Journal of Hazardous Materials 479 (2024) 135638

Contents lists available at ScienceDirect

Journal of Hazardous Materials

journal homepage: www.elsevier.com/locate/jhazmat

Potentially pathogenic bacteria in the plastisphere from water, sediments, and commercial fish in a tropical coastal lagoon: An assessment and management proposal

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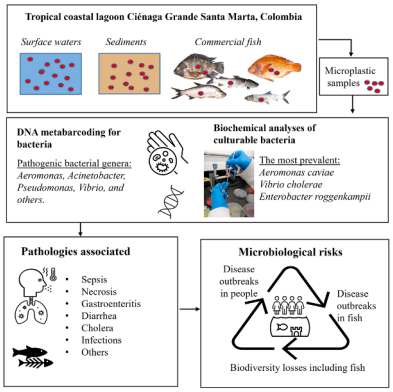
HIGHLIGHTS

- Microplastics (MPs) in the investigated coastal lagoon harbor over 1760 bacterial genera.
- At least 19 potentially pathogenic bacterial species (PPBS) live on these MPs.
- *Aeromonas caviae* is the most prevalent, occurring on MPs from all environmental matrices.
- PPBS are more abundant in areas near population centers and with high fishing activity.

GRAPHICAL ABSTRACT



ARTICLE INFO

Keywords:
Microplastic pollution
DNA metabarcoding
Bacterial diversity

ABSTRACT

Microplastics in aquatic ecosystems harbor numerous microorganisms, including pathogenic species. The ingestion of these microplastics by commercial fish poses a threat to the ecosystem and human livelihood. Coastal lagoons are highly vulnerable to microplastic and microbiological pollution, yet limited understanding of the risks complicates management. Here, we present the main bacterial groups, including potentially pathogenic

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https://doi.org/10.1016/j.jhazmat.2024.135638
Received 21 April 2024; Received in revised form 6 August 2024; Accepted 22 August 2024
Available online 30 August 2024

Microbiological risk
Environmental management

species, identified on microplastics in waters, sediments, and commercial fish from Ciénaga Grande de Santa Marta (CGSM), the largest coastal lagoon in Colombia. DNA metabarcoding allowed identifying 1760 bacterial genera on microplastics, with *Aeromonas* and *Acinetobacter* as the most frequent and present in all three matrices. The greatest bacterial richness and diversity were recorded on microplastics from sediments, followed by waters and fish. Biochemical analyses yielded 19 species of potentially pathogenic culturable bacteria on microplastics. *Aeromonas caviae* was the most frequent and, along with *Pantoea* sp., was found on microplastics in all three matrices. *Enterobacter roggenkampii* and *Pseudomonas fluorescens* were also found on microplastics from waters and fish. We propose management strategies for an Early Warning System against microbiological and microplastic pollution risks in coastal lagoons, illustrated by CGSM. This includes forming inter-institutional alliances for research and monitoring, accompanied by strengthening governance and health infrastructures.

1. Introduction

Pollution of aquatic ecosystems is a recurrent issue, primarily caused by the discharge of sewage and solid waste from domestic and industrial activities. Such waste materials contain various pollutants, including microplastics (1-μm – 5-mm in size) and microorganisms able to cause disease [1-3]. These types of pollution degrade environmental quality in aquatic ecosystems, disrupting the biotic networks and impacting the well-being of human communities along their shores [1,4,5].

Recent studies have demonstrated the role of microplastics in aquatic ecosystems as substrata, niches, or vectors for various microorganisms [6-9]. The microbial community inhabiting microplastics and forming biofilms on them is known as the "plastisphere" [10,11], which includes harmless, beneficial, and potentially pathogenic species for fish and humans [12-16]. These biofilm-coated microplastics resemble planktonic organisms, which leads to their ingestion by aquatic species, including commercial fish [17-20]. Understanding the relationship between microplastics and pathogenic microorganisms is crucial for assessing their environmental and human health impacts [15].

Coastal lagoons are aquatic ecosystems of critical environmental value, characterized by high productivity and biodiversity [21]. However, they are highly vulnerable to the above-mentioned pollution types largely due to their unique characteristics as shallow, closed, or semi-closed systems with limited water circulation and renewal [22-24]. Moreover, the watersheds and shores of many coastal lagoons, especially at mid and low latitudes, face increasing urbanization and industrial activities, which produce large amounts of waste that is often discharged directly or indirectly into the lagoons [23-25].

In the Colombian Caribbean, the Ciénaga Grande de Santa Marta (CGSM) lagoon system is recognized as a Ramsar site, a Biosphere Reserve, and a natural park, highlighting the need for strict protection to maintain its environmental status [26]. However, CGSM faces significant threats, including high levels of microbiological and microplastic pollution, which compromise habitat quality, commercial fisheries, and local food security [23,27,28]. Potentially pathogenic bacteria, such as *Vibrio* spp. and *Aeromonas* spp., have been detected in the water and muscle tissue of commercial fish species in CGSM [28,29]. At least nine fish species ingest microplastics from their habitat in CGSM [30,31], which may pose a risk to the health of the ecosystem and the local population through the consumption of contaminated seafood or wound contact with polluted water [32-34]. This situation is likely mirrored in other coastal lagoons worldwide.

There is a major gap in understanding the environmental and public health risks arising from interactions between microplastics and pathogenic microorganisms in coastal lagoons like CGSM, particularly regarding their impact on fisheries. This knowledge deficiency hampers effective responses to these challenges in such critical coastal ecosystems [15,23]. Therefore, it is imperative to conduct dedicated research to improve our understanding of pollution-related issues in these environments and develop effective strategies for managing the associated environmental risks.

Management strategies for addressing microbiological risks heightened by microplastic pollution in coastal lagoons should consider the implementation of Early Warning Systems based on regular monitoring of water bodies for microplastic and bacterial concentrations. This way, pollution hotspots and trends can be quickly identified, and potential outbreaks of infectious diseases can be timely anticipated. Such systems are crucial for preventing or reducing harm to local communities by providing timely and precise information for sound decision-making and the implementation of proactive measures [35-37]. An effective Early Warning System involves several key phases, including risk identification, monitoring, threat analysis, and forecasting, which can be centralized or community-based [38,39]. These systems also require efficient alert communication mechanisms and a collaborative approach, integrating local communities, scientific institutions, and healthcare establishments to assess and mitigate risks, safeguarding public health [35,37,39].

The identification of microorganisms in environmental samples has traditionally relied on phenotypic and chemical methods [40,41]. Nowadays, these conventional approaches are augmented by advanced molecular biology techniques, notably metabarcoding. This method uses the amplification of specific DNA sequences to identify bacteria, eukaryotes, or archaea, creating detailed taxonomic profiles and determining the relative abundances of microorganisms in samples [41,42]. Comprehensive DNA metabarcoding analysis complements traditional methods, enhancing our understanding of microbial communities [3,42].

The present study aims to identify the main bacterial groups, including potentially pathogenic species, on microplastics sampled from waters, sediments, and the digestive tracts of commercial fish from CGSM, using molecular biology and biochemical techniques. It is a follow-up to the Garcés-Ordóñez et al. [31] paper, which focused on microplastic pollution levels in the above-mentioned environmental matrices from the CGSM lagoon complex. Samples provided by that study were subsequently analyzed (i.e., framed within the research reported here) for plastisphere characterization purposes and to assess the potential environmental and public health risks associated with bacteria on microplastics. The current study also provides a reference approach that could be applied to other coastal lagoons worldwide.

The specific questions now addressed are: (1) What is the taxonomic composition of the bacterial community on sampled microplastics from waters, sediments, and fish in CGSM? (2) Which genera or species of potentially pathogenic bacteria occur on these microplastics? (3) Which are the environmental and public health risks that microplastic pollution and these microorganisms may pose to the local fishery resource and local residents? And (4) What could be done to address and reduce such environmental risks in the coastal lagoon under study and beyond? The present article provides a baseline for exploring how microplastics and pathogens interact in coastal lagoons, which constitutes vital knowledge for risk assessment, fisheries protection, and the development of strategies to conserve such a vulnerable ecosystem and protect local human communities from the threats of pollution.

2. Materials and methods

2.1. Study area

CGSM is the largest (1321 km^2), shallow (1–1.8 m) lagoon system on

the Colombian Caribbean coast (Fig. 1). Ciénaga Grande (450 km^2; hereafter CG) and Pajarales (120 km^2) are the largest lagoons in the CGSM system, which receive freshwater from four rivers and marine water from the Caribbean Sea through a 120 m wide inlet channel in the northeastern part of CG (Fig. 1; [43]). The climate in the area is semi-arid with two rainy seasons (April–May and September–November) and two dry seasons (June–August and December–March; [44,45]). Total annual precipitation, average air temperature, and solar radiation vary from 500–1000 mm, 26–34 °C, and 4.5–6.0 Wh m^{-2}, respectively [45,46].

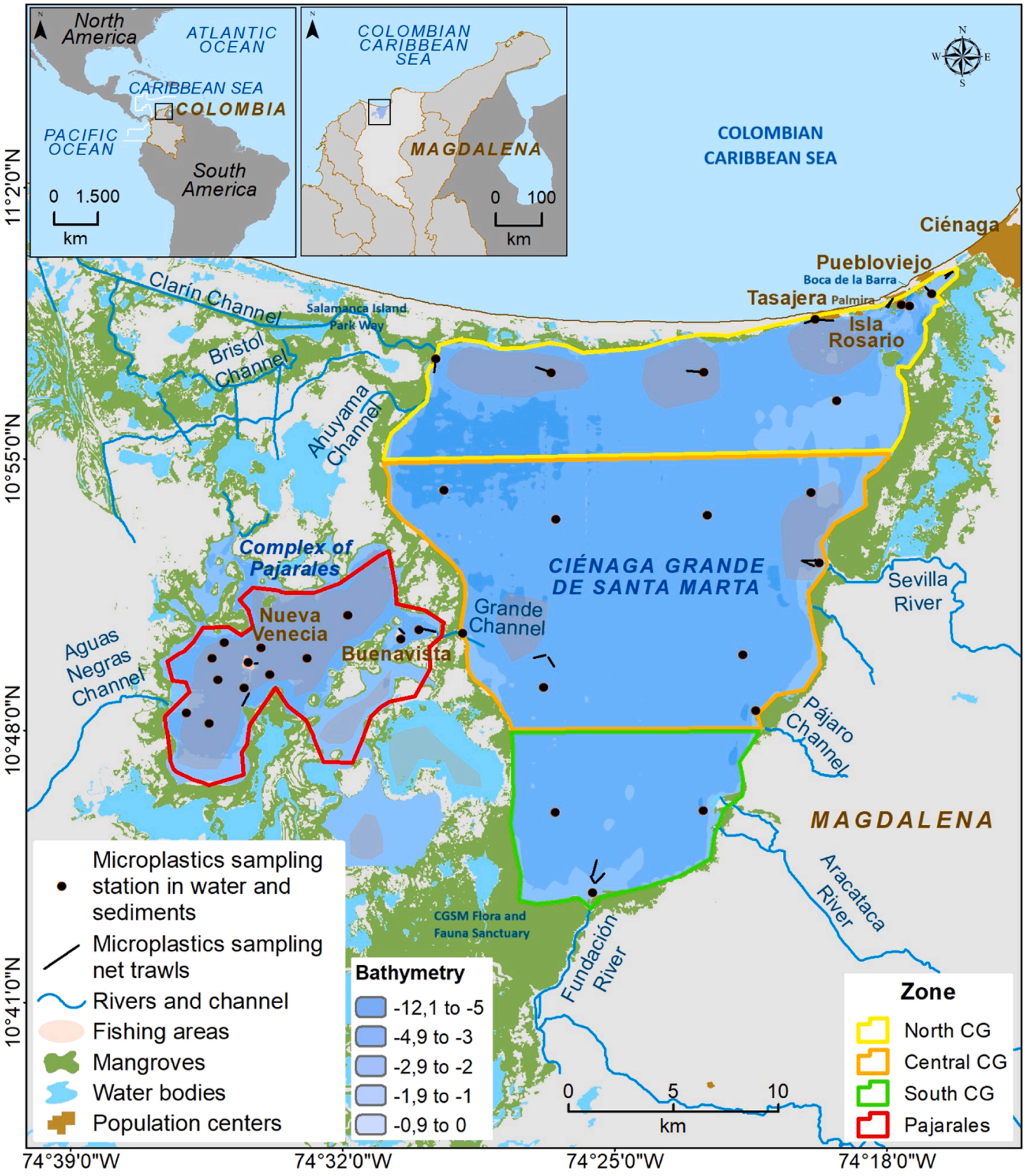

Fig. 1. Ciénaga Grande de Santa Marta lagoon system in the Colombian Caribbean. Four main zones are identified within the lagoon system (yellow, orange, green, and red polygons) and point stations for microplastics sampling in water and sediments (black dots), conducted by Garcés-Ordóñez et al. [31], are shown, together with plankton net trawling transects for surface water sampling of microplastics (short black lines) carried out in this study. Fishing areas information is from Carrasquilla-Henao et al. [47].

In the CGSM lagoons, water salinity ranges from 0.1 to 12 units in river-dominated areas and gets close to 30 units in marine-influenced areas [26]. Daytime temperatures vary from 23 to 34 °C, with dissolved oxygen concentrations between 4 and 9 mg L^{-1} and oxygen saturation from 53 to 121 %, the highest values (i.e., oxygen supersaturation) due to photosynthetic activity during periods of high phytoplankton densities [26]. Eutrophication events are frequent due to high nutrient concentrations from domestic wastewater discharges and agricultural runoff [48,49]. The four villages on the northeastern shores of CG are home to ~13,200 people, whereas about 3000 persons live in the two villages within the Pajarales complex [50]. These communities are highly vulnerable, as they suffer from a lack of very basic household and urban services, and around 70 % of the total population is below the average poverty line [50].

For the current study, we considered the same zonation of the overall study area and sampling stations as in Garcés-Ordóñez et al. [31]. The lagoon system has been divided into four main study zones, which are referred to as North CG, Central CG, South CG, and Pajarales, with 33 microplastic sampling stations distributed among them (Fig. 1). Sampling stations were selected using the "Create Fishnet" tool in ArcGIS 10.8 software. The North CG and Pajarales zones are shallow (~1 m), support high fishing intensity, and are close to population centers, while the Central CG and South CG zones are slightly deeper (1–2 m), have low fishing intensity, and are far from population centers (Fig. 1).

2.2. Sampling and isolation of microplastics in waters, sediments, and fish

Two expeditions were conducted to the CGSM for microplastic sampling in surface waters and sediments aboard a small boat (Fig. S1 in Section 1 of the supplementary material –SM–). The first expedition took place from March 8th to 11th, 2021 (dry season), and the second from May 10th to 13th, 2021 (rainy season). One sampling day was assigned per study zone (Fig. 1), with sample collection carried out in the morning, followed by isolation of the microplastics needed for biochemical analysis within 24 h by a research team of six. Additionally, microplastic analysis was performed on 474 individuals of nine commercial fish species bought from local fishermen during the expeditions, including *Megalops atlanticus*, *Oreochromis* sp., *Cathorops mapale*, *Elops smithi*, *Centropomus undecimalis*, *Ariopsis canteri*, *Eugerres plumieri*, *Mugil incilis*, and *Oreochromis niloticus*.

The sampling and isolation of microplastics in surface waters, bottom sediments, and fish digestive tracts followed the methods used by Garcés-Ordóñez et al. [31]. Briefly, at each of the 33 stations, a sample of 100 L of surface water was collected down to a maximum depth of 0.3 m using a 20 L metal bucket (five individual samples per station that were subsequently integrated) to increase the probability of obtaining microplastics based on point sampling aimed at visualizing their abundance and spatial distribution in the lagoon, optimizing logistical resources, time, and materials [51]. This volume was then reduced by passing the sample through a 300-μm sieve. The retained material was deposited into a previously sterilized glass bottle, which was kept refrigerated at less than 6 °C until analysis.

At the same sampling stations, ~500 g of sediment was collected and homogenized. A 200 g aliquot of the homogenized sample was then placed into a sterilized glass bottle. To this, we added 450 mL of sterile buffered peptone water (density at 20 °C is ~1020 g/L) that had been filtered through an 8-μm pore Whatman™ filter, stirred the solution for 10 min, and passed it through 5.0-mm and 500-μm sieves. The material retained by the 300-μm and 500-μm sieves from both water and sediment samples was directly examined under Leica EZ4 Microsystems binocular stereomicroscopes to isolate microplastics. Similarly, the digestive tract contents of all fish individuals were extracted and meticulously examined under stereomicroscopes for microplastics.

To obtain the necessary quantities of microplastics for DNA metabarcoding analysis (see the Section 2.4 below), two to six trawl nets were deployed per zone using a Hydro-Bios plankton net with a mesh size of 300 μm (Fig. 1). The net was towed along the water surface at a depth of 0 to 20 cm for 10 min at a constant speed of 1 knot, following the methodology described by Kovač et al. [52]. The starting and ending points of each trawl were georeferenced using a handheld Garmin GPS device. The materials collected were then transferred to sterilized glass bottles, transported under refrigeration to the laboratory, and subsequently examined under a binocular stereomicroscope to isolate the microplastics. The procedures for preventing sample contamination are described in Section 2 of the SM.

2.3. Selection and distribution of microplastic samples for analyses

In total, 1499 microplastics were isolated: 311 from integrated surface water samples, 955 from net trawls in surface water, 75 from bottom sediments, and 158 from the digestive tracts of nine fish species. These particles were conveniently divided for polymer characterization, biochemical analysis of cultivable bacteria, and DNA metabarcoding analyses (see Section 3 of the SM; Table S1). The abundances, distribution (Fig. S2 in Section 4 of the SM), and characteristics (shapes, colors, and polymer type) of the microplastics in the referred samples are detailed in Garcés-Ordóñez et al. [31] except for those collected with trawl nets.

The size range of microplastics isolated in water was 5.0 mm to 300 μm, while for sediments and fish it was 5.0 mm to 500 μm, which aided their visual identification, minimizing confusion with non-plastic materials [53,54]. These sizes of microplastics can be examined in greater detail under the stereoscope, as some may retain characteristics of the original product. Additionally, they are easy to review using identification criteria such as the absence of cellular structures, performing the hot needle test to confirm the plastic material [55], and confirming the polymer type with FTIR.

2.4. DNA metabarcoding analysis for bacteria

The microplastics selected for DNA metabarcoding analysis to identify bacteria were grouped based on environmental matrices (i.e., waters, sediments, and fish). The samples were considered representative of the entire CGSM system since they included microplastics from all four main study zones (Fig. 1) and the nine fish species combined. Such grouping was essential to ensure sufficient quantity and quality of DNA for the analysis (>2 ng of DNA μL^{-1}; four times higher than the minimum—500 pg—suggested by Abellan-Schneyder et al. [56]). The chosen microplastic samples were cryopreserved at −70 °C until analysis. All molecular analyses, along with their respective quality controls, were conducted at the National Center for Genomic Sequencing at the University of Antioquia, Colombia. Sequencing services were provided by MACROGEN from Seoul, South Korea.

Metabarcoding analysis was performed by high-throughput sequencing of fragments of the 16S rRNA gene (variable regions V3-V4) [57]. Bacterial DNA extraction from microplastic samples was performed using the QIAGEN DNeasy PowerLyzer PowerSoil Kit, with two control blanks using the elution buffer from the same kit. After the extraction process, DNA quantification was performed by the spectrophotometric method using NanoDrop™ 2000-Thermo Scientific™ (absorption spectrum at 260 nm), recording DNA concentrations from 2.6 to 10.2 ng μL^{-1} with absorbance ratios of 260/280 values between 1.8 and 1.9, which are indicative of high quality for 16S rRNA gene sequencing (V3-V4) [56]. Extracted DNA samples were preserved at −20 °C and sent to the MACROGEN sequencing center. For sequencing of the 16S rRNA gene (variable regions V3-V4), the oligonucleotides Bakt_341F (CCTACGGGNGGCWGCAG) and Bakt_805R (GACTACHVGGGTATCTAATCC) were used. These sequencing procedures were performed on the Illumina MiSeq platform, generating paired end reads of 300 bases each.

2.5. Biochemical identification of potentially pathogenic culturable bacteria

The microplastics selected for the identification of potentially pathogenic cultivable bacteria were grouped according to the environmental matrix (water and sediments) in each climatic season (dry and rainy), as well as by fish species (*E. smithi*, *E. plumieri*, and *M. incilis*). Each microplastic was held with fine-tipped metal forceps and carefully rinsed with sterile buffered peptone water to remove any loose bacterial cells on the plastic surface.

Subsequently, the microplastics from each grouping category were separately submerged in BD™ Brain Heart Infusion (BHI) Agar broth, a general-purpose medium effective in culturing a wide variety of microorganisms, including many types of pathogenic bacteria [58]. The BHI with the immersed microplastics was then incubated for 18 ± 4 h at 35 °C in a 35 L Binder incubator to obtain young cells that usually are metabolically more active, which would be used for subsequent isolations in selective culture media and biochemical tests.

At the end of the above incubation period, samples were taken from each of the broths using inoculation loops and streaked onto selective media, including CHROMAgar™ Vibrio (CHROMagar™, France), ENDO Agar (Merck KGaA, Germany), Glutamate Agar GSP (Merck KGaA, Germany), M-PAC-BBL Agar (BD™), Cetrimide Agar (Merck KGaA, Germany), Brilliant Green Agar (Merck KGaA, Germany), and CN Pseudomonas Agar (Merck KGaA, Germany), in order to isolate enterobacteria and bacteria of the *Vibrio*, *Aeromonas*, and *Pseudomonas* genera, which include potentially pathogenic species. The cultured colonies were purified through successive streaking until obtaining axenic cultures of the bacterial strains of interest.

Subsequently, these bacterial colonies were phenotypically characterized (size, color, border, and shape) and identified using biochemical tests, including the oxidase test to determine whether the microorganism possesses the cytochrome oxidase system [59], and the Analytical Profile Index (API) 20E kit. This widely accepted kit for enterobacteria identification consists of 21 microtubes containing dehydrated substrates, which after an incubation period allows positive or negative reactions to be observed depending on the ability of bacteria to degrade these substances, thus generating unique biochemical profiles for each species [60]. Later, these profiles along with oxidase test results were analyzed using the APIWEB™ (https://val.apiweb.biomerieux.com) to identify the bacterial species. The identification of the biochemical profile and the assignment of each bacterial species was considered reliable when scores exceeded 75 %.

Finally, ten bacterial strains were selected from the most prevalent cultured species in the analyzed samples considering their significant health interest as potential pathogens for both fish and humans according to scientific literature. These strains underwent further confirmation through molecular analysis using taxonomic analysis average nucleotide identity (ANI) and based on sequencing and phylogenetic analysis of genes (16S, dnaA, gyrB, infC, rplM, rpoB, and secY). The results of these confirmatory analyses are presented in the Section 5 in the SM.

2.6. Data analysis

The DNA sequence quality analysis, taxonomic classification, and calculation of the Chao1 richness and Shannon and Inverse Simpson diversity indices [61] were performed using the MOTHUR platform, version 1.44.3. Additionally, a descriptive analysis was conducted, and graphical representations were generated in Excel to display the most prevalent taxonomic groups from microplastics extracted from surface waters, sediments, and fish from CGSM. A list of potentially pathogenic bacterial genera found on sampled microplastics was compiled and prioritized. To that end, a literature review was conducted on isolation matrices and main diseases associated with the identified bacteria.

Conceptual and background information from international and national guides [37,62,39], some of the existing Early Warning Systems [63,64] and scientific articles (e.g., [35,36,38]) were consulted and analyzed to identify key aspects in order to adapt them to the risk posed by microbiological and microplastic pollution in CGSM. These elements are all of relevance to the environmental condition of CGSM and useful for eventual disease outbreak management.

The data were also analyzed using test statistics to compare the data groups. The assumptions of normality and homoscedasticity for the abundance data of bacterial species in plastispheres were verified using Shapiro-Wilk and Levene's tests, respectively, which help in selecting the appropriate statistical tests. As the data did not meet these assumptions, non-parametric tests were applied:

(1) Mann-Whitney U tests for two independent samples (bacterial abundance in dry and rainy seasons; bacterial abundance in North CG and Pajarales zones) were used to determine if their distributions differ significantly, based on the hypothesis that the means of the two variables are not equal ($H_a\ \mu \neq \mu$). In this test, the effect size (r) was calculated using the bivariate rank correlation test, providing a measure of the strength of the statistical relationship between two variables. Bacterial communities on microplastics from water were compared between the confined Pajarales lagoon, which receives wastewater from two villages, and the larger, marine-influenced North CG zone (Fig. 1).
(2) Kruskal-Wallis chi-square tests were used to determine if the abundances of groups categorized by matrix (water, sediment, fish) differ significantly. When this test showed statistical significance, a Dwass-Steel-Crichlow-Fligner post-hoc test for pairwise comparisons was applied to identify which specific groups differ from each other, adding depth to the analysis. All these statistical analyses were conducted using Jamovi® 2.4.14 software with a 95 % confidence interval.

3. Results

3.1. Bacterial taxa identified with DNA metabarcoding

The analyzed microplastic samples had sufficient DNA in optimal quality conditions required for a comprehensive study of bacterial diversity, with sequencing coverage exceeding 98 % (Table 1). The dataset comprised a total of 213,865 sequences, allowing the identification of bacteria distributed across 65 phyla, with Proteobacteria (52 %), Firmicutes (15 %), and Bacteroidetes (8 %) being the most prominent. At the class level, 160 taxa were determined, with a higher representation of Gammaproteobacteria (33 %), Alphaproteobacteria (15 %), and Clostridia (10 %). At the order level, 420 taxa were recorded, with Clostridiales (10 %), Aeromonadales (9 %), and Pseudomonadales (9 %) being the most represented. At the family level, 746 taxa were found, with Aeromonadaceae (9 %), Moraxellaceae (8 %), and Peptostreptococcaceae (7 %) as the most abundant. Finally, 1760 genera were identified, with *Aeromonas* (9 %), *Romboutsia* (6 %), *Acinetobacter* (6 %) and *Exiguobacterium* (3 %) as the most frequent (Fig. 2).

In the microplastics from surface waters of the North CG and Pajarales zones, bacteria from the genera *Aeromonas* and *Acinetobacter* stood out in abundance, representing 43.7 % and 25.4 % of the analyzed sequences, respectively, followed by the genera *Exiguobacterium* and *Sphingomonas* (Fig. 2A-B). In microplastics extracted from the sediments of the CGSM lagoon system, bacteria from the Rhodocyclaceae family were predominant (Fig. 2C). In microplastics recovered from the digestive tract of fish, the genera *Romboutsia*, *Mesorhizobium*, *Allorhizobiumes*, *Neorhizobium*, *Pararhizobium* and *Rhizobium* were the dominant ones (Fig. 2D). The Chao1, Shannon and Inverse Simpson indices showed that microplastics extracted from sediments had the highest richness and diversity of bacterial species, followed by microplastics from surface waters of North CG and Pajarales zones. In contrast, microplastics extracted from the digestive tracts of fish had the lowest

Table 1
General results of the sequencing of the 16S ribosomal gene, V3-V4 regions, and the analysis of bacterial richness and diversity associated with microplastics extracted from surface waters, sediments and the digestive tract of nine commercial fish species from the Ciénaga Grande de Santa Marta lagoon complex. Nseqs: number of sequences.

Sample code	Raw reads	Q30 (%)	Nseqs	Coverage	Observed (Sobs)	Chao1	Shannon	Inv. Simpson
Waters – North CG	227,592	90.23	53504	0.996	1625	1698	4.5	14.5
Waters – Pajarales	217,554	90.13	53487	0.993	1595	1799	4.7	32.2
Sediments	145,084	88.62	53435	0.999	2134	2144	6.8	339.8
Fish	174,670	86.88	53439	0.999	458	460	4.0	15.2

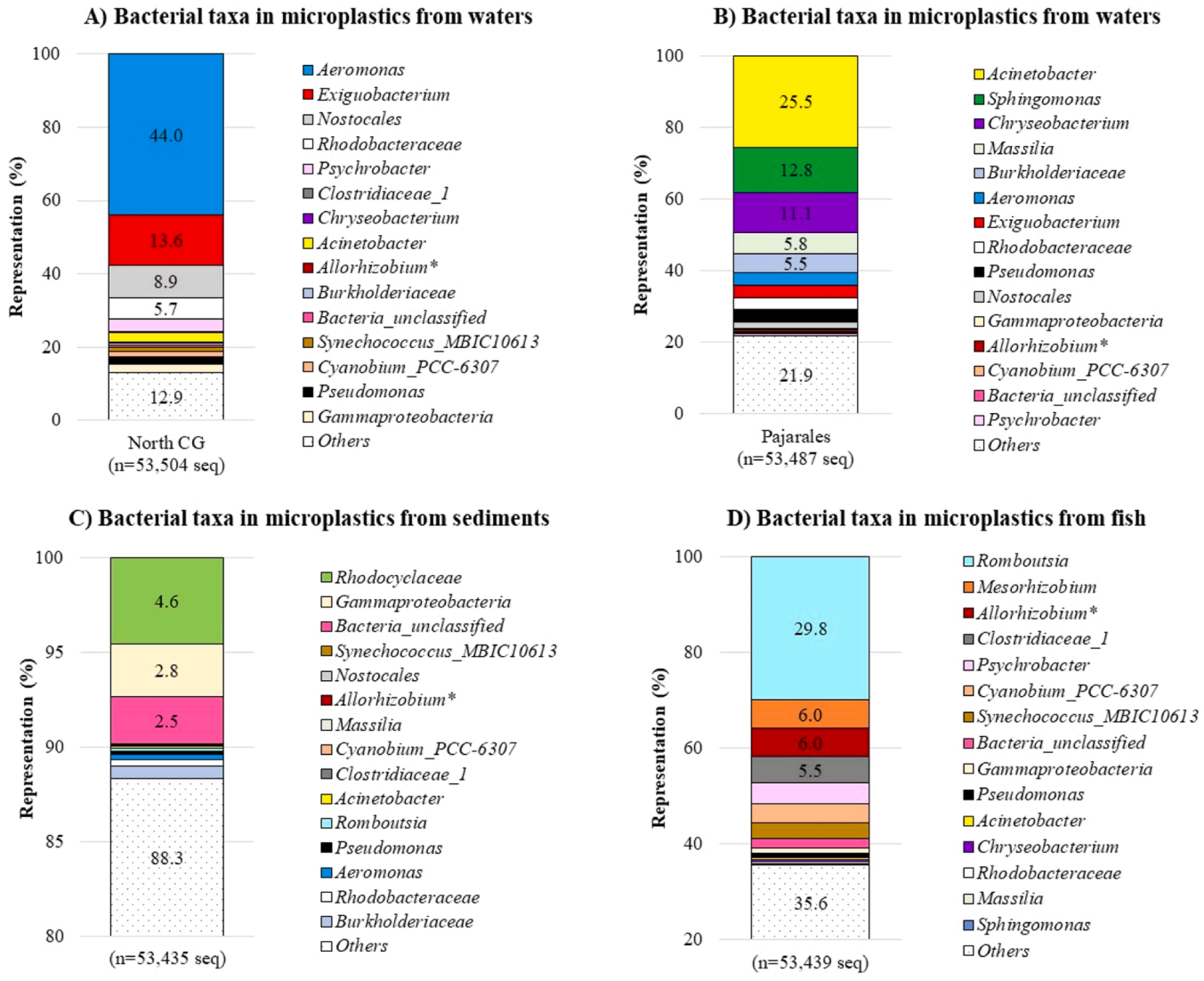

Fig. 2. Top 15 bacterial taxa identified on microplastics from the Ciénaga Grande de Santa Marta lagoon system within (A) surface waters from the North Ciénaga Grande (North CG) zone, (B) surface waters from the Pajarales zone, (C) sediments from the entire lagon system, and (D) digestive tracts of commercial fish from the entire lagon system. Taxa with * represent more than one taxon. Further information can be found in the Supplementary material. See zones of analysis en Fig. 1.

estimated richness and species diversity (Table 1).

A significant statistical difference was found when comparing the bacterial community abundance on microplastics from water between the North CG and Pajarales zones (Mann-Whitney U = 1,260,000, p-value = 0.043, effect size r = 0.0397). Significant differences were also found between the bacterial community abundances on microplastics from the three environmental matrices (Kruskal-Wallis χ^2 test = 598, df = 2, p-value = <0.001). The post-hoc analyses of pairwise comparisons showed significant differences between bacterial communities on microplastics from all matrices: water-sediments (W = −10.1, p = <0.001), water-fish (W = −35.5, p = <0.001), and sediments-fish (W = −20.1, p = <0.001).

3.2. Potentially pathogenic culturable bacteria identified after biochemical analysis

130 bacterial colonies were isolated from the microplastics analyzed in the selective culture media. Reliable biochemical identification was achieved for 105 colonies belonging to 19 species, 13 genera, eight families, and six different orders (Table 2). 51 colonies of 13 culturable

Table 2
Prevalence (%) of bacterial species reliably identified in the 105 colonies isolated from microplastics in the Ciénaga Grande de Santa Marta (CGSM) lagoon system using biochemical tests. The percentages on the number of colonies (n) are presented according to the seasons (dry vs. rainy) and the environmental matrices investigated in CGSM. The most frequent bacterial species are in bold, and those found in more than one environmental matrix are gray shaded. The species with * were confirmed using molecular biology tests (cf. Section 5 in the SM – Table S2-S4, and Fig. S3-S7).

Order	Family	Identified culturable bacteria	Season (%)		Environmental matrix (%)		
			Dry (n = 51)	Rainy (n = 54)	Water (n = 80)	Sediments (n = 14)	Fish (n = 11)
Aeromonadales	Aeromonadaceae	***Aeromonas caviae****	47	50	50	72	9
Alteromonadales	Shewanellaceae	*Shewanella algae* *	2	0	1	0	0
Enterobacterales	Enterobacteriaceae	*Cronobacter* spp	0	2	1	0	0
		Enterobacter kobei *	4	0	0	14	0
		Enterobacter roggenkampii*	2	9	3	0	37
		Escherichia coli *	2	0	1	0	0
		Klebsiella pneumoniae	0	7	5	0	0
		Proteus mirabilis	8	2	6	0	0
		Proteus vulgaris group	5	0	4	0	0
		Raoultella ornithinolytica	2	0	1	0	0
	Erwiniaceae	***Pantoea* spp**	4	6	1	7	27
	Yersiniaceae	*Serratia odorifera*	0	2	0	0	9
Pseudomonadales	Pseudomonadaceae	*Pseudomonas aeruginosa* *	0	5	4	0	0
		Pseudomonas fluorescens/putida	2	2	1	0	9
		Pseudomonas luteola	0	2	0	0	9
Vibrionales	Vibrionaceae	*Vibrio alginolyticus*	2	2	3	0	0
		Vibrio cholerae*	14	7	14	0	0
		Vibrio parahaemolyticus *	6	2	4	7	0
Xanthomonadales	Xanthomonadaceae	*Stenotrophomonas maltophilia*	0	2	1	0	0

bacterial species were identified from microplastics collected in the dry season, while 54 colonies of 14 species were found on microplastics from the rainy season (Table 2). No significant differences were encountered regarding the number of colonies by species amongst seasons (Mann-Whitney U = 306, p-value = 0.895, r = 0.0224).

Out of the 105 identified bacterial colonies, 76 % (from 16 species), 13 % (from four species) and 11 % (from six species) appeared on microplastics from surface water, sediments, and fish digestive tracts, respectively (Table 2). Significant differences in bacterial composition were found among environmental matrices (Kruskal-Wallis χ^2 test = 31.6, df = 2, p-value = <0.001). The post-hoc analyses revealed significant differences in bacterial abundance between water and sediment samples (W = −6.668, p = <0.001), and between water and fish samples (W = −6.442, p = <0.001), while no significant difference was found between sediment and fish samples (W = 0.826, p = 0.829).

The most prevalent bacterium was *Aeromonas caviae*, representing 47 % and 50 % of the isolated colonies from microplastics collected in the dry and rainy seasons, respectively. This bacterium dominated in colonies obtained from microplastics in waters (50 %) and sediments (72 %), whereas it was much less dominant in those from fish digestive tracts (9 %) (Table 2). *Vibrio cholerae* was the second most prevalent bacterium in both the dry (14 %) and rainy (7 %) seasons, but it was found only on microplastics from surface waters.

Enterobacter roggenkampii was the third most prevalent bacterium during the rainy season (9 %), occurring on microplastics from surface waters (3 %) and fish digestive tracts (37 %). During the dry season, *Proteus mirabilis* was the third most prevalent bacterium (8 %), which was identified on microplastics from surface waters (6 %) (Table 2). The prevalence of *Vibrio parahaemolyticus* and *Pantoea* spp was low but both were present on microplastics from all three environmental matrices. Finally, *Pseudomonas fluorescens/putida* occurred, also with low prevalence, on microplastics from surface waters and fish digestive tracts (Table 2).

In total, 12 bacterial species were identified in both North CG and Pajarales zones, with a relatively large number of colonies (47 and 43, respectively) (Fig. 3A). In contrast, only four bacterial species were distinguished in each of the two other zones, Central CG and South CG, with eight and seven colonies, respectively (Fig. 3A). The Chao1 index reflected these findings, indicating high species richness in North CG (Chao1 = 12.67) and Pajarales (Chao1 = 13.25) zones, and a more limited richness in Central CG and South CG (Chao1 = 4 in both zones).

Microplastics from surface waters in North CG and Pajarales zones showed the highest number of culturable bacterial species (Fig. 3B). *Aeromonas caviae* and *V. cholerae*, which were found on microplastics from all sampling zones, were particularly noticeable, indicating a widespread distribution of these two species in the CGSM lagoon system. In North CG and Pajarales, these bacteria were found on microplastics collected in both seasons, dry and rainy, while in South CG they were only identified on microplastics collected during the dry season. In Central CG, *A. caviae* was found on microplastics collected in both seasons, while *V. cholerae* was identified on microplastics collected in the rainy season (Fig. 3B).

We were able to biochemically isolate and identify only the bacterial colonies associated with microplastics from sediments in the North CG and Pajarales zones, with a higher number of species found in the latter zone (Fig. 3C). *Aeromonas caviae* was the most common culturable bacterium on microplastics from both sampling zones. Microplastics extracted from the fish *E. smithi* and *M. incilis* yielded colonies of four bacterial species, while only one bacterial species was identified on microplastics of the fish *E. plumieri* (Fig. 3D). *Enterobacter roggenkampii* was common on microplastics from all these three fish species (Fig. 3D).

4. Discussion

4.1. Bacterial community and potentially pathogenic species on microplastics

Since the first documented microorganisms on marine plastic litter in 1972 [65,66], research into the plastisphere of aquatic ecosystems has grown significantly, enhancing our understanding of these microbial communities [67,68,8,11]. However, knowledge of the plastisphere in coastal lagoons remains limited [23]. The results presented here provide new insight into the plastisphere in an internationally significant lagoon system in the tropical Caribbean region.

This is the first study to characterize, mainly with an exploratory character, the bacterial community on microplastics sampled from waters, sediments, and commercial fish of Colombia's largest coastal lagoon system, which is a crucial area for biodiversity and fisheries [47, 69,43]. The current research combined molecular identification of bacterial genera using DNA metabarcoding techniques (without

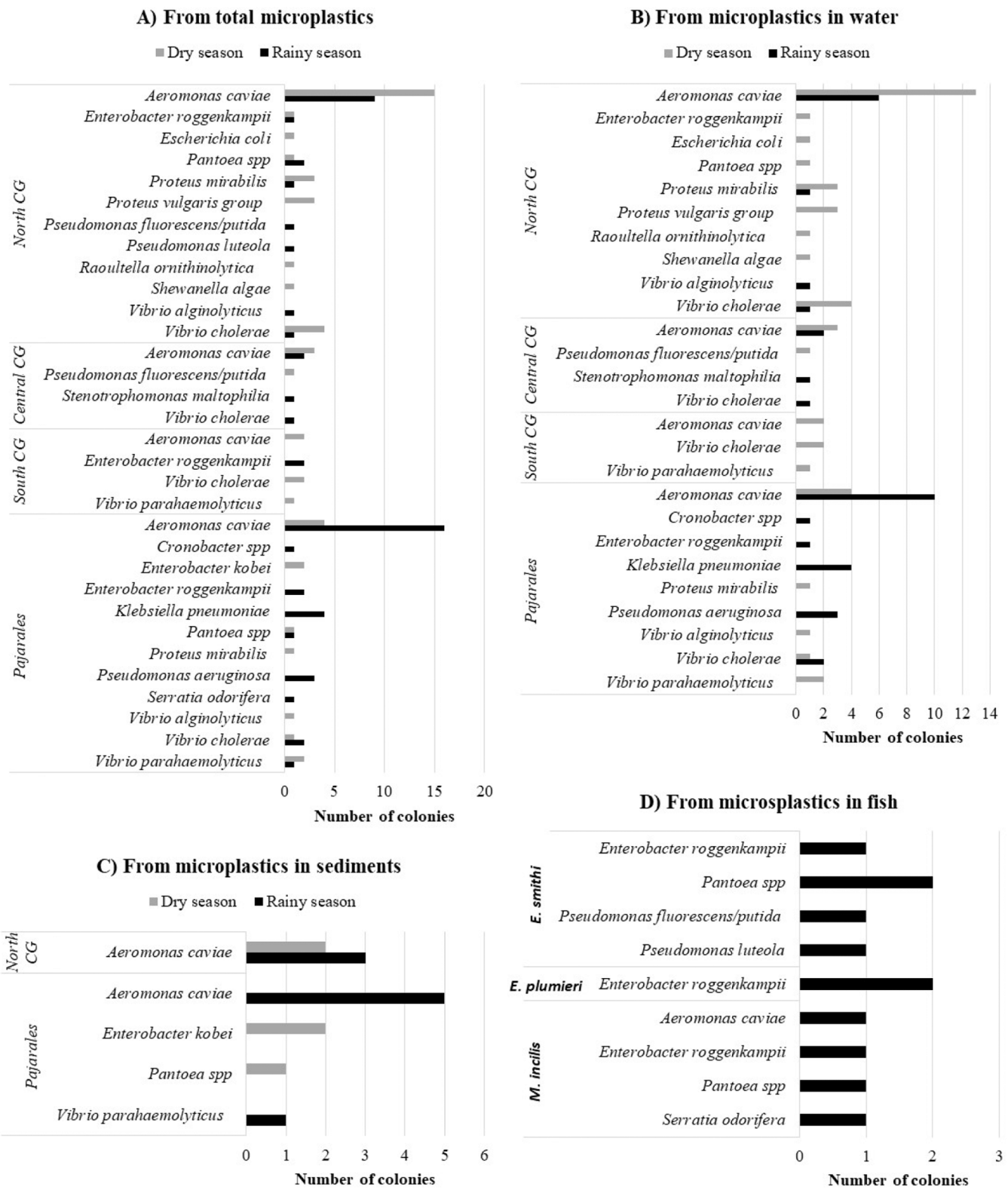

Fig. 3. Spatial (by zones of analysis) and seasonal (dry vs. rainy seasons) distribution of bacterial species identified from the 105 colonies isolated on microplastics from the Ciénaga Grande de Santa Marta lagoon system using biochemical tests. The general species richness profile (A) and detailed species profiles for samples extracted from waters (B), sediments (C) and the digestive tract of three fish species are shown (D).

distinguishing between living or dead states) with traditional microbiological and biochemical techniques to identify potentially pathogenic living species cultured in the laboratory. These complementary methods helped establishing a baseline to enhance our understanding of threats, identify risks, and assist in developing strategies to mitigate the impacts of microplastic pollution and associated potential pathogens on the coastal lagoon ecosystem and local communities [40,41].

Our results indicate that microplastics in CGSM are a habitat for a

significant diversity of bacteria, encompassing 1760 genera across 65 phyla. Notably, Proteobacteria, Firmicutes, and Bacteroidetes are the predominant phyla, which are recognized as the primary and most abundant colonizers of plastic surfaces in marine environments [9]. This observation aligns with previous research documenting microbial communities on microplastics from coastal waters in France [70], Singapore [71], South Korea [72], Colombia [73] and a lake in China [74]. All these bacterial phyla are naturally found in surface waters, sediments, and soils of different ecosystems, as well as in sewage, and are associated with humans, fish, and other aquatic and terrestrial animals and plants [75-78] (Table S5).

Given that these bacteria are ubiquitous and abundant, it is not surprising that they are also found on microplastics. Indeed, eliminating plastics would likely not significantly alter their abundance, as there would still be enough natural substrata for these bacteria to thrive. However, most of these microplastics are positively buoyant polymers (polyethylene and polypropylene; [31]) that might maintain the associated bacterial colonies in the water column or near the sea surface, exposing them to particular environmental conditions (oxygen, light, nutrients). Furthermore, due to their specific characteristics (buoyancy, specific density) that differ from most natural particles, these microplastics might serve as vectors facilitating the transfer of microplastics from environmental matrices (sediment, water) into fish.

Framed in the wide variety of bacteria found on microplastics, which can be harmless, beneficial, or harmful, this study sought to identify potentially pathogenic living species, emphasizing the need to detect and confirm the presence of species that may pose health risks to fisheries and local communities dependent on those fish resources. Our research identified numerous bacterial genera, such as *Aeromonas*, *Shewanella*, *Cronobacter*, *Enterobacter*, *Escherichia*, *Klebsiella*, *Proteus*, *Raoultella*, *Pantoea*, *Serratia*, *Pseudomonas*, *Vibrio*, and *Stenotrophomonas*, among others (Table S5). Biochemical and molecular techniques allowed identifying at least 15 species of potentially pathogenic culturable bacteria for fish and humans.

To cause disease, potentially pathogenic species must have the necessary virulence genes [78]. Therefore, from a precautionary viewpoint, it would be advisable to consider possible risks according to the nature of the given bacterial genus. The genus *Vibrio* includes 12 known human pathogenic species and has a high potential for horizontal transfer of virulence and resistance genes. Non-pathogenic *Vibrio* may act as reservoirs for these types of genes [79], and microplastics provide surfaces where intense interactions and gene exchange through horizontal transfer can occur [80].

Bacterial pathogenicity, determined by virulence, ranges from avirulent to highly virulent forms, depending on specific DNA segments encoding virulence factors [81,78,82]. These factors include proteins for adhesion, invasion, toxin secretion, immune system inhibition, and biofilm formation [83]. The interaction between bacteria and their host hinges on both host resistance and bacterial virulence [78,81]. In the case of CGSM, further investigation into the virulence of the potentially pathogenic species identified on microplastics is recommended.

Fish can be infected or act as transport vectors for pathogenic bacteria, resulting in the accumulation of toxins and subsequently posing a risk to both the ecosystem health and the people who consume them [84, 85]. The diseases associated with the presence of potentially pathogenic bacteria include sepsis, necrosis, and poisoning in fish, as well as gastroenteritis, diarrhea, cholera, and food poisoning in humans following the consumption of contaminated seafood. Additionally, they can cause eye, respiratory, skin, and soft tissue infections in humans after contact, wound exposure, or use of contaminated water (Table S5).

While many of the potentially pathogenic bacterial genera are native to the CGSM ecosystem, their presence in the water, sediments, and fish from the lagoons relates to the constant input of fecal waste [26], mainly in the North CG and Pajarales zones, where the main population centers, and fishing and aquaculture activities, are located (Fig. 1). All of them suffer from severe deficiencies in waste and wastewater management [26,49]. However, according to some studies it is also likely that the environmental conditions in the lagoons, such as high solar radiation, high water temperatures (23.4–34.7 °C) and highly variable salinity (>28 units), could act as limiting factors for the proliferation of certain pathogenic bacterial species [86,29,87,76].

As a matter of fact, the presence of microplastics in the ecosystem helps create a favorable environment for the associated bacteria to survive through the formation of biofilms on the particles' surfaces [88-90]. These biofilms enable the bacteria to withstand unfavorable environmental conditions [88], which in the case of the CGSM lagoon system often occur during the dry season when the influx of freshwater from rivers significantly decreases and the marine influence increases [91,29,26].

During the two annual rainy seasons, salinity conditions decrease due to a higher freshwater inflow into the lagoon system, which also carries nutrients, organic matter and many microorganisms that are indicative of fecal contamination [26], jointly with microplastics [31]. This likely results in enhanced pathogen concentrations in the water and, thus, in an increased potential for disease outbreaks [76,92]. Córdoba-Meza et al. [29] found that the culturable species *V. cholerae* increases in density and frequency in the water of the CGSM lagoon system during the months with lower salinities (0.1–10 units).

Living cells of bacteria *A. caviae*, *Pantoea* spp., *E. roggenkampii, P. fluorescens/putida*, and *V. parahaemolyticus* were found on microplastics extracted from water and sediments collected in CGSM. Except for *V. parahaemolyticus*, the other species occurred in water and sediments, and in fish. Studies by INVEMAR [26] and Córdoba-Meza et al. [29] identified these bacteria in water, and Garcés-Ordóñez et al. [31] noticed commercial fish ingesting microplastics from their habitat. The presence of these potentially pathogenic bacterial species on microplastics points to the likelihood of infection of the CGSM's fishery resources, as observed in previous studies where strains of these pathogenic bacteria were encountered in muscle tissues of commercial fish in CGSM [26,93].

Furthermore, culturable *A. caviae* and *V. cholerae* appeared on microplastics from all zones within the CGSM lagoon system, with higher numbers of isolated colonies during the dry season. There are two possible explanations to this, namely that (i) microplastic particles serve as a common niche for these bacteria due to their widespread distribution in the lagoons, potentially facilitating microorganism dispersion within and also beyond the CGSM system, and (ii) these bacteria colonize microplastics in the waters more easily and frequently during the dry season and under unfavorable conditions such as higher salinity. The latter behavior was observed in *A. caviae* and *V. cholerae*, as well as in other culturable species within the North CG zone (Fig. 3), which displays a higher salinity due to seawater influence [26].

4.2. Potential environmental and public health risks

The CGSM lagoon system, due to its semi-closed character and the various sources of pollutants entering it [49], becomes highly vulnerable to the detrimental effects of contamination. Due to inadequate sanitation services, communities around the CGSM lagoon system often dispose waste directly in the water and along shores, causing microplastic and microbiological pollution, which affects mangroves, waters, sediments, and aquatic life, including fish, which are a vital local food source (Calderón et al., 2019; [94,23,26]). The presence of potentially pathogenic bacteria on microplastics that are transferred from the environment to fish [31] involves clear environmental and public health risks, eventually threatening ecosystem biodiversity, fisheries, and local populations (Fig. 4).

Microbiological risks identified in the CGSM ecosystem can lead to outbreaks of infectious diseases in fish (Fig. 4), impacting their populations and the broader ecosystem, especially when combined with overfishing and pollution [48,26,95]. These issues also pose health and economic threats to local communities dependent on fishing and

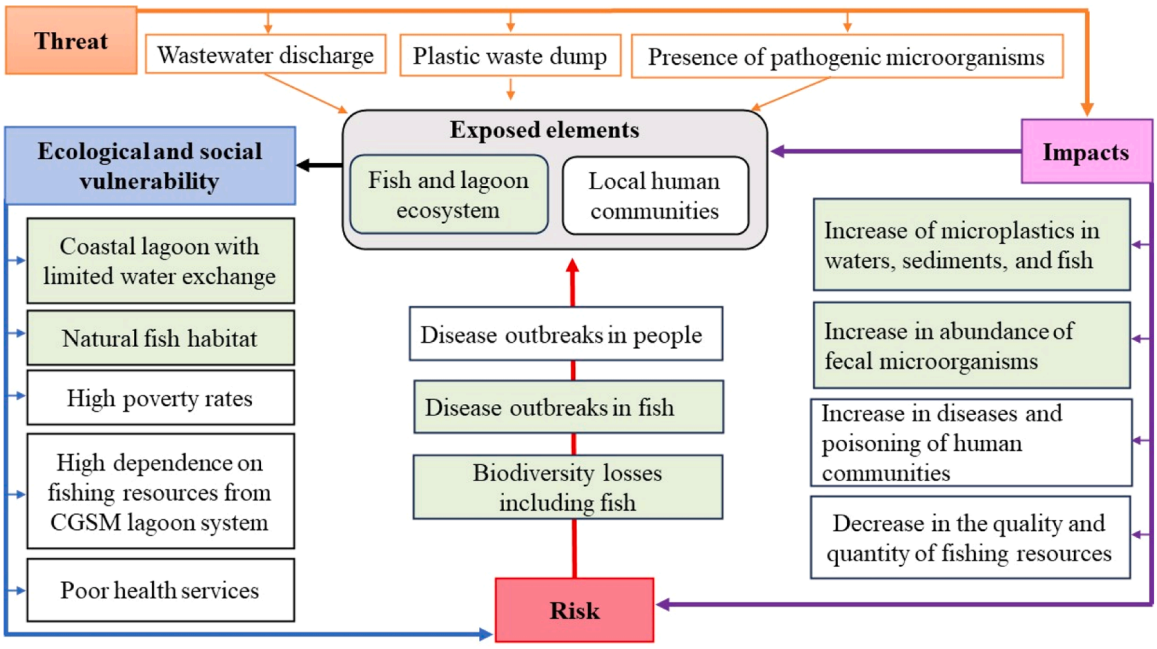

Fig. 4. Conceptual model of microbiological risk over the fishery resources and local human communities in Ciénaga Grande de Santa Marta (CGSM) lagoon system. The orange, purple, blue and red arrows and boxes represent threats, impacts, vulnerability and risks, respectively. The green and white boxes represent features of the lagoon ecosystem and the local human communities, respectively.

aquaculture [47,69], forcing people to travel to distant cities for healthcare due to local facility shortages [96], thus underscoring the need for integrated environmental and health strategies.

Pollution in the CGSM lagoon has already led to fish mortality events, often linked to water anoxia [48], but the potential synergistic effects of poor water quality and potentially pathogenic microorganisms warrant further investigation. This includes examining whether bacteria with virulence and antibiotic resistance genes occur in the plastisphere of CGSM. This is highly relevant because wastewater introduces bacteria and resistance genes into ecosystems that also colonize microplastics and form biofilms, where gene transfer among bacteria is facilitated [80, 97,10,98].

Currently, there are no records of possible infectious disease outbreaks in the fisheries resource and local communities due to consumption of contaminated food or exposure to polluted water. Whereas this information gap highlights the urgent need to establish systematic health records, our findings also point to the necessity of developing prevention measures based on management strategies aimed at easing data collection on health threats and risks. Only through the gathering and analysis of accurate data can effective prevention and mitigation actions be advanced in the CGSM area.

4.3. *Proposal for microbiological risk management*

The key elements needed for managing microbiological risk in the CGSM lagoon system include: (1) long-term monitoring involving stakeholders to understand risk patterns over time and space, (2) threat analysis and forecasting using an Early Warning System that engages both the community and healthcare services, and (3) prompt alert communication linked with emergency protocols, involving scientific, healthcare, and local communities. Based on the above, a series of management strategies were assessed, including six lines of action with their respective objectives and activities. Key players for CGSM were identified, encompassing inter-institutional partnerships, capacity building, monitoring, and strengthening of governance and infrastructures for sanitation, monitoring and research (Table 3).

We identified a high level of difficulty for implementing 50 % of the suggested activities, a medium level of difficulty for 30 %, and a low level of difficulty for 20 % (see Table 3 and Table S6). The implementation difficulty categories for the lines of action and activities described in Table 3 generally depend on the willingness, available resources (financial, material, and human), skills, implementation time in the short (1–2 years), medium (3–5 years), and long term (>5 years), and on effective collaboration and coordination efforts among the stakeholders identified for each activity.

It is also convenient highlighting the progress made and the opportunities arising that will likely ease the implementation of management strategies to prevent microbiological and microplastic risk in the CGSM lagoon system. Institutional efforts primarily aimed at monitoring environmental conditions in the CGSM lagoon system have already resulted in scientific data regarding indicators of fecal contamination and microbial pathogens [26]. This monitoring was carried out in response to the negative impacts caused by the construction of inter-municipal roads and the interruption of water flows, which have significantly deteriorated the mangrove and lagoon ecosystems [26]. Such a monitoring effort, which continues to this day, provides a solid foundation for the design and implementation of an Early Warning System for future pathogen and disease outbreaks.

Despite the above-mentioned advancements, more specialized research is needed to assess key aspects for which critical information gaps still exist. For instance, there is an absolute necessity to understand the diseases affecting fishery resources, encompassing all commercially important species, and the frequency and intensity of disease outbreaks. It is also essential to gather health records of individuals after having been exposed to polluted waters, sediments, and fish in the CGSM lagoon system.

Education, training, and environmental awareness among the inhabitants of the CGSM system are fundamental elements and should be integrated into environmental management and an Early Warning System [29,37,95]. Such an integration will enable the local communities, researchers, healthcare professionals and government officers to identify pollution-led issues affecting the ecosystem and, consequently, take timely action [39]. This training and awareness among the involved stakeholders should lead to significant behavioral changes, enabling the trained personnel to take action and participate in long-term prevention and monitoring activities. Mapping risks in the ecosystem could be a

Table 3
Proposed management strategies to support the implementation of an Early Warning System for responding to potential outbreaks of pathogens and infectious diseases in the Ciénaga Grande de Santa Marta lagoon system, Colombian Caribbean. The level of implementation difficulty is classified as high, medium, and low, considering the required resources, skills, implementation time, and coordination amongst stakeholders (see Table S6 in the SM).

Action lines	Activities	Level of difficulty - main requirements	Advisable stakeholders
1. Monitoring and research: Establish guidelines for continuous monitoring of potentially pathogenic microorganisms and the conditions that favor their presence and growth in the lagoons.	• Redesign the monitoring of microbiological pollution together with the environmental conditions that promote such pollution and disease outbreaks in the ecosystem.	• Medium - Requires revising and updating existing monitoring protocols.	Government, educational centers, environmental and healthcare organizations, local communities, and private sector.
	• Perform research on the virulence and antibiotic resistance of microorganisms isolated from the environment, fishery resources and clinical cases in the area.	• High - Requires extensive laboratory work and scientific research.	
	• Investigate and diagnose diseases resulting from microbiological pollution of water and fishery resources for human consumption.	• High - Needs advanced diagnostic facilities and expertise.	
	• Identify high-risk areas for prioritized monitoring.	• Low - Relatively straightforward, can be done using existing data and minimal resources.	
	• Develop mechanisms for knowledge transfer regarding microbiological risk.	• Low - Involves communication and education strategies.	
2. Infrastructures: Technical strengthening of stakeholder's capabilities for environmental research and emergency response.	• Provide key stakeholders with tools for the identification of microorganisms causing infections.	• Medium - Involves some training and distribution of diagnostic tools.	Government, environmental and healthcare organizations, providers of basic services, private sector, and local communities.
	• Establishing regional centers for the diagnosis of infectious diseases.	• High - Involves significant investment in infrastructure and training.	
	• Developing a permanent communication system with local communities for alert communication, knowledge transfer and capacity building.	• High - Requires developing and maintaining a robust communication network.	
3. Control and surveillance: Establish epidemiological surveillance programs to monitor infectious disease outbreaks in the area.	• Define symptoms and warning signs for each disease.	• Low - Requires medical and epidemiological expertise, which is achievable with standard protocols.	Government, environmental and healthcare organizations, and local communities.
	• Train community members to recognize symptoms and warning signs, so that appropriate measures could be applied.	• Medium - Requires organizing and conducting training sessions.	
	• Report cases and integrate information with environmental conditions easing the development of given diseases.	• Medium - Needs systematic data collection and analysis.	
4. Governance: Strengthening mechanisms for addressing and preventing pathogen outbreaks.	• Generate a map of critical areas based on the coverage of basic services such as drinking water supply, sewerage, solid waste collection and health care.	• Medium - Involves data gathering and GIS mapping.	Government, environmental and healthcare organizations, and local communities.
	• Design projects for the practical implementation of waste and wastewater treatment systems in different communities, or to improve the existing ones whenever required.	• High - Involves complex engineering and significant financial resources.	
5. Partnerships, cooperation: Establish partnerships between environmental and healthcare organizations.	• Mapping of key stakeholders to establish a network of alliances and cooperation at local, regional, and international scales, along with a work plan.	• High - Requires extensive coordination and strategic planning.	Government, environmental and healthcare organizations, industries, educational centers, local communities.
	• Formulating projects to characterize the risk and build technical capacity and continuous monitoring systems on infectious diseases in the area.	• High - Involves comprehensive project design and implementation.	
6. Education, training, and awareness: Provide training and raise awareness about the risks and diagnosis of outbreaks of diseases caused by pathogenic microorganisms.	• Create awareness spaces for the prevention of infectious diseases, especially those associated with food and water consumption, as well as exposure during recreational and fishing/aquaculture activities.	• Medium/High - Requires organizing workshops and public meetings and sustained effort and resources.	Government, educational centers, environmental and healthcare organizations, local communities.
	• Train technical personnel and local community members in the detection of pathogens and infectious outbreaks.	• High - Involves designing and implementing specialized training programs for qualified personnel to take action, change behaviors, and participate in long-term prevention or monitoring activities.	
	• Create and disseminate informative brochures about the most common diseases.	• Low - Involves creating educational materials and distributing them.	

valuable tool for the early detection of threatening situations and the establishment of mechanisms for response, prevention, and mitigation [99].

Communication facilities should deserve attention too as they can vary substantially across communities, with some having better access than others. Therefore, it is essential to improve infrastructure also in terms of communication to (and from) the population. Limitations in the availability of communication installations and devices should be addressed directly. For example, telecommunication signals do not reach the stilt house settlements of Nueva Venecia and Buenavista, in the Pajarales zone (Fig. 1), thus highlighting the need to strengthen connectivity, eventually through a community information network. It is

also important to utilize existing institutional information services, such as the marine environmental information system managed by INVEMAR and other Early Warning System for natural events managed by the Colombian *Instituto de Hidrología, Meteorología y Estudios Ambientales* (IDEAM) and *Instituto Nacional de Salud* (INS).

5. Conclusions

Ciénaga Grande de Santa Marta (CGSM) is an internationally recognized coastal lagoon system of high importance for biodiversity conservation in the Colombian Caribbean encompassing fishing and aquaculture activities of local relevance. Unfortunately, the CGSM system is being impacted by interacting microplastics and microbiological pollution, in addition to other anthropogenic impacts that are not addressed here. Microplastics are home to a highly diverse community of bacteria, some of which are potentially pathogenic for both fish and humans. Thus, microplastics become a reservoir for these microorganisms in CGSM and, very likely, in other coastal lagoons around the world.

DNA analyses have revealed the presence of 1760 bacterial genera on the microplastics of the CGSM system, among which 19 potentially pathogenic species belonging to 15 cultivable bacterial genera have been identified. These bacteria live on microplastics found in water and sediments, as well as in the digestive tracts of commercial fish within the CGSM system. Although these bacteria grow on different substrata in the natural environment, they are also introduced into the lagoon ecosystem through the discharge of wastewater. Among the most common cultivable species are *Aeromonas caviae*, *Vibrio cholerae*, *Proteus mirabilis*, and *Enterobacter roggenkampii*. The virulence of the potentially pathogenic bacterial species identified needs to be investigated.

Potentially pathogenic bacteria represent a microbiological risk for the ecosystem and its biodiversity, and for the quality and safety of the fishery resource, as well as for the health of local human communities that eat lagoon fish. These bacteria can cause infections, intoxications, and diseases in fish and in humans exposed to them. The assessment of the results obtained in terms of management implications points to the necessity of implementing strategies that include infrastructure strengthening and the creation of an integrated Early Warning System in the CGSM lagoon system framed within interinstitutional partnerships. Such a framework should actively promote continuous monitoring, education, and training activities, and ultimately ease a sound governance of the unique CGSM lagoon system for current and future generations. The findings presented here also lay the groundwork for future studies aiming to deepen the understanding of microbial community interactions and the risks they pose to the lagoon's wild and cultivated organisms, as well as to public health.

Environmental implication

Our study addresses the serious threat posed by microplastics and potentially pathogenic bacteria (PPB) in tropical coastal lagoons, ecosystems that are crucial and highly vulnerable to these hazardous materials, as exemplified by the Ciénaga Grande de Santa Marta (Ramsar site and Biosphere Reserve). Microplastics, as habitats for PPB, threaten the fishing resources that ingest these particles. This study highlights the interaction between microplastics and PPB, analyzing environmental risks and developing management proposals to raise awareness and reduce this issue affecting biodiversity and vulnerable communities. The study offers a model approach that could be applicable to coastal lagoons globally.

CRediT authorship contribution statement

Ostin Garcés-Ordóñez: Writing – review & editing, Writing – original draft, Visualization, Validation, Supervision, Project administration, Methodology, Investigation, Funding acquisition, Formal analysis, Data curation, Conceptualization. **Miquel Canals:** Writing – review & editing, Visualization, Supervision, Resources. **Martin Thiel:** Writing – review & editing, Visualization, Supervision. **Alejandra P é rez-Duque:** Writing – review & editing, Validation. **Luisa F. Espinosa-Díaz:** Writing – review & editing, Resources, Project administration, Funding acquisition. **Lina Blandón:** Writing – review & editing, Validation, Methodology, Conceptualization. **Sol Sáenz-Arias:** Writing – original draft, Investigation, Formal analysis. **Tania Córdoba-Meza:** Writing – original draft, Visualization, Validation, Supervision, Methodology, Investigation, Funding acquisition, Formal analysis, Data curation, Conceptualization.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data availability

Data will be made available on request.

Acknowledgments

The authors would like to express their gratitude for the support provided by their respective institutions. They are grateful to INVEMAR and MinCiencias Colombia for support through research project "*Risk assessment of microplastics as vectors of potentially pathogenic microorganisms for three commercially important fish species in the Ciénaga Grande de Santa Marta, Colombian Caribbean*" funded by Francisco José de Caldas Fund (grant agreement number 2105 −852 −71858); and to the University of Barcelona for framing this study within its Doctorate Program on Marine Sciences. We also extend our gratitude to the Research Group on Innovation in BioGeosciences, Nature, and Sustainability – InBiGS of INGEOS S.A. (Colombia), led by Dr. Grace Montoya-Rojas, who were also a part of this project. Additionally, we thank Juan Saldarriaga, Kevin Mejía, Laura Fragozo, and Janet Vivas for their assistance in field, laboratory and administrative activities, and Felipe Valencia for map production. Miquel Canals and Ostin Garcés acknowledge *GRC Geociències Marines*, which is funded by the Catalan Government (grant 2021 SGR 01195) as part of its program for excellence research groups. Scientific contribution of INVEMAR No. 1381.

Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at doi:10.1016/j.jhazmat.2024.135638.

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