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# Isolation, Identification and Antibiogram of Bacteria from Imported Frozen Fish at Public Markets in Mosul City, Iraq

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**Abstract**

THE PREVALENCE of infections caused by antibiotic-resistant bacteria is increasing globally. A total of 100 frozen fish samples were randomly obtained from several public markets in Mosul, Iraq. Biochemical assays and the VITEK 2 system were used to analyze the samples and assess the antibiotic resistance patterns of the bacterial species. The study yielded a total of ten genera and thirteen bacterial species, which were identified as *E. coli*, *Citrobacter braakii, Citrobacter freundii*, *Staphylococcus aureus*, *Enterobacter aerogenes*, *Enterobacter cloacae* complex, *Aeromonas spp*., *Leuconostic citreum*, *Enterococcus durans*, *Pseudomonas spp*., *Klebsiella spp*. and *Proteus mirabilis*. There was a total of 108 isolates. *Escherichia coli* was the most often isolated bacterium, accounting for 48.1% of the isolates. *Citrobacter spp*. was the second most common, with a frequency of 24.0%. The least frequent isolates were *Leuconostic citreum*, *Enterococcus durans*, *Pseudomonas spp*., *Klebsiella spp*., and *Proteus mirabilis*, each accounting for 1.9% of the isolates. The VITEK 2 system as used to conduct an antibiotic sensitivity test. The bacterial isolates that were examined exhibited different levels of resistance to sixteen drugs. *Pseudomonas spp*. exhibited total resistance (100%) to fourteen antibiotics, whilst *Klebsiella spp* shown full resistance to around six medicines. *Enterobacter spp*, on the other hand, showed varied degrees of resistance to most of the antibiotics tested. However, *E. coli* and all other bacterial species that were examined exhibited varying rates of resistance. Ciprofloxacin had the highest efficacy against the studied bacteria, although the effectiveness of the other antibiotics varied depending on the bacterial species. All of the isolates exhibited multidrug resistance, meaning they were resistant to a minimum of three or more drug classes that were examined. *Aeromonas spp* ad a MAR value of 0.2, whereas the other bacteria tested had MAR values ranging from 0.3 to 0.8.

**Keywords:** Bacteria, MDR, MAR, Frozen fish. Antibiotics.

## Introduction

Fish is an influential source of excellent quality proteins for human beings [1]. There has been a growth in the demand for such adequate quality protein over the last decade worldwide [2]. It contributes nearly 60% of the world's outfit of protein and about two-thirds of the growing world originates from extra than 30% of their every year protein from fish [3]. In tropical countries, any shortfall in fish availability will affect the animal protein consumption of human beings [4].

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Microbiologically speaking, fish and associated items provide a possible risk to human health due to their ability to host significant pathogenic microorganisms either inside or externally. Bacterial infections may arise from incorrect handling and eating of inadequately cooked seafood. Diverse bacterial genera such as *Escherichia, Pseudomonas*, *Klebsiella,* and *Salmonella* have been proposed as contaminants of fish and can point out multi-sourced pollution [5,6]. The majority of populations get infections via direct contact with water or other components of the fish's habitat. The occurrence of bacterial infections is significantly influenced by the physiological state of the individual consuming them. For instance, individuals who have weakened immune systems or are under significant stress are very vulnerable to opportunistic infections. This is seen in patients who have HIV and AIDS [7].

Antibiotic-resistant bacteria are causing an increase in the incidence of illnesses globally [8]. Some bacterial infections, such as salmonellosis, do not necessitate medication; nevertheless, if the disease is aggressive or invasive, antibacterial medications are usually given [8,9]. Furthermore, the excessive use of medications to protect or cure infections in humans and veterinary medicine participates in the accelerated recurrence and spread of AMR [10]. The nonsensical utilization of antibacterial is associated to multiplied selective pressures on microbial populations as nicely as priorities for the survival and proliferation of resistant bacteria. Antimicrobial resistance is a naturally going on phenomenon, and resistance ratios are saved reasonably low. Grown-up AMU, on the other hand, can cause resistance to increase. Antimicrobial resistance in bacteria derived from the natural environment, which would not be influenced by antibacterial drug selection pressures, is thought for being weak. Despite this, Levy and Marshall [8] argued suggested outgrowing resistant bacteria with sensitive bacteria is a more efficient approach of getting rid of them.

Typically, fish respond to opportunistic microbial invasion as a result of functional imbalance. Pressure determinants such as food deficiency, reduced water quality, and overfilling all have a role in developing of fish bacterial infections. Pathogenic microorganisms are classified as either indigenous or external. *Aeromonas species*, which are prevalent in water in their freshwater environs, are pathogenic bacteria frequent in fish [11]. According to the same source, endogenous bacteria such as *Clostridium, Vibrio, and Aeromonas* are dispersed in aquatic ecosystems in warm tropical areas and estuarial regions. A multitude of variables influence the persistence of *E. coli*, *Salmonella* and *Shigella* bacteria in water, including biological (interaction with other bacteria) and physical elements such as temperature. The presence of indigenous bacteria like as *Salmonella, E. coli*, and *Shigella*. *coli*, and *Shigella dysenteriae* in fishes is routinely a consequence of faecal contamination. As a result, it has been strongly advised that programmers to monitor antimicrobial medication use the prevalence of antimicrobial resistance in animals and humans be created [12]. This has been done in certain nations; however, a key hurdle has been a lack of consultation and consistency, both across time and across borders, confusing comparisons. The prevalence of antimicrobial resistance among bacteria from animals has piqued the public's interest due to the possibility of resistant harmful and commensal bacteria are transferred to the human population [13]. The protection of eating fish from the casual market has no longer been established. As a result, there is a want to observe and analyze the viable danger to human fitness furnished by means of consuming fish from the casual market [14].

The reason of the present study used to be isolation and identification bacterial contaminants from fish at the local casual market in Mosul city, Iraq, as properly as to determine the antimicrobial resistance patterns of the contaminating microorganism towards sixteen antibiotics.

## Material and Methods

### Study Design and Sample Collection

The current investigation was conducted as a cross-sectional study, where in samples were randomly obtained from various public marketplaces in Mosul city, Iraq, spanning from 1st September to mid-December 2021. One hundred fish samples were gathered in a random manner. A total of twenty fish samples were obtained on the initial visit, and this process was repeated five times. Fish were purchased from marketplaces and gathered in sterile plastic bags labelled with IDs derived from the site of collection. The collected samples were promptly sent to the microbiology laboratory at Mosul University's College of Science for cultivating and isolating bacteria using primary culture media on the same day

they were collected. Mosul is an urban area characterized by a high population density and a significant presence of informal marketplaces and stores.

**Preparation of Samples and Isolation of Bacteria**

A total of twenty grams of fish was sliced into little pieces and then put in a vial that was labelled and filled with peptone water and buffered peptone water. The little fragments were standardized. The peptone water was streaked over mannitol salt, MacConkey, chocolate, and blood agars using a sterile loop. The plates with streaks were subjected to incubation under both aerobic and anaerobic conditions at a temperature of 37°C for a duration 4 hours [15].

**Morphologic, Biochemical and VITEK 2 Identification of Isolates**

Each individual colony that was found was recognized by analyzing its morphological features, doing Gram staining, and performing biochemical assays, as shown in Figure (1). Additionally, some colonies were further cultivated on selecting differential medium [15]. Subsequently, the VITEK 2 system as used to validate the identity of every purified biochemical test colony. Several biochemical assays, including IMVIC, oxidase, catalase, motility, coagulase, lysine decarboxylase, urease, and triple sugar iron (TSI), as well as several sugar fermentations, were conducted. The negative control consisted of fish and medium that were sterilized using an autoclave and were not infected. The positive controls consisted of five ATCC standard strains: *Staphylococcus aureus* TCC 29213, *Escherichia coli* ATCC 25922, *Klebsiella pneumonia* ATCC 70603, *Citrobacter freundii ATCC 8090, ATCC 8090,* and *Pseudomonas aeruginosa ATCC 27853* [16, 17].

**Antibiotic Resistance Profile**

The antibiotic susceptibility of the isolates was once assessed the use of the Kirby-Bauer disc-diffusion breakpoint assay on Mueller-Hinton agar. Oxoid discs (obtained from Hi-Media, India) have been used, following the recommendations encouraged by way of the Clinical and Laboratory Standards Institute (CLSI, previously recognized as NCCLS) in their 2007 suggestions [18]. In brief, 4-5 well-isolated and purified colonies with identical morphological characteristics were chosen and obtained from a 24-hour incubated bacterial culture and swabbed with a sterile cotton swab [19]. The colonies were transferred to a sterile solution of 0.85% phosphate buffer saline (PBS), and the bacterial colonies were well mixed until the cloudiness resembled that of a tube containing the 0.5 McFarland standard. Another aseptic swab was immersed in PBS, and then pressed against the inner walls of the flask above the liquid surface to eliminate any surplus fluid. Subsequently, the swab was systematically dragged in three distinct orientations over the surface of the Mueller-Hinton agar (MHA) plate, resulting in a consistent and evenly distributed inoculation. The plates that were infected were left undisturbed for a duration of 4-5 minutes, allowing the inoculum to become dry. The user has provided a list of sixteen standard antibiotic discs (Oxoid) with their respective dosages. The antibiotics include piperacillin PIP (100 µg), piperacillin/tazobactam TZP (110 µg), ceftazidime CAZ (30 µg), cefixime CFM (30 µg), aztreonam AZT (30 µg), imipenem IPM (10 µg), meropenem MER (10 µg), amikacin AMK (30 µg), gentamycin GEN (10 µg), netilmicin NET (30 µg), tobramycin TOB (10 µg), ciprofloxacin CIP (5 µg), levofloxacin LEV (5 µg), tetracycline TET (30 µg), and tigecycline TGC (15 µg). The SXT combination of sulfamethoxazole-trimethoprim (25 µg) was applied to labeled infected MHA plates using a disc dispenser. The plates have been then let to stand for a brief duration of time and incubated at 37°C for 24 hours inside 15 minutes of utility [14]. Antibiotic sensitivity was once evaluated by way of measuring the region of inhibition (zone of clearance) from the rear of the plate to the closest mm the use of a calliper.

**Multiple Antibiotic Resistance (MAR) among Bacterial Isolates**

The multiple antibiotic resistance index (MARI) is represented as a/b, where "a" indicates the number of antibiotics to which the isolate was resistant, and "b" indicates the total number of drugs tested against the isolate. If the isolate was treated to sixteen antibiotics and showed tolerance to eight of them, the isolate's index would be calculated as 16/2 or 0.50 [20]. The MAR index was computed for each of the bacterial isolates.

**Data Analysis**

The prevalence rate of bacterial isolates was determined by dividing the number of diagnoses of a specific bacterial species by the total number of identified bacterial species. The resistance rates for each bacterial isolate and antibiotic were determined by dividing the

number of resistant isolates by the total number of isolates examined. The overall resistance rates for each antibiotic were determined by dividing the number of bacteria that showed resistance to the antibiotics by the total number of bacterial isolates that were examined.

## Results and Discussion

### Isolation and Identification of Bacterial Isolates

The total number of bacterial isolates in the present study was 108. Table (1) shows that thirteen bacterial species were isolated and identified, and they were *Escherichia coli*, *Citrobacter braakii*, *Citrobacter freundii*, *Staphylococcus aureus*, *Enterobacter aerogenes*, *Enterobacter cloacae* complex, *Aeromonas spp*., *Leuconostic citreum*, *Enterococcus durans*, *Pseudomonas spp*., *Klebsiella spp*., *CNS, and Proteus mirabilis*. Among them, *Escherichia coli* was isolated most frequently 52 (48.1%), the second was *Citrobacter spp.* 26 (24.0%); as *Citrobacter braakii* 15 (13.9%) and *Citrobacter freundii* 11 (10.1%), followed by *Staphylococcus aureus* 8 (7.4%), *Enterobacter spp*. 7 (6.5%); as *Enterobacter aerogenes* 4 (3.7%), and *Enterobacter cloacae* complex 3 (2.7%), and *Aeromonas spp*. 3 (2.7%). While the least frequent isolates were *Leuconostic citreum, Enterococcus durans, Pseudomonas spp., Klebsiella spp*., CNS, and *Proteus mirabilis*, with 2 (1.9%) for each one.

### Resistance to Antimicrobial agents

The results of the resistance of the tested bacterial species to antimicrobial agents are detailed in Table 2 and figure 2 (A&B). Bacterial isolates appeared to have different resistance proportions towards tested antimicrobials. *Pseudomonas aeruginosa* was the most resistant, as the two isolates showed absolute resistance to 14 antibiotics, while only one of them was resistant to CIP and GEN. *Escherichia coli* had high resistance towards TGC, TZP, and PIP at rates of 96.1%, 80.8%, and 76.9%, respectively, and more than half of its isolates were resistant to NET, TOB, and LEV with a percentage of 63.5%, while all of its isolates were sensitive to CIP. *Klebsiella aerogenes* and *Enterococcus durans* howed 100% resistance to all antibiotics, including NET, TOB, LEV, TET, TGC, and SXT, but only half of the isolates of these two species were resistant to TZP, IPM, MER, and GEN. *Citrobacter spp*. isolates were completely resistant to AZT and TET, while their resistance was very low to PIP, TGC, and MER, and they were resistant to the rest of the antibiotics. All of the *Staphylococcus aureus* isolates were 100% resistant to SXT, and all of them were absolutely sensitive to CIP. Its resistance to other antibiotics is shown in table 2 and figure 2 (A & B). The rest of the tested bacteria in the present study revealed different resistance rates, as in table 2 and figure 2 (A & B). Table 3 explains the MDR of all tested isolates, where all the isolated bacterial species were multidrug resistant (resistant to at least one antimicrobial agent in three or more antimicrobial categories). Table 3 also shows that the MAR indexes of all the isolated bacteria ranged from 0.2 to 0.8. *Citrobacter spp*., *Pseudomonas spp*., and *Klebsiella spp*. have the highest MAR index value of 0.8, followed by *Escherichia coli* with a MAR index value of 0.7, and *Aeromonas spp*. with the lowest MAR index value of 0.2.

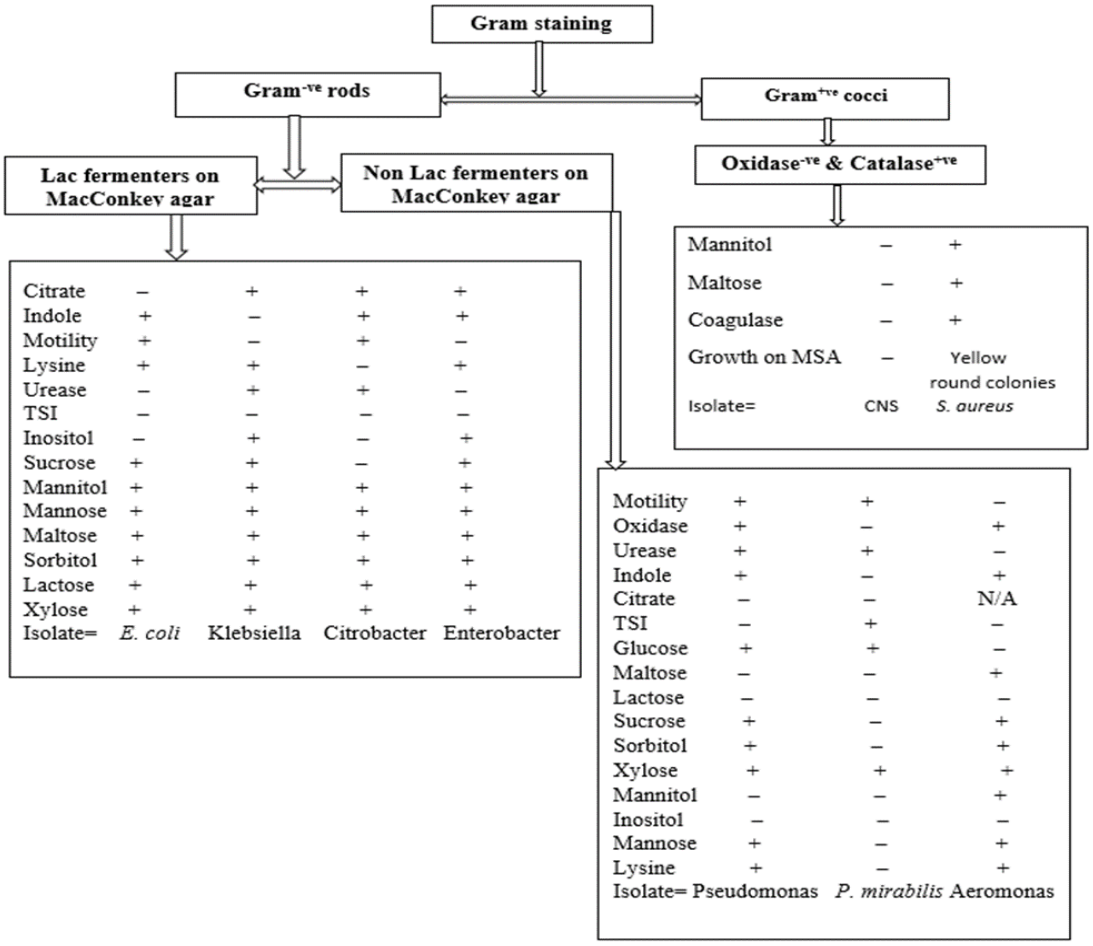


**Fig.1. Morphological and biochemical identification flow diagram of bacterial isolates.**

**TABLE 1. Prevalence rates of bacterial isolates.**

| Bacterial Isolates | Number | % |
|---|---|---|
| *Escherichia coli* | 52 | 48.1 |
| *Citrobacter braakii* | 15 | 13.9 |
| *Citrobacter freundii* | 11 | 10.1 |
| *Staph. aureus* | 8 | 7.4 |
| *Enterobacter aerogenes* | 4 | 3.7 |
| *Enterobacter cloacae complex* | 3 | 2.7 |
| *Aeromonas spp.* | 3 | 2.7 |
| *Leuconostic citreum* | 2 | 1.9 |
| *Enterococcus durans* | 2 | 1.9 |
| *Pseudomonas spp.* | 2 | 1.9 |
| *Klebsiella spp.* | 2 | 1.9 |
| *Proteus spp.* | 2 | 1.9 |
| *CNS* | 2 | 1.9 |
| **Total** | **108** | **100** |

**TABLE 2. Antibiotics resistance rates of bacterial isolates.**

| Bacterial isolates | PIP | TZP | CAZ | CFM | AZT | IPM | MER | AMK |
|---|---|---|---|---|---|---|---|---|
| *Escherichia coli* | 76.9 | 80.8 | 7.7 | 7.7 | 7.7 | 9.6 | 11.5 | 9.6 |
| *Citrobacter spp.* | 7.7 | 76.9 | 15.4 | 11.5 | 100 | 11.5 | 7.7 | 19.2 |
| *Staph. Aureus* | 37.5 | 37.5 | 37.5 | 37.5 | 37.5 | 37.5 | 37.5 | 50.0 |
| *Enterobacter spp.* | 42.9 | 71.4 | 42.9 | 100 | 100 | 71.4 | 71.4 | 85.7 |
| *Aeromonas spp.* | 0.0 | 33.3 | 0.0 | 0.0 | 33.3 | 33.3 | 33.3 | 33.3 |
| *Leuconostic citreum* | 0.0 | 0.0 | 0.0 | 50.0 | 50.0 | 50.0 | 0.0 | 50.0 |
| *Enterococcus durans* | 0.0 | 50.0 | 0.0 | 0.0 | 0.0 | 50.0 | 50.0 | 0.0 |
| *Pseudomonas spp.* | 100 | 100 | 100 | 100 | 100 | 100 | 100 | 100 |
| *Klebsiella spp.* | 0.0 | 50.0 | 0.0 | 0.0 | 0.0 | 50.0 | 50.0 | 0.0 |
| *Proteus spp.* | 50.0 | 0.0 | 50.0 | 50.0 | 50.0 | 50.0 | 50.0 | 0.0 |
| *CNS* | 0.0 | 0.0 | 50.0 | 0.0 | 0.0 | 0.0 | 0.0 | 50.0 |

| Bacterial isolates | GEN | NET | TOB | CIP | LEV | TET | TGC | SXT |
|---|---|---|---|---|---|---|---|---|
| *Escherichia coli* | 19.2 | 63.5 | 63.5 | 0.0 | 63.5 | 17.3 | 96.1 | 26.9 |
| *Citrobacter spp.* | 42.3 | 23.1 | 26.9 | 23.1 | 19.2 | 100 | 7.7 | 11.5 |
| *Staph. Aureus* | 25.0 | 37.5 | 37.5 | 0.0 | 37.5 | 50.0 | 37.5 | 100 |
| *Enterobacter spp.* | 28.5 | 42.9 | 85.7 | 14.2 | 42.9 | 85.7 | 85.7 | 65.7 |
| *Aeromonas spp.* | 33.3 | 33.3 | 33.3 | 0.0 | 33.3 | 33.3 | 33.3 | 33.3 |
| *Leuconostic citreum* | 50.0 | 0.0 | 0.0 | 0.0 | 0.0 | 100 | 100 | 100 |
| *Enterococcus durans* | 50.0 | 100 | 100 | 0.0 | 100 | 100 | 100 | 100 |
| *Pseudomonas spp.* | 50.0 | 100 | 100 | 50.0 | 100 | 100 | 100 | 100 |
| *Klebsiella spp.* | 50.0 | 100 | 100 | 0.0 | 100 | 100 | 100 | 100 |
| *Proteus spp.* | 0.0 | 0.0 | 50.0 | 0.0 | 0.0 | 50.0 | 50.0 | 50.0 |
| *CNS* | 50.0 | 50.0 | 50.0 | 0.0 | 50.0 | 50.0 | 50.0 | 50.0 |

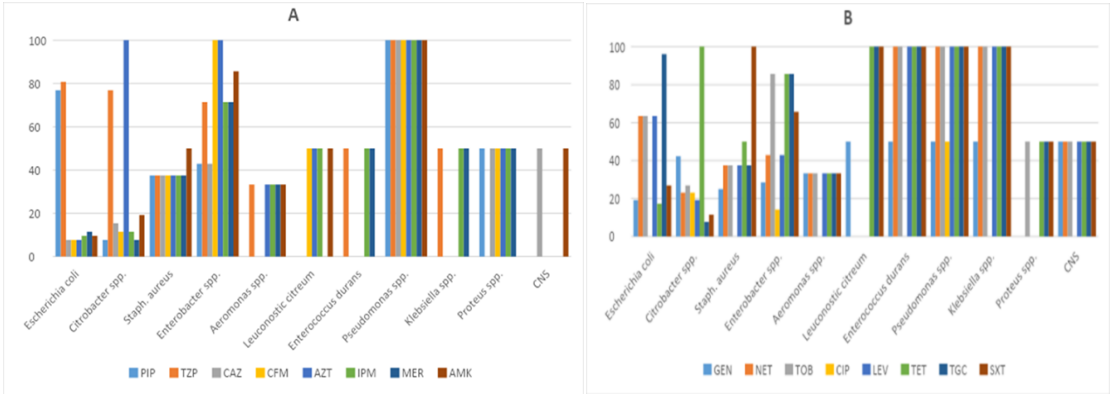


**Fig. 2 (A & B). Antibiotics resistance rates of bacterial isolates**

**TABLE 3. Multiple drug resistance (MDR) and multiple antibiotic resistance (MAR) index of bacterial isolates.**

| Bacterial isolates | Number of tested bacteria | No. of MDR of each bacterial species | % of MDR of each bacterial species | Overall MAR Index |
|---|---|---|---|---|
| *Escherichia coli* | **52** | **40** | **76.9** | **0.7** |
| *Citrobacter spp.* | **26** | **18** | **69.2** | **0.8** |
| *Staph. Aureus* | **8** | **4** | **50.0** | **0.5** |
| *Enterobacter spp.* | **7** | **6** | **85.7** | **0.6** |
| *Aeromonas spp.* | **3** | **1** | **33.3** | **0.2** |
| *Leuconostic citreum* | **2** | **1** | **50.0** | **0.5** |
| *Enterococcus durans* | **2** | **2** | **100** | **0.6** |
| *Pseudomonas spp.* | **2** | **2** | **100** | **0.8** |
| *Klebsiella spp.* | **2** | **2** | **100** | **0.8** |
| *Proteus spp.* | **2** | **1** | **50.0** | **0.3** |
| *CNS* | **2** | **1** | **50.0** | **0.3** |

## Discussion

Fish is a popular food item in international trade, but it spoils quickly, especially when storage facilities are limited. It is well known as an excellent source of protein and other nutrients essential for maintaining a healthy body [21]. The presence of microorganisms in frozen fish was investigated. According to the findings of this investigation, frozen fish offered on the market has a significant level of contamination. Possible causes for this phenomenon include temperature preferences of certain organisms, inadequate personal hygiene practices by the fish handler, consumption of contaminated water by the fish, which may contain fecal matter in their environment, leading to the presence of enteric organisms like *E. coli*, as well as other microorganisms such as *Staphylococcus aureus*, which can produce harmful substances when consumed by humans. This is in accordance with a previous study by [22], on the bacteriological and chemical features of rural water sources, as well as an earlier one by [23], both studies discovered significant levels of coliform bacteria in the water ecosystem, which may explain the presence of *E. coli* in the fish examined. It is crucial to note that water samples with high coliform levels and viable bacterial counts are not safe for human consumption. In addition to harmful enteric pathogens, this investigation also identified *Staphylococcus aureus*, a well-known producer of enterotoxins and a hazardous microorganism. These findings align with previous research [24 , 25].

The most common isolates were *E. coli*, *Citrobacter spp*., *Enterobacter spp.*, *Enterococcus durans*, *Klebsiella spp.,* and *Proteus mirabilis*, which were all isolated from randomly chosen fish. Similar organisms were identified in fish and fish products by [26,27]. According to [28], the microbiological quality of the tilapia suggested that all tissue samples were infected with fecal coliform except muscle tissues. The most prevalent contamination is *E. coli* which is frequently found in large numbers. Some additional researchers looked at the existence of *E. coli* and Vero toxigenic *E. coli* O157:H7 in fish meal [29,30]. *Pseudomonas spp*. was isolated from the fish samples obtained from the two locations in this investigation. The recovery of *Pseudomonas spp*. from fish samples is critical since this bacterium serves as a possible pathogenic bacterium for humans as well as a food quality indicator as a rotting organism. This is in line with what [27,31] earlier stated, who found pseudomonads as an useful spoiling index.

Cross-contamination from the environment, source, and seller's handling might all be factors in the presence of contaminating bacteria in sea foods [32]. The microbes identified in this study are comparable to those reported in numerous studies like [33-36]. It was observed that the organisms identified from frozen indicate a significant degree of contamination in the water body where these fish were collected, implying that the body of water is contaminated with bacteria. The isolates collected in this work are comparable to those described in [37] prior work on frozen fish, which included *Escherichia coli, and Staphylococcus spp.*

The microbial composition of fish is determined by the microbial levels present in the water they inhabit. The skin and internal organs of recently captured, healthy fish from tropical and temperate waters are often devoid of microorganisms. This is due to the presence of scales and slime on the fish, which serve as natural barriers preventing the entrance of microbes [37]. Although there is no epidemiological evidence of a foodborne illness epidemic, there are signs that foods may be contaminated with high levels of air flora and other microbes at the point of consumption. This contamination may occur from handlers, equipment/utensils, and raw food ingredients [38]. To assure acceptable levels of contamination and minimize the negative human health effects of food borne disease, effective hygiene management through bacteriological testing is essential [39]. Food handlers and retailers that offer these goods to the public for ingestion may, however, contaminate the fish [40].

Antibiotic resistance in fish pathogenic bacteria is relevant because it may reveal the extent to which anthropogenic activities have altered water ecosystems. Water bacteria might be native to aquatic settings or exogenous, i.e., bacteria that have been shed from animal, vegetal, or soil surfaces and are present in the water on a temporary basis. The isolates' antibiotic resistance can be attributed to the extensive utilization of these compounds in aquaculture, particularly those that are non-biodegradable. This practice intensifies the selective pressure on antibiotics in water, facilitating the transmission of antibiotic-resistant traits among aquatic bacteria, including those that are harmful to fish and humans. Additionally, it permits the persistence of residual antibiotics in commercially available fish and shellfish products [41,42]. The isolates that were discovered exhibited resistance to many antibiotics that were used. Several antibiotics shown greater efficacy compared to

others. The antibiotics that shown the most efficacy were ciprofloxacin, piperacillin, and gentamicin, which aligns with the findings of a previous research [5]. The findings of [43] indicated that gentamicin was effective against several of the tested bacteria, which was consistent with the bacterial species examined in the present study. Antimicrobials in waste water are becoming more common, and they may play a key role in the emergence and selection of antimicrobial resistance in the environment [41]. All isolates had a MAR index greater than 0.2, with the exception of *Aeromonas spp*., which had a MAR index of 0.2. Multidrug-resistant bacteria with MAR indices larger than 0.2 are intended to arise from a high-risk source, such as feces, where antibiotics are routinely administered. Antibiotic resistance may have emerged among bacteria as a result of indiscriminate antibiotic usage.

**Conclusion:**

The present study concluded that *E. coli* and *Citrobacter spp.* were the most frequent bacterial species that have isolated from examined one hundred fish samples. All 108 isolates that belong to thirteen bacterial species revealed multidrug resistance of at least three different classes of antibiotics. Ciprofloxacin was the most effective antibiotic against all tested bacteria. *Aeromonas spp*. had a MAR value of 0.2, whereas the other bacteria tested had MAR values ranging from 0.3 to 0.8.

*Conflict interest.* The authors have no conflict interest to be announced.

*Authors' contribution :* Jassim Fatehi Ali: Conception and design of the study, wrote the first draft of the manuscript and design figures. Rawaa Ghanim Mohammed and Semaa F.H. Al-Abedi critically revised the manuscript, funding acquisition.

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## عزل وتشخيص والمضادات الحيوية ضد البكتيريا من الأسماك المجمدة المستوردة في الأسواق العامة في مدينة الموصل، العراق

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**الخلاصة**:

يتزايد انتشار حالات العدوى التي تسببها البكتيريا المقاومة للمضادات الحيوية على مستوى العالم. تم الحصول بشكل عشوائي على 100 عينة من الأسماك المجمدة من عدة أسواق عامة في مدينه الموصل، العراق. تم استخدام الفحوصات البيوكيميائية ونظام VITEK 2 لتحليل العينات وتقييم أنماط مقاومة المضادات الحيوية للأنواع البكتيرية باستخدام نظام2 VITEK .

أسفرت الدراسة عن عشرة أجناس وثلاثة عشر نوعًا بكتيريًا تم تحديدها وهي : *E. coli, Citrobacter braakii*, *Citrobacter freundii, Staphylococcus aureus, Enterobacter aerogenes, Enterobacter cloacae complex, Aeromonas spp., CNS, Leuconostic citreum, Enterococcus durans, Pseudomonas spp., Klebsiella spp. and Proteus mirabilis.* كان هناك ما مجموعه 108 عزلات. كانت E. coli هي البكتيريا الأكثر عزلة، حيث شكلت 48.1% من العزلات *Citrobacter spp*. كان الثاني الأكثر شيوعاوبنسبة 24.0٪. كانت الانواع الأقل شيوعا هي *Leuconostic citreum, Enterococcus durans, Pseudomonas spp*., *Klebsiella spp., and Proteus mirabilis*، حيث شكلت كل منها 1.9% من العزلات.

تم استخدام نظام VITEK 2 لإجراء اختبار الحساسية للمضادات الحيوية. أظهرت العزلات البكتيرية التي تم فحصها مستويات مختلفة من المقاومة لستة عشر دواء. أبدت *Pseudomonas spp*. مقاومة كاملة (100%) لأربعة عشر مضادًا حيويًا، بينما أظهرت *Klebsiella spp*. مقاومة كاملة لستة أدوية. من ناحية أخرى، أظهرت بكتيريا *Enterobacter* درجات متفاوتة من المقاومة لمعظم المضادات الحيوية التي تم اختبارها. ومع ذلك، أظهرت *E. coli* وجميع الأنواع البكتيرية الأخرى التي تم فحصها معدلات مقاومة متفاوتة. كان للسيبروفلوكساسين أعلى فعالية ضد البكتيريا المدروسة، على الرغم من أن فعالية المضادات الحيوية الأخرى تختلف باختلاف الأنواع البكتيرية. أظهرت جميع العزلات مقاومة متعددة للأدوية، مما يعني أنها كانت مقاومة لما لا يقل عن ثلاث فئات أو أكثر من الأدوية التي تم فحصها. بلغت قيمة MAR للنوع *Aeromonas spp.* 0.2. في حين أن البكتيريا الأخرى التي تم اختبارها كانت لها قيم MARتتراوح من 0.3 إلى 0.8.