

Revista Facultad de Ingeniería



Title: Situational status of antibiotic resistance of *E. coli* in the Escalerilla WWTP, Arequipa, Peru



Authors: Isaac Yanqui-Morales, Ricardo León-Vásquez, Kusisqa Saqra, Danitza DelCha and Renzo Aguirre

DOI: 10.17533/udea.redin.20241252

To appear in:

Revista Facultad de Ingeniería Universidad de Antioquia

Received:	January 29, 2024
Accepted:	December 05, 2024
Available Online:	December 09, 2024

This is the PDF version of an unedited article that has been peer-reviewed and accepted for publication. It is an early version, to our customers; however, the content is the same as the published article, but it does not have the final copy-editing, formatting, typesetting and other editing done by the publisher before the final published version. During this editing process, some errors might be discovered which could affect the content, besides all legal disclaimers that apply to this journal.

Please cite this article as: I. Yanqui-Morales, R. León-Vásquez, K. Saqra, D. DelCha and R. Aguirre-Guillen. Situational status of antibiotic resistance of *E. coli* in the Escalerilla WWTP, Arequipa, Peru, *Revista Facultad de Ingeniería Universidad de Antioquia*. [Online]. Available: https://www.doi.org/10.17533/udea.redin.20241252



Situational status of antibiotic resistance of *E. coli* in the Escalerilla WWTP, Arequipa, Peru Estado situacional de la resistencia antibiótica de *E. coli* en la PTAR Escalerilla, Arequipa, Perú

Isaac Yanqui-Morales https://orcid.org/0000-0001-9144-6320, Renzo Kusisqa Saqra https://orcid.org/0009-0003-2197-6646, Danitza DelCha https://orcid.org/0009-0001-9144-6320, Renzo Aguirre https://orcid.org/0009-0001-9144-6320, Renzo Aguirre https://orcid.org/0009-0003-2197-6646, Danitza DelCha https://orcid.org/0009-0003-2197-6646, Danitza DelCha https://orcid.org/0009-0009-9900-6843, Renzo https://orcid.org/0009-0001-1689-3937

Universidad Nacional de San Agustín de Arequipa. Santa Catalina # 117. C. P. 04001. Arequipa, Perú.

KEYWORDS

E. coli; AMR; ARB; antimicrobial resistance; CLSI; WWTP; AGISAR *E. coli*, RAM, ARB, resistencia antimicrobianos, CLSI, PTAR, AGISAR

Corresponding author: Isaac Yanqui-Morales E-mail: iyanqui@unsa.edu.pe

ABSTRACT: During the COVID-19 pandemic in Peru, a notable increase in self-medication with antibiotics has been observed, raising concerns about the increase in bacterial resistance. In this context, we evaluated the situation in wastewater treatment plants (WWTPs) using biochemical methods and sensitivity tests, such as the Kirby-Bauer assay. The results of our study show a high sensitivity to antibiotics in most of the strains analyzed, particularly towards β -lactams. However, this sensitivity appears to be influenced by seasonal patterns of medication consumption, supported by studies indicating that its contribution to the total flow is minimal. We analyzed 49 strains of *Escherichia coli*, 27% of which showed no resistance to any antibiotic, while the highest resistance was observed against tetracycline (63%). High levels of resistance to fluoroquinolones, such as ciprofloxacin and levofloxacin, were also recorded. In contrast, amikacin and piperacillin-tazobactam showed minimal resistance, with only one strain resistant to each. Multiresistance, defined as resistance to a and 10 antibiotics, respectively.

RESUMEN: En Perú, durante la pandemia de COVID-19, se ha observado un notable incremento en la automedicación con antibióticos, lo que ha generado preocupación por el aumento de la resistencia bacteriana. En este contexto, evaluamos la situación en las plantas de tratamiento de aguas residuales (PTAR) utilizando métodos bioquímicos y pruebas de sensibilidad, como el ensayo de Kirby-Bauer. Los resultados de nuestro estudio muestran una alta sensibilidad a los antibióticos en la mayoría de las cepas analizadas, especialmente hacia los β -lactámicos. Sin embargo, esta sensibilidad parece estar influenciada por los patrones estacionales de consumo de medicamentos, respaldado por estudios que indican que su contribución al caudal total es mínima. Se analizaron 49 cepas de *Escherichia coli*, de las cuales el 27% no presentó resistencia a ningún antibiótico, mientras que la mayor resistencia se observó frente a la tetraciclina (63%). También se registraron altos niveles de resistencia a fluoroquinolonas,



como ciprofloxacina y levofloxacina. En contraste, la amikacina y la piperacilina-tazobactam presentaron una resistencia mínima, con solo una cepa resistente a cada una. La multirresistencia, definida como la resistencia a al menos dos antibióticos, se identificó en el 35% de las cepas, y dos de ellas mostraron resistencia a 8 y 10 antibióticos, respectivamente.

1. Introduction

Antibiotic resistance has become an imminent global problem. Research has identified resistant bacteria and resistance genes in various settings, including clinical analyses, livestock, and wastewater [1]. Currently, wastewater analysis is emerging as a reliable and complementary epidemiological tool to monitor pharmacological substances like antibiotics, providing real-time data and enabling the identification of geographical variations and temporal trends in their consumption [2]. Wastewater treatment plants (WWTPs) are recognized as major drivers of antibiotic resistance since most of these drugs, both from human and veterinary use, are excreted unmetabolized and reach WWTPs via urine and feces, entering the sewage system [3].

Bioaccumulation of pharmacological substances like antibiotics occurs in WWTPs due to their limited or absent elimination. This constant flow towards receiving water sources can negatively impact human health and ecosystems, promoting the proliferation of resistant bacteria and their genes [4]. Studies have shown that the selection and transfer of antibiotic resistance occur even with exposures to very low concentrations, below the minimum inhibitory concentration, in various environmental settings [5].

The increase in antimicrobial resistance is an imminent threat to public health. Lack of intervention could lead us into a post-antibiotic era, severely limiting the effectiveness of these treatments against common and severe infections. Human migration and globalization have contributed to the spread of resistant bacteria [6]. According to a report from the United Kingdom, it is projected that by 2050, deaths due to drug-resistant infections could surpass 10 million, exceeding even those related to cancer. Global economic losses to antimicrobial resistance could reach \$100 trillion [7].

Multi-drug resistant (MDR) *Enterobacteriaceae* and their genes show significant prevalence, possibly linked to intensive animal farming, contributing to their frequency in soil and nearby aquatic ecosystems. It's crucial to maintain constant surveillance of zoonotic bacteria to address this issue [8]. Further research is needed to thoroughly understand the mechanisms of selection, transfer, propagation, and impact of antimicrobial-resistant bacteria, both at environmental and operational levels. Additional studies are essential to develop effective mitigation and control strategies [9].

The COVID-19 pandemic has disproportionately affected low- and middle-income countries (LMICs). Therefore, it is essential to conduct ongoing studies to better understand antimicrobial resistance (AMR) and nosocomial infections in these countries [10].

This study aimed to investigate the prevalence of specific antibiotic resistance in *E. coli* strains at five different points within the Escalerilla Wastewater Treatment Plant (WWTP), from its influent to the final



effluent. The main goal was to identify the antibiotics to which these strains showed higher resistance, using *E. coli* as a common indicator of water quality according to national regulations [11]. Additionally, for the "Tricycle Protocol" developed by the World Health Organization (WHO) under the "One Health" approach [12], the supervision of antibiotic resistance in humans, animals, and the environment was considered. Thus, the aim was to establish a solid informational basis for conducting environmental epidemiological surveillance of wastewater in the city of Arequipa, Peru.

2. Methodology

2.1. Study Location

The Escalerilla WWTP is located at coordinates 219125.74m E, 8188306.97m N, characterized by scarce humidity occasionally reaching up to 50%. High solar radiation leads to an evaporation rate between 4 and 6 times greater than the precipitation rate, resulting in a dry and arid climate with intense sun exposure. Winds range from 6 m/s to 20 m/s, peaking around 1 PM. This treatment plant manages effluents from the Northern Cone of Metropolitan Arequipa, covering the rapidly growing districts of Cerro Colorado and Yura. Furthermore, it has a projected design horizon extending until the year 2036 [13]





Figure 1. Zones contributing wastewater flow

In **Figure 1**, the districts of Yura, Cerro Colorado, and Cayma are clearly distinguished. The Escalerilla WWTP is marked with a green dot, while the drainage areas, highlighted in blue, represent the zones contributing wastewater flow to this treatment plant. The white areas correspond to uninhabitable zones.

2.2. Hydraulic and Physicochemical Characteristics

The primary collector sewer system directing flows towards the Escalerilla Wastewater Treatment Plant is mainly composed of recently constructed PVC pipes. This system plays a crucial role in treating urban wastewater, covering approximately 9.48% of the city's total area. The treatment method employed is extended aeration, designed to remove between 85% and 95% of contaminants present in the wastewater. The preliminary treatment process includes screening, grit removal, degreasing, as well as fats and oils



removal. On the other hand, secondary treatment occurs through various stages such as the distribution chamber, biological reactor, secondary sedimentation, and external sludge recirculation. Currently, the operation of the biological reactors is alternated, so that one is on standby. In its first phase, the operating reactor supports a maximum mass load of 0.093 kgBOD5/kg SS per day and has a concentration of 4.5 kg/m³ (**Table No. 1**). Each reactor has a total volume of 12.87 m³, with 20% dedicated to anoxia and 80% to aeration [13].

Phase	Year	Average Flow (l/s)	Maximum Flow (l/s)	Mass Load kg BOD5/kg SS per day
F1	2013	260	327	0.930
F2	2017	336	423	0.108
F3	2025	390	491	0.126
F4	2036	403	509	0.130

 Table No. 1
 Flow and Load Variation Over the Years According to Design

To obtain a representative overview, 5 monitoring points were selected among the main treatment units. These specific points are detailed in **Table No. 2** and were calculated based on an average flow rate of 145 liters per second measured at the treatment plant. The lower treated flow compared to the projected flow is partly due to the ongoing execution of the sanitation projects for "Reservoirs N39 and N31". These projects will complete the missing collectors, allowing their connection to the existing Escalerilla collector.

Table No. 2	Hydraulic	Retention	Time
-------------	-----------	-----------	------

	No.	Label	Hydraulic Component	Accumulated Retention Time	Unit
	P1	A1	Debris Screen - Influent	2.08	min
C	P2	MR	Distribution Manhole	34.63	min
	P3	B1	Bioreactor Point 1	42.32	min
	P4	B2	Bioreactor Point 2	1290.51	min
9	P5	C1	Secondary Clarification	1818.59	min

Table 3 shows the contaminant removal efficiency obtained through monitoring conducted for the National Urban Sanitation Program (PNSU) of Peru at the end of 2020 in an accredited laboratory, using standardized and validated methods. The Wastewater Treatment Plant (WWTP) exhibits the following



removal efficiencies, defined as the difference between the initial and final concentrations, divided by the initial concentration: more than 98% for Settleable Solids, Total Suspended Solids, Oils and Greases, Biochemical Oxygen Demand (BOD5), Chemical Oxygen Demand, Thermotolerant Coliforms, and Total Coliforms. However, the removal efficiency for Total Solids was 68.23%. This difference is due to the WWTP not being specifically designed to remove dissolved solids, as Total Solids are the sum of suspended, settleable, and dissolved solids. The removal of dissolved solids requires other types of processes, such as coagulation-flocculation and/or reverse osmosis.

Parameter	Detection Limit	Unit	Inlet Concentration (P1)	Outlet Concentration (P5)	Removal Efficiency (%)
рН	-	pH units at 25 °C	7.87	7.06	-
Temperature	-	°C	22.6	25.6	-
Dissolved Oxygen	-	mg/L	0.03	3.79	-
Settleable Solids	0.1	mL/L	33.5	< 0.1	99.70%
Total Suspended Solids	2.5	mg/L	1038	2.83	99.73%
Total Solids	2.5	mg/L	2902	922	68.23%
Oils and Greases	0.5	mg AyG /L	201	4	98.01%
Biochemical Oxygen Demand	2	mg/L	999	10.2	98.98%
Chemical Oxygen Demand	2.5	mg/L	2424	34.7	98.57%
Thermotolerant Coliforms	1.8	NMP/100 mL	54,000,000	70,000	99.87%
Total Coliforms	1.8	NMP/100 mL	240,000,000	350,000	99.85%

Table No. 3 Contaminant Removal Efficiency

2.3. Sample Collection

Samples were collected between 9:00 a.m. and 9:30 a.m. the last Monday of every month, from November 2022 to February 2023. Each composite sample was obtained by mixing three individual samples. Using a steel sampler, samples were collected and stored in sterile 100 ml plastic bottles. The collection process began at point P5 and sequentially continued to point P1, ensuring the sampler was cleaned between each sample collection. Additionally, in-situ pH data were recorded using ISOLAB TM indicator paper strips, which yielded values ranging between 7 and 7,5. The collected samples were properly packaged, and the cold chain was maintained for transportation to the Microbiology Laboratory of the Faculty of Medicine at the National University of San Agustin, where their analysis would be conducted [14].

It is important to highlight that each year CLSI updates the diameter ranges used to analyze antimicrobial sensitivity and resistance. In this study, in addition to the routinely evaluated antimicrobials, penicillin, amoxicillin, cephalexin, oxacillin, and clindamycin were included, which are not commonly used for *E*.



coli infections. Vancomycin, erythromycin, and azithromycin were also evaluated, although no breakpoints are established for these in the CLSI guidelines. This underscores the importance of establishing specific breakpoints for environmental studies on antimicrobial resistance.

2.4. Microbial Isolation

The determination of *E. coli* was conducted using the Most Probable Number (MPN) technique, as outlined in the 'Standard Methods for the Examination of Water and Wastewater' (APHA) Ed. 2017 [15]. A non-selective enrichment with Buffered Peptone Water was used for the presumptive test, aimed at revitalizing bacteria possibly damaged by storage conditions. To determine the optimal dilution range, 1 ml of the sample was inoculated into a tube containing 9 ml of GranuCultTM Buffered Peptone Water, creating a 10^{-1} dilution. Subsequently, serial dilutions were prepared until achieving a 10^{-3} dilution.

From this dilution, 1 ml was inoculated into 3 tubes with GranuCultTM Lactose Lauril Sulfate broth with Durham tubes to detect gas production. These tubes were incubated for 48 hours at 37 °C. Tubes showing turbidity and gas production in the Durham tube were subjected to the confirmatory test. For this stage, a selective enrichment was performed using GranuCultTM Brilliant Green Bile Lactose broth (BRILA) at 37°C for 48 hours for total coliforms and GranuCultTM EC broth (*Escherichia coli*) at 44°C for 48 hours for fecal coliforms, both mediums containing Durham tubes. Turbidity and gas production in the Durham tubes were considered as positive results. To confirm the presence of *E. coli*, Kovac's reagent was added to positive EC broth tubes. The appearance of a turquoise ring on the medium surface indicated a positive result for *E. coli*, enabling further selective isolation.

Selective isolation was performed on MacConkey agar GranuCultTM, as it allows differentiation of Gramnegative bacteria and the *Enterobacteriaceae* family. Suspected colonies of *E. coli*, identified by their pinkish-red color, underwent biochemical tests using GranuCultTM Lysine Iron Agar (LIA), Triple Sugar Iron (TSI) Agar GranuCultTM, and Simmons Citrate Agar GranuCultTM [16]

2.5. Antibiotic Susceptibility Test

The Kirby-Bauer disk diffusion technique was employed to evaluate antibiotic susceptibility (**Table No. 4**). An inoculum of colonies obtained from previous plates was transferred to a tube containing peptone water. Upon reaching a turbidity equivalent to $1.5 \times 10-8$ CFU/ml (No. 0.5 on the Mac Farlan scale), it was seeded onto the surface of plates with Mueller Hinton NutriSelect® agar. Subsequently, antibiotic disks were placed on these plates, which were then incubated for 24 hours at 37°C. The zones of inhibition surrounding the antibiotics were measured, classifying them as Resistant (R), Susceptible (S), or Intermediate (I), based on standard halo patterns for *E. coli* outlined in the CLSI M100, 2020 Edition, March 2020 - Performance Standards for Antimicrobial Susceptibility Testing [17].

Table No. 4Antibiotics by groups and sub groups



Groups	Subgroup	Antibiotic		
Aminoglycosides	-	Gentamicin (GM)		
	-	Amikacin (MK)		
Beta-lactams	Beta-lactamase inhibitors	Ampicillin sulbactam (SAM)		
	Penicillins	Penicillin (P)		
	3GEN cephalosporins	Cefotaxime (CTX)		
	Penicillins - aminopenicillins	Amoxicillin (AMX)		
	Penicillins - aminopenicillins	Ampicillin (AM)		
	Beta-lactamase inhibitors	Amoxicillin + ac. clavulanic (AMC)		
	1GEN cephalosporins	Cephalexin (CFL)		
	Penicillins - isoxazolylpenicillins	Oxacillin (OX)		
	Beta-lactamase inhibitors	Piperacillin – tazobactam (PTZ)		
	Cephalosporins – 3GEN	Ceftriazone (CRO)		
Cefuroxime	2GEN cephalosporins	Cefuroxime (CXM)		
Glycopeptides	-	Vancomycin(VA)		
Lincosamides	-	Clindamycin(CC)		
Macrolides	14atm	Erythromycin (E)		
	15atm	Azithromycin (AZM)		
Quinolones	3GEN	Levofloxacin (LEV)		
	2GEN	Ciprofloxacin (CIP)		
Sulfonamides	-	Trimethoprim sulfamethoxazole (SXT)		
Tetracycline	1GEN	Tetracycline (TE)		

2.6. Statistical Analysis

The results of this study were obtained through a multivariate analysis of variance (MANOVA) to evaluate significant differences at each analysis point across different monitoring dates. This analysis was performed using IBM SPSS Statistics 7.0.1 IF026 (x64) software.

A total of 49 strains of *Escherichia coli* collected at different points and sampling dates (**Table No. 02**) were analyzed, of which 13 showed no resistance to any antibiotic. Twenty-seven percent of the strains were sensitive to all evaluated antibiotics. The highest resistance was observed against tetracycline, with 63% of the total strains and 86% of the 36 strains that showed resistance to at least one antibiotic. Fluoroquinolones, such as ciprofloxacin and levofloxacin, showed the next highest resistance rates.

The antibiotics with the lowest resistance were amikacin and piperacillin-tazobactam, with only one resistant strain for each. It is important to note that the strain resistant to amikacin was not multidrug-resistant, while the strain resistant to piperacillin-tazobactam showed resistance to four antibiotics.



Strains that showed resistance to at least two antibiotics were considered multidrug-resistant; it was found that 35% of the strains were multidrug-resistant. Additionally, a strain resistant to 10 antibiotics was identified at point P3 and another resistant to 8 antibiotics at point P5, both isolated on the same date during the first month of sampling. A strain resistant to 6 antibiotics was also found at point P1, corresponding to a sampling conducted during the rainy season (February).

The proportion of resistant strains at point P5 was lower compared to other points, representing 50% (5 out of 10) of the strains. At the other points, the proportions were 73% at P4 (8 out of 11), 70% at P3 (7 out of 10), 71% at P2 (5 out of 7), and 100% at P1 (11 out of 11). During the rainy season months, no resistant strains were detected in the final phase of the wastewater treatment plant (WWTP). This could be because the rainiest months coincide with the highest temperatures, which implies a lower consumption of antibiotics due to a reduction in respiratory infections. Additionally, the location of the Escalerilla WWTP means that the flow received from rain is not significant, as even during the rainy season, it does not reach the plant. This could indicate that exposure to lower concentrations of antibiotics, along with competition among different bacteria present in the sludge, reduces the population of antibiotic-resistant bacteria.



Table No. 5 Percentage of Antimicrobial Resistance Level by E. coli according to the sampling point

									~						~	
		S	27,3	36,4	63,6 e1 e	0 <u>-</u> 0	6 ⁰ 6	6'06	100,0	81,8	45,5	6'06	45,5	81,8	100,0	
ıt	P4	_	0'0	18,2	27,3 18.2	10,2	0'0	9,1	0,0	9,1	18,2	9,1	9,1	9,1	0'0	
ling Poir		R	72,7	45,5	0,1 1	0	9,1	0,0	0,0	9,1	36,4	0'0	45,5	9,1	0'0	X
y Samp		N3	1 0	10	66	2	10	10	10	10	9	10	10	10	10	• •
istance b		S	30,0	60,0	70,0	00,001	80,0	80,0	80,0	70,0	60,0	70,0	80,0	100,0	60,0	
obial Res	P3	_	10,0	10,0	0,0	o O	10,0	10,0	0,0	20,0	30,0	20,0	10,0	0,0	10,0	
ge of Micr		R	60,0	30,0	30,0	o O	10,0	10,0	20,0	10,0	10,0	10,0	10,0	0,0	30,0	
centag		N2	7	7	~ ~	-	~	7	7	7	~	7	7	7	7	
Per		S	28,6	71,4	85,7 71 1	- - t	85,7	100,0	100,0	100,0	71,4	85,7	71,4	100,0	100,0	
	P2	_	14,3	14,3	14,0 2,4,0	1 0	14,3	0,0	0'0	0'0	14,3	0'0	14,3	0,0	0,0	
		R	57,1	14,3	0,0	<u>+</u>	0,0	0,0	0,0	0,0	14,3	14,3	14,3	0,0	0'0	
		LN	÷	5	55	=	-	10	10	10	9	7	5	5	5	
		S	9,1	72,7	63,6 00 0	90'9	90,9	90'0	80,0	90'0	60,0	81,8	81,8	100,0	81,8	
	P.	_	0'0	27,3	36,4 0 1	ົ	0,0	10,0	0'0	0'0	20,0	0'0	9,1	0'0	9,1	
		R	6'06	0'0	0,0	0	9,1	0,0	20,0	10,0	20,0	18,2	9,1	0,0	9,1	
			Tetracycline	Ciprofloxacin	Gentamicin	Ampicillin-	sulbactam	Trimethoprim Sulfamethoxazole	Cefotaxime	Cefuroxime	Levofloxacin	Ampicillin	Amoxicillin + clavulanic acid	Piperacillin- tazohactam	Ceftriaxone	

Note: The percentages were calculated between the types of resistance (R=resistance, I = intermediate and S=sensitive) per monitoring point.

In the MANOVA statistical analysis, no significant differences were found between the sampling points. However, multivariate tests revealed a significant difference, suggesting that the date on which the samples are taken influences the inhibition halos.



3. Results

In Peru, the self-medication rate with antibiotics before the Covid-19 pandemic stood at 27.6%. During the pandemic, these values increased to 39.2% for antibiotics/anti-inflammatories and specifically to 21.6% for antibiotics. A reduction in the average age of self-medicators was observed, decreasing from 46.5 years before the pandemic to 40.87 years during it [18]. This was mainly attributed to the dispensing of drugs without a prescription, guidance from pharmacists, occasional use of medications, and acquisition without proper consideration of their implications [19].

These factors suggest a probable increase in antimicrobial resistance in WWTPs, especially due to the high rate of self-medication and hospital discharges. The latter contribute to the alteration of the microbiota present in effluents, generating resistance that is affected by the persistence and solubility of the medications [20].

This could be due to the fact that, although hospitals would be expected to be the largest source of discharge in WWTPs, since they host a wide variety of multi-resistant bacteria, they do not represent a significant percentage of the flow to the plants, as confirmed by studies such as that of Verburg et al. which suggests that hospital discharges are 10% compared to other discharges [3]. Rahman et al., in their wastewater monitoring, identified carbapenem-resistant *Enterobacteriaceae* (CRE), vancomycinresistant *Enterococci* (VRE), and Methicillin-resistant *Staphylococcus aureus* (MRSA) in areas with 5.2 million residents, but evidenced that hospitals were not a predominant source of resistance [21].

This suggests that the major contribution of resistant bacteria may come from other discharges, such as urban, domestic, or livestock wastewater. In urban environments, WWTPs present considerable diversity [22]. The sources of contamination in these facilities include fluoroquinolones, trimethoprim, aminoglycosides, sulfonamides, beta-lactams, tetracyclines, cephalosporins, and carbapenems in extracellular (exDNA) and intracellular (inDNA) DNA [23], [24]. Resistance to broad-spectrum antibiotics such as aminoglycosides, which inhibit protein synthesis in gram-negative infections resistant to β -lactams and other first-line antibiotics [25], can propagate antimicrobial resistance in aquatic environments through horizontal gene transfer, posing a risk for the selection of resistant bacteria in treated wastewater [23].

Our study demonstrated higher sensitivity to antibiotics, mostly belonging to the β -lactam group (**Table No. 5**). This trend could be linked to the rapid hydrolysis of these antibiotics in bodies of water, which could limit their ability to effectively promote resistance [26]. However, it was observed that *E. coli* showed higher resistance to Oxacillin, Penicillin, and Tetracycline. In the case of the latter, various studies have shown a constant prevalence of resistance, as *E. coli* harbors at least 40 tetracycline resistance genes. These genes encode enzymatic inactivation, ribosomal protection, or efflux pumps such as the tetA pump, known for its role in tetracycline resistance in *Enterobacteriaceae* [27].



Revista Facultad de Ingeniería, Universidad de Antioquia, No.117, pp. x-xx, xxx-xxx 2025

I. Yanqui-Morales et al.; Revista Facultad de Ingeniería, No. 117, pp. x-x, 2025

According to our analysis, no significant differences were found between the sampling points. However, a significant variation (p<0.05) was observed in the mean values of each sampling point across the different monitoring dates. Likewise, there wasn't a pronounced prevalence of resistance during the analyzed months. These results align with several studies, demonstrating that the relationship between antibiotic concentration, Wastewater Treatment Plant (WWTP) treatments, and antibiotic resistance is not always strictly positive or negative. This suggests that, while WWTPs might stress bacteria, they aren't always a hotspot for resistance gene proliferation. However, they may increase the relative abundance of mobile resistance genes, such as plasmids [28]. Despite the reduction in *E. coli* population density achieved by some WWTPs, as found in our study (**Table No. 6**), they don't ensure the effective elimination of bacterial DNA, leaving residual fractions in the environment attached to particles, degraded, or absorbed through natural transformation into competent cells [24].

Table No. 6 E. coli MPN values from the five sampling points of the Escalerilla WWTP

IVIIN	while per sampling day at the ve wire Escalerina								
P1	P2	Р3	P4	P5					
1500	1600	1200	900	700					
5300	>110000	>110000	24000	1500					
15000	9300	1900	2400	600					
900		>110000	5300	300					
	P1 1500 5300 15000 900	P1 P2 1500 1600 5300 >110000 15000 9300 900	P1 P2 P3 1500 1600 1200 5300 >110000 >110000 15000 9300 1900 900 >110000	P1 P2 P3 P4 1500 1600 1200 900 5300 >110000 >110000 24000 15000 9300 1900 2400 900 >110000 5300					

MNP ner	sampling day	y at the W	WWTP	Fscalarilla
	sampning ua	at the v		Escalerma

Other studies have reported a higher prevalence of antibiotic-resistant bacteria in facilities with more invasive treatments, such as WWTPs utilizing a modified activated sludge process, followed by a laminar settler for nutrient removal, and a final UV disinfection step at an estimated dose of 16 mJ/cm2 [29]. Our results do not support their findings, which could be due to the fact that the monitoring point 'P5' is located before the disinfection process. Antibiotic resistance prevalence is also influenced by how these treatments might alter the abundance of elements carrying resistance genes, such as integrons or plasmids [28].

Despite the development of microbial isolation and molecular methodologies more sensitive than the biochemical methods used in this study, no substantial difference in results has been evidenced between the two approaches in different studies; instead, similar studies have shown comparable percentages when using conventional methods akin to those employed here [30]. Additionally, it has been demonstrated that methods like qPCR have limitations in detecting some bacteria that are identified by culture-based methods, which can incur higher economic costs if multiple targets need detection [31]. Hence, it's crucial to pay attention to these conventional methods, especially in countries with fewer resources where modern methods might not be as accessible.



All of this underscores the importance of epidemiological surveillance of wastewater, integrating technical and business information from Sanitation Service Providing Companies. It's considered crucial to characterize antimicrobial resistance in specific population groups through surveillance at WWTPs, health centers, schools, and strategic sampling points. These data will effectively monitor antibiotic consumption characteristics in the population, aiming to prevent resistance issues in the future.



4. Conclusions

The study did not find significant differences between the monitoring points through the MANOVA analysis. However, a significant variation in average values was observed over the monitoring dates, suggesting that seasonal changes influence the resistance of the collected strains. This highlights the importance of conducting seasonal monitoring to better understand the dynamics of antimicrobial resistance (AMR) and how environmental conditions impact its spread, a central aspect of the environmental monitoring in the Tricycle protocol.

The *E. coli* strains showed higher resistance to tetracycline (63%), followed by fluoroquinolones, emphasizing the need for specific monitoring of these antibiotics. Additionally, 35% of the isolated strains were multidrug-resistant, with some resistant to up to 10 antibiotics. These antibiotics, identified with high resistance rates, require strict public health surveillance to anticipate possible hospital complications. It is essential to exercise greater caution when prescribing these agents to vulnerable patients, ensuring prior identification of the pathogen and its antimicrobial sensitivity.

Although advanced molecular techniques exist, culture-based methods remain effective and costefficient for AMR surveillance, especially in resource-limited settings. The Tricycle protocol promotes their use, demonstrating that conventional methods can provide valuable data for monitoring antimicrobial resistance.

A biannual antibiotic resistance surveillance is proposed, with reviews during warmer (summer) and colder (winter) periods. It is also crucial to consider natural phenomena such as El Niño and the impact of global warming in these analyses. This should be reflected in public policies to improve wastewater management and evaluate technologies to reduce the load of resistant bacteria released into the environment.

Finally, it is recommended to conduct additional studies incorporating advanced microbial identification methods, such as proteomics or genomics, in conjunction with biochemical methods, aiming to establish correlations between environmental factors such as temperature, hydraulic retention time, and cell retention time.

Declaration of competing interest

We declare that we have no significant competing interests including financial or non-financial, professional, or personal interests interfering with the full and objective presentation of the work described in this manuscript.



Acknowledgment

The authors wish to express their gratitude to the National University of San Agustin de Arequipa for their support under contract IBA-IB-15-2020-UNSA within the project "Physicochemical and microbiological characterization of effluents from wastewater treatment plants in the Arequipa region". Additionally, we would like to thank the Sanitation Service Provider SEDAPAR SA and National Urban Sanitation Program (PNSU) for their collaboration and the facilities provided during the execution of this research.

Funding

The authors wish to express their gratitude to the National University of San Agustin de Arequipa for their support under contract IBA-IB-15-2020-UNSA within the project "Physicochemical and microbiological characterization of effluents from wastewater treatment plants in the Arequipa region".

Author contributions

- Isaac Yanqui Morales: Conceptualization, Funding Acquisition, Methodology, Project Administration, Writing Original Draft Preparation, Writing.
- Ricardo León Vásquez: Conceptualization, Methodology, Resources, Writing Original Draft Preparation.
- Kusisqa Saqra: Conceptualization, Writing Original Draft Preparation.
- Danitza DelCha: Methodology, Writing Original Draft Preparation.
- Renzo Aguirre: Formal Analysis, Investigation, Data Curation.

Data availability statement

The data used in this study can be viewed at the following link https://drive.google.com/drive/folders/1xk1nItLtmU2Ie5SAmhzdRaQ4sr68R9R5?usp=sharing

References

T. U. Berendonk *et al.*, *Tackling antibiotic resistance: The environmental framework*, vol. 13, no.
 Nature Publishing Group, 2015. doi: 10.1038/nrmicro3439.

[2] E. Pocurull *et al.*, "Wastewater-based epidemiology: present and future in Spain," 2020.

[3] I. Verburg, S. García-Cobos, L. H. Leal, K. Waar, A. W. Friedrich, and H. Schmitt, "Abundance and antimicrobial resistance of three bacterial species along a complete wastewater pathway," *Microorganisms*, vol. 7, no. 9, Sep. 2019, doi: 10.3390/microorganisms7090312.

[4] M. Á. Mueses, "Las tecnologías de tratamiento de aguas un atractivo de la investigación en ingeniería," *Revista Ing-Nova*, vol. 1, no. 2, pp. 149–151, Jul. 2022, doi: 10.32997/rin-2022-3998.

[5] E. Gullberg, L. M. Albrecht, C. Karlsson, L. Sandegren, and D. I. Andersson, "Selection of a multidrug resistance plasmid by sublethal levels of antibiotics and heavy metals," *mBio*, vol. 5, no. 5, Oct. 2014, doi: 10.1128/mBio.01918-14.



[6] K. L. Schwartz and S. K. Morris, "Travel and the Spread of Drug-Resistant Bacteria," *Current Infectious Disease Reports*, vol. 20, no. 9. Current Medicine Group LLC 1, Sep. 01, 2018. doi: 10.1007/s11908-018-0634-9.

[7] J. O'Neill, "Tackling Drug-Resistant Infections Globally: Final Report And Recommendations The Review On Antimicrobial Resistance Chaired By Jim O'neill," 2016.

[8] P. Amador, R. Fernandes, C. Prudêncio, and I. Duarte, "Prevalence of antibiotic resistance genes in multidrug-resistant enterobacteriaceae on portuguese livestock manure," *Antibiotics*, vol. 8, no. 1, Mar. 2019, doi: 10.3390/antibiotics8010023.

[9] H. Bürgmann *et al.*, "Water and sanitation: An essential battlefront in the war on antimicrobial resistance," *FEMS Microbiol Ecol*, vol. 94, no. 9, Sep. 2018, doi: 10.1093/femsec/fiy101.

[10] P. Dey, D. Parai, S. T. Hossain, and S. K. Mukherjee, "The aftermath of corona virus disease on antimicrobial resistance across low and middle-income countries," Universitas Scientiarum, vol. 28, no. 2, pp. 183–199, 2023. Available: https://doi.org/10.11144/Javeriana.SC282.taoc

[11] MINAM, Aprueban Estándares de Calidad Ambiental (ECA) para Agua y establecen Disposiciones Complementarias. Perú, 2017.

[12] World Health Organization, "Global Tricycle Surveillance", WHO, march 2023. [Link: https://iris.who.int/bitstream/handle/10665/340079/9789240021402-eng.pdf?sequence=1]

[13] J. Maldonado and L. López, "Construcción De Emisor Y Sistema De Tratamiento De Aguas Residuales Del Sector Denominado Cono Norte De Arequipa Metropolitana," Arequipa, 2012.

[14] B. A. Body, *Quality control of microbiological transport systems : approved standard*. National Committee for Clinical Laboratory Standards., 2003.

[15] American Public Health Association, American Water Works Association, and Water Environment Federation, *Standard Methods for the Examination of Water and Wastewater*, 23RD EDITION. 2017. doi: 10.2105/SMWW.2882.216.

[16] A. M. Hammad, A. Eltahan, H. A. Hassan, N. H. Abbas, H. Hussien, and T. Shimamoto, "Loads of Coliforms and Fecal Coliforms and Characterization of Thermotolerant *Escherichia coli* in Fresh Raw Milk Cheese," *Foods*, vol. 11, no. 3, Feb. 2022, doi: 10.3390/foods11030332.

[17] M. P. Weinstein and Clinical and Laboratory Standards Institute, *Performance standards for antimicrobial susceptibility testing*, 30th Edition. 2020.

[18] P. J. Navarrete-Mejía, J. C. Velasco-Guerrero, and L. Loro-Chero, "Self-medication in time of pandemic: Covid-19," *Revista del Cuerpo Medico Hospital Nacional Almanzor Aguinaga Asenjo*, vol. 13, no. 4, pp. 350–355, 2020, doi: 10.35434/rcmhnaaa.2020.134.762.

[19] J. B. Pari-Olarte *et al.*, "Factors associated with non-responsible self-medication in Peru," *Revista del Cuerpo Medico Hospital Nacional Almanzor Aguinaga Asenjo*, vol. 14, no. 1, pp. 29–34, Mar. 2021, doi: 10.35434/rcmhnaaa.2021.141.867.

[20] S. G. Rizvi and S. Z. Ahammad, "COVID-19 and antimicrobial resistance: A cross-study," *Science of the Total Environment*, vol. 807. Elsevier B.V., Feb. 10, 2022. doi: 10.1016/j.scitotenv.2021.150873.



[21] Z. Rahman *et al.*, "Wastewater-based monitoring reveals geospatial-temporal trends for antibiotic-resistant pathogens in a large urban community," *Environmental Pollution*, vol. 325, May 2023, doi: 10.1016/j.envpol.2023.121403.

[22] I. Bueno *et al.*, "Quantifying and predicting antimicrobials and antimicrobial resistance genes in waterbodies through a holistic approach: a study in Minnesota, United States," *Sci Rep*, vol. 11, no. 1, Dec. 2021, doi: 10.1038/s41598-021-98300-5.

[23] M. Haenni *et al.*, "Environmental contamination in a high-income country (France) by antibiotics, antibiotic-resistant bacteria, and antibiotic resistance genes: Status and possible causes," *Environment International*, vol. 159. Elsevier Ltd, Jan. 15, 2022. doi: 10.1016/j.envint.2021.107047.

[24] D. Calderón-Franco *et al.*, "Metagenomic profiling and transfer dynamics of antibiotic resistance determinants in a full-scale granular sludge wastewater treatment plant," *Water Res*, vol. 219, Jul. 2022, doi: 10.1016/j.watres.2022.118571.

[25] Y. Javvadi and S. V. Mohan, "Understanding the distribution of antibiotic resistance genes in an urban community using wastewater-based epidemiological approach," *Science of the Total Environment*, vol. 868, Apr. 2023, doi: 10.1016/j.scitotenv.2023.161419.

[26] O. Tenaillon *et al.*, "Tempo and mode of genome evolution in a 50,000-generation experiment," *Nature*, vol. 536, no. 7615, pp. 165–170, Aug. 2016, doi: 10.1038/nature18959.

[27] D. O. Perewari, K. Otokunefor, and O. E. Agbagwa, "Tetracycline-Resistant Genes in *Escherichia coli* from Clinical and Nonclinical Sources in Rivers State, Nigeria," *Int J Microbiol*, vol. 2022, 2022, doi: 10.1155/2022/9192424.

[28] R. Pallares-Vega *et al.*, "Determinants of presence and removal of antibiotic resistance genes during WWTP treatment: A cross-sectional study," *Water Res*, vol. 161, pp. 319–328, Sep. 2019, doi: 10.1016/j.watres.2019.05.100.

[29] E. C. Machado *et al.*, "Antibiotic resistance profile of wastewater treatment plants in Brazil reveals different patterns of resistance and multi resistant bacteria in final effluents," *Science of the Total Environment*, vol. 857, Jan. 2023, doi: 10.1016/j.scitotenv.2022.159376.

[30] M. Azab El-Lathy, G. E. El-Taweel, W. Morsy El-Sonosy, F. A. Samhan, and T. A. A. Moussa, "Determination of pathogenic bacteria in wastewater using conventional and PCR techniques," 2009.

[31] E. Yergeau *et al.*, "Comparison of Methods to Identify Pathogens and Associated Virulence Functional Genes in Biosolids from Two Different Wastewater Treatment Facilities in Canada," *PLoS One*, vol. 11, no. 4, Apr. 2016, doi: 10.1371/journal.pone.0153554.

