

Aquatic Microbiota: A Systematic Review

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Abstract

Freshwater environments are the main ecosystems subjected to various anthropogenic impacts, which have caused the waterborne transmission of diseases caused mainly by bacteria. The main objective of this work was to carry out a systematic analysis through the literature on the main microorganisms found in impacted aquatic environments and to relate the data with the risks to public health. This review was planned, conducted and reported following the PRISMA protocol, which was used the PECO strategy. There performed searches for studies using the electronic databases *PubMed*, *Medline* and *LILACS* in September 2021, using the controlled search strategy: “Bacteria” and “Ecosystem” and “Environment” and “Aquatic” and “Impacted. The studies that met the eligibility criteria were considered eligible, with the participation of two independent reviewers. There found 1058 studies, of which were chosen only 31 to compose the results of this systematic review. Because of the results, there observed that the predominant bacterial genera in freshwater are: *Pseudomonas*, *Aeromonas*, and *Escherichia*, with the Asian continent presenting more varieties of bacterial species detected. These microorganisms are responsible for causing diseases that can lead to death, which shows the importance of constantly monitoring these ecosystems.

Keywords

Water, Microorganisms, Pathogenicity, Monitoring

1. Introduction

Water is one of the essential resources for sustaining life. However, anthropogenic activities have caused dangerous pollution problems, especially in freshwater environments [1]. One of the main factors that cause deterioration in

these ecosystems is the release of effluents without treatment, mainly by agricultural, industrial, and livestock activities, which can cause damage to the health of people and the organisms that live there [2].

Water can carry harmful bacteria to health since these microorganisms can cause waterborne diseases capable of leading to death, known to adapt to most different environments in isolation or groups [3]. These microorganisms, in turn, play a fundamental role in providing resistance and resilience against changes/pollution, which can measure the environmental stressors present by the practice of either-or inadequate management of these ecosystems [2].

According to the United Nations (UN), most diseases and deaths in developing countries are caused by microorganisms waterborne diseases, mainly due to the lack of sanitation, which can increase expenses with hospital admissions [4]. Therefore, these bacteria represent a risk to human health, causing approximately 870,000 deaths per year [5] [6].

For this reason, the microorganisms investigation in freshwater aquatic environments is essential to assess changes in these ecosystems. Thus, the main objective of this article was to carry out a systematic analysis through the literature on the main microorganisms found in impacted aquatic environments and to relate the data with the risks to public health.

2. Methodology

Protocol

This investigation was performed according to the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) and was organized into the planning, conducting, and reporting data phases.

Eligibility criteria

There used the PECO strategy to conduct this investigation: Population—Microorganisms, Exposure—Freshwater aquatic environments, Comparison—not applicable, and Outcomes—Main microorganisms found in freshwater environments.

Studies that considered the main microorganisms isolated in freshwater environments without year and-or language restrictions were eligible. The exclusion competed with editorial files, typical discussion documents, comments, letters, incomplete or insufficient data studies (studies that did not contain information on microorganism identification methodology), duplicates and titles that do not corroborate with the theme.

Information and Research Sources

The searches were carried out in the electronic databases PubMed, Medline, and LILACS. There selected the definition of descriptors and synonyms from the Medical Subject Headings (MeSH) and Decs (Descriptors of Health Sciences) and were also used keywords to assist in the controlled search strategy of scientific studies. Therefore, the resulting terms for the search strategy were: “Bacteria” and “Ecosystem” and “Environment” and “Aquatic” and “Impacted”.

Selection of studies

The selection of studies had the participation of two independent reviewers, which became reliable, separately and blindly, since the following variables were considered: Reasons for inclusion and exclusion of studies. The 1st stage consisted of studies analysis by title, so duplicates were eliminated. The 2nd stage consisted of the eligibility criteria discussion with the relationship of the PECO strategy since those studies that were not related to the proposed strategy were eliminated. The 3rd and last stage included the studies elimination after reading the abstract and total studies, which did not provide sufficient information and data to conduct this systematic review.

Data collection process

Soon after the selection of studies, there extracted information through a form created by the authors to record the selected studies' data, which there used a defined protocol. The included items consisted of the First author, year of publication, place of study, genus and species of the isolated microorganism, and type of environment in which the author(s) carried out the study; thus, they were tabulated in an Excel spreadsheet. Any necessary calculations for the data were performed by two researchers, and if there were discrepancies, they would be resolved through group discussion.

Risk of Bias

The risk of bias was assessed using the Joanna Briggs Institute (JBI) Critical Assessment Checklist for Qualitative Research [7]. Risk classification consisted of High (greater than 49% of studies scoring "yes"), Moderate (studies achieving 50% to 69% of "yes" scores), and Low (studies reaching higher than 70% of "yes" scores); thus, there excluded those with high publication bias. Because of this, two reviewers independently evaluated each study. Then, the information was verified so that in the event of ambiguity, a third reviewer was involved in the assessment of bias in the studies.

3. Results

According to the searches carried out in the electronic databases, there obtained 1058 studies in total, of which 173 were eliminated by duplication, 716 by title, and 103 because they did not meet the eligibility criteria, accounting for a total of 31 studies included in this systematic review. **Figure 1** corresponds to the flowchart showing the respective quantitative and qualitative data for the exclusion and inclusion articles.

Seeing the eligible studies, there performed the first analysis to identify the microorganism predominance in aquatic environments distributed on different continents. As a first result, there observed that the North American and Asian continents had the highest number of published studies on this topic, of which China and the United States were the most contemplated publications in the area. About the Latin American continent, Brazil stands out as the country with the highest number of publications. The data synthesis related to publications on

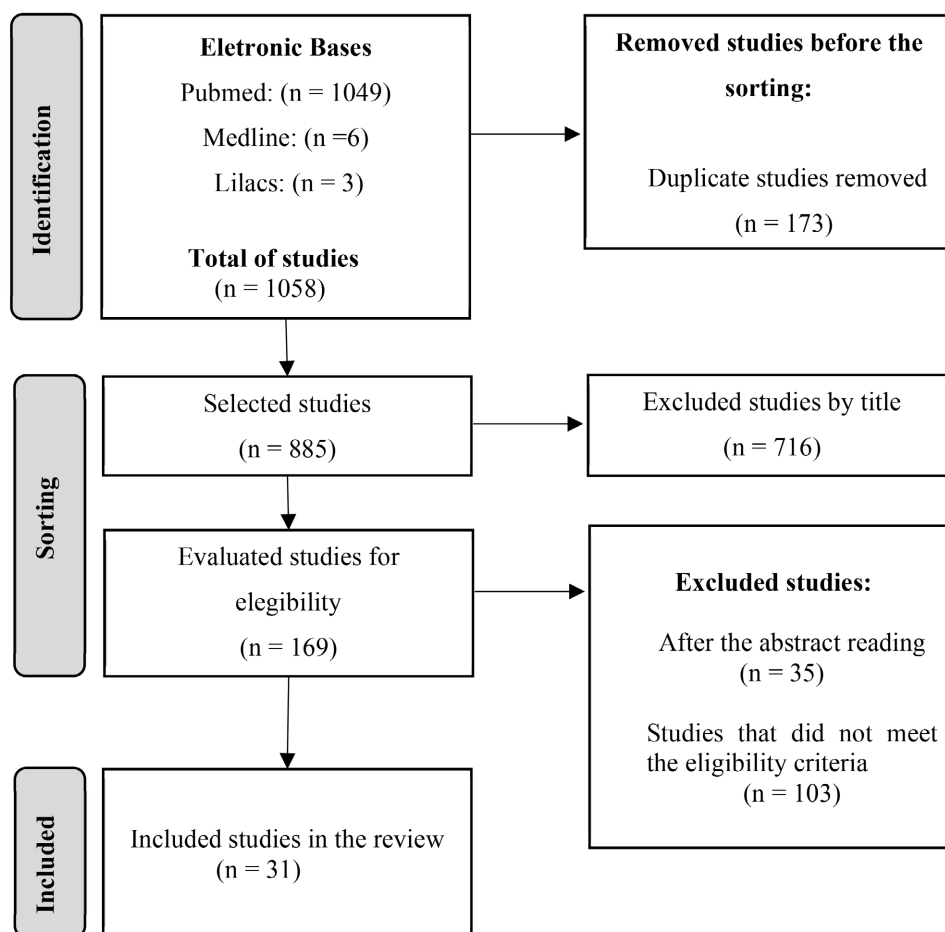


Figure 1. Source: Authors, 2023.

the subject by continent and their respective countries can be seen in **Table 1**, **Figure 2**.

Regarding the main genera and species of microorganisms found in these environments, the qualitative distribution can be seen in **Table 2**. There observed a total of 99 different bacterial genera and 150 species.

The bacterial genera that were found with the highest incidence were: *Pseudomonas* (n = 15), *Aeromonas* (n = 11), *Escherichia* (n = 9), and the most abundant species were: *Pseudomonas*—*P. putida*, *P. aeruginosa*, *P. taiwanensis*, *P. geniculata*, *P. otitidis*, *Aeromonas*—*A. veronii*, *A. caviae*, *A. hydrophila*; *Bacillus*—*B. licheniformis*; *Enterobacter*—*E. clocae*, *E. asburiae*; *Escherichia*—*E. coli*, and *Klebsiella*—*K. pneumoniae*.

Regarding the assessment of the risk of JBI bias, there observed that most of the responses to the critical evaluation questionnaire of the 31 studies consisted of “Yes” answers (>70%), indicating that the respective studies had a low risk of bias. Therefore, they have a high methodological quality.

4. Discussions

Aquatic environments are formed by marine and/or freshwater ecosystems.

Table 1. Quantitative synthesis of publications by continent and countries.

CONTINENT	COUNTRIES	STUDIES	N°	Total
Africa	Democratic Republic of Congo	Laffite <i>et al.</i> , 2016 [8]	1	1
North America	Canada	Gromala; Neufeld; Mcconkey, 2021 [9]	1	9
	USA	Williams <i>et al.</i> , 2018 [10], Choi; Dunams; Jiang, 2010 [11], Chu <i>et al.</i> , 2018 [12], Skwor <i>et al.</i> , 2020 [13], Harmon <i>et al.</i> , 2019 [14], Londono <i>et al.</i> , 2019 [15], Bared <i>et al.</i> , 2013 [16]		
	Mexico	Brito <i>et al.</i> , 2015 [17]	1	
South America	Brazil	Carvalho <i>et al.</i> , 2007 [18], Conte <i>et al.</i> , 2021 [19], Regina <i>et al.</i> , 2021 [20], Purificação <i>et al.</i> , 2017 [21]	4	6
	Colombia	Perlaza <i>et al.</i> , 2019 [22]	1	
	Chile	Leon <i>et al.</i> , 2012 [23]	1	
Asia	China	Chen <i>et al.</i> , 2019 [24], Li <i>et al.</i> , 2019 [25], Liang <i>et al.</i> , 2020 [26], Liao <i>et al.</i> , 2018 [27], Niu <i>et al.</i> , 2019 [28], Xiao <i>et al.</i> , 2013 [29], Xie <i>et al.</i> , 2021 [30], Zhang <i>et al.</i> , 2020 [31]	8	9
	Japan	Miyagi <i>et al.</i> , 2019 [32]	1	
Europe	Spain	Piedra <i>et al.</i> , 2017 [33]	1	6
	France	Devarajan <i>et al.</i> , 2015 [34], Girlich, Poirel, Nordmann, 2011 [35]	2	
	Italy	Adelowo; Akinlabi; Fagade, 2012 [36]	1	
	Portugal	Tacao; Correia; Henriques, 2015 [37]	1	
	Switzerland	Corno <i>et al.</i> , 2014 [38]	1	

Source: Authors, 2023.

Table 2. Qualitative synthesis of the main genera and species of microorganisms found in impacted freshwater environments.

GENUS	SPECIES	TYPE OF ENVIRONMENT	STUDIES
<i>Aeromonas</i>	<i>Aeromonas spp.</i>	River, Pond	Chu <i>et al.</i> , 2018 [12], Liang <i>et al.</i> , 2020 [26], Regina <i>et al.</i> , 2021 [20], Girlich; Poirel; Nordmann, 2011 [35]
	<i>A. veronii</i>	Residual waters, River, Pond	Brito <i>et al.</i> , 2015 [17], Skwor <i>et al.</i> , 2020 [13], Harmon <i>et al.</i> , 2019 [14], Tacao; Correia; henriques, 2015 [36], Conte <i>et al.</i> , 2021 [19]
	<i>A. caviae</i>	Residual waters	Conte <i>et al.</i> , 2021 [19], Skwor <i>et al.</i> , 2020 [13]
	<i>A. sanarelli</i>	Residual waters	Conte <i>et al.</i> , 2023 [19]
	<i>A. hydrophila</i>	Residual waters, Pond, River	Conte <i>et al.</i> , 2023 [19], Corno <i>et al.</i> , 2014 [38], Skwor <i>et al.</i> , 2020 [13], Tacao; Correia; henriques, 2015 [36]
	<i>A. jandaiei</i>	River	Skwor <i>et al.</i> , 2020 [13], Tacao; Correia; henriques, 2015 [36]
	<i>A. média</i>		Skwor <i>et al.</i> , 2020 [13]

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<i>Acidovorax</i>	<i>Acidovorax</i> spp.	Stream	Londono et al., 2019 [15]
<i>Acinetobacter</i>	<i>Acinetobacter</i> spp.	Pond, River, Stream	Chu et al., 2018 [12], Gromala; Neufeld; Mcconkey, 2021 [9], Liao et al., 2018 [27], Londono et al., 2019 [15], Regina et al., 2021 [20], Zhang et al., 2020 [31]
<i>Alkaliphilus</i>	<i>Alkaliphilus</i> spp.	River	Niu et al., 2019 [28]
<i>Anammoxglobus</i>	<i>Anammoxglobus</i> spp.		Chen et al., 2019 [24]
<i>Aquabacterium</i>	<i>Aquabacterium</i> spp.	Pond	Li et al., 2019 [25]
<i>Arenimonas</i>	<i>Arenimonas</i> spp.		Li et al., 2019 [25]
<i>Arcicella</i>	<i>Arcicella</i> spp.	Stream	Londono et al., 2019 [15]
<i>Arcobacter</i>	<i>Arcobacter</i> spp.	Pond	Li et al., 2019 [25]
<i>Armatimonas</i>	<i>Armatimonas</i> spp.	Stream	Londono et al., 2019 [15]
<i>Bacillus</i>	<i>Bacillus</i> spp.	Pond, River	Li et al., 2019 [25], Niu et al., 2019 [28]
	<i>B. cereus</i>	Stream	Adelowo; Akinlabi; Fagade, 2012 [36]
	<i>B. subtilis</i>		Adelowo; Akinlabi; Fagade, 2013 [36]
	<i>B. licheniformis</i>		Adelowo; Akinlabi; Fagade, 2014 [36], Purificação et al., 2017 [21]
	<i>B. pumilis</i>		Purificação et al., 2017 [21]
<i>Bacteroides</i>	<i>Bacteroides</i> spp.	River, Pond	Perlaza et al., 2019 [22], Regina et al., 2021 [20], Williams et al., 2018 [10]
<i>Brevundimonas</i>	<i>Brevundimonas</i> spp.	Pond	Gromala; Neufeld; Mcconkey, 2021 [9]
	<i>B. intermedia</i>		Corno et al., 2014 [38]
	<i>B. vesiculares</i>	Stream	Londono et al., 2019 [15]
<i>Brocadia</i>	<i>Brocadia</i> spp.	River	Chen et al., 2019 [24]
<i>Burkholderia</i>	<i>B. cepacia</i>	Stream	Adelowo; Akinlabi; Fagade, 2017 [36]
<i>Chromobacterium</i>	<i>C. haemolyticum</i>	River	Tacao; Correia; henriques, 2015 [37]
<i>Citrobacter</i>	<i>C. diversus</i>	Stream	Miyagi et al., 2019 [32]
<i>Clostridium</i>	<i>Clostridium</i> spp.	Pond	Li et al., 2019 [25]
<i>Cronobacter</i>	<i>Cronobacter</i> spp.	River	Niu et al., 2019 [28]
<i>Cryobacterium</i>	<i>Cryobacterium</i> spp.	Stream	Londono et al., 2019 [15]
<i>Cupriavidus</i>	<i>C. gilardii</i>	Pond	Harmon et al., 2019 [14]
<i>Delftia</i>	<i>D. tsuruhatensis</i>	Stream	Londono et al., 2019 [15]
<i>Desulfatiglans</i>	<i>Desulfatiglans</i> spp.	Pond	Li et al., 2019 [25]
<i>Desulfatirhabdium</i>	<i>D. butyrivorans</i>		Williams et al., 2018 [10]
<i>Desulfobacca</i>	<i>Desulfobacca</i> spp.		Li et al., 2019 [25]
<i>Dolichospermum</i>	<i>Dolichospermum</i> spp.	River	Liao et al., 2018 [26]
<i>Enterobacter</i>	<i>Enterobacter</i> spp.		Regina et al., 2021 [20]

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	<i>E. cloacae</i>	Stream, River	Purificação <i>et al.</i> , 2017 [21], Miyagi <i>et al.</i> , 2019 [32], Piedra <i>et al.</i> , 2017 [33]
	<i>E. aerogenes</i>	Stream	Miyagi <i>et al.</i> , 2019 [32]
	<i>E. asburiae</i>	Pond, River	Harmon <i>et al.</i> , 2019 [14], Tacao; Correia; henriques, 2015 [37]
	<i>E. ludwigii</i>	River	Tacao; Correia; henriques, 2015 [37]
Enterococcus	<i>Enterococcus spp.</i>	Pond, Residual waters	Devarajan <i>et al.</i> , 2015 [34], Laffite <i>et al.</i> , 2016 [8]
Escherichia	<i>Escherichia spp.</i>	Pond	Chu <i>et al.</i> , 2018 [12]
	<i>E. coli</i>	River, Residual waters, Pond	Adelowo; Akinlabi; Fagade, 2014 [36], Bared <i>et al.</i> , 2013 [16], Perlaza <i>et al.</i> , 2019 [22], Purificação <i>et al.</i> , 2017 [21], Miyagi <i>et al.</i> , 2019 [32], Piedra <i>et al.</i> , 2017 [33], Laffite <i>et al.</i> , 2016, Devarajan <i>et al.</i> , 2015 [34]
	<i>E. coli enterohemorrágica</i>	River	Xiao <i>et al.</i> , 2013 [29]
Exiguobacterium	<i>Exiguobacterium spp.</i>	River, Pond, Stream	Zhang <i>et al.</i> , 2020 [31], Liao <i>et al.</i> , 2018 [27], Purificação <i>et al.</i> , 2017 [21]
Faecalibacterium	<i>Faecalibacterium Spp.</i>	River	Perlaza <i>et al.</i> , 2019 [22]
Flavobacterium	<i>Flavobacterium spp.</i>	Pond, River, Stream	Li <i>et al.</i> , 2019 [25], Liao <i>et al.</i> , 2018 [37], Londono <i>et al.</i> , 2019 [15], Xie <i>et al.</i> , 2021 [30]
	<i>F. aquatile</i>	Stream	Adelowo; Akinlabi; Fagade, 2014 [36]
	<i>F. rigense</i>		
Fluoribacter	<i>F. dumoffii</i>	River	Carvalho <i>et al.</i> , 2007 [18]
Fluviicola	<i>Fluviicola Spp.</i>	River, Stream	Liao <i>et al.</i> , 2018 [27], Londono <i>et al.</i> , 2019 [15]
Francisella	<i>Francisella Spp.</i>	Pond	Chu <i>et al.</i> , 2018 [12]
Gaiella	<i>Gaiella Spp.</i>		Li <i>et al.</i> , 2019 [25]
Geobacter	<i>Geobacter Spp.</i>		Williams <i>et al.</i> , 2018 [10]
Haliangium	<i>Haliangium Spp.</i>		Li <i>et al.</i> , 2019 [25]
Helicobacter	<i>Helicobacter spp.</i>		Chu <i>et al.</i> , 2018 [12]
Jetternia	<i>Jetternia spp.</i>	River	Chen <i>et al.</i> , 2019 [24]
Klebsiella	<i>K. pneumoniae</i>	Stream, River	Adelowo; Akinlabi; Fagade, 2014 [36], Purificação <i>et al.</i> , 2017 [21], Piedra <i>et al.</i> , 2017 [33], Miyagi <i>et al.</i> , 2019 [32]
	<i>K. aerogenes</i>	Stream	Adelowo; Akinlabi; Fagade, 2014 [36]
	<i>K. ozaenae</i>		Miyagi <i>et al.</i> , 2019 [32]
	<i>K. oxytoca</i>	River	Piedra <i>et al.</i> , 2017 [33]
Kuenenia	<i>Leclercia Spp.</i>	River	Liang <i>et al.</i> , 2020 [26]
Leclercia	<i>Legionella Spp.</i>	Pond	Chu <i>et al.</i> , 2018 [12]
Legionella	<i>L. pneumophila</i>	River	Carvalho <i>et al.</i> , 2007 [18]

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	<i>L. birminghamensis</i>		
	<i>L. bozemonil</i>		
	<i>L. lytica</i>		
<i>Liminohabitans</i>	<i>Liminohabitans spp.</i>	River, Pond	Liang et al., 2020 [26], Perlaza et al., 2019 [22], Xie et al., 2021 [30], Zhang et al., 2020 [31]
<i>Luteolibacter</i>	<i>Luteolibacter spp.</i>	River	Liao et al., 2018 [27]
	<i>L. agae</i>	Stream	Londono et al., 2019 [15]
<i>Malikia</i>	<i>Malikia spp.</i>	Pond	Li et al., 2019 [25]
<i>Massilia</i>	<i>Massilia spp.</i>		
<i>Methylobacter</i>	<i>M. tundripaludum</i>		Williams et al., 2018 [10]
<i>Methylobacterium</i>	<i>M. tardum</i>	Stream	Londono et al., 2019 [15]
<i>Methylocaldum</i>	<i>Methylocaldum spp.</i>		
<i>Methylosinus</i>	<i>Methylosinus spp.</i>	River	Perlaza et al., 2019 [22]
<i>Methylotenera</i>	<i>M. mobilis</i>		Liao et al., 2018 [27]
<i>Methyloterna</i>	<i>M. versitalis</i>	Pond	Williams et al., 2018 [10]
<i>Micrococcus</i>	<i>M. luteus</i>		Corno et al., 2014 [38]
<i>Microcystis</i>	<i>Microcystis spp.</i>	River	Liao et al., 2018 [27]
<i>Moraxella</i>	<i>Moraxella spp.</i>	Pond	Chu et al., 2018 [12]
<i>Mycobacterium</i>	<i>Mycobacterium spp.</i>	River, Pond	Zhang et al., 2020 [31]
	<i>M. smegmatis</i>	River	Brito et al., 2015 [17]
<i>Neisseria</i>	<i>Neisseria spp.</i>	Pond	Chu et al., 2018 [12]
<i>Nitrospira</i>	<i>N. briensis</i>		Williams et al., 2018 [10]
<i>Nitrospira</i>	<i>Nitrospira spp.</i>	River, Pond	Li et al., 2019 [25], Zhang et al., 2020 [31]
<i>Novosphingobium</i>	<i>Novosphingobium spp.</i>	Pond	Li et al., 2019 [25]
	<i>N. subterraneum</i>	Stream	Londono et al., 2019 [15]
<i>Opitutus</i>	<i>Opitutus spp.</i>		
<i>Paenibacillus</i>	<i>Paenibacillus spp.</i>	River	Niu et al., 2019 [28]
<i>Pantoea</i>	<i>Pantoea spp.</i>		Liao et al., 2018 [27]
<i>Phenylobacterium</i>	<i>Phenylobacterium spp.</i>	Stream	Londono et al., 2019 [28]
<i>Polynucleobacter</i>	<i>Polynucleobacter spp.</i>	River	Liang et al., 2020 [26], Perlaza et al., 2019 [22]
<i>Proteus</i>	<i>P. vulgaris</i>	Stream	Adelowo; Akinlabi; Fagade, 2014 [36]
	<i>P. mirabilis</i>		Purificação et al., 2017 [21], Miyagi et al., 2019 [32]
<i>Providencia</i>	<i>P. alcaligenes</i>	River	Tacao; Correia; henriques, 2015 [37]
<i>Pseudomonas</i>	<i>Pseudomonas spp.</i>	Pond, Residual waters, River	Devarajan et al., 2015 [34], Gromala; Neufeld; Mcconkey, 2021 [9], Laffite et al., 2016 [8], Leon et al., 2012 [23], Li et al., 2019 [25], Liang et al., 2020 [26], Liao et al., 2018 [27], Regina et al., 2021 [20], Girlich; Poirel; Nordmann, 2011 [35]

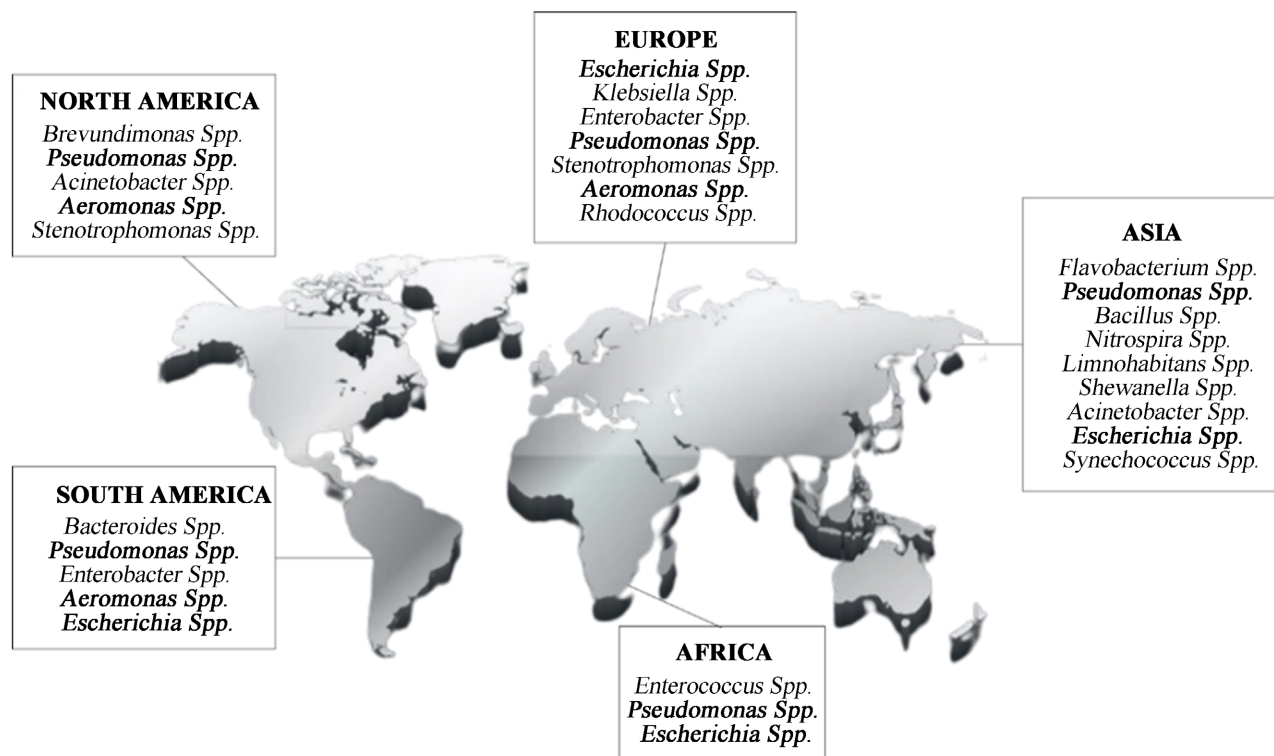
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	<i>P. putida</i>	Pond, Stream, River	Adelowo; Akinlabi; Fagade, 2014 [36], Leon et al., 2012 [23], Purificação et al., 2017 [21]
	<i>P. aeruginosa</i>	River	Brito et al., 2015 [17], Tacao; Correia; henriques, 2015 [37]
	<i>P. taiwanensis</i>	Stream, River	Londono et al., 2019 [15], Tacao; Correia; henriques, 2015 [37]
	<i>P. cedrina</i>	Pond	Harmon et al., 2019 [14]
	<i>P. geniculata</i>	Pond, River	Harmon et al., 2019 [14], Tacao; Correia; henriques, 2015 [37]
	<i>P. otitidis</i>		
	<i>P. stutzeri</i>	Pond	Harmon et al., 2019 [14]
	<i>P. beteli</i>	River	Tacao; Correia; henriques, 2015 [37]
	<i>P. hibiscicola</i>		
	<i>P. protegens</i>		
<i>Pseudoxanthomonas</i>	<i>Pseudoxanthomonas spp.</i>	River	Liang et al., 2020 [26]
<i>Psychrobacter</i>	<i>Psychrobacter spp.</i>	Pond	Gromala; Neufeld; Mcconkey, 2021 [9]
<i>Rahnella</i>	<i>R. aquatilis</i>	Stream	Miyagi et al., 2019 [32]
<i>Raoultella</i>	<i>R. ornithinolytica</i>	River	Piedra et al., 2017 [33]
<i>Rhodobacter</i>	<i>Rhodobacter spp.</i>	Pond, River	Li et al., 2019 [25], Perlaza et al., 2019 [22], Liao et al., 2018 [27]
<i>Rhodococcus</i>	<i>Rhodococcus spp.</i>	Pond	Corno et al., 2014 [38]
	<i>R. equi</i>	Stream	Adelowo; Akinlabi; Fagade, 2014 [36]
<i>Rhodoferax</i>	<i>Rhodoferax spp.</i>	River	Liang et al., 2020 [26]
	<i>R. ferrireducens</i>	Pond	Williams et al., 2018 [10]
<i>Rhodoluna</i>	<i>Rhodoluna spp.</i>		Xie et al., 2021 [30]
<i>Rickettsia</i>	<i>Rickettsia spp.</i>		Chu et al., 2018 [12]
<i>Roseburia</i>	<i>Roseburia spp.</i>	River	Perlaza et al., 2019 [22]
<i>Ruminococcus</i>	<i>Ruminococcus Spp.</i>		Perlaza et al., 2019 [22]
<i>Salmonella</i>	<i>Salmonella Spp.</i>		Xiao et al., 2013 [29]
<i>Scalindua</i>	<i>Scalindua Spp.</i>		Chen et al., 2019 [24]
<i>Sediminibacterium</i>	<i>Sediminibacterium spp.</i>		Liao et al., 2018 [27]
<i>Serratia</i>	<i>S. rubidaea</i>	Stream	Miyagi et al., 2019 [32]
<i>Shewanella</i>	<i>Shewanella spp.</i>	River	Liang et al., 2020 [26], Liao et al., 2018 [27]
	<i>S. xiamenensis</i>		Tacao; Correia; henriques, 2015 [37]
<i>Sideroxydans</i>	<i>S. lithotrophicus</i>	Pond	Williams et al., 2018 [10]
<i>Sphingomonas</i>	<i>Sphingomonas Spp.</i>		Leon et al., 2012 [23]
	<i>S. panni</i>	Stream	Londono et al., 2019 [15]
<i>Sphingopyxis</i>	<i>Sphingopyxis spp.</i>	River	Liang et al., 2020 [26]

Continued

<i>Sporacetigenium</i>	<i>Sporacetigenium spp.</i>	Pond	Li et al., 2019 [25]
<i>Staphylococcus</i>	<i>S. aureus</i> <i>S. epidermidis</i>	Stream	Adelowo; Akinlabi; Fagade, 2014 [36]
<i>Stenotrophomonas</i>	<i>S. pavanii</i> <i>S. maltophilia</i> <i>S. pavanii</i>	Stream Pond, River Pond	Londono et al., 2019 [15] Harmon et al., 2019 [14], Girlich; Poirer; Nordmann, 2011 [35], Tacao; Correia; henriques, 2015 [37] Harmon et al., 2019 [14]
<i>Streptococcus</i>	<i>S. agalactiae</i>	Stream	Adelowo; Akinlabi; Fagade, 2014 [46]
<i>Sulfuricella</i>	<i>S. denitrificans</i>	Pond	Williams et al., 2018 [10]
<i>Sulfuritalea</i>	<i>S. hidrogenivoros</i>		
<i>Synechococcus</i>	<i>Synechococcus spp.</i>	Pond, River	Xie et al., 2021 [30], Zhang et al., 2020 [31]
<i>Thiocapsa</i>	<i>Thiocapsa spp.</i>	River	Perlaza et al., 2019 [22]
<i>Trichococcus</i>	<i>Trichococcus spp.</i>	Pond	Gromala; Neufeld; Mcconkey, 2021 [9]
<i>Vibrio</i>	<i>VibRiver spp.</i> <i>V. cholerae</i>	River	Liang et al., 2020 [25] Choi; Dunams; Jiang, 2010 [11]
<i>Yersinia</i>	<i>Yersinia spp.</i>	Pond	Chu et al., 2018 [12]

Source: Author, 2023.



Source: Autores, 2023.

Figure 2. Distribution and predominance of microorganisms across continents.

However, freshwater is the primary environment in which there is a growing anthropogenic intervention, such as domestic, hospital, industrial, agricultural, and livestock effluents [2]; since rivers, streams, and water residues are among the leading sources that have suffered from the contamination of these emerging [39] [40].

Therefore, the continuous release of these organic compounds of anthropogenic origin has caused environmental degradation, in addition to increasingly resulting in the appearance of microorganisms [41]. These have as main characteristics high growth rates in addition to a higher metabolism, which also have particularities of being influenced by physicochemical changes and the introduction of organic, inorganic, and polluting compounds in the environment in which they inhabit [42].

The present research carried out a systematic review in which the Asian continent presented greater microbial diversity when compared to other continents, with China being the country with the highest bacterial representation. Considering the population and development characteristics that have been taking place over time in their areas, especially urban areas [1] [43], it is likely that these events have contributed to water pollution in freshwater environments and, consequently, greater bacterial diversity.

A point that deserves attention is that when identified in aquatic environments, these microorganisms can be used as a bioindicator of water contamination, reflecting the quality of the water, whether for bathing or drinking. An example of a bacterial species used to assess water quality is *E. coli*, one of the leading indicators of fecal contamination in freshwater aquatic environments, which has a strong relationship with risks of gastrointestinal diseases in humans [44].

Pseudomonas aeruginosa is a bacterium that is frequently isolated in lakes and rivers, in addition to wastewater, due to the high load of nutrients found in these environments. Recent studies give a fundamental role of water in the colonization of this microorganism in humans since these bacteria have multiple virulence factors that promote their high pathogenicity [45].

Klebsiella pneumoniae is a microorganism that can inhabit aquatic environments, soils, plants, and sewage. This bacterium can be isolated from the oropharynx, the gastrointestinal tract of humans and mammals, and the feces of healthy individuals, besides having the ability to colonize humans asymptotically. The most common leading infections are pneumonia, urinary tract infections, wounds, bacteremia, and meningitis [46].

Regarding the species of the genus *Aeromonas*, they are found in different habitats, particularly in aquatic environments, from which it is widespread. In freshwater environments, they are mainly present in wastewater, of which some species present themselves as relevant zoonotic pathogens. Among these, *A. veronii*, *A. caviae*, and *A. hydrophila* have been linked to diseases in humans, especially with symptoms of diarrhea, septicemia, and soft tissue infections of wounds after exposure to water, considered an emerging threat in different en-

vironments, mainly to human health [47].

Therefore, the contamination of pathogenic microorganisms in aquatic environments, mainly freshwater, has caused an extensive public health problem worldwide, especially concerning waterborne diseases, since many of these microorganisms are enteric and can lead to death [44] [48].

5. Conclusions

The findings and evidence showed that the genera *Pseudomonas*, *Aeromonas*, and *Escherichia* and their respective species were the main microorganisms isolated, that is, they proved to be the most predominant, which indicates that these pathogens can present themselves as leading indicators of quality in freshwater environments that are being impacted.

These data support the relevance of the continuous analysis of microorganisms in freshwater aquatic environments, mainly to assess the impact on the local fauna, the dynamics of water quality, and the survival of the beings that are there, helping to monitor this ecosystem and indicating the possible risks to the population that depends directly or indirectly on these places. The data presented reinforce that these environments not only harbor but spread pathogens, representing a risk to public health when not monitored or preserved.

Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

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