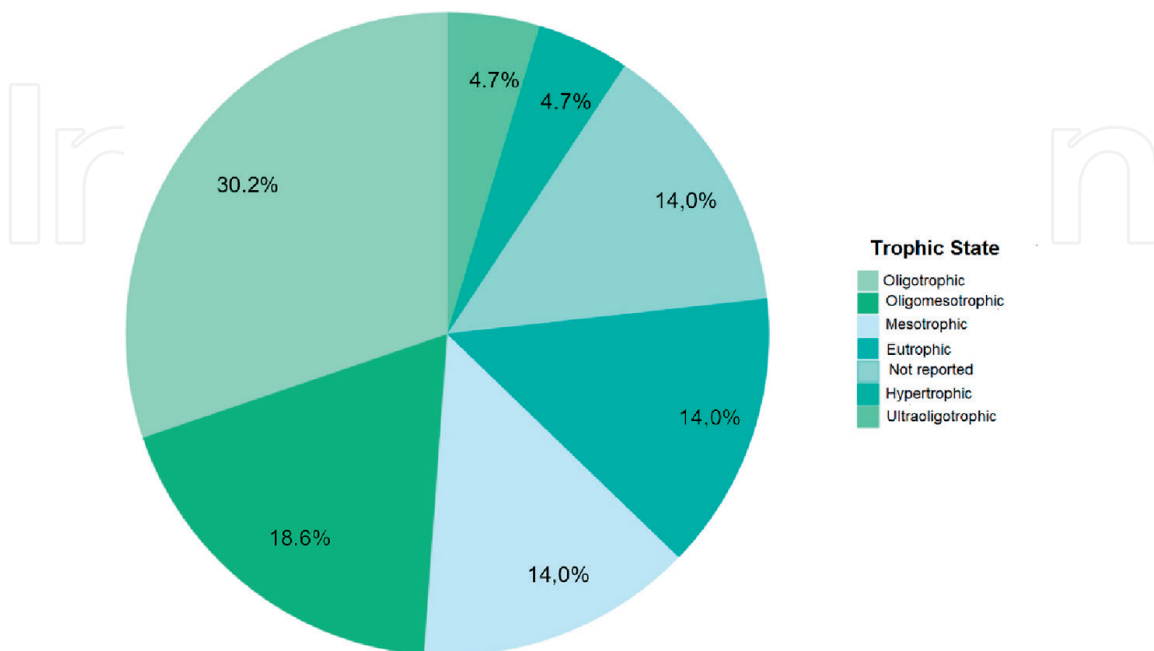
Figure 3.
Predominant picocyanobacteria in freshwater bodies. Source: own elaboration through the statistical tool RStudio.

As shown in **Figure 4** (see annex), oligotrophic lakes were the most studied for the identification of picocyanobacteria with a relative frequency of 32%, followed by oligomesotrophic lakes with 18.6% and mesotrophic and eutrophic lakes with 14% each.

3.3 Research topics on picocyanobacteria

The keyword mapping shows that the words: Cyanobacterium, Cyanobacteria, *Synechococcus*, Lake, Microbiology, 16S RNA, and Picocyanobacteria are the ones that

Figure 4.
Trophic state of the lakes studied in the articles of interest. Source: own elaboration through the statistical tool RStudio.

Figure 5.
Keyword mapping used in the search. Source: own elaboration through the application VOSviewer.

show the highest tendency in the present research with a frequency in the number of articles of 22, 18, 16, 14, 11, 11 and 10, respectively (**Figure 5**) see annex.

4. Discussion

The databases used in this systematic review were Scopus, Science Direct, and Scielo, as mentioned above. Scopus was chosen because it is widely known as one of the largest databases of abstracts and citations of peer-reviewed literature and has many records in the science area. In addition, it is easy to export bibliographic information for further analysis [25]. Likewise, ScienceDirect is a database with an extensive record of article records in various areas of science [26]. In the case of Scopus, this database focuses more on article records of researchers from South American countries [27]. With the choice of these three databases, the aim was to address the largest number of research studies on picocyanobacteria worldwide, since this is a subject that has not been studied extensively, as has been recognized by several authors.

In this regard, and after conducting the search strategy, it was found that the ScienceDirect and Scopus databases provided the largest number of publications due to their worldwide positioning as indexed databases and their mainly English-language journals. In addition, Scopus covers various areas of science, technology, medicine, social sciences, arts, and humanities [25]. Moreover, Sciencedirect is a database that also covers multidisciplinary scientific areas [28], however, it is limited to journals and books published directly by its publisher [29]. Therefore, although many of the articles included in this review were found, they did not exceed those found in Scopus [30].

In contrast, the Scielo open-access database, although it includes journals from all areas of science, only two articles associated with the topic were found in the search. This is since this database contains scientific articles published only in Latin America, and because it is a database that publishes mainly in Spanish and Portuguese [31].

There are different molecular techniques used for the identification of picocyanobacteria, in this review we found that the application of these techniques to characterize and amplify portions of the cyanobacterial genome has increased considerably in recent years. These techniques have proven to be valuable for comparing the structures of complex microbial communities, inferring phylogenetic relationships, and monitoring their dynamics in relation to environmental factors [32]. Cyanobacteria such as *Synechococcus* and *Cyanoothece* are particularly difficult to identify and classify [33], most molecular methods to identify them are based on total DNA or RNA extraction and amplification by PCR as shown in **Table 3**. However, there are biases related to the presence of PCR inhibitors and primer specificity and efficiency that can skew the results of community composition [33].

Concerning the number of annual publications obtained in the analyzed period (**Table 3**), there was consistency with the findings of Rousso et al. [4] in their research on predictive models for cyanobacterial blooms in freshwater lakes. They found that in the period between 2014 and 2019 the highest number of publications on cyanobacteria was reported, the same as this research, where it was found that between 2015 and 2019 the highest number of publications on picocyanobacteria was collected. However, the maximum number of publications found for the articles found that met the inclusion criteria was only 5 for the year 2019, indicating that there are still not many studies on picocyanobacteria [34]. Research on cyanobacteria appears to be strongly related to advances in monitoring technology, i.e., increased availability of data, knowledge of cyanobacterial ecology, physiology, and risks, among other factors [34]. Furthermore, due to the environmental problems associated with cyanobacteria and their potentially toxic blooms. Merel et al. [8] evidence that articles on cyanobacteria have increased significantly in the period 1995–2010, a trend that is expected to continue [8]. This systematic review shows that 2010 was a year where no significant reports on picocyanobacteria were found, which probably indicates that research is still focused on microplankton cyanobacteria instead of picocyanobacteria.

Regarding the countries where the studies were conducted, it was found that the United States and China have been outstanding countries for the number of scientific publications on cyanobacteria and their toxic blooms, this is demonstrated by the study conducted by Bertone [4], which analyzed the publications on CyanoHAB in different countries and found that most of the publications are focused on the United States, Northern Europe, Southeast China, Japan, and Oceania [4]. This result coincides with that found in this study (**Figure 2**), where the highest number of scientific articles on picocyanobacteria have been published in the United States and China.

The concentration of publications in developed countries such as these may be related to their economy and extensive scientific resources, the provision of funds for research and development, and the availability of data used for these purposes [35]. Also, these countries have managed to develop specialized monitoring and control procedures for CyanoHAB from research [8, 36]. On the other hand, Ndlela [37], made an overview of cyanobacterial bloom occurrences and research in Africa during the last decade and found that the amount of information available on the continent on the subject is limited probably due to the general inadequacy of the infrastructure and its relation to civil wars [37].

Regarding the most frequent genera, the genus *Synechococcus* was the most reported with a frequency of 24; this genus plays a fundamental role in the ecology of surface water bodies that are important human resources, being predominant in freshwater systems. Generally, picocyanobacteria of the genus *Synechococcus*, *Prochlorococcus,* and *Cyanobium* are designated as non-flourishing [38]. However, some strains of the genus *Synechococcus* can produce toxins such as β-N-methylamino-L-alanine (BMAA), and microcystin (MC) [39], which causes problems in the ecosystem and human health. Similarly, Gin [15] through his study showed that *Synechococcus* spp. could produce cylindrospermopsin (CYN) and anatoxin-a (ATX) which are alkaloids that can cause damage to mammalian organisms, this discovery has implications on the potential risk to freshwater resources that serve as drinking water supply [40].

Previous studies by Li [21] report that the prevalence of *Synechococcus* in water bodies is influenced by warm temperature, high nutrient level, and phosphorus limitation, comprising fractions of up to 80% of the total biomass of picocyanobacteria of a bloom [41]. Furthermore, the result obtained in this review agrees with that reported by Cabello [38], where it is confirmed that the genera *Synechococcus* and *Cyanobium* are the dominant picocyanobacteria in freshwater systems [42].

Prochlorococcus ranks third as one of the most frequently found picocyanobacteria in research. It inhabits the entire photic zone and can be found as deep as 200 m below the surface, being abundant in oligotrophic systems [43]. *Prochlorococcus* and *Synechococcus* can coexist in water bodies, but *Synechococcus* tolerates a wider temperature range, without being limited by temperatures as low as 2°C and is more ubiquitous and has a wider latitudinal distribution [32].

It has been shown that the trophic state of water bodies influences the composition and abundance of picocyanobacterial communities. It was observed that the most studied lakes were those in an oligotrophic state, these lakes are characterized by being poor in nutrients and having low primary productivity [44], which limits the presence of a high microbial density and only those taxa that have adapted to these conditions can survive. Thus, picocyanobacteria of the genus *Synechococcus* are predominant in these systems, this is due to the ability of these picocyanobacteria to adapt to low light conditions, their affinity for orthophosphate and other sources of inorganic phosphorus, as well as their ability to store nitrogen in phycobilins that increase the competition of *Synechococcus* against algae and other bacteria, as stated by Vanstein [45]. The above is consistent with that reported by Joachim Ruber et al. [46], who describe this important genus as dominant in oligotrophic conditions, concluding that *Synechococcus* could be used as a bioindicator in such environments [46]. Besides, authors such as Rousso et al. [4] reported in a systematic review on CyanoHAB that more than 50% of the lakes investigated were eutrophic or hypertrophic and only 8% of the lakes were oligotrophic, reporting that the occurrence of CyanoHAB is related to the levels of nutrients present in the lakes [47].

In **Figure 5**, it is evident that the distance between two keywords demonstrates relative strength and similarity of topic and circles in the same color group suggest that a similar topic is being addressed among the publications [48]. **Figure 5** shows that the most used keywords are: *Synechococcus*, microbial community, phylogeny, and 16S rRNA, this shows us that more molecular identification strategies have been used recently for the identification of picocyanobacteria as cited by Demoulin et al. [49], who indicate that since the late 1990's many phylogenetic studies based on 16S rRNA or specific protein have been published. Similarly, the results of the keywords are also observed in **Figure 5**, in which the most frequent words have been used a greater number of times in the articles. The total link strength attribute indicates when a

keyword is very important because it is identified to have had a lot of interaction with other keywords in the analyzed articles, the higher the value the stronger the link that exists between one word and another [50].

The findings of the current systematic review show the lack of research on picocyanobacteria in surface waters that allow understanding the importance they represent as beneficial microorganisms; standing out for being part of the primary producers, or harmful because they can produce toxic blooms. It was also evidenced that molecular identification methods of picocyanobacteria have recently begun to be highlighted in research methodologies, which shows a transition from traditional research to a more advanced one.

5. Conclusions

Although in the last two decades the identification of picocyanobacteria has increased due to the implementation of new automated methods and molecular techniques, studies aimed at identifying them in surface water bodies intended for recreational use or drinking water supply are still incipient, which is possibly explained by the difficulty in their characterization and rapid physiological plasticity. The predominant genus of picocyanobacteria in this systematic review was *Synechococcus*, a producer of toxic compounds, which generates an alert and highlights the importance of advancing in the implementation of protocols for sampling and identification of these bacteria for epidemiological surveillance.

The countries where more studies on cyanobacteria were conducted were the United States and China since these are developed countries that invest their resources in education and research and can develop specialized monitoring and control procedures for CyanoHAB from their scientific resources. Therefore, there is a need for further research in this area, to use the information for further studies and decision making.

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Conflicts of interest

There are no conflicts of interest disclosed for this publication.

Consent to publication

The authors involved gave their consent for publication.

Ethical approval and consent to participate

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