



Multi-Drug Resistant *Acinetobacter baumannii*; A Neglected Nosocomial Pathogen in the Veterinary Field as a Source of Human Infection



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BACKGROUND: One of the most important global warnings, according to the “World Health Organization (WHO)”, is the danger of multi-drug resistant microorganisms represent to human health. This study is intended to detect the precise *Acinetobacter baumannii* contamination rate in veterinary necessities, the possible method of *A. baumannii* transmission to human patients, and the extent of antibiotic resistance in these bacteria. **Methods:** From various areas in the Duhok governorate, 106 swabs were collected. Conventional microbiological, cultural, real-time PCR and “Vitek 2 system” tests were used to diagnose and confirm the *A. baumannii* isolates. The antimicrobial susceptibility test was performed by the standard disc diffusion method. ERIC PCR was used to determine the genetic similarity and DNA fingerprints of the retrieved isolates. **Results:** The total positive *A. baumannii* isolates were twenty-two samples (20.7%) ,18 (16.98%) were positive from 65 samples from slaughter houses, 2 (1.88%) out of 20 swabs from a private veterinary clinic and 2(1.88%) out of 20 swabs from a governorate veterinary centers). *Acinetobacter baumannii* strains that were isolated from veterinary necessities were genetically linked to some *A. baumannii* strains isolated from human patients (from Duhok Research Center). Moreover, none of the identified isolates were resistant to colistin and piperacillin, despite being multidrug resistant and demonstrating resistance to the most frequently tested antibiotics. **Conclusion:** The present findings suggest that *A. baumannii* resistance is potentially present in veterinary medicine, which requires a prompt and well-thought-out approach to contain the problem.

Keywords: *Acinetobacter baumannii*, Extensively drug-resistant, Genetic diversity, Zoonotic impact, Veterinary.

Introduction

Based on the World Health Organization (WHO), the resistance to antimicrobial drugs is estimated as one of the most serious worldwide warnings that threatening the health of humans [1]. *Acinetobacter baumannii* is one of the most severe multidrug resistant pathogens beside to “*Enterococcus faecium*, *Staphylococcus*

aureus, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, and *Enterobacter*” species that belong to the group that has been abbreviated “ESKAPE” [2]. *A. baumannii* is a dangerous concern among opportunistic bacteria for causing nosocomial and community-acquired infections in both humans [3] and animals [4], mainly due to its diverse antibiotic resistance mechanisms [5]. It

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is particularly concerning that *A. baumannii* has gotten little consideration in veterinary medicine given recent findings showing the existence of identical successful clones in both people and animals [5].

Even though some cases have been recently recorded, the data about *A. baumannii* from animals in veterinary medicine are still rare [6]. Mainly, *A. baumannii* was first labelled as an emerging pathogen in various European veterinary hospitals in 2011 [3]. Additionally, the possibility that animals might serve as a source of *A. baumannii* cannot be ruled out [7].

Acinetobacter baumannii has been isolated from different species of animals. Kimura and his colleagues isolated it from dogs and cats in 2018 from many sites of infection, such as the urinary tract, abscess, otitis, pneumonia, and sepsis [8]. Furthermore, it's also been noted that the incidence of *A. baumannii* in cattle varies within the same species [9]. *A. baumannii* prospective reservoirs are also environments for wildlife and farm birds, with variances in bird species and geographical regions [10]. Livestock poultry products, such as raw meat from turkey, are a source of concern since they may act as a vehicle for multidrug-resistant *A. baumannii* for human infection [11]. In addition, it was isolated from a horse with infection in eyes in Germany by [12].

A. baumannii has been discovered to have a resistance to various antibiotics that are frequently utilized such as penicillins, cephalosporins, carbapenems, and fluoroquinolones. The resistance is commonly caused by the generation of enzymes that break down the antibiotics or through modifications made to the bacterial cell wall, which prevents the antibiotics from accessing their intended targets [13]. Treatment options are also being limited by the introduction of *A. baumannii* strains that are resistant to a variety of antibiotics, even ones thought of as last resort, such as colistin [14]. Also, *A. baumannii* isolates can display a multidrug-resistant (MDR) phenotype by expressing the RND efflux pump, *AdeABC*, at high levels. The *AdeABC* pump is associated with resistance to a diverse range of antibiotics, such as chloramphenicol, tigecycline, macrolides/ lincosamides, beta-lactams, tetracyclines, and aminoglycosides [13].

The finding of *A. baumannii* isolates genotype is a crucial tool for containing the epidemic that has been brought on by this bacterium.

As a result, various DNA fingerprinting methods have been created to quickly and precisely classify *A. baumannii* isolates. To describe *A. baumannii* strains, various molecular genotyping techniques, including ribotyping, PFGE, MLST, and plasmid profiling, have been investigated [15]. Up to this point, much research has described various PCR-based techniques for typing multidrug resistant *A. baumannii*. In general, the ERIC-PCR method is a widely used, simple, and fast fingerprinting technique for identifying *A. baumannii* strains [16].

In this project, it tried for the first time to evaluate the incidence of "*A. baumannii*" contamination in veterinary necessities such as specialized governorate veterinary centers, private veterinary clinics, and slaughter houses in Duhok, Iraq. Also, to determine their rate of resistance to various antibiotics, which are mostly employed for therapeutic purposes in both humans and animals.

Material and Methods

Collection of Samples and Detection of A. baumannii

A total 106 swabs were collected from various veterinary regions in the Duhok governorate (slaughter houses 65, private veterinary clinics 20, and governorate veterinary centers 21). The collected swabs were transported in brain-heart infusion broth (Oxoid, USA), from both necessities and surrounding environments, and enriched by incubation at 37°C for 24 hours. In the "College of Veterinary Medicine microbiology lab", 10 µl of each incubated broth were cultured on CHROMagar™ *Acinetobacter* (CHROMagar, France) for 24 hours at 37°C. After that, the "MacConkey agar" used to differentiate between the fermented and non-fermented lactose colonies. On MacConkey agar, the pale-yellow (non-ferment lactose) colonies were verified to be *A. baumannii* by "VITEK®2 compact system (Bio-Mérieux, France)", depending on the manufacturer's procedure. Finally, all isolates were confirmed by amplification of the 16S-23S ribosomal DNA using applying the Realtime PCR. Then, The bacterial stocks were stored at -20°C using "brain heart infusion broth (Lab M, UK)" that enhanced with 30% glycerol [17].

Bacterial DNA Extraction

DNA extraction was performed based on [18]. A thermal separation technique was used to separate the DNA samples. After that, 200 µl of the supernatant was saved to be used as "PCR

DNA” templates, after the calculation of purity and quantity of all isolated DNA by using a “nanodrop (Thermo Scientific, USA)”.

Molecular Confirmation of A. baumannii

To confirm *A. baumannii* molecularly PCR technique was used by Real-time PCR to amplify the 16S ribosomal DNA using specific primers; “F 5’ CATTATCACGGTAATTAGTG and R 5’ AGAGCACTGTGCACTTAAG” [19]. The qPCR thermocycler (BIO RAD/Germany) was used to set up the amplification protocol as follows: Initial denaturation took place at 95 °C for 3 minutes, then there were 35 cycles of 95 °C for 45 seconds, followed by 45 seconds of annealing at 62 °C, and 45 seconds of extinction at 72 °C [11]. The positive control (*A. baumannii*) and negative control (*K. pneumoniae*) obtained from DRC, University of Duhok. The PCR solution was prepared in 0.2 ml PCR tubes containing a 20 µl volume (10 µl syber qPCR master mix (Addbio/Korea), 1 µl (10 pmol/µl) from each primer, 50–100 ng of sample DNA/µl) and 6 µl of nuclease-free distal water).

Antimicrobial susceptibility testing (AST)

The conventional disc diffusion method was used to evaluate the antimicrobial susceptibility of the confirmed *A. baumannii* isolates against 34 antibiotics on “Mueller-Hinton agar (Lab M, UK),” including erythromycin, aztreonam, clarithromycin, cefotaxime, meropenem, doxycycline, trimethoprim/sulfamethoxazole, levofloxacin, imipenem, gentamycin, norfloxacin, amoxicillin, ciprofloxacin, spiramycin, florfenicol, clindamycin, mecillinam, cefpodoxime, cinoxacin, ceftazidime, ticarcillin, amikacin, piperacillin, ceftazidime, netilmicin, colistin, tetracycline, tobramycin, piperacillin-tazobactam, fosfomycin, cefixime, cefotaxime, ampicillin, and streptomycin. To obtain the best therapeutic approaches that could be employed for both the medical and veterinary sectors, the used antibiotics were selected to cover all the possible therapeutic options. In order to identify the inhibition zone, the method that performed by some researchers [20, 21] was used. The labels “susceptible” and “resistant” were applied to isolates, depending on guidelines from the “Clinical and Laboratory Standards Institute (2015)”, Moreover, samples that were initially sensitive or somewhat resistant to one antibiotic may turn resistant after treatment. Therefore, isolates that intermediately susceptible to antibiotics were classified as resistant. Any isolate used in this investigation that showed

intermediate resistance to a specific antibiotic was considered an antibiotic-resistant isolate [21]. The term “multiple antibiotic resistant” describes to isolates that are resistant to three or more antibiotics, whereas the term “extensively drug resistant” refers to any isolate that is resistant to at least one agent from each antibiotic group but only two or fewer antimicrobials [22].

Clonal Relatedness and Diversity Analysis

For the detection of clonally related strains of *A. baumannii* and identification of variants, “ERIC-PCR” was applied, using specific sequences of universal ERIC primers “(ERIC1: 5’-ATGTAAGCTCCTGGGGATTAC-3’ and ERIC2:5’-AAGTAAGTGACTGGGGTGAGCG-3’)” that previously performed by Ahmed [23]. The technique of ERIC- PCR was achieved in a total volume of 25 µl, comprising 12.5 µl of “hot start master mix” (Addbio, Korea), 2 µl (10 pmol/µl) of each primer, 2 µl (30-100 ng/ µl) of DNA template and 6.5 µl of “nuclease-free water (Addbio, Korea) [17]. The “PCR system 9700 GeneAmp (Applied Biosystems, USA)” was used to perform the ERIC PCR. According to Taha et al.[24], the “PCR cycles” were employed. The PCR setting was start with initial denaturation 94°C for 5 minutes, followed by denaturation at 94°C for 1 minute, annealing for 1 minute at 54°C, then 10 minutes at 72°C extension for the 35 cycles, and the final extension 10 minutes at 72°C. Finally, the products of ERIC PCR were run in agarose at 2% with “1X Tris-acetate-EDTA buffer” and stained with “safe gel satin DNA (Addbio, Korea)”. The DNA marker that used in gel was a 100-base pair DNA ladder “(Genedirex, Taiwan)”.

ERIC-PCR Data Processing

The electrophoresis picture of ERIC PCR products, containing 26 isolates of *A. baumannii* (22 isolates from this study; veterinary sources and 4 from human sources; previously isolated in DRC, University of Duhok) was checked for the existence or absence of DNA bands in the gel, and then the “GelJ software version 2.0 (<https://sourceforge.net/projects/gelj/>)” was used to generate the dendrogram. The “Unweighted Pair Group Method with Arithmetic Mean (UPGMA)” method, which is based on 2% tolerance with the Dice similarity coefficient, was used to produce the strain genotyping. In ERIC-PCR, electrophoresis patterns that shared at least 80% of their similarities “(the limitation of similarity was 80% or above)” were assigned to the same

groups or genotypes [28]. According to sample source (human or veterinary field), the strains were clustered together.

Results

Occurrence of *A. baumannii*

The total 106 swabs (from the slaughter houses, private veterinary clinics, and governorate veterinary centers) from Duhok city were analyzed by cultural microbiological technique and the results confirmed by molecular methods for the detection of *A. baumannii*. Conventionally, *Acinetobacter* spp. isolated by cultural methods, based on appearing red colonies in “chromogenic agar (CHROMagar™ *Acinetobacter*)” (Fig. 1)

and colonies that were non-lactose fermenter in MacConkey agar (Fig. 2), showed that 22 (20.7%) out of 106 samples were positive for *Acinetobacter* spp. “The VITEK®2 compact system (Bio-Mérieux, France) using the Vitek 2 GN ID Card (Gram-Negative Identity Card)” to confirm that all 22 isolates were confirmed to be *A. baumannii*. Finally, “real-time PCR” assay were used to confirm all 22 samples, and it found that all isolates were *A. baumannii* (Fig. 3).

The maximum rate of *A. baumannii* isolation was recorded from slaughter houses 18 (16.98%), while only 2 isolates were detected with a percentage of about 1.88 for each of the private veterinary clinics and governorate veterinary centers (Fig. 4, Table1).

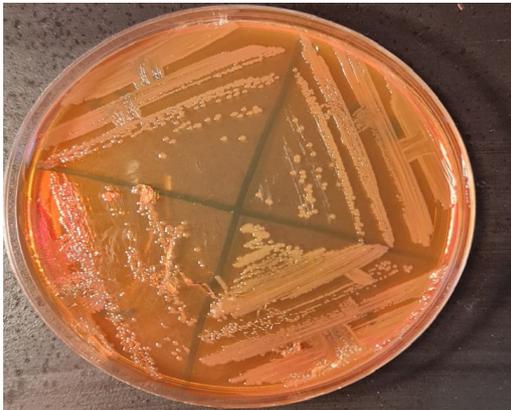


Fig. 2. Show the no lactose fermenter colonies of *A. baumannii* on MacConkey agar.



Fig.1. Show the specific red colonies of *A. baumannii* on CHROMagar™ *Acinetobacter*.

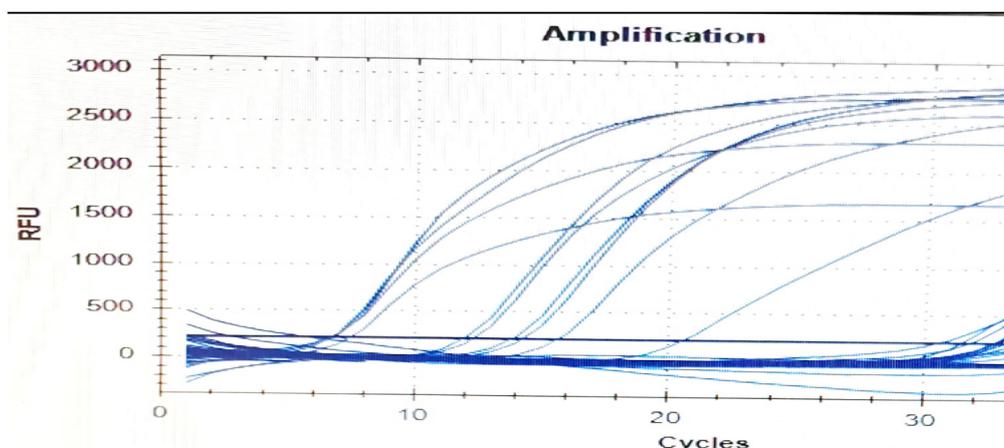
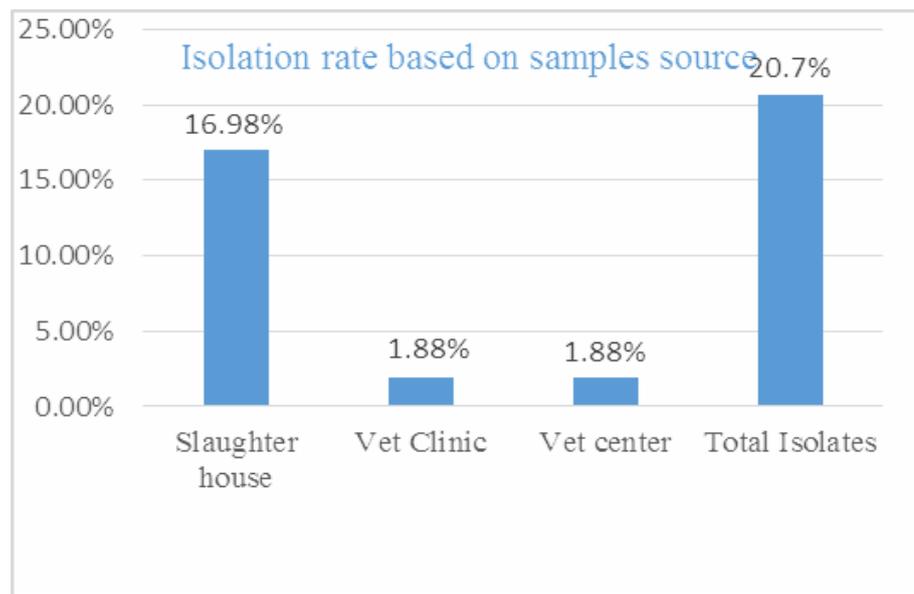


Fig.3. Shows the Real-time PCR amplification of 16S-23S ribosomal DNA in *A. baumannii* isolates. Negative control black arrow and positive control red arrow.

TABLE 1. The incidence rate of *A. baumannii* isolates from different veterinary sectors

	Total samples	Number of isolates	%
Slaughter houses	65	18	16.98
Private Veterinary Clinics	20	2	1.88
Governorate Veterinary Centers	21	2	1.88
Total	106	22	20.74

**Fig. 4. Incidence rate of *A. baumannii* isolated from different sources.**

Antimicrobial susceptibility test

The results of the antimicrobial susceptibility test showed that the twenty-two *A. baumannii* isolates were different in their sensitivity to studied antimicrobials. A total of 34 antibacterial agents were used, as shown in table 3. It is worth mentioning that all isolates were 100% resistant to 17 antibiotics, including erythromycin, aztreonam, cefotaxime, gentamycin, spiramycin, florfenicol, clindamycin, mecillinam, cefpodoxime, cinoxacin, ceftazidime, ticarcillin, ceftazidime, cefixime, cefotaxime, and ampicillin, and all of them were extensively drug resistant. Then the most next antibiotics that have a resistant rate are: Fosfomycin (95.5%), meropenem (90.8%), and clarithromycin (86.4%). In contrast, colistin and piperacillin showed a powerful effect (100% sensitive) on all 22 isolates (Fig. 4 Table2).

Regarding the sample source, isolates from slaughter houses showed a higher resistance rate (81.3%) when compared with other sources, including the governorate veterinary centers (9.8%) and private veterinary clinics (8.9%).

ERIC-PCR genotyping of Acinetobacter baumannii by

The results of ERIC PCR revealed that the *A. baumannii* isolates similarity ranged from 54 to 100% dependent on the size and number of bands and fingerprinting that was seen in each isolate. All of them were clustered into two main clusters (1 and 2), whereas the isolates were alienated into seven genotypes depending on a similarity limit of 80% (genotypes 1 to 7), in which, genotypes 6 was including the most prevalent clones and their variants among the isolates (Fig.s 5). The

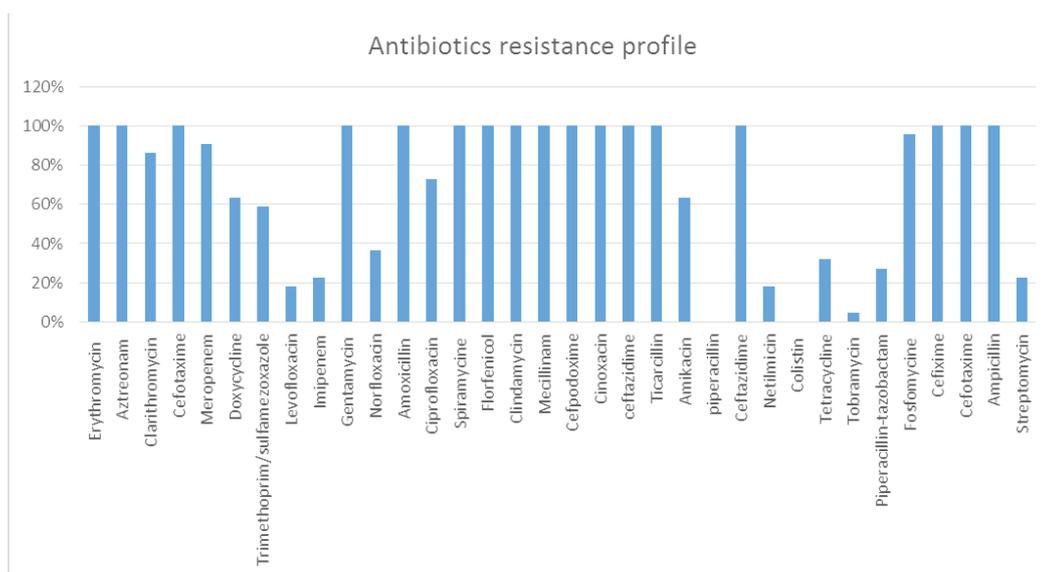


Fig.4. Total antibiotic resistant rate of 22 *A. baumannii* isolates from veterinary necessities.

largest group was genotype 6, containing 6 strains, including 2 isolates from human patients and 4 from slaughter houses. While four strains clustered in genotype 3 (composed of four isolates from slaughter houses) and genotype 2 (containing two from human sources, one from a private veterinary clinic, and one from a slaughter house). In contrast, genotype 1 consisted of only one strain from the slaughter house. These findings revealed that several strains collected from veterinary sources shared a genetic similarity with the isolates recovered from human patients. In addition, most strains from both private veterinary clinics and the governorate veterinary centers clustered within the same genetic profile.

Discussion

As far as it was known, there have been limited studies performed to track *A. baumannii* in veterinary field environments. Thus, this study provides valuable information for the fact that *A. baumannii*, which originated in the veterinary sector, could be regarded as a source of infection in humans. Additionally, the goal of this study was to ascertain the precise incidence rate of contamination of veterinary necessities by this infectious agent and to assess the rate of resistance of this pathogen to various antibiotics that are primarily used for therapeutic purposes in both animals and humans.

Reducing the danger of transmission to patients and animals by identifying the origins of organisms linked to veterinary settings is

essential [25]. In this study, *A. baumannii* was isolated at a rate of about 20.7%, and this may suggest the endemic occurrence of this pathogen on a veterinary level. The persistence and spread of *A. baumannii* may have been aided by the movement of animals from one veterinary clinic to another and from animal to human. This may be explained by the fact that transmission by hands or equipment should be taken into consideration because veterinarians, nurses, and stockmen go between the many clinics and departments [26]. Furthermore, the fact that it can form biofilms may help it survive in hospital settings and slaughter houses, which may in turn increase the risk of nosocomial infections and outbreaks [27]. Public health concerns about the existence of bacterial pathogens in veterinary settings highlight the necessity of implementing infection prevention and control strategies to get rid of these pathogens. The hospital environment, healthcare personnel, fomites, and patient microbiota were identified as potential sources of the microorganisms linked to hospital-acquired infections [28].

There was a considerable difference in the prevalence rate of *A. baumannii* between different sample types, as shown in present results: the slaughter houses had a higher rate of isolation than both private veterinary clinics and governorate veterinary centers, which could indicate that slaughter houses are the primary sources of infection for humans through meat processing plants [29] and environmental contamination [30]. These variations might be explained by the

TABLE 2. Antibiotics resistance rate of all 22 *A. baumannii* isolates from different veterinary sectors

Antibiotics	Slaughter houses No. (%)	Private veterinary clinics No. (%)	Governorate veterinary centers No. (%)	Total No. (%)
Erythromycin 15 mg	18 (100%)	2(100%)	2(100%)	22(100%)
Aztreonam 30 mg	18 (100%)	2(100%)	2(100%)	22(100%)
Cefotaxime 30 mg	18 (100%)	2(100%)	2(100%)	22(100%)
Gentamycin 10 mg	18(100%)	2(100%)	2(100%)	22(100%)
Clarithromycin 15 mg	15(83.4)	2(100%)	2(100%)	19(86.4)
Meropenem 10 mg	17 (94.4)	1(50%)	2(100%)	20(90.8)
Doxycycline 30 mg	12(66.7)	1(50%)	1(50%)	14(63.6)
Trimethoprim/ Sulfamezoxazole 25 mg	12(66.7)	0 (0%)	1(50%)	13(59.1)
Levofloxacin 5 mg	3(17.6)	0 (0%)	1(50%)	4(18.1)
Imipenem 10 mg	3(17.6)	1(50%)	1(50%)	5(22.7)
Norfloxacin 10 mg	6(33.3)	1(50%)	1(50%)	8(36.4)
Amoxicillin 25 mg	18 (100%)	2(100%)	2(100%)	22(100%)
Ciprofloxacin 5 mg	12(66.7)	2(100%)	2(100%)	16(72.8)
Spiromycine 30 mg	18 (100%)	2(100%)	2(100%)	22(100%)
Florfenicol 30 mg	18 (100%)	2(100%)	2(100%)	22(100%)
Clindamycin 2 mg	18 (100%)	2(100%)	2(100%)	22(100%)
Mecillinam 10 mg	18 (100%)	2(100%)	2(100%)	22(100%)
Cefpodoxime 10 mg	18 (100%)	2(100%)	2(100%)	22(100%)
Cinoxacin 100 mg	18 (100%)	2(100%)	2(100%)	22(100%)
Ceftazidime 30 mg	18 (100%)	2(100%)	2(100%)	22(100%)
Ticarcillin 75 mg	18 (100%)	100%)2	2(100%)	22(100%)
Amikacin 30 mg	11(61.1)	1(50%)	2(100%)	14(63.6)
Piperacillin 100 mg	0 (0%)	0 (0%)	0 (0%)	0 (0%)
Ceftazidime 30 mg	18 (100%)	2(100%)	2(100%)	22(100%)
Netilmicin 30 mg	4 (22.2)	0 (0%)	0 (0%)	4(18.2)
Colistin 10 mg	0 (0%)	0 (0%)	0 (0%)	0 (0%)
Tetracycline 30 mg	6(33.3)	1(50%)	0 (0%)	7(31.8)
Tobramycin 10 mg	1(5.6%)	0 (0%)	0 (0%)	1(4.5)
Piperacillin-tazobactam 100/10 mg	3(17.6)	1(50%)	2(100%)	6(27.2)
Fosfomicin 100 mg	17 (94.4)	2(100%)	2(100%)	21(95.5)
Cefixime 5 mg	18 (100%)	2(100%)	2(100%)	22(100%)
Cefotaxime 10 mg	18 (100%)	2(100%)	2(100%)	22(100%)
Ampicillin 10 mg	18 (100%)	2(100%)	2(100%)	22(100%)
Streptomycin 10 mg	4 (22.2)	0 (0%)	1(50%)	5(22.7)

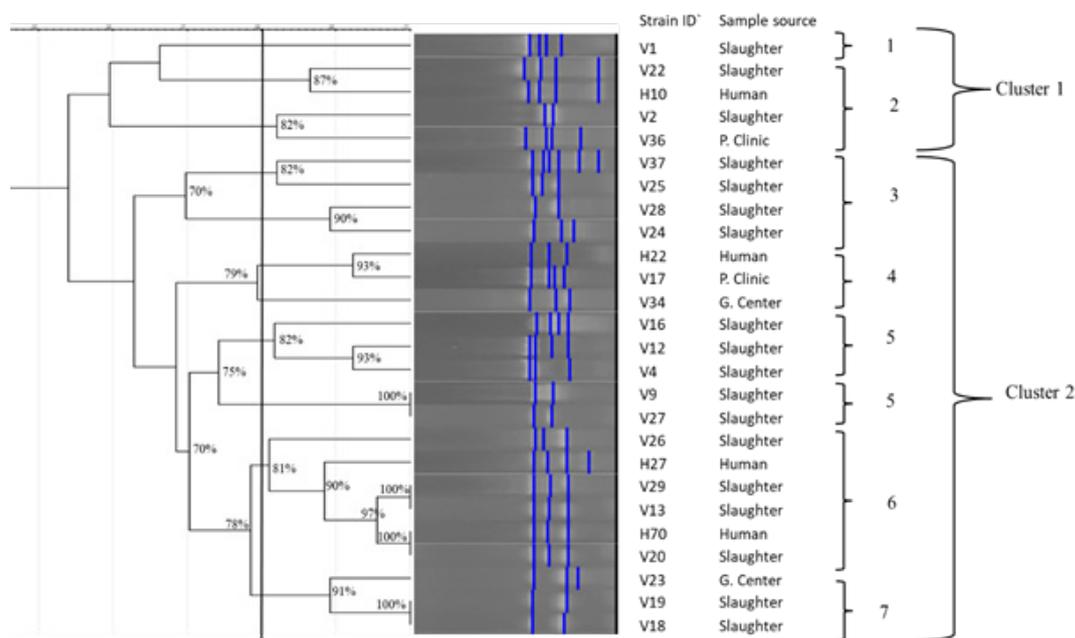


Fig. 5. Shows the pattern of bands from 26 *A. baumannii* strains isolated from the veterinary necessities (private veterinary clinics, governorate veterinary centers and samples from human patients).

P: Private, G: Governorate,

large number of processed animals as well as the fact that this bacterium is prevalent in corpse washing waters from various manufacturing stages in slaughter houses [31]. In addition, cleaning and disinfecting protocols may also be a reason for such differences, as different parts of the veterinary sector have different protocols for disinfection; therefore, these variances may have a considerable impact in terms of environmental contamination [32].

In contrast to the slaughter houses, the governorate veterinary centers and private veterinary clinics have fewer sources of contamination. Contact with the animal's hair, skin, limbs, stomach, blood, bile, and gut contents, as well as with facilities, equipment, hands, and worker apparel, are all potential sources of bacterial contamination throughout the process of slaughtering an animal [33]. Further, compared to the veterinary sector, slaughter houses typically receive an enormous number of animals for slaughter, which may raise the likelihood of contamination [34]. These are the main reasons why there is so much *A. baumannii* in the slaughter houses. Because of these things, hygiene and cleanliness have to be taken very seriously during the slaughtering process.

The rise of drug-resistant *A. baumannii* in *Egypt. J. Vet. Sci.* Vol. 54, No. 5 (2023)

hospitals and the nosocomial surrounding areas has raised concerns [4]. Worryingly, it became multi-drug resistant and resistant to carbapenems or last resort antimicrobial medicines like colistin [35]. Information on antibiotic resistance in *A. baumannii* of animal origin is still scarce. Since it is still unclear whether animals actually pose a risk as a reservoir for drug-resistant *A. baumannii* and whether this pathogen could carry resistant traits as a source of resistance in humans [36].

It is important to note that all of the *A. baumannii* isolates in this study were multidrug resistant, which means they were resistant to most of the common antibiotics used to treat both animals and people. This could be brought on by the improper use of antibiotics in animal husbandry as treatments and growth boosters, which has produced an increase in the transmission of antimicrobial resistance in bacteria linked to livestock and even the emergence of novel resistances [37]. Each gene is responsible for a specific antibiotic resistance, one gene may be accountable for resistance to a class of related antibiotics, or specific genes mutation that can extruding a large number of antibiotics, caused by the expression of a gene that encode for the protein that is responsible for drug resistance like efflux pump [19].

Scientists demonstrated that microbes between animals, the environment, and humans are constantly and reciprocally exchanged. Resistant gene transmission may be through the direct contact between people and animals, eating foods containing those animals, or environmental wastewater discharge [38]. Antibiotic resistance is an issue since these will build a great environment network for the co-transfer of various bacterial species and the acquisition of a variety of resistant genes amongst bacterial diversity [39].

The current results showed that isolates from slaughter houses exhibited a higher resistance rate compared to other sources. Many slaughtering processes can contaminate the environment and discharge multidrug resistant bacteria [40], in particular, defeathering and evisceration are thought to be the most significant ones because of the intestinal contents that are released during these processes [41]. In addition, animals have the ability to discharge antimicrobial-resistant bacteria into slaughter houses and transmit them across the environment process water, which is frequently contaminated with different multidrug-resistant bacteria and used at various stages of the slaughtering process, can constitute a potential cross-contamination route in this case [42]. Because of these things, wastewater from slaughter houses could carry antibiotic-resistant bacteria and contribute a lot to their spread in the environment [43].

Typically, slaughter houses have wastewater treatment facilities. Following treatment, the effluent is typically discharged into a sewer system or into a water body, such as a river. Therefore, This procedure might operate as a preserver for the spread of clinically significant, antibiotic-resistant bacteria into the environment, where they could ultimately have an impact on human general health through the risk of colonization and/or infection with ESKAPE bacteria [44]. However, some earlier research has demonstrated that farmers and slaughter houses employees may be more likely to develop and transmit antibiotic-resistant bacteria as a result of their regular contact with animals and/or contaminated working settings [45]. These strains are particularly prevalent in soil, plants, and surface water after being released into the environment through fecal material and wastewater, and they may therefore constitute a concern for the colonization of humans [46].

Regarding the genetic relatedness determined by ERIC-PCR fingerprinting, all strains from

human patients had the same genetic profile as some strains obtained from veterinary necessities, suggesting that *A. baumannii* emerged in the veterinary sector and may show that this pathogen is ubiquitous to these environments (the source for human infection was from the veterinary sector as indicated by their genetic relatedness). Thus, this study provides valuable information for the transmission of this bacterium between the veterinary field and humans. On the other hand, most strains isolated from both private veterinary clinics and governorate veterinary centers have the same genetic profile, indicating that the same clone is circulating in these two sectors, and cross transmission might be achieved through veterinarians and animal owners that circulate in both sectors [47].

Conclusions

According to this study, the slaughter houses had the most bacterial contamination when compared to other veterinary sectors, suggesting that it may be an environmental contamination pathway as well as a probable carrier for antibiotic-resistant *A. baumannii*. Because of this, the current study offers crucial data that brings up concerns about the possibility of zoonotic transmission of multidrug resistant *A. baumannii* from the veterinary sector to humans. This information helps the government create a systematic strategy for limiting the emergence and spread of this opportunistic pathogen and, ultimately, promoting public health. Animals do indeed pose a risk as reservoirs for multi-drug-resistant carrying traits of *A. baumannii*.

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Conflict of Interests

The authors declare no conflict of interest.

Funding statements

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Ethics

This paper performed under the regulation organized by general directorate of health (GDH), Duhok, Iraq, and they approved this study (GDH reference number: 2202021-6-4)

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بكتيريا *Acinetobacter baumannii* المقاومة للأدوية المتعددة؛ أحد مسببات الأمراض المهملة في المستشفيات في المجال البيطري كمصدر للعدوى البشرية

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خلفية الدراسة: واحدة من أهم التحذيرات العالمية، وفقاً لمنظمة الصحة العالمية (WHO)، هي خطورة الأحياء الدقيقة المقاومة للعديد من الأدوية على صحة الإنسان. كان الهدف من هذا الدراسة هو كشف معدل التلوث الدقيق بـ *Acinetobacter baumannii* في المراكز البيطرية (مجازر، عيادات خاصة، وحدات بيطرية)، وطريقة انتقال *A. baumannii* الممكنة إلى المرضى من البشر، ومدى مقاومة هذه البكتيريا للمضادات الحيوية.

طرائق العمل: تم جمع ١٠٦ مسحة من مناطق مختلفة في محافظة دهوك. تم استخدام الاختبارات المايكرو بيولوجية التقليدية والأوساط الزرعية وReal Time-PCR واختبار نظام "Vitek 2" لتشخيص وتأكيد عزلات *A. baumannii*. كذلك تم إجراء اختبار الحساسية للمضادات الحيوية باستخدام طريقة الانتشار القرصي القياسي. بالإضافة إلى استخدام اختبار البلمرة المتسلسل والتوافق الداخلي المتكرر بين الأنسجة البكتيرية ERIC PCR لتحديد التشابه الوراثي وبصمات الحمض النووي للعزلات المسترجعة.

النتائج: كان إجمالي عدد العزلات الإيجابية لـ *A. baumannii* هو ٢٢ عينة (٢٠,٧٪) وكانت موزعة كالتالي: (١٨) (١٦,٩٨٪) كانت إيجابية من بين ٦٥ عينة من المجازر، ٢ (١,٨٨٪) من بين ٢٠ مسحة من عيادة بيطرية خاصة، و٢ (١,٨٨٪) من بين ٢٠ مسحة من مراكز بيطرية في المحافظة). وقد كانت سلالات *A. baumannii* المعزولة من وحدات الطب البيطري مرتبطة وراثياً ببعض سلالات *A. baumannii* المعزولة من المرضى من البشر (من مركز دهوك للأبحاث). علاوة على ذلك، لم تكن أي من العزلات المحددة مقاومة للكولستين colistin والبيبيراسيلين piperacillin، على الرغم من كونها متعددة المقاومة وتظهر مقاومة لأكثر المضادات الحيوية المُختبرة بشكل متكرر.

الخلاصة: أظهرت النتائج الحالية إلى أن مقاومة *A. baumannii* يُحتمل أن تكون موجودة في مراكز الطب البيطري، الأمر الذي يتطلب نهجاً سريعاً ومدروساً لاحتواء هذه المشكلة.

الكلمات الدالة: «*Acinetobacter baumannii*»، مقاومة شديدة للأدوية، تنوع وراثي، تأثير حيواني، المنشأ، بيطري