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Wastewater from Social Housing Networks as a Reservoir of Antibiotic-Resistant *Vibrio*: Phenotypic Identification and Seasonal Variability in Yaoundé, Cameroon

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Abstract

A study was carried out to search for bacteria of the genus *Vibrio* in the effluents of the social housing networks (called SIC camps) in the city of Yaoundé. Wastewater samples were taken at various points in the SIC camps in selected locations in Yaoundé. In total, seven sampling points were selected. Bacteria were isolated on TCBS (Thiosulfate Citrate Bile Salts Sucrose) medium on a Petri dish using the surface spread technique. Standard analytical techniques were used to measure some abiotic parameters. Susceptibility testing to ten antibiotics was performed on 29 *Vibrio* isolates (19 dry season isolates and 10 wet season isolates). The species identified were *V. cholerae*, *V. alginolyticus*, *V. parahaemolyticus*, *V. vulnificus* and *V. mimicus*. The abundance of these bacteria varied between 0 and 4.40 log CFU/mL. *V. parahaemolyticus* was the most abundant species. Thus, their abundance has undergone spatio-temporal and seasonal variations and seems to be weakly influenced by the physico-chemical parameters considered in this study. The susceptibility of bacteria to ten antibiotics (ceftazidime, colistin, gentamicin, doxycycline, azithromycin, ciprofloxacin, nalidixic acid, chloramphenicol, amoxicillin + ac. clavulanic and cefotaxime) was carried out on 29 isolates (*i.e.*, 19 isolates in the dry season and 10 isolates in rainy season) of *Vibrio.* In the dry season, the highest resistance rate was that of

V. cholerae (60%) while in the rainy season, the highest resistance rate was that of *V. alginolyticus* (70%). In addition, the species identified have multi-resistance ranging from 2 to 7 different antibiotics.

Keywords

Wastewater, *Vibrio* Bacteria, Antibiotic Resistance, Abiotic Factors

1. Introduction

Wastewater is defined as water that has undergone physico-chemical and biological changes following anthropogenic use. The presence of this water in the environment poses a risk both to human health and to the environment. In developing countries, dirty water discharged after use is found in the environment due to a lack of collection and treatment networks [1]. This is the case in Yaoundé, Cameroon, where there are 13 social housing networks (called SIC camps) located in the city centre and on the outskirts. These dwellings are occupied by several households. These households produce significant amounts of domestic wastewater. The method of sanitation of this water through sewerage networks remains precarious and poorly managed by public authorities [2]. Thus, wastewater is most often discharged in an anarchic manner without prior treatment in the receiving environment (lakes, streets, rivers, etc.) [3]. The latter contains a wide range of substances as well as numerous micro-organisms, such as bacteria, that can pose health risks to humans and the environment in general [4] [5]. These waters may be the source of waterborne disease in a population caused by infectious agents responsible for morbidity and mortality [6]. Several diseases affecting the general population are caused by pathogens carried by untreated wastewater from human activities and released into the environment. Cholera morbidity is estimated at 2.9 million cases with 95,000 deaths per year worldwide [7]. In Cameroon, the first case was reported in 1971, followed by several outbreaks, the most recent from March to July 2023, with 19,488 cases and 465 deaths nationwide. In the Centre Region, the number of reported cases was 4,540, with 161 deaths. Studies conducted by some authors in tropical surface waters revealed the presence of 6 *Vibrio* species potentially pathogenic to humans (*Vibrio cholerae*, *V. parahaemolyticus*, *V. vulnificus*, *V. fluvialis*, *V. alginolyticus* and *V. mimicus*) [8]. Numerous studies on the impact of abiotic factors and antibiotic resistance have shown that parameters such as temperature and pH influence the antibiotic resistance of microorganisms in aquatic environments [9]. These findings underscore the need for further research in this area. Wastewaters discharged from social housing networks (SIC camps) in Yaoundé are often released into the environment without prior treatment. These wastewaters may contain pathogenic microorganisms, including *Vibrio* species, which are known to cause waterborne diseases such as cholera and other vibrioses. The presence of *Vibrio* in untreated wastewaters poses a significant public health risk, especially in urban communities with limited access to clean water and sanitation. Fur-

thermore, the increasing emergence of antibiotic-resistant bacteria is a major global concern. *Vibrio* species isolated from environmental sources may carry resistance genes, contributing to the spread of antimicrobial resistance in human populations through environmental exposure. Despite this, there is limited data on the phenotypic identification and antibiotic susceptibility profiles of *Vibrio* species in wastewaters from social housing networks in Yaoundé. Therefore, this study aims to phenotypically identify *Vibrio* species present in the wastewaters of social housing networks (SIC camps) discharged into the environment of Yaoundé, and to assess their susceptibility to selected antibiotics. The findings will provide valuable baseline data for public health interventions and wastewater management policies aimed at reducing the risks associated with *Vibrio* infections and the spread of antibiotic resistance in the community.

2. Material and Methods

2.1. Sampling Site Selection and Description

Seven social housing sites were selected based on specific criteria, including ease of access, population density, type of sanitation system, configuration of latrine pits, mode of effluent discharge into the environment, and spatial distribution. These criteria were applied to ensure the representativeness of various wastewater management practices and discharge conditions observed throughout the city's social housing network. Wastewater samples were collected from seven designated points: MDG, RPE, BIY, Cverte, MSI, MSII, and MFD. Those geographic coordinates are given in Table 1.

Table 1. Geographic coordinate of the sampling stations, sampling point description and observation.

Sampling point codes	Sics camp names	Geographic coordinates			Sampling point description and observation
		Latitude (N)	Longitude (E)	Altitude (m)	
MDG	Mendong	03˚83'60.48"	011˚46'92.93"	782	This point is a medium flow pit. It is more or less equipped.
RPE	Rond point express	03˚83'67.89"	011˚48'43.80"	715	The wastewater overflows the pit and moves through the environment at a medium speed.
BIY	Biyem-Assi	03˚83'87.50"	011˚48'60.85"	697	It is located on the site of the Biyem-Assi wastewater treatment plant.
Cverte	Cité-Verte	03˚87'62.19"	011˚48'94.59"	764	Wastewater is fed into a tank. It flows at a medium speed.
MSI	Messa I	03˚87'17.10"	011˚50'71.91"	733	Sewage is discharged into an overflow tank and, due to the high flow rate, the effluent is discharged directly into the environment.
MSII	Messa II	03˚87'12.26"	011˚50'68.95"	733	Wastewater is discharged into a pit. The wastewater flow is average.
MFD	Mfandena	03˚88'57.00"	011˚54'92.50"	756	Wastewater from this camp flows into a gully with an average flow rate.

2.2. Sampling Method and Measurement of Environmental Variables

The samples for the bacteriological analysis were collected in sterile glass bottles of 500 mL. Samples for physicochemical analyses were collected bubble-free by a diver in 250 ml double-capped polyethylene bottles following the techniques recommended by Rodier *et al*. [10]. At the level of each sampling station, the physicochemical analysis focused on 12 variables. Physico-chemical parameters (water Temperature (˚C), pH, electrical conductivity of the water (µS/cm), salinity (ppm), suspended solids (mg/L), total dissolved solid (ppm), water colour (Pt.Co), turbidity (FAU), nitrates (mg/L), nitrates (mg/L), orthophosphates (mg/L PO_4^{3-}) and ammonium ions (mg/L NH_4^+) were measured by colorimetry and/or spectrophotometry according to the techniques described by some authors [10] [11]. The various samples were then transported to the laboratory in a refrigerated chamber to undergo the various analyses and tests required. Bacteriological analysis begins within 4 hours of sampling.

2.3. Bacterial Isolation and Identification

The isolation of bacteria from the genus *Vibrio* was conducted through the utilisation of the surface spreading method. A volume of 100 µL of each sample was collected using a sterile micropipette and deposited onto the surface of Thiosulfate Citrate Bile Salts (TCBS) agar that had previously been poured into sterile Petri dishes (90 mm in diameter). The inoculum was distributed uniformly across the surface using a sterile rake or spreader until complete absorption was achieved. Subsequently, the plates were subjected to an incubation process at a temperature of 37˚C for a duration of 24 hours. The identification of *Vibrio* species commenced with a search for motility type and Gram staining. Gram staining is a method of staining bacteria that provides information on the morphology and structure of the bacteria wall. The colour, size and shape of colonies on TCBS agar were used as parameters. The process of classical biochemical identification has facilitated the identification of enzymes including oxidase, lysine decarboxylase, ornithine decarboxylase, urease, tryptophanase and β-galactosidase [12]. A suspension in sterile distilled water was prepared from a colony of the pure culture on an alkaline nutrient agar. The bacterial suspension was distributed in the capsules of the API 20E system (BioMérieux, France). After 24 hours of incubation at 37˚C, the metabolites formed were visualised by colour reactions or the addition of reagents. The APIDENT 2.0 software was used to numerically determine the corresponding bacterial species. The identification rate was maintained at least at 98%. Isolated bacteria were enumerated using an OSI brand colony counter. Bacterial abundances are expressed in decimal logarithmic units of colony forming units (CFU) per mL of water sample.

2.4. Antimicrobial Susceptibility Tests

We used agar diffusion to carry out the antibiograms [13]. It was based on the

presence or absence of an inhibition zone around an antibiotic-impregnated blotting paper (agar) disc. Antimicrobial susceptibility testing was performed on pure strains in accordance with the recommendations of the Antibiogram Committee of the French Society of Microbiology [14]. The antibiotics used belonged to several families. They were in the form of a disc of blotting paper, 6 mm in diameter, impregnated with well-determined quantities of active substances and rigorously controlled for the diffusion method. Table 2 lists the antibiotics used, their groups and their characteristics. The test results were only validated in those cases where the diameters of the inhibition zones of the control strains were within the performance ranges. Inhibition zone diameters of bacteria isolates were measured and then compared to National Committee of Clinical Laboratory Standards [15]. The sensitive (S) category means that the strain is susceptible to the antibiotic treatment given at the normal dose. In the intermediate category (I), the success of the therapy is not predictable. If the antibiotic is used at a higher dose than usual, the treatment will be effective. Intermediate means moderately susceptible or moderately resistant. The resistant (R) category means that there is a high probability of treatment failure regardless of the type of antibiotic treatment, or that the strain will not be affected regardless of the type of treatment. Monthly changes in physicochemical parameters at the different sampling sites and the prevalence of resistant (R), intermediate (I) or sensitive (S) strains to each antibiotic were plotted using Microsoft Excel.

Table 2. Antibiotics, disc loads, and critical reference diameters for *Vibrio* [14]-[16].

Antibiotic families	Standards	Antibiotics tested	Antibiotic concentration en µg	Critical reference diameter en mm		
				Sensible	Intermediate	Resistant
Beta-lactams	CLSI (2018)	Ceftazidime (CAZ30)	30	≥21	18-20	≤17
Polymyxines		Colistin (CT10)	10	-	-	-
Aminosides		Gentamicin (GEN10)	10	≥15	13-14	≤12
phenicol		Chloramphenicol (C30)	30	≥18	13-17	≤12
Beta-lactams	NCCLS (2023)	Cefotaxime (CTX30)	30	≥26	23-25	≤22
Beta-lactams		Amoxicillin + clavulanic acid (AMC30)	30	≥21	14-20	<14
Quinolones		Nalidixic acid (NA30)	30	≥20	15-19	<15
Cyclines		Doxycycline (DOX30)	30	≥19	17-18	<17
Macrolides	CASFM (2023)	Azithromycin (AT15)	15	≥16	-	<16
Quinolones		Ciprofloxacin (CIP5)	5	≥23	-	<23

2.5. Data Presentation and Statistical Analysis

The Principal Component Analysis (PCA) performed on the physico-chemical and bacteriological parameters facilitated the characterisation of the distinct

groups that were formed. The purpose of PCA was to extract the primary information representative of the typical characteristics of the water environment from a database and to represent it as a new set of independent principal component variables [17].

3. Results and Discussion

3.1. Biochemical Characteristics of Isolated Bacteria

Bacteriological analysis helped to identify five species belonging to the genus *Vibrio*. These are: *V. cholerae*, *V. alginolyticus*, *V. parahaemolyticus*, *V. vulnificus* and *V. mimicus*. The biochemical profiles of the strains studied, and the different species identified are shown in **Table 3**. The cultural characteristics of the different *Vibrio* species listed were yellow and flat colonies of 2 mm in diameter for the presumptive of *V. cholerae*, then yellow and large colonies (5 mm in diameter) presumptive of *V. alginolyticus*, large and green colonies (5 mm in diameter) presumptive of *V. parahaemolyticus*, small and green colonies (2 mm in diameter) presumptive of *V. vulnificus* and finally those which were medium and green colonies (3 mm in diameter) presumptive of *V. mimicus*. **Table 3** shows the biochemical profiles of the strains studied, as well as these different species identified.

Table 3. Biochemical characteristics of different species isolated.

Biochemical tests	Colony color on TCBS and Biochemical characteristics				
	MYC (Ø: 2 mm)	LYC (Ø :5 mm)	LGC (Ø: 5 mm)	SGC (Ø: 2 mm)	MGC (Ø: 3 mm)
Catalase	+	+	+	+	+
Glucose	+	+	+	+	+
Lactose	−	−	−	−	±
Sucrose	+	+	−	±	±
H_2S	−	−	−	−	−
Gas	−	−	+	−	−
Citrate	+	−	−	−	+
Mannitol	+	+	+	−	+
Mobility	+	+	+	+	+
Urease	−	−	−	−	−
Indole	+	+	+	+	+
Oxydase	+	+	+	+	+
Nitrates	+	+	+	+	+
Gelatinase	+	+	+	+	+
LDC	+	+	+	+	+

Continued

ODC	+	+/−	+	+/−	+
ADH	−	−	−	−	−
Bacteria Species identified	*V. cholerae*	*V. alginolyticus*	*V. parahaemolyticus*	*V. vulnificus*	*V. mimicus*

MYC = medium yellow colony; LYC = large yellow colony; LGC = large green colony; SGC = small green colony; MGC = medium green colony; +: Positive for 90 to 100 % of strains ; −: Negative for 90 to 100% of strains ; +/−: variable.

3.2. Spatio-Temporal Variations of Studies Bacteria

Several species of the genus *Vibrio* have been isolated and identified from water samples collected at all sampling stations. These are *V. parahaemolyticus* , *V. alginolyticus* , *V. cholerae* , *V. mimicus* and *V. vulnificus*. These species, known for their role in infectious diarrhea in humans, especially *Vibrio cholerae* and *Vibrio parahaemolyticus*, have been regularly isolated from the wastewaters of social housing networks (SIC camps). Some studies carried out in the aquatic environment of the central and coastal regions of Cameroon [18]-[20] have identified strains belonging to *Vibrio* species similar to those found in our study. The spatio-temporal variations in the abundance of bacterial germs are presented in **Figure 1** and **Figure 2**. The abundances of *V. cholerae* cells, expressed in decimal logarithmic units (CFU/ mL), ranged from 0 to 3.20 log CFU/mL. Undetectable bacterial load (0 log CFU/mL) was observed mainly during the month of February at all sampling points. The highest value (3.20 log CFU/mL) was noted at point BIY (**Figure 1**). Concentrations of *V. alginolyticus* ranged from 0 to 3 log CFU/mL. Undetectable bacterial load (0 log CFU/mL) was observed mainly at the Cverte and MSII points in March, April and May. The highest value (3 log CFU/mL) in the month of April at the MFD point (**Figure 1**). *V. parahaemolyticus* concentrations ranged from 0 to 4.40 log CFU/mL. Undetectable bacterial load (0 log CFU/mL) was observed in March at point MDG, in April at points RPE, MSI and MSII and in May at points MDG, MSI and MSII. The highest value (4.40 CFU/mL) was in February at point BIY (**Figure 1**).

Concentrations of *V. vulnificus* ranged from 0 to 2 log CFU/mL. Undetectable bacterial load (0 log CFU/mL) was observed mainly at the MDG, BIY, Cverte and MSI points throughout the study period. The highest value (2 log CFU/mL) in March at the MFD point (**Figure 2**). And the densities of *V. mimicus* varied from 0 to 2 log CFU/mL. Undetectable bacterial load (0 log CFU/mL) was observed mainly at the MDG, BIY, Cverte and MSI points throughout the study period. The highest (2 log CFU/mL) in March at the RPE point (**Figure 2**).

As illustrated in **Figure 3**, the recovery frequency of bacteria isolated during the course of the study is demonstrated. Of the species identified, *Vibrio parahaemolyticus* was the most prevalent, accounting for 91% of the total. This was followed by *Vibrio cholerae* (6%), *Vibrio alginolyticus* (3%), *Vibrio vulnificus* (0%) and *Vibrio mimicus* (0%) (**Figure 3**). It has been asserted by certain authors that the aforementioned species, which are distinguished by their role in the causation of

infectious diarrhoea in humans, most notably *Vibrio cholerae* and *Vibrio parahaemolyticus*, have been frequently isolated with spatial and temporal occurrence rates of 100% each [6].

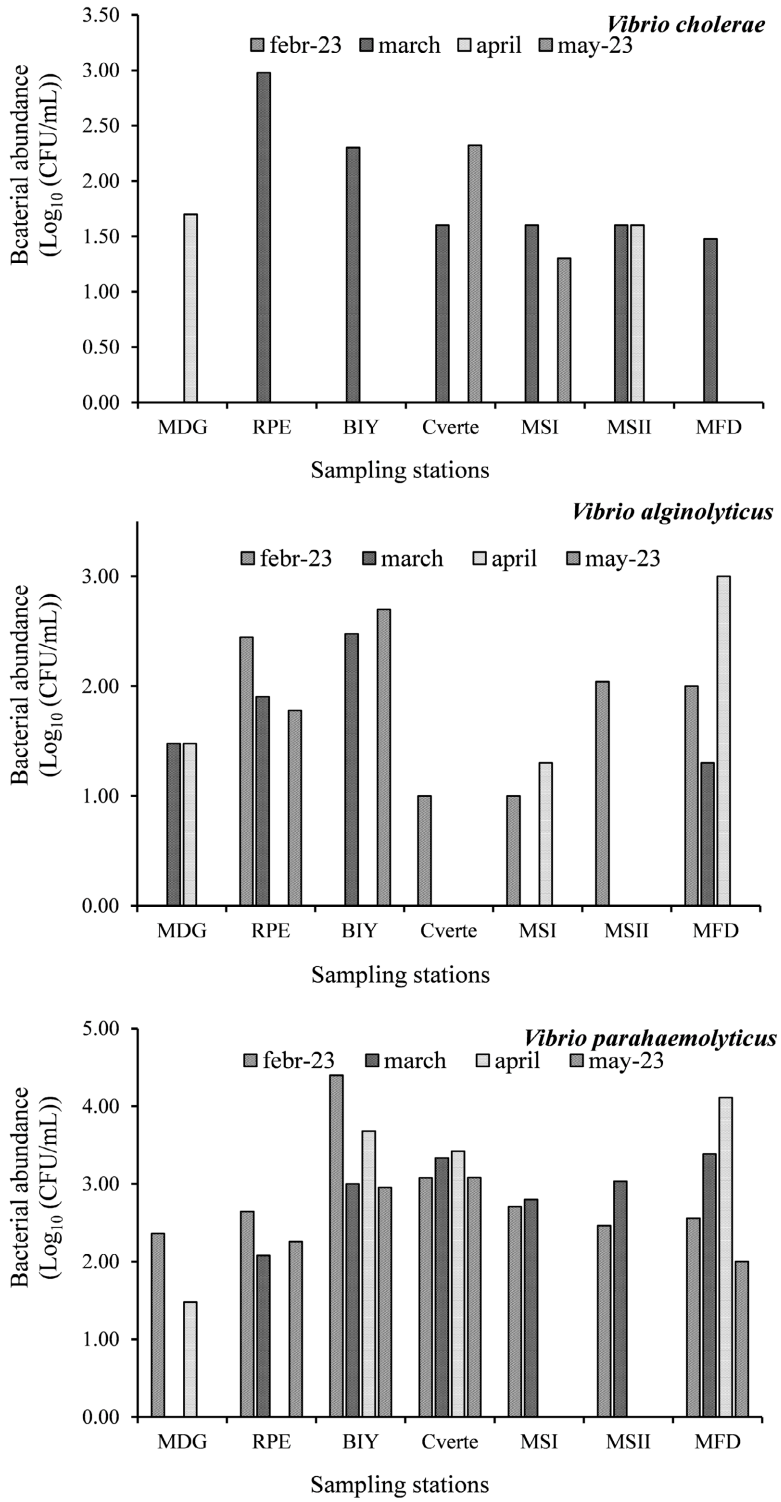

Figure 1. Spatially and temporally resolved variations in the abundance of *Vibrio cholerae*, *Vibrio alginolyticus* and *Vibrio parahaemolyticus* isolated during the study period.

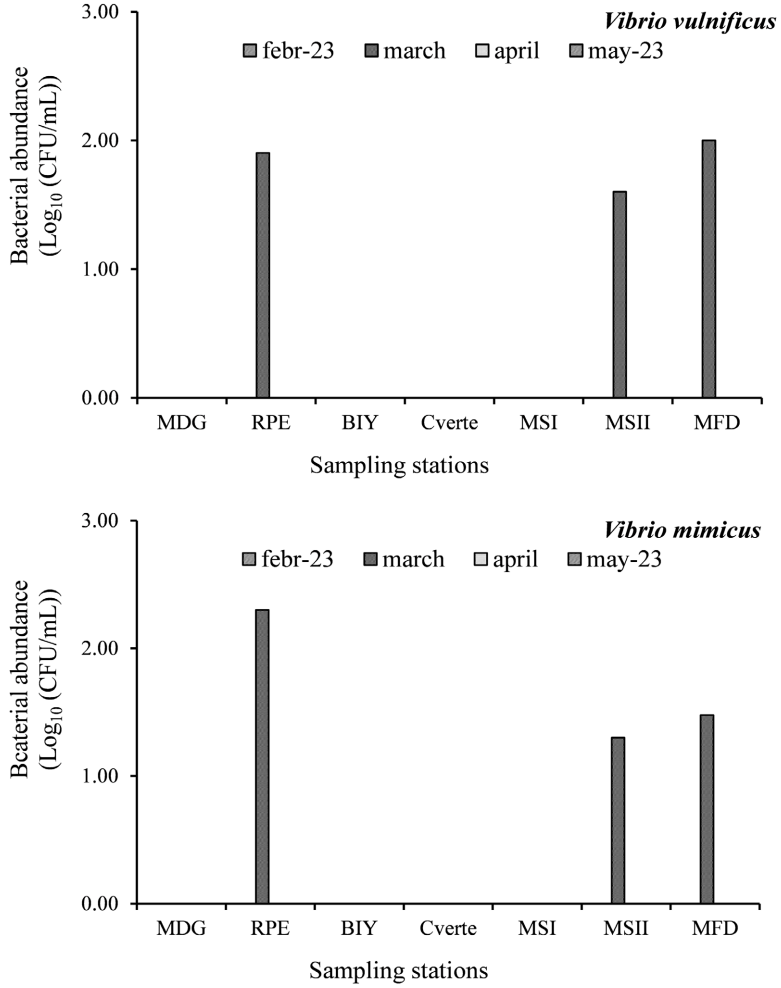

Figure 2. Spatially and temporally resolved variations in the abundance of *Vibrio vulnificus* and *Vibrio mimicus* isolated during the study period.

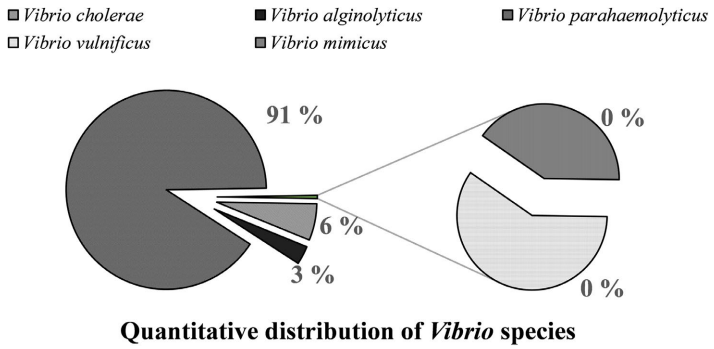

Figure 3. Rates of isolation of *Vibrio* species isolated from different points.

3.3. Antimicrobial Susceptibility Patterns among *Vibrio* Strains Isolated

In the context of the dry season, strains of *V. parahaemolyticus* and *V. cholerae* exhibited the highest levels of resistance to six antibiotics that were subjected to testing. These were *V. parahaemolyticus* resistance to amoxicillin/clavulanic acid, cefo-

taxime, colistin, azithromycin, nalidixic acid and doxycycline, and *V. cholerae* resistance to amoxicillin/clavulanic acid, cefotaxime, colistin, azithromycin, nalidixic acid and doxycycline. The *V. alginolyticus* species was resistant to two antibiotics: colistin and ciprofloxacin. In general, *V. parahaemolyticus* and *V. cholerae* were resistant to beta-lactams, polymyxins, macrolides, quinolones and partially to cyclins. *V. alginolyticus* was resistant to polymyxins and quinolones (Figure 4). During the

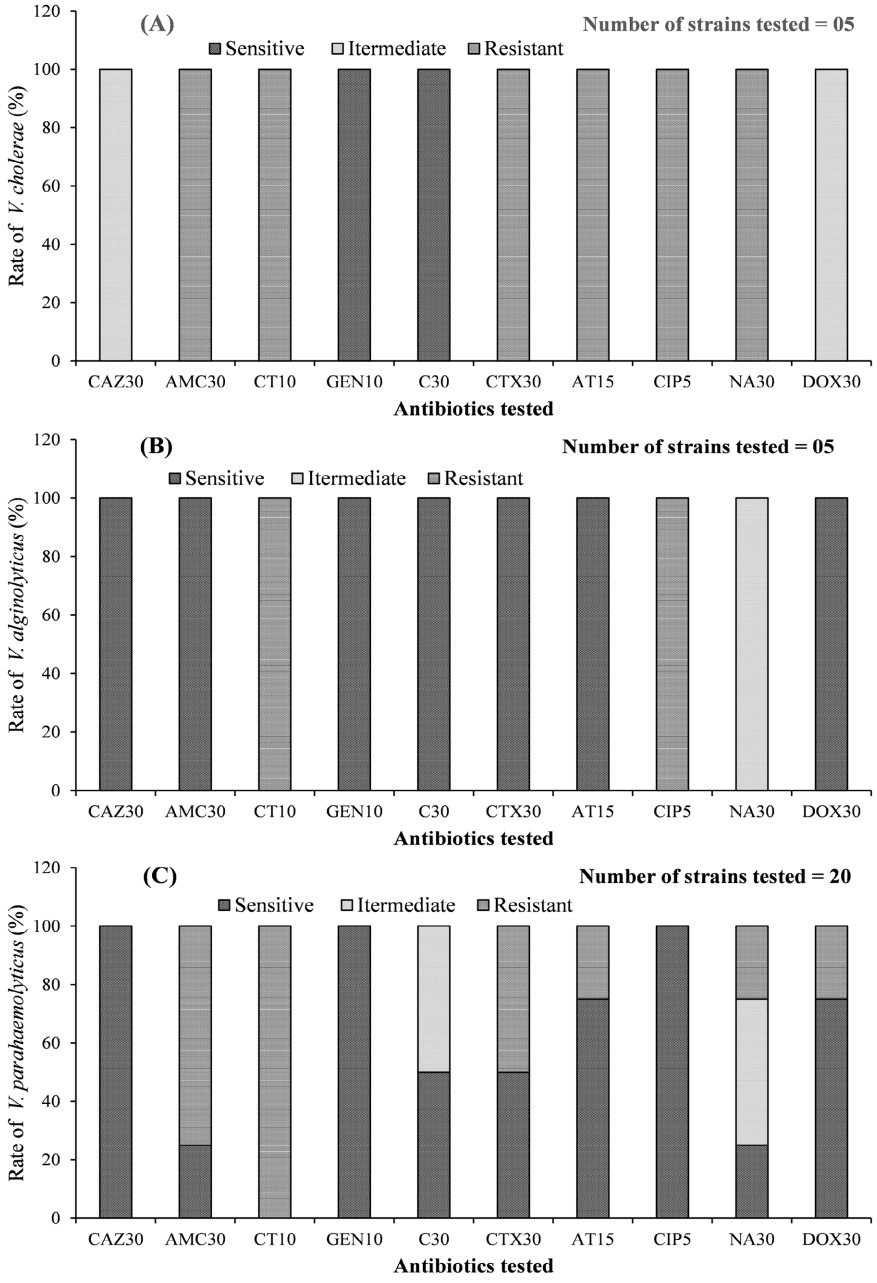

Figure 4. Antimicrobial susceptibility patterns among *Vibrio cholerae* strains (A), *Vibrio alginolyticus* (B) and *Vibrio parahaemolyticus* (C) isolated from the effluents of the social housing networks during dried season (CAZ: Ceftazidime, AMC: Amoxicillin + clavulanic acid, CT: Colistin, GEN: Gentamicin, C: Chloramphenicol, CTX: Cefotaxime, AT: Azithromycin, CIP: Ciprofloxacin, NA: Nalidixic acid, DOX: Doxycycline).

same season, *V. mimicus* strains showed maximum resistance (*i.e.*, 100%) to three antibiotics tested: amoxicillin-clavulanic acid, colistin and ceftazidime. *V. vulnificus* strains were resistant to five antibiotics: amoxicillin-clavulanic acid, cefotaxime, colistin, nalidixic acid and doxycycline (Figure 5).

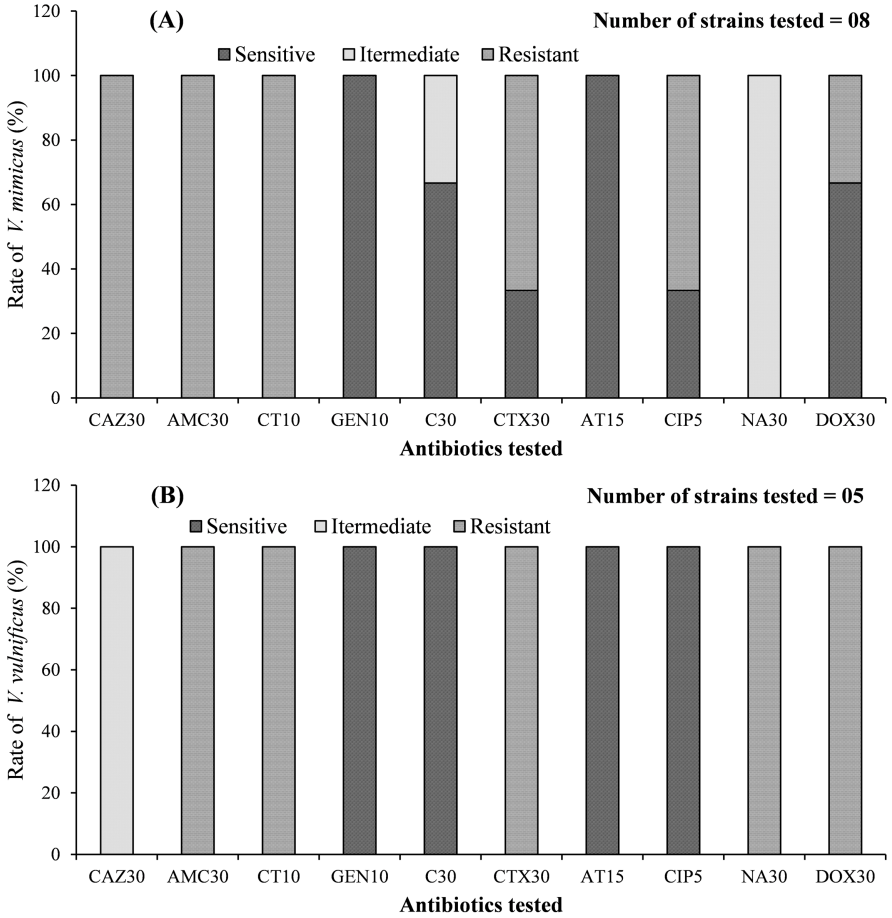

Figure 5. Antimicrobial susceptibility patterns among *Vibrio mimicus* (A) and *Vibrio vulnificus* (B) isolated from the effluents of the social housing networks during dried season (CAZ: Ceftazidime, AMC: Amoxicillin + clavulanic acid, CT: Colistin, GEN: Gentamicin, C: Chloramphenicol, CTX: Cefotaxime, AT: Azithromycin, CIP: Ciprofloxacin, NA: Nalidixic acid, DOX: Doxycycline).

During the rainy season, strains of *V. parahaemolyticus* and *V. alginolyticus* species showed maximum levels of resistance to seven of the same antibiotics tested: amoxicillin-clavulanic acid, cefotaxime, ceftazidime, colistin, ciprofloxacin, nalidixic acid and doxycycline. Whereas *V. cholerae* species were resistant to two antibiotics: amoxicillin-clavulanic acid and colistin. In general, *V. parahaemolyticus* and *V. alginolyticus* were resistant to beta-lactams, polymyxins, macrolides, quinolones and cyclins. *V. cholerae,* on the other hand, was resistant to beta-lactams and polymyxins (Figure 6).

Overall, *V. cholerae* showed the highest resistance rate in the dry season (60%) and the lowest in the wet season (20%), and *V. alginolyticus* showed the highest

resistance rate in the wet season (70%) and the lowest in the dry season (20%). Table 4 below shows the overall percentage of resistance, susceptibility and intermediary of the strains tested for susceptibility according to season.

Antibiotic susceptibility testing of isolates revealed multiresistant strains depending on the antibiotic used. *V. cholerae* was the most resistant species, followed by *V. vulnificus* in the dry season, while *V. alginolyticus* was the most resistant of six species in the wet season, with resistance rates above 50%.

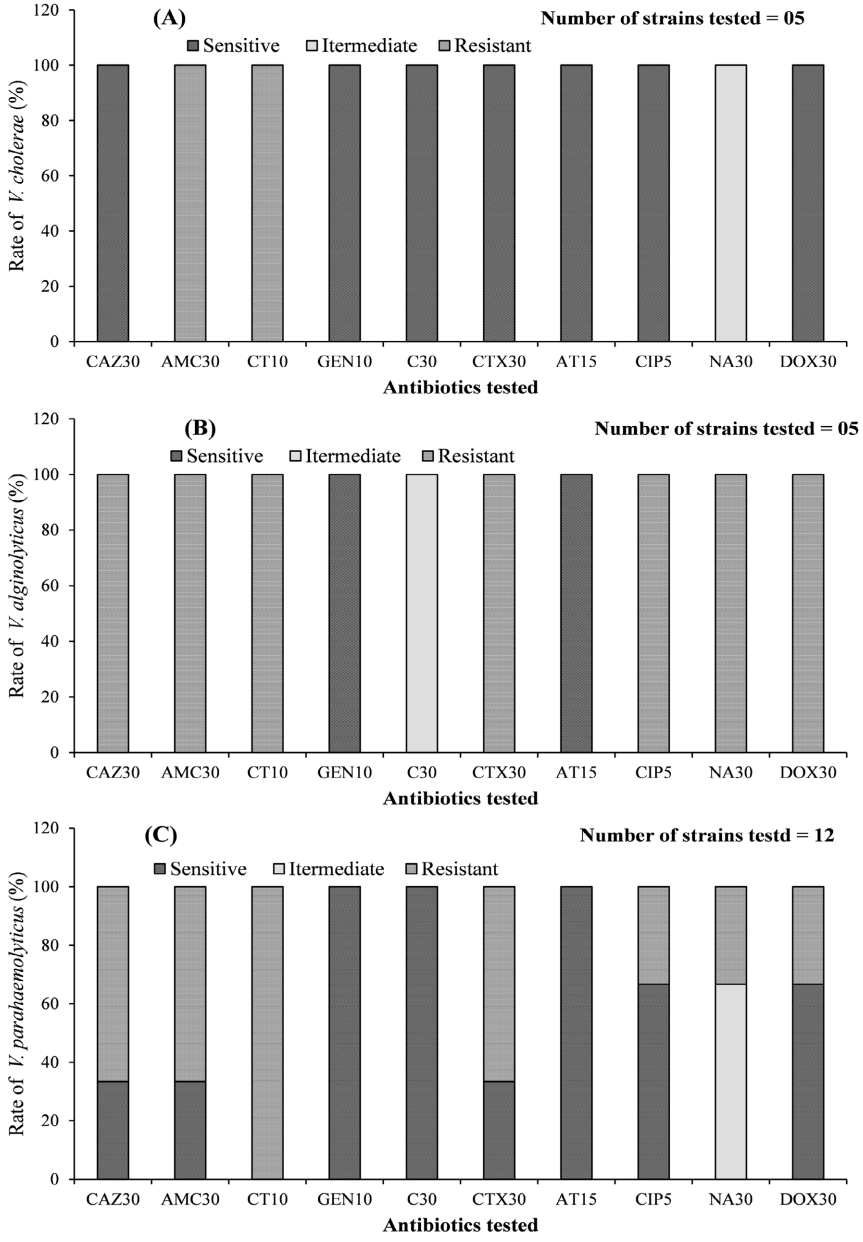

Figure 6. Antimicrobial susceptibility patterns among *Vibrio cholerae* strains (A), *Vibrio alginolyticus* (B) and *Vibrio parahaemolyticus* (C) isolated from the effluents of the social housing networks during rainy season (CAZ: Ceftazidime, AMC: Amoxicillin + clavulanic acid, CT: Colistin, GEN: Gentamicin, C: Chloramphenicol, CTX: Cefotaxime, AT: Azithromycin, CIP: Ciprofloxacin, NA: Nalidixic acid, DOX: Doxycycline).

Table 4. Total percentage of susceptibility to antibiotics of the bacterial species isolated during the dry season and the rainy season.

Sampling season and bacterial species		Percentage of resistance, sensitivity and susceptibility to the antibiotics tested (%)		
		Sensitive	Intermediate	Resistant
Dried Season	*V. cholerae*	20	20	60
	V. alginolyticus	70	10	20
	V. parahaemolyticus	60	10	30
	V. mimicus	40	13	47
	V. vulnificus	40	10	50
Rainy Season	*V. cholerae*	70	10	20
	V. alginolyticus	20	10	70
	V. parahaemolyticus	53	7	40

Furthermore, certain bacterial species of the *Vibrio* genus demonstrated sensitivities that were contingent on the presence of the antibiotic. In the dry season, *V. alginolyticus* (70%) demonstrated the highest level of sensitivity, followed by *V. parahaemolyticus* (60%). Conversely, in the rainy season, *V. cholerae* (70%) and *V. parahaemolyticus* (53%) exhibited the highest levels of sensitivity, with resistance rates exceeding 50%. With regard to resistance, the use of antibiotics in both human and veterinary medicine exerts selection pressure on commensal or pathogenic bacteria of humans or animals that can spread to the natural environment (continental and coastal waters or soil via livestock effluent or domestic wastewater). This has the potential to result in the emergence and subsequent dissemination of genetic determinants of antibiotic resistance to other environmental microbial communities [21]. This spread is facilitated by the common phylogeny within the bacterial world. According to some authors, *Vibrio* resistance is due to multiple mechanisms, including transferable plasmid and chromosomal resistance [22]. Indeed, the documented resistance exhibited by *Vibrio* strains to beta-lactam antibiotics is attributable to a plasmid that carries genes which also encode for a multitude of other antibiotics [23] [24]. As a result, transferable genetic elements within Vibrionaceae often lead to the acquisition of multidrug resistance, justified by their genetic proximity [25] [26]. What's more, the penicillinase phenotype is easily detected by beta-lactam resistance [21]. This explains, on the one hand, the resistance of *V. cholerae* and *V. vulnificus* to amoxicillin + clavulanic acid and cefotaxime, and the resistance of *V. alginolyticus* to these same antibiotics in addition to ceftazidime. On the other hand, *Vibrio* resistance could be explained by the formation of biofilms in the piping of the sanitary sewage systems in Yaoundé's SIC camps. Indeed, undecontaminated wastewater, stagnant water or water from industry is generally water containing bacteria and is generally a reservoir for microbial proliferation and biofilm development.

Still on the subject of bacterial susceptibility, *Vibrio* are usually sensitive to beta-lactams, aminoglycosides, quinolones, tetracyclines, chloramphenicol, sulfonamides, trimethoprim, furans, nalidixic acid and fluoroquinolones [21]. Other studies have confirmed that *Vibrio cholerae* is sensitive to beta-lactam antibiotics (amoxicillin, amoxicillin-clavulanic acid, and cefotaxime), aminoglycosides (gentamicin), tetracyclines (doxycycline), fluoroquinolones (ciprofloxacin), and quinolones (nalidixic acid). These findings are consistent with the results of the present study, which showed that *V. parahaemolyticus* are sensitive to ceftazidime, amoxicillin-clavulanic acid, gentamicin, chloramphenicol, cefotaxime, ciprofloxacin, nalidixic acid, and doxycycline, while *V. alginolyticus* is more sensitive to ceftazidime, amoxicillin-clavulanic acid, gentamicin, chloramphenicol, cefotaxime, and doxycycline [18]. Furthermore, the study also revealed that *V. parahaemolyticus* and *V. cholerae* are sensitive to ceftazidime, amoxicillin-clavulanic acid, gentamicin, chloramphenicol, cefotaxime, ciprofloxacin, and doxycycline.

3.4. Wastewaters Physicochemical Characteristics

The mean values physico-chemical variables of the effluent over the course of the study are shown in **Figure 7**. The average water temperature is 25.6 ˚C (±1.7 ˚C), with values ranging from 22.2 ˚C to 26.9 ˚C depending on the site. This moderate variation likely reflects differences in exposure or depth. The highest value was recorded at the MFD sampling point during the short rainy season and the lowest value at the RPE sampling point during the same season (**Figure 7(A)**). Studies have shown that some pathogens grow extremely well at a mesophilic temperature range of 15˚C - 45˚C for most strains [27] [28]. The pH is generally alkaline, with an average of 7.73 (±0.43), ranging from 7.21 to 8.23. These values indicate a slightly basic environment, compatible with a good ecological status for most aquatic organisms. The highest value was recorded at point MDG during the long dry season and the lowest value was recorded at point MSII during the same season (**Figure 7(A)**). This alkalinity of water is due to the nature of the chemical substances present in the grey water of the SIC camps. The pH measured is ideal for growth of bacteria belonging to the *Vibrionaceae* family. According to some authors pH values between 6 and 8.5 are favourable for the expression of the biological potential of several groups of bacteria [29].

Turbidity shows strong disparities: the average is 1015.8 FAU (±872.2), ranging from 226.5 to 2589 FAU. The highest value was recorded at sampling site MFD. As for the water color, the mean values ranged from 597.8 to 5657.8 Pt.Co, with the MFD site having the highest value (**Figure 7(B)**). These values are obtained at the MFD during the long rainy season.

The mean values of total suspended solids recorded during the study period ranged from 121 mg/L to 1609 mg/L. The Total dissolved solids values (TDS) varied between 295 and 1080 ppm with an average of 582 mg/L (±250.7). The highest value was recorded at point BIY during the long dry season and the lowest value at point MSI during the short rainy season (**Figure 7(C)**).

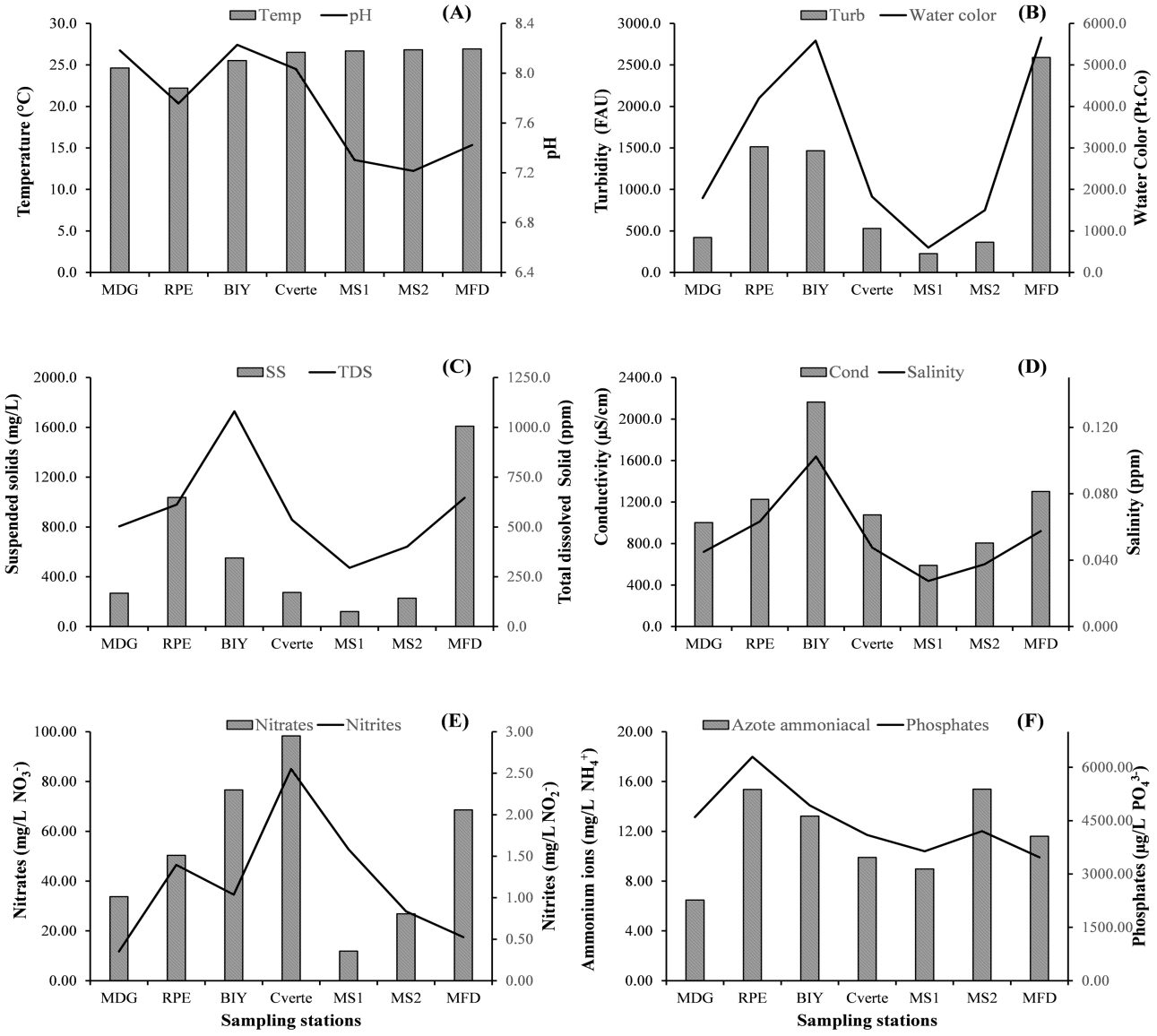

Figure 7. Temporal variation with respect to the sampling site of the Temperature & pH (A), turbidity & water color (B), suspended solid & total dissolved solids (C), electrical conductivity & salinity (D), nitrates & nitrites (E) and ammoniums ions & phosphates (F).

The electrical conductivity values varied between 590.3 and 2163 µS/cm. The highest value was recorded at the BIY point during the long dry season and the lowest value was recorded at the MSI point during the short rainy season. The electrical conductivity values varied considerably. The values obtained indicate that these waters are highly mineralised. In fact, minerals are important factors for bacterial growth. The high pH and electrical conductivity would favour the growth and spread of these bacteria, especially as their values coincide with the dry season, when epidemics are also documented [30].

Salinity values ranged from 0.025 to 0.12 ppm with an average of 0.053 ppm. The highest value was recorded at point BIY during the long dry season and the lowest at point MSI during the short rainy season (**Figure 7(D)**). In addition, re-

gions exposed to relatively high temperatures experience water losses through evapotranspiration, which indirectly affects the salinity of their waters. Identifying interactions between temperature and salinity may explain some of the variability in *Vibrio* distribution. Indeed, significant differences in *Vibrio* growth rates due to salinity were only observed at low temperatures [31]. The values for nitrate and nitrite ions are between 11.90 - 98.33 mg/L and 0.35 - 2.55 mg/L respectively. The highest values were recorded at point Cverte during the long dry season regarding nitrate and nitrite ions and the lowest values were recorded at point MS1 for nitrate ions and at a point MDG for nitrite ions during the short rainy season (**Figure 7(E)**). Ammoniacal nitrogen values ranged from 6.48 to 15.39 mg/L, with a mean value of 11.56 ± 0.68 mg/L. The highest value was recorded at the MS2 point during the long dry season and the lowest value at the MDG point during the rainy season. The values of the phosphate ions reached 6294.67 mg/L at the point of RPE during the long dry season (**Figure 7(F)**). Studies have shown that microbial diversity varies following changes in water chemistry that are caused by phosphate enrichment [32].

3.5. Relationships between Bacterial Abundance and Abiotic Factors

A grouping of the parameters into 2 kernels is shown by the PCA applied to the different biological and physico-chemical variables. Most of the total variance is provided by the first two factorial axes F1 (51.89%) and F2 (17.79%), which explain 69.69% of the total inertia (**Figure 8**). The factorial map shows a distribution of the seven sampling points with respect to their physicochemical and bacteriological characteristics. On the F1-F2 plane, active variables are grouped according to their correlations. Electrical conductivity, salinity, and total dissolved solids (TDS) are strongly associated and aligned along the positive side of F1, suggesting that they co-vary across certain stations. Conversely, variables such as turbidity, suspended solids (SS), water color, ammonium (NH_4^+), nitrate (NO_3^-), and phosphate (PO_4^{3-}) are grouped toward the negative side of F1, forming a second cluster indicative of organic and nutrient-rich conditions. This opposition on axis F1 thus reflects a physicochemical gradient separating mineralized or saline waters from more organically polluted ones.

The *Vibrio* species show ecological associations aligned with this gradient. *Vibrio parahaemolyticus*, *V. vulnificus*, and *V. alginolyticus* are positioned on the positive side of F1, close to salinity and conductivity vectors, suggesting a preference for saline environments. In contrast, *V. cholerae* and *V. mimicus* appear on the negative side of F1, aligned with nutrient-rich and turbid conditions. These associations are consistent with established ecological patterns: halophilic species like *V. alginolyticus* and *V. vulnificus* are typically linked to higher salinity, while *V. cholerae* and *V. mimicus* are known to thrive in freshwater or wastewater environments rich in organic matter.

The spatial distribution of the sampling stations further supports this interpretation. Stations MSI, MSII, and MFD are located on the positive side of F1, asso-

ciated with higher salinity and conductivity, and correlate with halophilic *Vibrio* species. In contrast, stations MDG, RPE, BIY, and Cverte fall on the negative side of F1, characterized by higher levels of nutrients and suspended matter, and show a greater presence of *V. cholerae* and *V. mimicus*. This separation may reflect the distinct environmental conditions associated with the two wastewater networks (labeled N1 and N2), each exhibiting specific physicochemical and microbial profiles. Principal component analysis suggests that physico-chemical and biological variables interact in a complex way, reflecting the complex processes that occur in the natural environment [6].

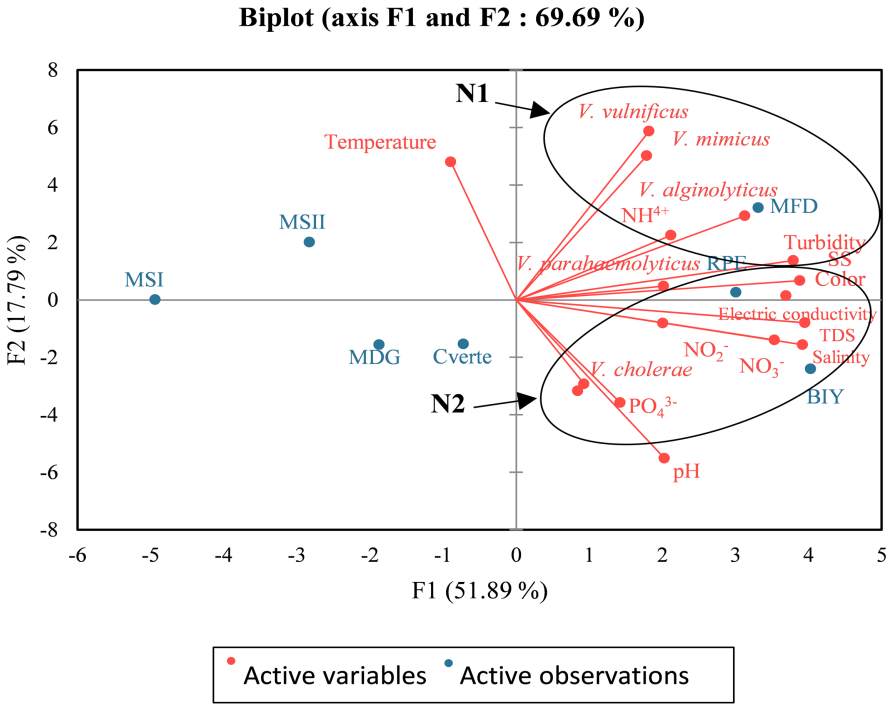

Figure 8. Result of the Principal Component Analysis (PCA) carried out on the physico-chemical and bacteriological variables measured in the different stations during the study period: The Biplot showing the distribution of the stations with respect to their physico-chemical and bacteriological characteristics in the factorial plane F1 X F2.

The results of the correlations between the abiotic and bacteriological variables show that among the physicochemical parameters analyzed, certain variables significantly influenced the population and distribution of bacteria throughout the study. This would result in the fact that bacteria react differently to chemical compounds. Indeed, the influence of chemical compounds on the microflora of the soil and subsoil varies depending on the ability of the bacterial species to degrade this chemical compound, either to neutralize its toxicity or to make the nutrients available. and the energy source, which are necessary for its biosynthesis. Environmental factors that positively correlate recovery rates of *Vibrio isolates* from waters include temperature, electrical conductivity, and air flow, although bacterial strains can be actively disseminated during flooding [21].

4. Conclusions

This investigation into the diversity, abundance, and antibiotic resistance profiles of *Vibrio* species in wastewater from Social Housing Network (SIC) camps in Yaoundé has yielded several critical insights with implications for both environmental safety and public health. Firstly, the qualitative and quantitative analyses confirmed that SIC camp wastewater, discharged untreated into the urban environment, constitutes a reservoir for a broad spectrum of pathogenic *Vibrio* species. The following *Vibrio* species were identified: *V. cholerae*, *V. parahaemolyticus*, *V. mimicus*, *V. alginolyticus* and *V. vulnificus*. The densities of the bacteria under investigation varied in relation to key abiotic factors, particularly pH, mineral content, organic load and seasonal temperature fluctuations. This indicates that environmental conditions prevalent in Yaoundé's waste streams are conducive to the proliferation of the bacteria. Most notably, the study demonstrated high levels of antibiotic resistance among the isolates. The overall resistance rates attained a maximum of 70%, with *V. alginolyticus* exhibiting the highest levels of resistance during the rainy season and *V. cholerae* reaching its peak in the dry season. The present study found that resistance to third-generation cephalosporins (ceftazidime), β-lactam/β-lactamase inhibitor combinations (amoxicillin-clavulanic acid), and polymyxins (colistin) was especially pronounced across all species. These patterns underscore an urgent need to curb indiscriminate antibiotic use, both in clinical settings and local communities, to stem the further emergence and dissemination of multidrug-resistant *Vibrio* strains.

The consistently alkaline pH, high mineralization, and elevated organic matter content provide an optimal milieu for *Vibrio* survival and growth. Seasonally stable temperatures in Yaoundé's tropical climate likely facilitate year-round persistence of these pathogens once introduced into the environment. Without any form of wastewater treatment, SIC camp effluents thus act as continuous point sources, enabling *Vibrio* species and their resistance determinants to enter surface waters, agricultural lands, and ultimately human populations through drinking water, irrigation, and recreational contact. Taken together, these results highlight significant public health risks. Inhabitants of neighborhoods receiving SIC wastewater are potentially exposed to *Vibrio*-associated illnesses ranging from cholera and acute gastroenteritis to wound infections and septicemia compounded by the difficulty of treating infections caused by antibiotic-resistant strains. Moreover, the environmental release of antimicrobial-resistant *Vibrio* may facilitate horizontal gene transfer to other Gram-negative pathogens, amplifying the overall burden of resistance within the urban microbial ecosystem.

Conflicts of Interest

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

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