

Anthropogenic Drivers of Antibiotic Resistance in *Aerococcus viridans* from Urban Mangrove Waters of Grand Libreville (Gabon): Environmental and Public Health Implications

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Abstract

Mangrove waters are essential ecosystems, serving as nurseries for fish and crustaceans. Investigating bacterial antibiotic resistance in these waters is crucial for assessing potential risks to human health and the safety of food resources derived from these environments. This study highlights the antibiotic resistance profiles associated with *Aerococcus viridans* strains isolated from mangrove waters in Grand Libreville, Gabon, and examines their geographical variability. The study was conducted from July to September 2025 across nine urban mangrove sites within the four municipalities that make up Grand Libreville: Ambowe, Ondongo, Rouger, Alenakiri, Lowe, Bizango, Angondje, Ozoughe, and Okala. Water samples were collected at low tide from five sampling points per site, yielding a total of 45 wastewater samples. Bacterial cultures were performed on D-Cococcel agar (BioMérieux, France) at 37.0 ± 0.5°C for 48 hours. Each colony underwent Gram staining, as well as oxidase and catalase testing. Biochemical identification was carried out using API 20 Strep galleries (BioMérieux, France). Antibiotic susceptibility testing was performed using the Kirby-Bauer disk diffusion method with fourteen antibiotic discs. The prevalence of antibiotic resistance was highest for penicillin (100%)

and erythromycin (60%), representing a potential public health risk. Moreover, resistance patterns exhibited notable geographical disparities. Higher resistance levels and multidrug resistance scores were observed in sites exposed to multiple sources of anthropogenic pollution, particularly Lowe (76.2%) and Ambowe (61.9%). In contrast, lower resistance levels and multidrug resistance scores were recorded in Okala (16.6%) and Alenakiri (10.71 %), where human activities are less intense. These findings suggest that anthropogenic activities contribute to the contamination of mangrove waters in Lowe and Ambowe. Although the overall situation does not appear alarming, identified hotspots of resistance, as well as intermediate zones such as Bizango, Rouger, and Ozoughe, warrant continued monitoring.

Keywords

Mangrove Wastewaters, *Aerococcus viridans*, Antibiotic Resistance, Anthropogenic Pressures, Health Risks

1. Introduction

With increasing urbanization, pollution levels in many aquatic ecosystems have risen significantly [1], particularly in mangrove waters. These ecotones often serve as primary habitats for commercially important seafood species [2] [3]. They are also subject to intense anthropogenic pressures that contribute to their degradation. Mangroves play a crucial role as natural filters for nutrients and pollutants; however, they are increasingly recognized as reservoirs of antibiotic-resistant bacteria (ARB) and antibiotic resistance genes (ARG) in water, sediments, and biota [4]-[6]. These ecosystems support fisheries resources such as crabs and shrimp that are highly valued for human consumption, and many local populations depend on these resources for their livelihoods [7].

Aerococcus viridans (*A. viridans*) has been identified as one of the bacterial contaminants in mangrove wastewater [8]. This microorganism has been associated with several infections in aquatic animals, including gaffkaemia in lobsters, septicemia in sea turtles, and mortality in tilapia [9] [10]. It has also been reported to infect shrimp and crabs, causing numerous bacterial disease outbreaks [9] [11] [12]. In addition, *Aerococcus* species such as *A. urinae*, *A. sanguinicola*, and *A. viridans* are known to cause urinary tract infections (UTIs) in humans [13], as well as bacteremia, endocarditis, para-aortic abscesses, meningitis, spondylodiscitis, and septic arthritis [14] [15].

It is therefore plausible that this bacterium may be transmitted to humans through the consumption of aquatic organisms harvested from mangrove environments [16]. Consequently, the presence of this bacterium in mangrove waters may indirectly pose a risk to human health, particularly through seafood consumption, highlighting the urgent need to monitor these ecosystems. The aim of this study is to determine the prevalence of antibiotic-resistant *Aerococcus viri-*

dans in mangrove wastewater from Grand Libreville (Gabon) and to assess its spatial distribution.

2. Materials and Methods

2.1. Study Area and Sampling Period

The study area comprised nine sampling sites located within Grand Libreville, including the municipalities of Libreville, Owendo, Akanda, and Ntoun (Figure 1). Four sites were located in Libreville (Ondongo, Ambowe, Lowe (Mindoube), and Ozoughe). Additional sites included Alenakiri and Rouger (in Owendo), Okala (Avolé-Zamé village) and Angondje (in Akanda), and Bizango (in Ntoun). At each site, five sampling points were selected. This design resulted in a total of 45 water samples collected for analysis.

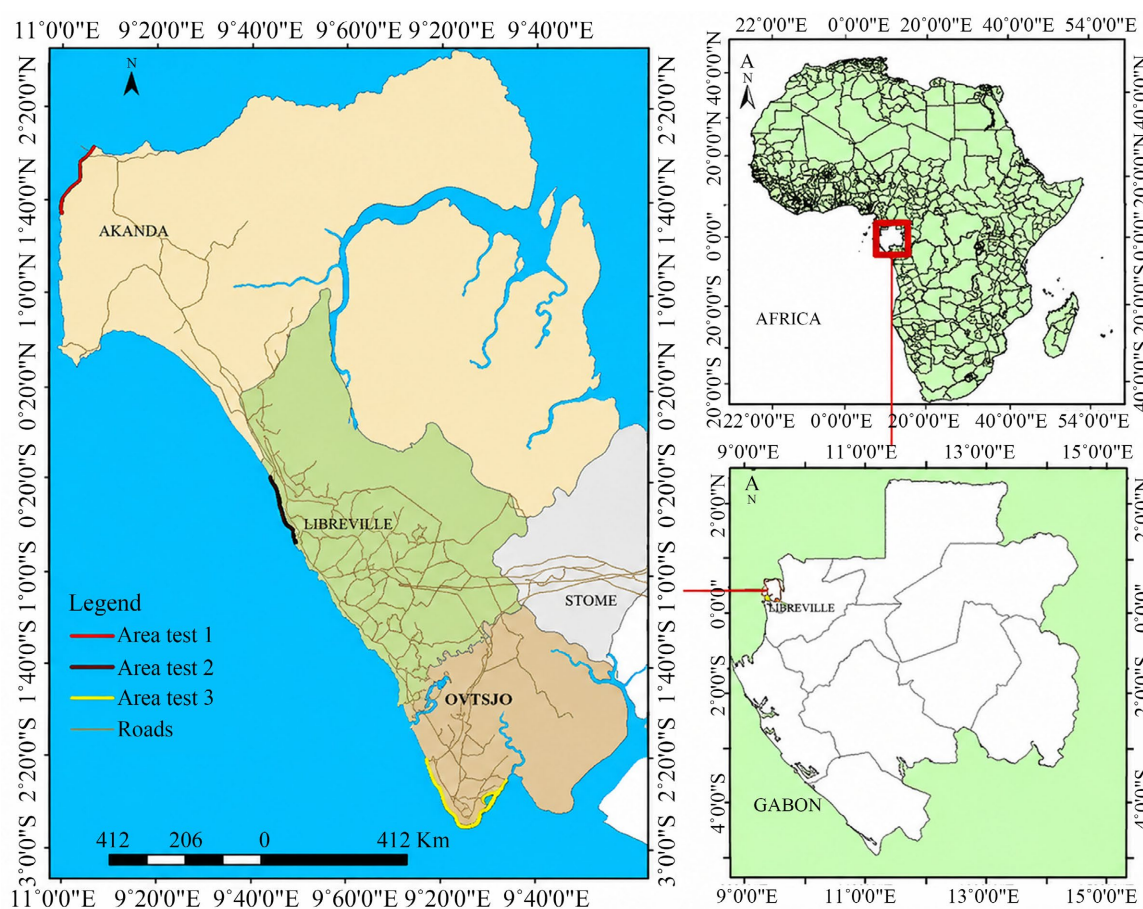


Figure 1. Location of the study area (adapted from [17]).

Among all these sites, those of Lowe, Ambowe, and Ozoughe were particularly affected by anthropogenic activities. The Lowe site is characterized by unregulated stilt constructions within the mangrove ecosystem, established by foreign communities engaged in fishing activities in these waters. As a result, traditional latrines and bathing facilities have been built, leading to the direct discharge of domestic

wastewater into the mangrove environment. A similar situation is observed at the Ozoughe and Ambowe sites, where the distinguishing feature is the disposal of all types of waste into the ecosystem, resulting in multiple forms of pollution [18] [19].

In contrast, sites such as Okala and Ondongo benefit from significant conservation efforts aimed at protecting the ecosystem. For instance, at Okala, a non-governmental organization actively works toward ecosystem preservation, ensuring that the area remains clean.

The sampling period extended from July to September 2025. During this period, surface water samples were collected at ebb tide from five points at each site. For each of the 45 water samples analyzed, the sampling unit consisted of 500 mL of surface water. Samples were collected using sterile polyethylene containers. These containers were immediately stored in a light-protected isothermal bag containing ice packs (-4°C) and transported to the laboratory for analysis.

2.2. Culture and Isolation of Bacterial Colonies

Upon arrival at the laboratory, each water sample underwent four successive serial dilutions up to 10^{-4} . Subsequently, 1 mL of each original sample and its dilutions were spread onto D-Cococcel agar plates (bioMérieux, France) using a sterile 10 μL inoculation loop, and incubated at $37.0 \pm 0.5^{\circ}\text{C}$ for 48 hours. After incubation, all bacterial colonies exhibiting distinct morphology and coloration were isolated on the same medium under identical conditions.

2.3. Identification of Bacterial Colonies

From each plate, only grey colonies on a black background suspected to belong to the genus *Aerococcus* were selected. Culturing of the 45 wastewater samples resulted in a total of 51 colonies. Each colony was subjected to Gram staining, as well as oxidase and catalase tests. Final identification was performed using API 20 Strep galleries (bioMérieux, France). Results were interpreted using the ApiWeb software.

2.4. Antibiotic Susceptibility Method

Antibiotic susceptibility testing was carried out using the disk diffusion method on Mueller-Hinton agar (bioMérieux, France), as described by [20]. To ensure a comprehensive assessment for this taxon, CLSI standards (2024) were utilized to supplement EUCAST (2023) criteria where data were limited. This approach precluded the use of surrogate criteria, thereby ensuring a rigorous interpretation of inhibition zone diameters. A total of 14 antibiotics were tested to determine the susceptibility profiles of the isolates, including: oxacillin (5 μg), penicillin (10 μg), erythromycin (10 μg), chloramphenicol (30 μg), azithromycin (30 μg), vancomycin (30 μg), teicoplanin (30 μg), streptomycin (10 μg), gentamicin (30 μg), amikacin (30 μg), tetracycline (30 μg), linezolid (30 μg), cefotaxime (30 μg), and ciprofloxacin (30 μg).

2.5. Statistical Analysis

Overall and site-specific resistance/susceptibility proportions were compared us-

ing Pearson's Chi-square test or Fisher's exact test when expected cell counts were below 5. Multidrug resistance (MDR) score, defined as the number of distinct antibiotic classes to which an isolate exhibited resistance, was compared across sites using the Kruskal-Wallis test. All analyses were performed with statistical significance set at $\alpha = 0.05$.

3. Results

3.1. Prevalence of *Aerococcus viridans*

The identification of the 51 colonies selected on D-coccocel agar resulted in the detection of *Aerococcus viridans* with excellent and very good confidence levels. The proportion of the 51 selected suspect colonies identified as *A. viridans* was 100%. Only a single isolate per positive sample was selected for antimicrobial susceptibility testing to ensure the statistical independence of observations.

3.2. Antibiotic Susceptibility

The overall resistance observed across the entire sample was 38.40%, whereas the overall susceptibility reached 61.60%. The overall resistance and susceptibility rates were calculated using the total number of individual susceptibility tests as the explicit denominator. Accordingly, the overall resistance percentage was defined as the total number of results classified as 'Resistant' (R) divided by the total count of isolates tested.

Table 1. Overall antibiotic susceptibility.

Indicator	Value
Overall resistance	38.40%
Overall susceptibility	61.60%

The results (**Table 1**) highlight two major trends among *Aerococcus viridans* strains isolated from mangrove waters. Overall susceptibility (61.6%): the majority of the isolates remained susceptible to the antibiotics tested, and overall resistance (38.4%), where more than one-third of the isolates exhibited resistance. In microbiology, resistance levels approaching 40% are generally considered high.

The presence of approximately 38% resistance in *A. viridans* within this specific environment suggests two main hypotheses. First, it may reflect strong selective pressure, likely due to anthropogenic pollution such as domestic, agricultural, or hospital wastewater discharge. Second, the presence of antibiotics in aquatic ecosystems may drive bacterial adaptation. Thus, proximity to human activities is likely a key factor in this observed resistance. Such resistance levels in *A. viridans* could potentially impact the survival of certain mangrove species if infections occur.

3.3. Site-Specific Antibiotic Susceptibility Profiles

Resistance levels varied markedly between sampling sites. The highest resistance rates were recorded at Lowe (76.19%) and Ambowe (61.90%), whereas the lowest

were observed at Alenakiri (10.71%) and Okala (16.67%) (see **Figure 2**). This spatial analysis provides critical geographical insight, demonstrating that *Aerococcus viridans* resistance is not uniformly distributed across mangrove ecosystems in Grand Libreville, but instead varies significantly depending on the sampling location.

Two sites exhibited particularly concerning resistance profiles, in which resistance exceeded susceptibility.

Lowe (76.2% resistance) represents the most critical point in the study. The inversion of the susceptibility/resistance ratio (only 23.8% susceptible) suggests a strong and continuous contamination source, potentially linked to nearby hospital, industrial, or dense urban discharge. Ambowe (61.9% resistance), where resistance is also predominant at this site. Together, Lowe and Ambowe may act as hotspots for the dissemination of resistance genes within the mangrove ecosystem. These sites are the “High-Risk Areas” (Resistance-Dominated Zones).

Additionally, there are transition areas (moderate risk): Bizango, Ondongo, Ozoughe, and Rouger. These areas showed intermediate profiles, with susceptibility remaining dominant (57% - 75%) but with resistance already well established (approximately 30% - 40%). These findings raise the possibility of a correlation with human activity. For instance, are Lowe and Ambowe located near residential areas or waste disposal sites? Alternatively, could this reflect localized pollution events rather than intrinsic resistance patterns of the species?

Finally, there are “high-sensitivity” areas. In contrast, some sites show a much healthier microbiological profile. Alenakiri (89.3% susceptibility) appears to be the least impacted, with a low resistance rate (10.7%), and could serve as a reference for physicochemical comparisons. Okala (83.3%) and Agondje (76.8%) seem relatively less affected by antibiotic selective pressure.

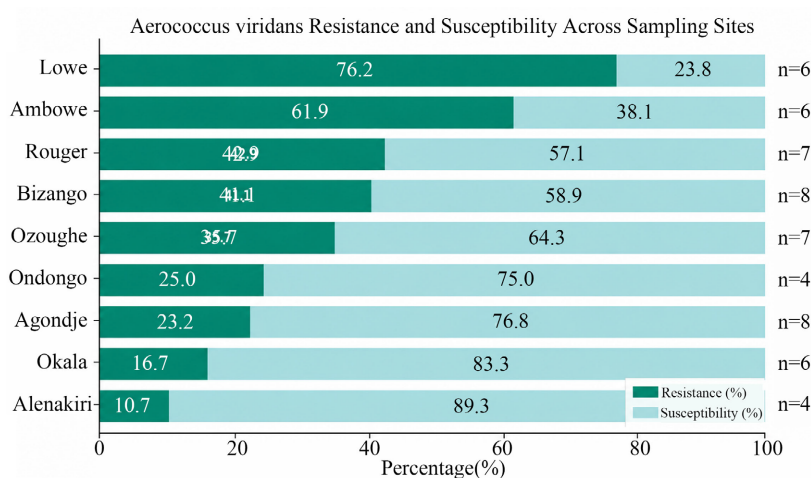


Figure 2. Resistance and sensitivity of *A. viridans* by location.

Resistance prevalence to penicillin (P) reached 100% at all nine sites, confirming this antibiotic as ineffective against *A. viridans* across the entire study area, while linezolid (LZ) remained fully effective (0% resistance) at every site. Beyond

these two extremes, resistance profiles diverged sharply by location: Lowe and Ozoughe exhibited near-complete resistance (67-100%) to most antibiotic classes tested, including vancomycin, teicoplanin, azithromycin and erythromycin, whereas Alenakiri, Okala and Ondongo showed resistance limited to one or two antibiotics (mainly erythromycin or streptomycin), with 0% resistance to the remaining twelve (see **Figure 3**).

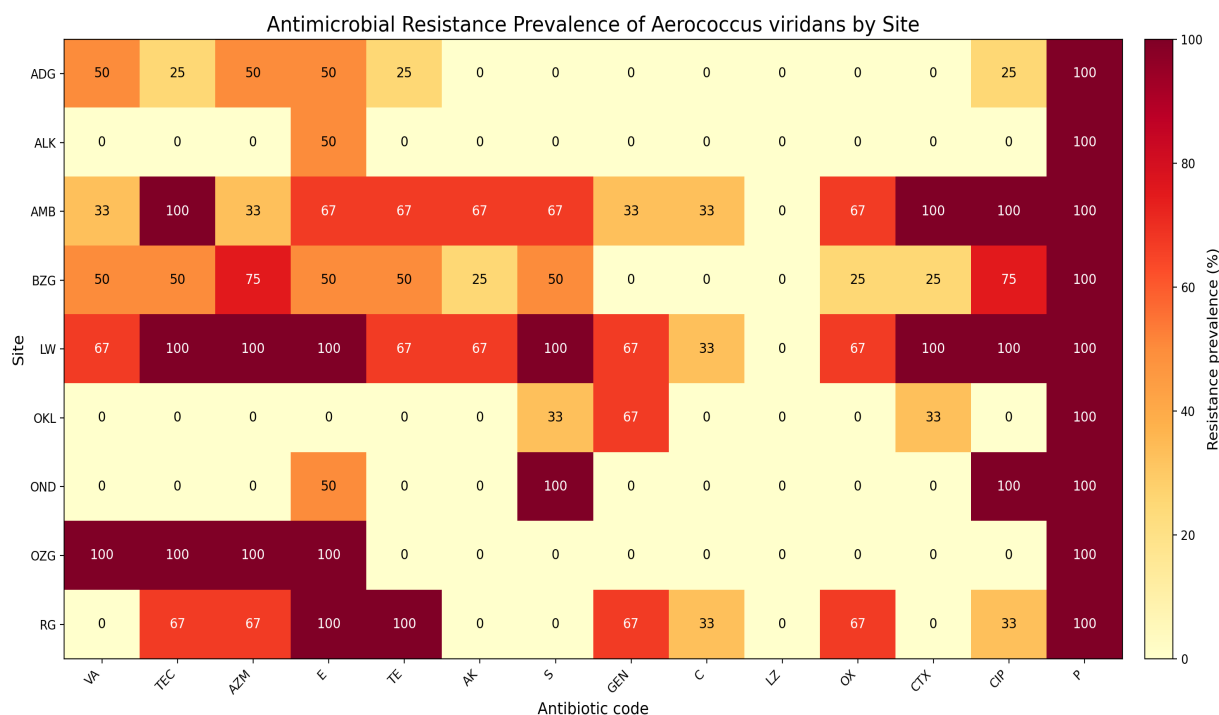


Figure 3. Prevalence of antibiotic resistance (%) of *A. viridans* by location. Legend: Vancomycin (VA); Teicoplanin (TEC); Azithromycin (AZM); Erythromycin (E); Tetracycline (TE); Amikacin (AK); Streptomycin (S); Gentamicin (GEN); Chloramphenicol (C); Linezolid (LZ); Oxacillin (Ox); Penicillin (P); cefotaxime (CTX), and ciprofloxacin (CIP).

3.4. Comparison between Site Groups

Group 1 exhibited a mean resistance of 64.30%, compared to 28.60% in Group 2. Conversely, mean susceptibility was 35.70% in Group 1 versus 71.40% in Group 2 (as shown in **Figure 4**). Overall, isolates from Lowe, Ambowe, and Ozoughe were more resistant than those from Okala, Ondongo, Rouger, Bizango, Alenakiri, and Agondje.

High anthropogenic influence (Group 1), comprising the Lowe, Ambowe, and Ozoughe sites, exhibits critical levels of antibiotic resistance. This group shows a complete reversal of the standard microbiological profile of *Aerococcus viridans*, with resistance predominating (64.3%) and susceptibility becoming a minority trait (35.7%). By combining Lowe, Ambowe, and Ozoughe, a distinct “red zone” of the mangrove ecosystem can be identified. The fact that resistance reaches nearly two-thirds of the isolates suggests that these three sites may share highly pronounced ecological or geographical characteristics. This group most likely corresponds to mangrove sectors located closest to urban discharge outlets

and wastewater drainage channels, where antibiotic residues accumulate and exert strong selective pressure favoring resistant strains.

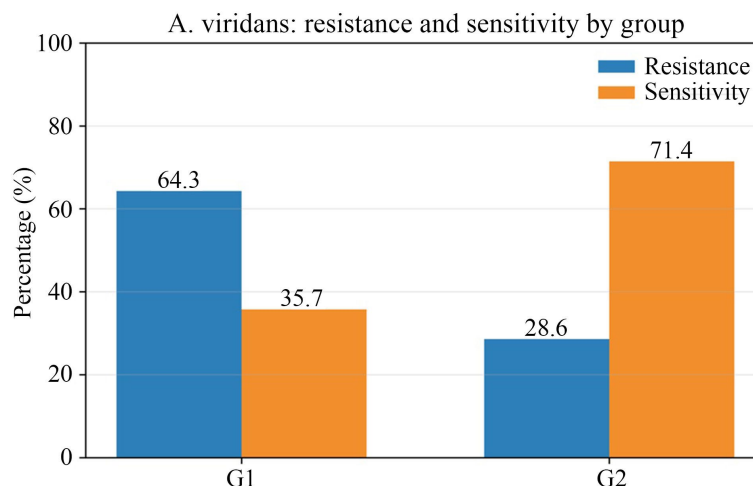


Figure 4. Resistance and sensitivity of *A. viridans* by location.

Low anthropogenic influence (Group 2) includes the Okala, Ondongo, Rouger, Bizango, Alenakiri, and Agondje sites. The microbial dynamics observed in these sites are markedly reversed compared with Group 1 and more closely resemble a natural environmental profile, characterized by a clear predominance of susceptible isolates (71.4%) and a lower residual level of resistance (28.6%). A susceptibility rate exceeding 70% indicates that the ecological resilience of the mangrove ecosystem remains largely functional in these areas. These sites are likely situated in more remote zones, distant from direct anthropogenic pressures. Nevertheless, the presence of 28.6% resistant isolates indicates that chemical contamination and/or the transport of resistance genes through water circulation are not entirely absent, even in the least impacted areas.

These findings demonstrate that antibiotic resistance in the mangrove ecosystem is not randomly distributed, but rather follows a clear pattern of spatial compartmentalization. Comparison of the mean resistance rates per isolate between Groups 1 and 2 revealed a highly significant difference according to both the Chi-square and Fisher's exact tests ($p < 0.001$). This result confirms that the observed difference in resistance levels between the two groups cannot be attributed to simple random variation.

3.5. *A. viridans* Multidrug Resistance (MDR) by Location

Figure 5 shows the distribution of multidrug resistance scores among *Aerococcus viridans* isolates across the nine sampling sites. The MDR score represents the number of antibiotic classes to which each isolate exhibited resistance. It varied significantly between sites (Kruskal-Wallis test, $p = 1.19 \times 10^{-5}$), indicating substantial spatial heterogeneity in antimicrobial resistance profiles. While some sites exhibited relatively low and homogeneous MDR scores (Group 1),

others showed higher median values and a broader dispersion of scores (Group 2). The observed variability suggests that local environmental and anthropogenic factors may influence the selection and dissemination of antimicrobial resistance. Sites characterized by higher MDR scores may be exposed to stronger selective pressures, potentially associated with antimicrobial use, wastewater contamination, livestock activities, or other human-related inputs. Conversely, sites with lower MDR scores may represent environments subjected to reduced antibiotic pressure.

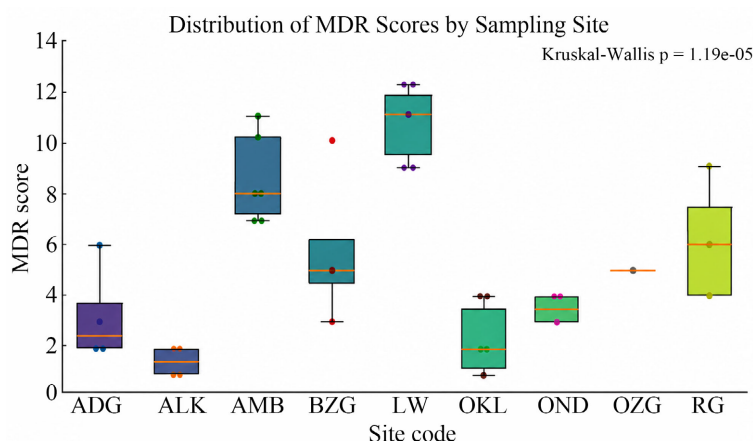


Figure 5. Distribution of MDR scores by sampling location (Kruskal-Wallis test, $p = 1.19 \times 10^{-5}$).

4. Discussion

4.1. Occurrence and Impact of *Aerococcus viridans* in Mangrove Wastewaters

The occurrence of *A. viridans* in the environment constitutes a significant indicator of contamination of human origin, although its precise sources may sometimes be complex to identify [16] [21]. Moore *et al.*, [22] reported that the isolation of *A. viridans* at high frequencies exclusively in polluted marine water samples (Avalon Bay, USA), but not in wastewater effluents or urban runoff, could be attributed to the existence of alternative sources of this bacterium in marine environments, even though such sources remain poorly documented to date. Nevertheless, its presence in the oral cavity [21] or among domestic fauna [23]–[25] may contribute to indirect environmental contamination.

4.2. Antibiotic-Resistant *A. viridans*: A Dangerous Zoonotic Pathogen

A. viridans, a fastidious Gram-positive coccus associated with a wide range of diseases in both humans and animals, has been isolated from environmental samples, aquatic organisms, wildlife, livestock, and animal-derived products [21] [26]. To our knowledge, this is the first study investigating *A. viridans* in wastewater samples from urban mangrove aquatic ecosystems. Our results indicate that the prev-

alence of antibiotic resistance is higher in the Lowe and Ambowe sites, which correspond to areas with greater anthropogenic pressure, consistent with findings from previous studies [27]. Urbanization and industrialization contribute to increased loads and adverse effects associated with antibiotic discharge into aquatic environments [28]. As reported by several authors, a high prevalence of antibiotic-resistant bacteria in the environment often serves as an indicator of anthropogenic pressure, such as antibiotic pollution or urban discharge [29] [30]. Several studies corroborate our findings. For instance, in India, the highest abundance of antibiotic-resistant bacteria was recorded in mangrove ecosystems receiving human waste discharge [31], suggesting that these sites were the most polluted by anthropogenic activities, including untreated domestic, commercial, industrial, and agricultural effluents. This supports the hypothesis that the relatively high levels of antibiotic resistance may result from the exchange of resistant bacteria between humans, aquatic fauna, and the environment [28] [32]. Overall, these findings suggest that antibiotic-resistant *A. viridans* should be considered a zoonotic bacterial pathogen [21] [33]. Furthermore, its presence may also be regarded as an indicator of human-derived contamination [4].

4.3. Health Risks Associated with Antibiotic-Resistant *A. viridans* Strains in Mangrove Ecosystems

The presence of antibiotic-resistant *A. viridans* strains in mangrove ecotones may pose significant public health concerns [5]. This bacterium is frequently isolated in hospital settings and has also been identified as a marine pathogen responsible for fatal diseases in several aquatic species, including sea turtles, fish, and lobsters [34] [35]. Available data indicate that *A. viridans* can be highly pathogenic to certain aquatic animals, representing both ecological and economic risks in coastal ecosystems [35] [36]. This ecological risk is compounded by a direct threat to human populations, particularly those relying on subsistence fishing in these waters. Comparison with existing literature highlights that seafood consumption constitutes a well-documented route of human infection by *A. viridans* [12]. Mangroves serve as nurseries for crabs and shrimp, which, once contaminated, may transmit the pathogen to humans [37]. A clinical case in India linked *A. viridans* infection to lobster consumption two weeks prior to symptom onset [38].

In our study, resistance rates to penicillin and erythromycin were 100% and 60%, respectively. These values are comparable to those reported in Burkina Faso, China, and Algeria, where penicillin resistance reached 83.3% [14] [39] [40], oxacillin 83.3%, chloramphenicol 80%, and erythromycin 66.7% [21] [40]. Contrary to some earlier findings [40], *A. viridans* was previously considered susceptible to commonly used hospital antibiotics. However, recent studies indicate that it often remains susceptible to β -lactam antibiotics, particularly penicillin, which is regarded as the treatment of choice for infections caused by this bacterium [21]. The observed resistance to penicillin and erythromycin may be explained by their frequent use in treating Group B Streptococcus (GBS) infections, with erythromycin

serving as an alternative to penicillin [41]. Variations in resistance and MDR across study sites may be attributed to differences in antibiotic usage patterns between geographical regions and other anthropogenic pressures [30]. Indeed, several reports indicate considerable diversity in antibiotic resistance profiles among isolates from different locations [10]. Moreover, published data on the antibiotic susceptibility of environmental *A. viridans* isolates remain limited. The presence of this rare environmental pathogen is likely to pose public health challenges. Transmission to humans may occur through foodborne or environmental exposure [21] [38]. Numerous studies have reported infections in fish and crustaceans caused by this bacterium [36] [42], which may subsequently lead to human infection following seafood consumption.

Mangrove ecosystems provide suitable habitats for many of these seafood species [43] [44], including mud crabs and shrimp [45] [46]. Notably, *A. viridans* has been detected in mangrove mud crabs [45]. These organisms represent an essential source of nutrients, such as proteins, lipids, and minerals, for human populations in many regions [44] [47].

Consequently, this situation may lead to significant health risks, particularly in developing countries where resources for managing public health crises are often limited.

5. Conclusion

Aerococcus viridans is a bacterium widely distributed in mangrove ecosystems in Gabon. This bacterium may be transmitted to humans through the consumption of seafood, including crustaceans and fish harvested from these mangrove waters, thereby posing a potential health risk to consumers, particularly when the bacterium carries antibiotic resistance traits. Our study showed that antibiotic-resistant *A. viridans* is of anthropogenic origin, as resistance prevalences were markedly higher in the most anthropized areas, namely Lowe, Ambowe, and Ozoughe, where human activities are more intense, compared with the more preserved sites of Okala and Ondongo.

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Author Contributions

Conceptualization, D.T.K.K. and P.P.N.M.; data curation and formal analysis,

D.T.K.K. and J.C.O.M.; investigation, D.T.K.K., E.A.A.L., and S.B.M.I.; funding acquisition, D.T.K.K., C.R.Z.K., and E.A.A.L.; methodology, P.P.N.M. and G.R.N.A.; original draft preparation, D.T.K.K. and P.P.N.M.; writing, review, and editing, D.T.K.K., P.P.N.M., E.A.A.L., and S.B.M.I.; visualization, D.T.K.K., E.A.A.L., and C.R.Z.K.; supervision, C.R.Z.K., P.P.N.M., and G.R.N.A.; validation, P.P.N.M. and C.R.Z.K.; project administration, D.T.K.K. and C.R.Z.K.

All authors have read and approved the published version of the manuscript.

Conflicts of Interest

The authors declare no conflicts of interest.

References

- [1] Parveen, S. and Malviya, A. (2022) Analytical Review on Membrane Water Filter Using Different Materials to Prevent Microbial Activities. *Journal of Pure and Applied Microbiology*, **16**, 2352-2362. <https://doi.org/10.22207/jpam.16.4.68>
- [2] Hamilton, S. (2013) Assessing the Role of Commercial Aquaculture in Displacing Mangrove Forest. *Bulletin of Marine Science*, **89**, 585-601. <https://doi.org/10.5343/bms.2012.1069>
- [3] Zamora-Tovar, C. (2021) The Fishing Communities Involved in Mangrove Restoration Promote the Productivity of Its Artisanal Fisheries. *Oceanography & Fisheries Open Access Journal*, **13**, Article 555865. <https://doi.org/10.19080/ofoaj.2021.13.555865>
- [4] Palacios, O.A., *et al.* (2021) Antibiotiques, bactéries multirésistantes et gènes de résistance aux antibiotiques: Indicateurs de contamination dans les ma. <https://doi.org/10.3390/antibiotics10091103>
- [5] Lertcanawanichakul, M., Bhoopong, P. and Horpet, P. (2025) Mangrove Ecosystems as Reservoirs of Antibiotic Resistance Genes: A Narrative Review. *Antibiotics (Basel)*, **14**, Article 1022.
- [6] Tresor Kassa-Kassa, D., Mbehang Nguema, P.P., Zinga Koumba, C.R., Apinda Legnouo, E.A., Lendamba, R.W., Loïc Bekale Obame, A.L., *et al.* (2026) Summary of Recent Research on Antibiotic-Resistant Microbial Pollutants in Mangrove Wastewater Ecosystems: Public Health and Environmental Risks. *International Journal of Plant, Animal and Environmental Sciences*, **16**, 21-29. <https://doi.org/10.26502/ijpaes.4490189>
- [7] Sivan, G., Sukumaran, D.P., Ezhuthanikkunel, A.P. and Ammanamveetil Abdulla, M.H. (2023) Prevalence of Extended-Spectrum Beta-Lactamase Resistance and CTX-M-Group 1 Gene in *Escherichia coli* from the Water and Sediment of Urbanized Mangrove Ecosystems of Kerala. *Microbial Drug Resistance*, **29**, 582-588. <https://doi.org/10.1089/mdr.2023.0089>
- [8] Obire, O., Ogan, A. and Okigbo, R.N. (2008) Impact of Fertilizer Plant Effluent on Water Quality. *International Journal of Environmental Science & Technology*, **5**, 107-118. <https://doi.org/10.1007/bf03326003>
- [9] Ke, X., Lu, M., Ye, X., Gao, F., Zhu, H. and Huang, Z. (2012) Recovery and Pathogenicity Analysis of *Aerococcus viridans* Isolated from Tilapia (*Oreochromis niloticus*) Cultured in Southwest of China. *Aquaculture*, **342**, 18-23. <https://doi.org/10.1016/j.aquaculture.2012.02.012>
- [10] Liu, G., Liu, Y., Ali, T., Ferreri, M., Gao, J., Chen, W., *et al.* (2015) Molecular and

- Phenotypic Characterization of *Aerococcus viridans* Associated with Subclinical Bovine Mastitis. *PLOS ONE*, **10**, e0125001. <https://doi.org/10.1371/journal.pone.0125001>
- [11] Cawthorn, R.J. (2011) Diseases of American Lobsters (*Homarus americanus*): A Review. *Journal of Invertebrate Pathology*, **106**, 71-78. <https://doi.org/10.1016/j.jip.2010.09.010>
- [12] Stewart, J.E. (2021) Infectious Diseases of Marine Crustaceans. In: *Pathobiology of Marine and Estuarine Organisms*, CRC Press, 319-342. <https://doi.org/10.1201/9781003069058-12>
- [13] Le Brun, C., Robert, S., Bruyere, F. and Lanotte, P. (2015) Emerging Uropathogens: Point for Urologists and Biologists. *Progrès en Urologie*, **25**, 363-369. <https://doi.org/10.1016/j.purol.2015.01.021>
- [14] Zhou, W., Nanci, V., Jean, A., Salehi, A.H., Altuwaijri, F., Cecere, R., *et al.* (2013) *Aerococcus viridans* Native Valve Endocarditis. *Canadian Journal of Infectious Diseases and Medical Microbiology*, **24**, 155-158. <https://doi.org/10.1155/2013/470413>
- [15] Tiwari, S. (2020) Penicillin-Resistant *Aerococcus viridans* Septicemia in an Immunocompetent Person: An Unusual Case Report OPEN ACCESS. *American Journal of Clinical Microbiology and Antimicrobials*, **3**, Article 1046.
- [16] Ezechukwu, I., Singal, M. and Igbinosa, O. (2019) *Aerococcus viridans*: Case Report, Microbiology, and Literature Review. *American Journal of Case Reports*, **20**, 697-700. <https://doi.org/10.12659/ajcr.914866>
- [17] Manomba-Mbadinga, N., Niculescu, S., Zaabar, N., Mombo, J. and Xie, G. (2023) Grand Libreville (Gabon) Coastline Machine Learning and Convolutional Neural Network Detection and Automatic Extraction of the Methods. *Earth Resources and Environmental Remote Sensing/ GIS Applications XIV*, Amsterdam, 3-7 September 2023, Article 1273402. <https://doi.org/10.1117/12.2678897>
- [18] Okanga-Guay, M., Guylia, R.L., Emmanuel, O.A., Aline, L.B., Igor, A.A. and Jean-Bernard, M. (2022) Les moteurs de la déforestation des mangroves urbaines du Grand Libreville (Gabon). *VertigO - la revue électronique en sciences de l'environnement*, **22**. <https://doi.org/10.4000/vertigo.35668>
- [19] Saint Bickolard, M.I., Rodrigue, S.T., Arnaud, B., *et al.* (n.d.) Modification of the Chemical Composition and the Natural Durability of Avicennia Germinans (Linné) Mangrove Tree of the Estuary Region of Gabon Exposed to Marine Hydrocarbons Pollution. <https://doi.org/10.1016/j.marpolbul.2024.116196>
- [20] Bauer, A.W., Kirby, W.M.M., Sherris, J.C. and Turck, M. (1966) Antibiotic Susceptibility Testing by a Standardized Single Disk Method. *American Journal of Clinical Pathology*, **45**, 493-496. https://doi.org/10.1093/ajcp/45.4_ts.493
- [21] Razali, K., Nalbone, L. and Giarratana, F. (2023) *Aerococcus viridans* and Public Health: Oral Carriage and Antimicrobial Resistance in Stray Dogs and Cats in Algeria. *Microbial Drug Resistance*, **29**, 576-581. <https://doi.org/10.1089/mdr.2022.0165>
- [22] Moore, J.E., Mason, C.K., Coulter, W.A., McCarron, P., Leggett, P., Montgomery, J., *et al.* (2008) Comparison of Clustered, Regularly Interspaced Short Palindrome Repeats (CRISPRs) in Viridans Streptococci (*Streptococcus gordonii*, *S. mutans*, *S. sanguinis*, *S. thermophilus*) and in *S. pneumoniae*. *British Journal of Biomedical Science*, **65**, 104-108. <https://doi.org/10.1080/09674845.2008.11978109>
- [23] Saishu, N., Morimoto, K., Yamasato, H., Ozaki, H. and Murase, T. (2015) Characterization of *Aerococcus viridans* Isolated from Milk Samples from Cows with Mastitis

- and Manure Samples. *Journal of Veterinary Medical Science*, **77**, 1037-1042. <https://doi.org/10.1292/jvms.15-0100>
- [24] Khafagy, A., El-TarabiliSuez, R.M., Yousseff, F.M.A., *et al.* (2023) Emergence of MDR *Aerococcus viridans* in Diarrhea in Chickens in Egypt as the First Study. *Suez Canal Veterinary Medicine Journal*, **28**, 167-172.
- [25] Kang, H.J., You, J., Kim, S.H., Moon, J., Kim, H., Kim, J., *et al.* (2025) Association with Elevated Somatic Cell Counts and Characterization of *Aerococcus viridans* Isolates from Bovine Mastitis Milk in South Korea. *Current Microbiology*, **82**, Article No. 325. <https://doi.org/10.1007/s00284-025-04291-1>
- [26] Zseni, A., Miseta, R. and Németh, B. (2019). Microbiological Testing of Drinking Water in the Western Transdanubian Region of Hungary Using API Tests. *WIT Transactions on Ecology and the Environment*, **239**, 193-203. <https://doi.org/10.2495/ws190171>
- [27] Nappier, S.P., Liguori, K., Ichida, A.M., Stewart, J.R. and Jones, K.R. (2020) Antibiotic Resistance in Recreational Waters: State of the Science. *International Journal of Environmental Research and Public Health*, **17**, Article 8034. <https://doi.org/10.3390/ijerph17218034>
- [28] Mohanta, T. and Goel, S. (2014) Prevalence of Antibiotic-Resistant Bacteria in Three Different Aquatic Environments over Three Seasons. *Environmental Monitoring and Assessment*, **186**, 5089-5100. <https://doi.org/10.1007/s10661-014-3762-1>
- [29] Bhattacharyya, A., Haldar, A., Bhattacharyya, M. and Ghosh, A. (2019) Anthropogenic Influence Shapes the Distribution of Antibiotic Resistant Bacteria (ARB) in the Sediment of Sundarban Estuary in India. *Science of the Total Environment*, **647**, 1626-1639. <https://doi.org/10.1016/j.scitotenv.2018.08.038>
- [30] Foysal, M.J., Neilan, B.A. and Timms, V. (2025) The Impact of Anthropogenic Activities on Antimicrobial and Heavy Metal Resistance in Aquatic Environments. *Applied and Environmental Microbiology*, **91**, e02317-24. <https://doi.org/10.1128/aem.02317-24>
- [31] Behera, B.C. *et al.* (2014) Physico Chemical Properties of Water Sample Collected From Mangrove Ecosystem of Mahanadi River Delta, Odisha, India. *American Journal of Marine Science*, **2**, 19-24. <https://pubs.sciepub.com/marine/2/1/3/>
- [32] Larsson, D.G.J. (2014) Pollution from Drug Manufacturing: Review and Perspectives. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **369**, Article 20130571. <https://doi.org/10.1098/rstb.2013.0571>
- [33] Xi, H., Ji, Y., Fu, Y., Chen, C., Han, W. and Gu, J. (2024) Biological Characterization of the Phage Lysin AVPL and Its Efficiency against *Aerococcus viridans*-Induced Mastitis in a Murine Model. *Applied and Environmental Microbiology*, **90**, e00461-24. <https://doi.org/10.1128/aem.00461-24>
- [34] Parrey, A.H., Sofi, F., Ahmad, M. and Kuchay, A. (2016) *Aerococcus viridans* Infection Presenting as Cutaneous Vasculitis in an Immunocompetent Patient. *Rheumatology*, **54**, 318-320. <https://doi.org/10.5114/reum.2016.64909>
- [35] Getzner, M. and Islam, M.S. (2020) Ecosystem Services of Mangrove Forests: Results of a Meta-Analysis of Economic Values. *International Journal of Environmental Research and Public Health*, **17**, Article 5830. <https://doi.org/10.3390/ijerph17165830>
- [36] Sanz, J.C., Fernández-García, A., Echevarría, J.E. and de Ory, F. (2021) Valuation of a Commercialized RT-PCR Kit for the Diagnosis of Infection Caused by the Measles Virus. *Enfermedades Infecciosas y Microbiología Clínica*, **39**, 155-156.
- [37] Kathiresan, K. and Bingham, B.L. (2001) Biology of Mangroves and Mangrove Eco-

- systems. In: *Advances in Marine Biology*, Elsevier, 81-251.
[https://doi.org/10.1016/s0065-2881\(01\)40003-4](https://doi.org/10.1016/s0065-2881(01)40003-4)
- [38] Yadav, K., Sharma, M., Agarwal, S., Bhatia, N. and Yadav, N. (2018) Aortic Pseudoaneurysm & Endocarditis Caused by *Aerococcus viridans*: A Case Report and Literature Review. *Cardiovascular Revascularization Medicine*, **19**, 201-203.
<https://doi.org/10.1016/j.carrev.2017.08.011>
- [39] Uh, Y., Son, J.S., Jang, I.H., *et al.* (2002) Penicillin-Resistant *Aerococcus viridans* Bacteremia Associated with Granulocytopenia. *Journal of Korean Medical Science*, **17**, 113-115.
- [40] Wad, K., Konaté, A., Dembélé, R., Konaté, K., *et al.* (2016) Occurrence and Antibiotic Susceptibility of *Aerococcus* and *Enterococcus* Strains Isolated from Acute and Chronic Cellulites of Dental Origin in Ouagadougou, Burkina Faso. *Journal of Dentistry and Oral Care Medicine*, **2**, 1-7.
<https://doi.org/10.15744/2454-3276.2.104>
- [41] Mambu, M., Kouegnigan Rerambiah, L., Abdoulaye, S., *et al.* (2012) Low Carriage of *Streptococcus agalactiae* in Pregnant Women in Libreville-Gabon.
<https://doi.org/10.4236/ojog.2012.21001>
- [42] Wu, M., Fan, Y., Gong, C., Chen, X., Li, L. and Yuan, J. (2024) Pathogenicity and Risk of Cross-Species Transmission of *Aerococcus viridans* Isolated from Tian-E-Zhou National Reserve for Lipotes Vexillifer in Shishou, China. *Aquaculture and Fisheries*, **9**, 776-784. <https://doi.org/10.1016/j.aaf.2022.12.003>
- [43] Moh, H.H., Chong, V.C. and Sasekumar, A. (2015) Distribution and Burrow Morphology of Three Sympatric Species of *Thalassina* Mud Lobsters in Relation to Environmental Parameters on a Malayan Mangrove Shore. *Journal of Sea Research*, **95**, 75-83. <https://doi.org/10.1016/j.seares.2014.10.006>
- [44] Murugan, S. and Anandhi, D.U. (2016) An Overview of Crustacean Diversity in Mangrove Ecosystem. In: *Arthropod Diversity and Conservation in the Tropics and Subtropics*, Springer, 81-99. https://doi.org/10.1007/978-981-10-1518-2_5
- [45] Australia, B. (2009) Generic Import Risk Analysis Report for Prawns and Prawn Products. Biosecurity Australia.
- [46] Vishwanathan, B. and Ramalingam, P.V. (2023) Deciphering the Bacterial and Archaeal Communities Colonizing the Rhizospheres of Mangrove Spp. of Pichavaram Wetlands by ARDRA and PCR-DGGE Analysis.
<https://doi.org/10.2139/ssrn.4408186>
- [47] Leboulanger, C., Kolanou Biluka, L., Nzigou, A., Djuidje Kenmogne, V., Happi, J.L.M., Ngohang, F.E., *et al.* (2021) Urban Inputs of Fecal Bacteria to the Coastal Zone of Libreville, Gabon, Central Western Africa. *Marine Pollution Bulletin*, **168**, Article 112478. <https://doi.org/10.1016/j.marpolbul.2021.112478>