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Isolation and identification of some pathogenic bacteria from water samples in Qalubiya Governorate

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Abstract:

Microbial activity in water can lead to various challenges, including the contamination of drinking water, deterioration of overall water quality, and the proliferation of harmful pathogens. In Egypt, this issue is particularly significant due to the country's heavy reliance on the Nile River, which is potentially contaminated with bacteria, parasites, and other pollutants. In the present study, thirty-five bacterial isolates were isolated from untreated water samples collected from four water stations (El-Filal Station, El-Haras station, Bata station and Qalyub Station). Distinct colonies obtained from these samples were subjected to preliminary identification based on morphological and biochemical characteristics Among the isolates, four bacterial strains demonstrated resistance to 100% of the tested antibiotics, qualifying them as multi-drug resistant (MDR) bacteria. Advanced identification using the VITEK 2 compact system classified these MDR isolates as *Escherichia coli*, *Klebsiella pneumoniae*, *Staphylococcus aureus* and *Enterobacter aerogenes.*

Keywords: Egypt, Water stations, Pathogenic bacteria, Bacterial identification, multidrug-resistant (MDR) bacteria, water quality.

1. Introduction:

Water is a fundamental necessity for life, serving as the source of all biological activity and providing essential nutrition. Ensuring the availability of safe drinking water is a critical public health concern, particularly in developing nations[6]. Egypt faces significant challenges in this regard, as its water resources are limited, and the growing demand for clean water is placing considerable strain on this vital resource.[8]. The Nile River, a primary water source for the country, is increasingly burdened by rapid population growth, land reclamation projects, and industrial waste production, which exceed its natural capacity for self-purification. This situation has profound implications for public health and the economy. Water contaminated with pathogenic bacteria is classified as unsafe for consumption and poses a serious risk to human health[5] [9].

Access to safe and high-quality drinking water is essential for human survival. The physical, chemical, and biological properties of water significantly influence its impact on health. Unprotected water sources are vulnerable to contamination by microbes, often introduced through rainfall runoff, agricultural activities, sewage infiltration, or fecal deposits from wildlife. Such contamination renders the water unsafe for human consumption. A primary source of microbial contamination is fecal waste from warm-blooded animals, including humans. While some bacteria are harmless, others, such as *Escherichia coli*, *Salmonella sp.*, *Shigella spp.*, *Bacillus spp.*, *Pseudomonas spp.*, *Streptococcus spp.*, and *Vibrio spp.*, are pathogenic and can cause diseases like diarrhea, enteric fever, dysentery, and other serious illnesses[3; 10].

Water is considered unsafe for consumption when it contains harmful microorganisms. The bacteriological safety of water is typically assessed by detecting coliform bacteria, which serve as indicators of fecal contamination. Infants, immunocompromised individuals, and others with vulnerable health conditions are particularly at risk of infection from contaminated water, emphasizing the importance of proper water treatment[12]. Bacteria such as *Escherichia coli*, *Salmonella* sp., *Shigella* spp., *Bacillus* spp., *Pseudomonas* spp., *Streptococcus* spp., and *Vibrio* spp. are known to cause diseases like diarrhea, enteric fever, dysentery, and other serious illnesses[14].

In recent years, the presence of antibiotic-resistant bacteria (ARB) in treated and untreated drinking water has garnered growing attention, highlighting an emerging public health concern. This study aims to isolate and identify pathogenic bacteria from untreated water samples collected from various water stations in Qalyubiya Governorate, Egypt—specifically El-Filal station, El-Haras station, Bata station, and Qalyub station. The research seeks to evaluate the microbiological quality of untreated commercial drinking water and provide insight into potential health risks.

2. Material and Methods:

2.1. Study Location and Sample Collection

The study was conducted in Qalubiya Governorate, Egypt. Untreated water samples were collected from four different water stations: El-Filal, El-Haras, Bata, and Qalyub stations.

2.2. Bacterial isolates and selection:

Bacterial isolates were obtained using the serial dilution and agar streaking methods. The diluted water samples were plated onto nutrient agar, which served as the standard medium for observing growth and colonial characteristics. Blood agar was also used for isolating specific bacterial types. The plates were incubated at 37°C for 24 hours under both aerobic and anaerobic conditions.

Following incubation, bacterial colonies were purified through repeated inoculation onto various selective media. After further incubation, colonies from different samples were selected for primary identification based on their morphological and biochemical characteristics.

2.3. Morphological and Biochemical identification:

Bacterial isolates were grown on nutrient agar, blood agar, MacConkey agar and Mannitol salt agar. After 24 hours of incubation, the pure cultures were Gram-stained and examined microscopically. The cultures were then inoculated into slants for further identification. Isolates preserved on slants were selected for identification using conventional biochemical methods described earlier[(4)].

Biochemical characterizations were performed and included the following tests: Catalase activity, Slide and tube coagulase tests, Cytochrome oxidase test, Carbohydrate fermentation, Nitrate reduction test, Methyl Red (MR) test, Indole production test, Voges-Proskauer (V-P) test (using glucose-peptone medium and glucose-salt medium), Citrate utilization test (using citrate utilization medium), Urease production test (using

urease production medium), and Motility test.

2.4. Antibiotic Susceptibility Testing:

The antibiotic susceptibility of bacterial isolates was determined using the Kirby-Bauer disk diffusion method following the Clinical and Laboratory Standards Institute (CLSI) guidelines. Briefly, overnight bacterial cultures were prepared in nutrient broth and adjusted to a turbidity equivalent to 0.5 McFarland standard. Mueller-Hinton agar plates (15 mL per plate) were poured, allowed to solidify, and surface-dried at 37°C for 30 minutes.

Five hundred microliters of the standardized bacterial suspension were spread evenly onto the surface of the dried agar plates using a sterile glass spreader. The inoculum was allowed to absorb into the agar for 10 minutes before placing antibiotic disks on the agar surface. Fifteen antibiotic disks from various classes (obtained from Sigma-Aldrich, Germany) were used for testing. The plates were incubated at 37°C for 24 hours under aerobic conditions. Following incubation, the zones of inhibition were measured in millimeters (mm) using a calibrated ruler. The results were interpreted according to CLSI criteria to determine the susceptibility or resistance of the isolates to each antibiotic.

2.5. Automated Identification using VITEK2 compact system:

The bacterial isolates were identified using the VITEK 2 Compact system (bioMérieux, France), an automated microbial identification platform. This system uses colorimetric reagent cards that assess biochemical and metabolic activities of microorganisms. Pure bacterial cultures were prepared by inoculating isolates onto nutrient agar and incubating them at 37°C for 24 hours. Colonies from these cultures were suspended in sterile saline to achieve the required turbidity, as specified by the manufacturer's protocol.

The prepared suspensions were loaded into reagent cards specific for bacterial identification, which were inserted into the VITEK 2 Compact instrument. The system automatically incubates the cards, measures biochemical reactions at defined intervals, and interprets the results using an integrated database. This approach ensures high-throughput and accurate identification of bacterial species based on their metabolic profiles.

3. Results

3.1. Bacterial isolation and identification:

A total of 35 bacterial isolates were isolated from different water samples which were collected from four water stations in Qalyubiya Governorate: El-Filal, El-Haras, Bata, and Qalyub stations. The distribution of bacterial isolates was as follows: 13 isolates from El-Filal station (37.1%), 7 isolates from El-Haras station (20.0%), 10 isolates from Bata station (28.6%), and 5 isolates from Qalyub station (14.3%) **(Table 1)**.

Table (1): Number of bacterial isolates and its Location

No.	Sample source	Number of Bacterial isolates	Percentage
1	El-Filal station	13	37.1%
2	El-Haras station	7	20%
3	Bata station	10	28.6%
4	Qalyub station	5	14.3%
Total		35	100%

Bacterial isolates were obtained from water samples and cultured on various media. All isolates grew successfully on nutrient agar and blood agar. Additionally, 20 out of 35 isolates grew on MacConkey agar, while 15 isolates were able to grow on Mannitol salt agar **(Table 2)**. Based on Gram staining, 20 isolates were identified as Gram-negative, while the remaining isolates were Gram-positive **(Table 3)**.

Table (2): Primary identification of bacterial isolates

Specimen Code	Nutrient Agar	Blood Agar	MacConky Agar	Manitol Agar	Gram Stain	KOH Test
SARA 1	+Ve	+Ve	-Ve	+Ve	+Ve	-Ve
SARA 2	+Ve	+Ve	+Ve	-Ve	-Ve	+Ve
SARA 3	+Ve	+Ve	-Ve	+Ve	+Ve	-Ve
SARA 4	+Ve	+Ve	-Ve	+Ve	+Ve	-Ve
SARA 5	+Ve	+Ve	+Ve	-Ve	-Ve	+Ve
SARA 6	+Ve	+Ve	+Ve	-Ve	-Ve	+Ve
SARA 7	+Ve	+Ve	+Ve	-Ve	-Ve	+Ve
SARA 8	+Ve	+Ve	-Ve	+Ve	+Ve	-Ve
SARA 9	+Ve	+Ve	-Ve	+Ve	+Ve	-Ve
SARA 10	+Ve	+Ve	+Ve	-Ve	-Ve	+Ve
SARA 11	+Ve	+Ve	+Ve	-Ve	-Ve	+Ve
SARA 12	+Ve	+Ve	-Ve	+Ve	+Ve	-Ve
SARA 13	+Ve	+Ve	+Ve	-Ve	-Ve	+Ve
SARA 14	+Ve	+Ve	-Ve	+Ve	+Ve	-Ve
SARA 15	+Ve	+Ve	+Ve	-Ve	-Ve	+Ve
SARA 16	+Ve	+Ve	-Ve	+Ve	+Ve	-Ve
SARA 17	+Ve	+Ve	+Ve	-Ve	-Ve	+Ve
SARA 18	+Ve	+Ve	+Ve	-Ve	-Ve	+Ve
SARA 19	+Ve	+Ve	+Ve	-Ve	-Ve	+Ve
SARA 20	+Ve	+Ve	+Ve	-Ve	-Ve	+Ve
SARA 21	+Ve	+Ve	-Ve	+Ve	+Ve	-Ve
SARA 22	+Ve	+Ve	-Ve	+Ve	+Ve	-Ve
SARA 23	+Ve	+Ve	+Ve	-Ve	-Ve	+Ve
SARA 24	+Ve	+Ve	+Ve	-Ve	-Ve	+Ve
SARA25	+Ve	+Ve	-Ve	+Ve	+Ve	-Ve
SARA 26	+Ve	+Ve	+Ve	-Ve	-Ve	+Ve
SARA 27	+Ve	+Ve	-Ve	+Ve	+Ve	-Ve
SARA 28	+Ve	+Ve	+Ve	-Ve	-Ve	+Ve
SARA 29	+Ve	+Ve	+Ve	-Ve	-Ve	+Ve
SARA 30	+Ve	+Ve	-Ve	+Ve	+Ve	-Ve
SARA 31	+Ve	+Ve	+Ve	-Ve	-Ve	42.8%+Ve
SARA 32	+Ve	+Ve	+Ve	-Ve	-Ve	+Ve
SARA 33	+Ve	+Ve	-Ve	+Ve	+Ve	-Ve
SARA 34	+Ve	+Ve	+Ve	-Ve	-Ve	+Ve
SARA 35	+Ve	+Ve	-Ve	+Ve	+Ve	-Ve

Table (3): Types of bacterial isolates according to Gram staining

No.	Bacterial Type	Total number	Percentage
1	Gram Positive (G+**Ve)**	15	42.8%
2	Gram Negative (G-**Ve)**	20	57,1%
Total		35	100%

Further characterization and identification of the 35 isolates were conducted using a series of biochemical tests **(Table 4)** along with the motility test. All isolates demonstrated catalase activity, and all but 5 isolates were capable of fermenting carbohydrates. Coagulase activity was detected in 10 isolates, specifically isolates 1, 3, 8, 9, 12, 21, 25, 27, 30, and 33.

Table (4): Secondary identification of bacterial isolates

Test / Code No.	Motility	Catalase	Oxidase	Carbohydr-ate Fermentation	Nitrate Reduction	Methyl Red	Voges Proskour	Indol Production	Citrate Utilization	H2S Production	Ureas Test	Coagulase
SARA 1	-Ve	+Ve	-Ve	+Ve	+Ve	+Ve	+Ve	-Ve	+Ve	-Ve	+Ve	+Ve
SARA 2	+Ve	+Ve	-Ve	+Ve	+Ve	-Ve	+Ve	-Ve	+Ve	-Ve	-Ve	-Ve
SARA 3	-Ve	+Ve	-Ve	+Ve	+Ve	+Ve	+Ve	-Ve	+Ve	-Ve	+Ve	+Ve
SARA 4	-Ve	-Ve	-Ve	+Ve	+Ve	+Ve	+Ve	-Ve	-Ve	-Ve	-Ve	-Ve
SARA 5	-Ve	+Ve	-Ve	+Ve	+Ve	+Ve	-Ve	-Ve	+Ve	-Ve	+Ve	-Ve
SARA 6	-Ve	+Ve	-Ve	-Ve	-Ve	+Ve	-Ve	-Ve	+Ve	-Ve	-Ve	-Ve
SARA 7	-Ve	+Ve	-Ve	+Ve	+Ve	+Ve	-Ve	-Ve	+Ve	-Ve	+Ve	-Ve
SARA 8	-Ve	+Ve	-Ve	+Ve	+Ve	+Ve	+Ve	-Ve	+Ve	-Ve	+Ve	+Ve
SARA 9	-Ve	+Ve	-Ve	+Ve	+Ve	+Ve	+Ve	-Ve	+Ve	-Ve	+Ve	+Ve
SARA 10	-Ve	+Ve	-Ve	+Ve	+Ve	+Ve	-Ve	-Ve	+Ve	-Ve	+Ve	-Ve
SARA 11	+Ve	+Ve	-Ve	+Ve	+Ve	+Ve	-Ve	+Ve	-Ve	-Ve	-Ve	-Ve
SARA 12	-Ve	+Ve	-Ve	+Ve	+Ve	+Ve	+Ve	-Ve	+Ve	-Ve	+Ve	+Ve
SARA 13	-Ve	+Ve	-Ve	-Ve	-Ve	+Ve	-Ve	-Ve	+Ve	-Ve	-Ve	-Ve
SARA 14	-Ve	+Ve	-Ve	+Ve	+Ve	+Ve	+Ve	-Ve	+Ve	-Ve	+Ve	-Ve
SARA 15	-Ve	+Ve	-Ve	-Ve	-Ve	+Ve	-Ve	-Ve	+Ve	-Ve	-Ve	-Ve
SARA 16	-Ve	-Ve	-Ve	+Ve	+Ve	+Ve	+Ve	-Ve	-Ve	-Ve	-Ve	-Ve
SARA 17	+Ve	+Ve	-Ve	+Ve	+Ve	+Ve	-Ve	+Ve	-Ve	-Ve	-Ve	-Ve
SARA 18	+Ve	+Ve	-Ve	+Ve	+Ve	+Ve	-Ve	+Ve	-Ve	-Ve	-Ve	-Ve
SARA 19	+Ve	+Ve	-Ve	+Ve	+Ve	+Ve	-Ve	+Ve	-Ve	-Ve	-Ve	-Ve
SARA 20	+Ve	+Ve	-Ve	+Ve	+Ve	+Ve	-Ve	+Ve	-Ve	-Ve	-Ve	-Ve
SARA 21	-Ve	+Ve	-Ve	+Ve	+Ve	+Ve	+Ve	-Ve	+Ve	-Ve	+Ve	+Ve
SARA 22	-Ve	+Ve	-Ve	+Ve	+Ve	+Ve	+Ve	-Ve	+Ve	-Ve	+Ve	-Ve
SARA 23	-Ve	+Ve	-Ve	+Ve	+Ve	+Ve	-Ve	-Ve	+Ve	-Ve	+Ve	-Ve
SARA 24	-Ve	+Ve	-Ve	-Ve	-Ve	+Ve	-Ve	-Ve	+Ve	-Ve	-Ve	-Ve
SARA25	-Ve	+Ve	-Ve	+Ve	+Ve	+Ve	+Ve	-Ve	+Ve	-Ve	+Ve	+Ve
SARA 26	+Ve	+Ve	-Ve	+Ve	+Ve	+Ve	-Ve	+Ve	-Ve	-Ve	-Ve	-Ve
SARA 27	-Ve	+Ve	-Ve	+Ve	+Ve	+Ve	+Ve	-Ve	+Ve	-Ve	+Ve	+Ve
SARA 28	+Ve	+Ve	-Ve	+Ve	+Ve	+Ve	-Ve	+Ve	-Ve	-Ve	-Ve	-Ve
SARA 29	-Ve	+Ve	-Ve	-Ve	-Ve	+Ve	-Ve	-Ve	+Ve	-Ve	-Ve	-Ve
SARA 30	-Ve	+Ve	-Ve	+Ve	+Ve	+Ve	+Ve	-Ve	+Ve	-Ve	+Ve	+Ve
SARA 31	-Ve	+Ve	-Ve	+Ve	+Ve	+Ve	-Ve	-Ve	+Ve	-Ve	+Ve	-Ve
SARA 32	-Ve	+Ve	-Ve	+Ve	+Ve	+Ve	-Ve	-Ve	+Ve	-Ve	+Ve	-Ve
SARA 33	-Ve	+Ve	-Ve	+Ve	+Ve	+Ve	+Ve	-Ve	+Ve	-Ve	+Ve	+Ve
SARA 34	-Ve	+Ve	-Ve	+Ve	+Ve	+Ve	-Ve	-Ve	+Ve	-Ve	+Ve	-Ve
SARA 35	-Ve	+Ve	-Ve	+Ve	+Ve	+Ve	+Ve	-Ve	+Ve	-Ve	+Ve	-Ve

3.2. Antibiotic susceptibility:

The antibiotic susceptibility of purified bacterial isolates was evaluated using 15 antibiotics from different classes. Among the Gram-negative isolates, three (SARA 2, SARA 11, and SARA 23) exhibited resistance to all tested antibiotics **(Table 5)**. In contrast, among the Gram-positive isolates, only one isolate (SARA 27) demonstrated complete resistance to all antibiotics **(Table 6)**.Overall, four isolates (SARA 2, SARA 11, SARA 23, and SARA 27) were identified as the most antibiotic-resistant strains, showing complete resistance to all applied antibiotics.

Table (5): Susceptibility of Gram Negative Isolates to Antibiotics.

.AB / Code No.	Tigecyclin	Imipenam	Cefotaxime	Cefuroxime	Amikacin	Levofloxacin	Colistine	Trimethoprime/ sulfomethoxazol	Meropenam	Pipracillin/Tazo bactam	Ceftazidime	Amoxacillin/ Clavulanic acid	Cefepime	Aztreonam	Ertapenem
SARA 2	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
SARA 5	R	R	R	R	R	R	S	R	R	R	R	S	R	R	R
SARA 6	I	S	R	R	S	R	S	R	S	R	R	I	R	R	R
SARA 7	R	I	R	R	R	R	S	R	R	R	R	S	R	I	R
SARA 10	R	S	I	R	S	R	I	S	S	R	R	R	S	I	I
SARA 11	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
SARA 13	I	R	R	R	R	R	R	I	R	R	R	R	R	R	R
SARA 15	R	R	R	R	R	R	S	R	R	S	R	R	R	S	R
SARA 17	R	S	I	R	S	R	I	S	S	R	R	R	S	I	I
SARA 18	S	S	R	R	S	I	S	S	S	I	R	S	S	R	R
SARA 19	R	S	R	R	S	R	I	R	S	R	R	I	R	R	S
SARA 20	R	I	I	R	I	R	I	S	S	R	R	R	S	R	R
SARA 23	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
SARA 24	R	R	R	R	S	R	S	S	S	S	I	I	I	R	S
SARA 26	R	R	R	R	S	I	S	R	R	I	S	S	S	I	S
SARA 28	R	S	R	R	S	R	I	S	S	S	R	I	I	R	S
SARA 29	R	R	R	R	S	R	S	S	S	S	I	I	I	R	S
SARA 31	R	R	R	R	R	R	S	R	R	R	S	R	R	S	R
SARA 32	R	S	I	R	S	I	S	R	S	R	S	R	R	S	R
SARA 34	R	S	R	R	R	R	S	R	R	R	R	R	R	R	R

(R=Resistance, I=Intermediate, S=Sensitive)

Table (6): Susceptibility of Gram Positive Isolates to Antibiotics.

AB / Code No	Trimethoprime/ sulfomethoxazole	Meropenam	Pipracillin/Tazobactam	Cefepime	Ciprofloxacin	Cefoxitin	Oxicillin	Linzolid	Erythromycin	Azithromycin	Vancomycin	Gentamycin	Tigecyclin	Tetracycline	Clindamycin
SARA 1	R	**S**	S	**S**	**R**	**S**	**R**	S	**R**	**R**	**S**	**I**	**R**	**R**	**R**
SARA 3	R	**S**	S	**S**	**R**	**I**	**S**	S	**R**	**R**	**S**	**S**	**S**	**I**	**R**
SARA 4	S	**R**	R	**R**	**R**	**S**	**R**	S	**R**	**R**	**I**	**I**	**R**	**I**	**R**
SARA 8	S	**S**	S	**S**	**R**	**R**	**R**	S	**R**	**R**	**S**	**I**	**R**	**R**	**R**
SARA 9	S	**R**	**R**	**R**	**R**	**R**	**R**	S	**R**	**I**	**I**	**I**	**R**	**R**	**R**
SARA 12	S	**S**	**R**	**S**	**R**	**I**	**R**	S	**R**	**I**	**I**	**S**	**S**	**I**	**S**
SARA 14	S	**S**	S	**S**	**R**	**R**	**R**	S	**R**	**R**	**S**	**I**	**R**	**R**	**R**
SARA 16	S	**S**	S	**S**	**R**	**R**	**R**	S	**R**	**R**	**S**	**I**	**R**	**R**	**R**
SARA 21	**R**	**S**	**S**	**R**	**R**	**S**	**R**	**S**	**R**	**R**	**S**	**R**	**S**	**R**	**I**
SARA 22	**I**	**S**	**S**	**R**	**R**	**S**	**R**	**S**	**R**	**R**	**S**	**S**	**S**	**R**	**21**
SARA 25	I	**S**	S	**R**	**I**	**S**	**R**	S	R	**R**	**S**	**S**	**S**	**R**	**S**
SARA 27	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**R**	**R**
SARA 30	I	**S**	R	**R**	**R**	**S**	**I**	**I**	I	**I**	**S**	**I**	**S**	**R**	**S**
SARA 33	**I**	**S**	**S**	**R**	**R**	**S**	**R**	**S**	**R**	**R**	**S**	**S**	**S**	**R**	**21**
SARA 35	**I**	S	**R**	**R**	**S**	**S**	**I**	**I**	I	**R**	**S**	**I**	**R**	**R**	**S**

(R=Resistance, I=Intermediate, S=Sensitive)

3.3. Identification of the Highest Multidrug-Resistant Isolates:

Four multidrug-resistant (MDR) isolates—SARA 2, SARA 11, SARA 23, and SARA 27—were identified from untreated water samples collected from El-Filal, El-Haras, Bata, and Qalyub stations. Of these, SARA 27 was the only isolate capable of growing on Mannitol Salt Agar and was Gram-positive, as confirmed by Gram staining.

The remaining three MDR isolates (SARA 2, SARA 11, and SARA 23) were Gram-negative and grew on MacConkey agar. All four isolates exhibited catalase activity **(Table 7)**.

Table (7): Primary identification of(MDR) bacterial isolates.

Isolate Code	Sample source	Manitol salt agar (MSA)	Gram stain	Catalase test	MacConkey Agar
SARA 2	**El-Filal station**	-ve	-ve	+ve	+ve
SARA 11	**El-Haras station**	-ve	-ve	+ve	+ve
SARA 23	**Bata station**	-ve	-ve	+ve	+ve
SARA 27	**Qalyub station**	+ve	+ve	+ve	-ve

The four most potent multidrug-resistant bacterial isolates were further identified biochemically through 14 tests **(Table 8)**. Notably, the coagulase test yielded a positive result only for SARA 27, suggesting its potential pathogenicity. None of the four isolates were able to ferment starch. According to the VITEK 2 Compact System, the high multidrug-resistant isolates were identified as *Escherichia coli*, *Klebsiella pneumoniae*, *Staphylococcus aureus*, and *Enterobacter aerogenes* **(Figure1)**.

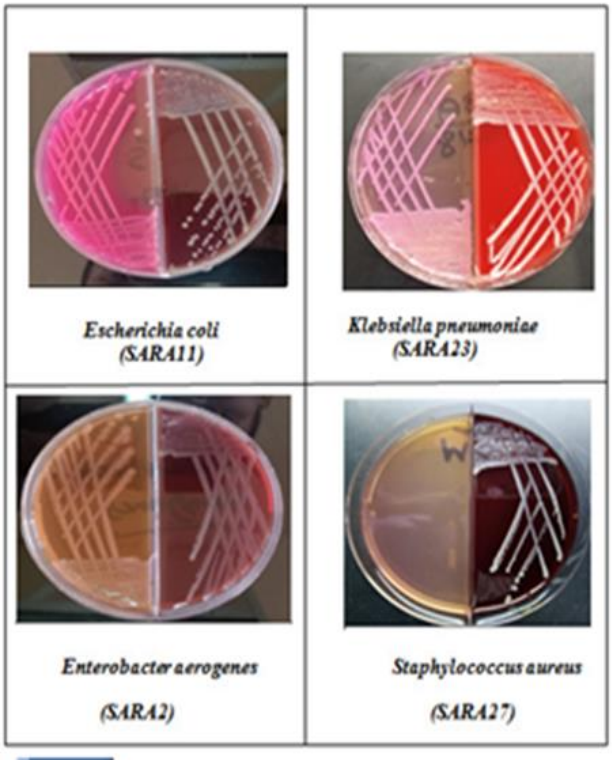

Figure (1): Identified bacterial isolates

Table (8): Biochemical analysis of bacterial isolates

NO	Organism / Tests	SARA 2	SARA 11	SARA 23	SARA 27
1	Catalase	+	+	+	+
2	Oxidase	-	-	-	-
3	Nitrate Reduction	-	+	+	+
4	Methyl Red Test	+	-	+	+
5	Voges Proskour	-	+	-	+
6	Indol Production	-	-	-	-
7	Citrate utilization	+	+	+	+
8	H_2S Production	+	-	-	-
9	Urease production	-	-	+	+
10	Starch Hydrolysis	-	-	-	-
11	GelatinH ydrolysis	+	-	-	+
12	Lipase Test	-	-	-	+
13	Carbohydrates fermentation	+	+	-	-
14	Coagulase test	-	-	-	+

4. Discussion

The primary objective of the present study was to isolate environmental bacterial contaminants from untreated water samples collected from various water stations in Qalyubiya Governorate, Egypt. Numerous studies have documented the presence of pathogenic microorganisms in drinking water and their association with waterborne disease concerns in public health today is antibiotic resistance. The emergence of bacteria that have developed resistance to virtually all commonly used antibiotics poses a significant threat. This resistance not only makes infections more severe and difficult to treat, but also increases healthcare costs. Furthermore, these antibiotic-resistant bacteria are transmissible, contributing to the spread of resistant infections. Preventative measures, such as reducing unnecessary antibiotic prescriptions, adhering to prescribed medication regimens, and practicing good hygiene and infection control, are crucial to combating antibiotic resistance.[10; 15; 18].

In this study, the most frequently isolated bacteria were Gram-negative bacilli and Gram-positive cocci, a finding

consistent with the study by Bhumbla [(1)] which also reported Gram-poci, Gram-positive bacilli, and Gram-negative bacilli as the predominant organisms.

Another key objective of this study was to analyze the antibiotic resistance profiles of the bacterial isolates. Four isolates exhibited resistance to 100% of the tested antibiotics, categorizing them as multidrug-resistant (MDR). These MDR isolates were identified as *Escherichia coli*, *Klebsiella pneumoniae*, *Enterobacter aerogenes*, and *Staphylococcus aureus* using the VITEK 2 Compact System. This is in agreement with the findings of Panneerselvam and Arumugam[(11)] who identified *Escherichia coli* as commonly isolated organisms with similar resistance patterns.

According to Touron et al.[(16)], published a study in the French Seine estuary, where water samples were analyzed for fecal coliforms, *E. coli*, enterococci, and *Clostridium perfringens* spores across nine locations over a nine-year period. Their results showed associations between fecal coliforms, *E. coli*, and enterococci, with significant correlations found near the estuary's mouth, specifically between Salmonella and enterococci counts at Honfleur. Similarly, Wilkes et al.[(17)] conducted a comparative study on the prevalence of pathogenic and indicator bacteria in the surface water of a Canadian river, finding strong correlations between various indicator organisms and pathogens over multiple years of data collection.

The presence of pathogenic microorganisms in untreated water sources poses significant health risks to consumers, especially to vulnerable populations such as infants and immunocompromised individuals. The reduction in bacterial numbers observed in water compared to untreated water can likely be attributed to the treatment process, underscoring the importance of water treatment in safeguarding public health.A better understanding of the ecology and behavior of pathogenic bacteria in environmental water is essential for managing and mitigating health risks. Such knowledge is crucial for directing financial resources toward improving water quality and public health interventions

5. References

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