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ERIC PCR-Based Genotyping and Antimicrobial Susceptibility of *Brucella melitensis* Isolates Recovered from Slaughtered Camels in Egypt

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Abstract

Brucellosis is a zoonotic disease affecting various animals, including camels. Our study aimed to isolate, identify, genotype the *Brucella* species circulating in camels and to test the antibiotic susceptibility of the *Brucella* isolates against 8 antibacterial agents commonly prescribed for human brucellosis. Lymph nodes (n = 350) were collected from camels from different Egyptian governorates. As identified by bacteriological and Abortus meltensis ovis suis PCR, 14 *Brucella* isolates recovered from 350 lymph nodes were identified as *B. melitensis* biovar 3 (4%). The results of antimicrobial susceptibility assays denoted that all *B. melitensis* strains tested in this study were susceptible to ciprofloxacin, tigecycline, gentamicin and rifampin whereas 28.6%, 28.6%, 21.4% and 7.1% of the isolates were resistant to doxycycline, tetracycline, trimethoprim-sulfamethoxazole and erythromycin, respectively Meanwhile, 21.4% and 7.1% of the isolates were resistant to trimethoprim-sulfamethoxazole and erythromycin, respectively. The genetic analyses based on ERIC-PCR indicated that *B. melitensis* isolates of the current study are almost identical to *Brucella* strains recovered from goats raised away from the study area. In conclusion, The emergence of resistance to the first and second lines of therapeutics prescribed for brucellosis limits the drug choices. Therefore, we strongly advise performing routine antibiotic sensitivity testing and updating zone diameter breakpoints for those drugs prescribed for treatment of human brucellosis. ERIC-PCR is a comparatively swift and affordable method for determining the genetic fingerprinting of *Brucella* species in developing countries that cannot finance sequence-based fingerprinting techniques. Our findings highlight the role of the mixed species husbandry system in *brucella* transmission between camels and other livestock.

Keywords: Antibiotics, Brucellosis, Camels, Epidemiology, ERIC-PCR, Resistance, Zoonoses.

Introduction

Brucellae are facultative intracellular bacteria that cause a worldwide zoonotic disease called brucellosis. *Brucella species* of zoonotic importance include *Brucella melitensis*, *Brucella abortus, Brucella suis*, and *Brucella canis* [1]. Camelids are mainly infected by *B. melitensis and B. abortus* [2]. The clinical signs of camel brucellosis are variable and can range from asymptomatic cases to severe abortion [3]. The recorded pathological conditions in camel brucellosis are granulomatous endocarditis, placental retention, and ovario-bursal adhesions. Males suffer from lameness due to arthritis and orchitis [4,5]. The economic importance of brucellosis is attributed to infertility, delayed first calving, mastitis, and decreased milk production [6, 7].

In Egypt, the first report of camel brucellosis was recorded in 1939 [8]. Camels are imported into Egypt from different eastern African countries. The seroprevalence of camel brucellosis in those countries is considerably high. Unfortunately, no proper quarantine measures are performed on the imported camels, posing a considerable risk to non-infected humans and livestock [9, 10].

Brucellosis is a worldwide zoonotic disease, with more than half a million confirmed human cases reported annually [11, 12].

Brucella species are transmitted from livestock animals to humans through direct contact with blood,

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fetal and uterine discharges, or through the consumption of contaminated raw milk and milk products [13].

In humans, brucellosis causes recurrent fever, headaches, muscle aches, and night sweats. Series complications include osteoarticular, cardiac malfunctions, and genital diseases [1, 14].

The brucellosis control is challenging due to the intracellular nature of Brucella spp. inside the macrophages, and the long course of antibiotic therapy [15]. The World Health Organization (WHO) recommends a 6-to-8-week oral doxycycline and rifampin course for treating human brucellosis. These antimicrobials effectively penetrate macrophages and work within the acidic intracellular environment. Other alternatives include doxycycline with either streptomycin or gentamicin [16, 17]. Tetracyclines, fluoroquinolones, trimethoprim-sulphamethoxazole, third-generation cephalosporins, and other aminoglycosides are used in combinations for the treatment of brucellosis. [18, 19]. In Egypt, studies about antibiotic sensitivity for Brucella isolates revealed susceptibilities to the most used antibiotics. However, ciprofloxacin, rifampin, and erythromycin resistances were detected [20–22].

The epidemiological traceback of camel brucellosis in Egypt is essential to determining the associations between different *Brucella* isolates recovered from camels and other proximate animals [23, 24]. The traceback can be achieved using various methods, including DNA fingerprinting. The most applicable fingerprinting methods are Random Amplified Polymerase Chain Reaction (RAPD PCR), Enterobacterial Repetitive Intergenic Consensus (ERIC PCR), and Repetitive-Element PCR (REP PCR) [25].

ERIC-PCR has been widely used to fingerprint members of the Enterobacteriaceae family (26) and other bacteria, including *Brucella* spp. ERIC-PCR uses a random primer pair that binds to non-specific genomic sites, producing strain-specific band patterns [27, 28].

Accordingly, our study aimed to isolate *Brucella* species from camels to determine the circulating species, the possible antibiotic susceptibility, and comparatively fingerprint strains with others isolated from sheep and goats to determine the epidemiological tracing of camel brucellosis in Egypt.

Material and Methods

Study area

Lymph node samples were collected from camels from different localities in Egypt, including Kerdasa slaughterhouse in Giza governorate, quarantines in border governorates such as Aswan and Red Sea, and household animals from Assiut and Beni Suef governorates. In Egypt, camels are native animals or imported through two main pathways: Somaliland and Ethiopia, or Sudan. Camels imported from Somaliland and Ethiopia are shipped from Dhijoboti through the Red Sea to Safaga or Suez ports, and this pathway has now ceased. Other camels are imported from the Sudan and are transported to Egypt through two routes. The first route is from west Sudan to Dongola quarantine and then alongside the Nile River. Camels cross the Egyptian border to Abu Simbel quarantine and then to Daraw camel market in Aswan. The second route is from east Sudan, where camels cross the borders from Kassala state to Halayeb and Shalateen quarantine. It is noteworthy that some animals don't enter the slaughter areas directly. They are smuggled to the markets and reared as household animals. These untested camels are highly likely to spread brucellosis to other animals and humans [10].

Samples' collection:

Retropharyngeal lymph nodes (350) were collected from Camels as the following: 100 lymph nodes from Kerdasa abattoir in Giza governorate, 175 lymph nodes from Abou-Simbel quarantine in Aswan, 50 lymph nodes from the Red Sea, and 25 lymph node samples from Beni-Suef (Fig. 1). The samples were collected over the period from October 2022 to January 2024. Camels were clinically normal with no vaccination record against brucellosis. Lymph node samples were collected in sterile bags and transported while cold to the laboratory with minimum delay.

Isolation and the identification of Brucella spp.

Lymph nodes were surface decontaminated by immersion in absolute ethanol and flaming. They were cut into small parts and homogenized in sterile phosphate-buffered saline. A loopful of the homogenate was cultured on tryptic-soy agar supplemented by antibiotic-selective supplements containing polymyxin B 2,500 IU, bacitracin 12,500 IU, cycloheximide 50.0mg, nalidixic acid 2.5mg, nystatin 50,000 IU and vancomycin 10.0mg (Oxoid, UK cat. no: SR0083). Plates were incubated at 37°C for up to 14 days with and without 10% carbon dioxide concentrations.

The suspected colonies were identified by their colonial morphology and biochemically through oxidase, catalase, and urease tests. The colonies were tested for their smoothness via the acriflavine test. The acriflavine is performed by dissolving a part of the colony in acriflavine reagent where the smooth colonies remain in suspension whereas rough colonies agglutinate [29].

DNA samples were extracted from *Brucella* colonies using the heat block method and amplified using the AMOS-PCR for *Brucella* species identification. The amplification mixture included

1X PCR master mix (Genedirex, South Korea cat. no: MB203-0100), a combination of primers with the sequences as depicted in Table 1 (0.2 µm concentration each), and 0.5 µL DNA (ten nanograms of DNA) per 25 µL reaction [30]. PCR products were separated on 1% electrophoresis agarose gel in 1X TAE buffer simultaneously with a DNA ladder (Genedirex, South Korea, Cat. No. DM101-0100).

The *Brucella* biovar was identified according to the requirement of CO_2, H_2S production, growth in the presence of thionin, and basic fuchsin (1/50000). Suspected *Brucella* colonies were typed using monospecific antisera with A and M *Brucella* antigens [29].

Antibiotic susceptibility of Brucella strains

Pure colonies of each of the 14 brucella isolates were suspended separately in sterile saline to match MacFarland turbidity tube number 0.5. The bacterial suspensions were spread using sterile swabs on Mueller-Hinton agar supplemented with 5% defibrinated sheep RBCs. The strains were tested against eight antibiotics via the disc diffusion method [31]. The tested antibacterials were doxycycline, tetracycline, erythromycin, ciprofloxacin, trimethoprim-sulfamethoxazole, tigecycline, rifampin, and gentamicin (Himedia, India). The selection of antibiotics for the antibiotic sensitivity test was based on several criteria. Primarily, antibiotics recommended by the World Health Organization (WHO) for the treatment of brucellosis are prioritized. These include doxycycline, streptomycin, rifampin, gentamicin, and trimethoprim-sulfamethoxazole [17]. Antibiotics such as tetracycline, erythromycin, and ciprofloxacin were selected due to their effective intracellular penetration [32]. Tigecycline was chosen for its broad spectrum and synergistic activity with doxycycline [33]. In each step of the antibiotic sensitivity test, *Brucella melitensis* Ether strain was used as a *B. melitensis* positive control.. The culture plates were incubated at 37 ℃ for 48 hours at ambient air. The breakpoints of *Brucella* against the tested antibiotics were established according to EUCAST (The European Committee on Antibiotic Susceptibility Testing) guidelines [34] Tigecycline breakpoint was determined according to manufacturer instructions with an inhibition zone ≤15 mm considered resistant according to manufacturer's instructions.

ERIC-PCR and phylogenetic analysis:

DNA samples were extracted from fourteen *Brucella* strains and compared with five DNA samples of *Brucella melitensis* isolated from goats and one from sheep using the ERIC-PCR fingerprinting technique. These strains were obtained through the routine work of the Brucellosis Research Department, Animal Health Research Institute, Dokki, Giza. The PCR mixture included 1X PCR mastermix (Genedirex, South Korea cat. no: MB203-0100), Two primer pairs (ERIC1 5' ATGTAAGCTCCTGGGGATTCAC-3' and ERIC2: 5' AAGTAAGTGACTGGGGTGAGCG-3') with 0.4 µm concentration each and 0.5 µL DNA (ten nanograms of DNA) per 25 µL reaction [35]. PCR products were separated on 1% electrophoresis agarose gel in 1X TAE buffer. A DNA ladder (Genedirex, Cat. No: DM101-0100) was used as a standard size determining bands. The gel was photographed by a gel documentation system (Alpha Innotech, Biometra, GmbH, Kasendorf, Germany), and the data was analyzed through computer software. A dendrogram was constructed with ERIC-PCR products with 1 % tolerance and 90% similarity coefficient using the Jaccard coefficient and the unweighted pair group method with arithmetic mean with GelJ software v.2.3 [36]. Simpson's diversity index for discrimination efficiency of ERIC-PCR genotyping of detected *B. melitensis* isolates was conducted as previously described [37].

Results

Concerning *Brucella* isolation, 14 *Brucella* isolates were recovered from 350 lymph nodes (4 %). The colonial morphology was distinctive, the colonies were round, translucent, honey coloured, 1-2 mm in diameter with smooth margins. The isolates were positive for oxidase, catalase, and urease tests and the colonies were smooth using the acriflavine test. AMOS-PCR revealed an amplicon of 731 bp, specific for *B. melitensis* in all isolates (Figures 2 and 3). *Brucella* isolates grew on media containing thionin and basic fuchsin dyes (1/50000). They grew without carbon dioxide and showed no hydrogen sulfide gas production. All isolates were agglutinated with monospecific anti-*Brucella* A and M sera. Phenotypic and molecular methods demonstrated that the isolates were all *B. melitensis* biovar 3 (Table 2).

The antibiotic sensitivity test results indicated that all strains were susceptible to rifampin, gentamicin, ciprofloxacin, and tigecycline. Resistance to doxycycline and tetracycline was observed in 28.6% of the isolates, while resistance to trimethoprim-sulphathiazole and erythromycin was conferred by 21.4% and 7.1% of the isolates, respectively [34] (Table 2).

ERIC-PCR was performed on *B. melitensis* reference strain, the fourteen isolates recovered in this study in addition to 6 isolates outside the study area. Based on the ERIC-PCR phylogeny, the strains were categorized into two mains clusters (clusters 1 and 2) with 68% homology. *Brucella melitensis* biovar 3 reference strain Ether (ATCC 23458) was included in cluster 2. The strains were discriminated into 17 distinct genotypes (M1-M17) along the reference strain Ether (M18). The discrimination index of the ERIC-PCR was 0.87.

The phylogenetic tree of *Brucella* strains revealed three identical strains (ID 11, 20, 21) represented by the M13 genotype and two identical strains (ID 6, 17) represented by the M14 genotype as shown in (Fig. 4).

Discussion

It is worth mentioning that camels are a significant source of income for nomadic communities in Egypt and many developing countries [2]. As urbanization increases, there has been a growing demand and market for camel milk and meat, which is an excellent source of low-cost meat due to their heavy carcasses and comparatively cheap husbandry [3, 7, 38].

Despite being investigated in many other countries, brucellosis in camels is considered a neglected zoonotic threat in Egypt [39], and they are still not incorporated in the national survey programs [40]. However, some published articles and theses from Egypt reported the detection of *Brucella* DNA in camels' sera and milk [23, 41], and few studies reported the isolation of Brucellae from camels in Egypt including one *B. melitensis* strain from camel [42] and two *B. melitensis* biovar3 strains from milk of she-camels [43].

Therefore, it was necessary to test camels for brucellosis through the isolation of brucellae to determine the most common species and biovars circulating in camels in Egypt. In addition, genotyping of the isolates was targeted for epidemiological tracing back the potential source of infection.

In the current study, all isolates were identified morphologically and biochemically as *Brucella melitensis* biovar 3, which is recorded as the predominant biotype in other livestock and humans in Egypt [42, 44-47].

The *Brucella* species was determined by AMOS-PCR, a multiplex PCR assay. Multiplex PCR assays are superior to the uniplex PCR ones that depend only on one primer pair due to their high discriminatory ability and the remarkable resemblance in the genome of *Brucella* species [48].

Concerning the results of the antibiotic susceptibility test, all isolates were susceptible to rifampin, gentamicin, and ciprofloxacin. Resistance was detected against doxycycline (28.6%), tetracycline (28.6%), trimethoprim-sulfamethoxazole (21.4%), and erythromycin (7.1%). The zone diameter breakpoints depend on the EUCAST guidelines for the disc diffusion method. Previous studies on antibiotic susceptibility of *Brucella* strains relied on CLSI guidelines for *Hemophilus spp*. or other agents of bioterrorism [34, 49, 50].

There are few studies about the antibiotic susceptibility of *Brucella* isolates in Egypt. In a study by Abdel Maksoud et al. 355 *Brucella spp.* strains were phenotypically susceptible to doxycycline, tetracycline, ciprofloxacin, and trimethoprim-sulfamethoxazole. A high resistance rate was observed for rifampin (64%) [20].

In another study, *Brucella melitensis* isolates were sensitive to gentamicin and tetracycline, while the resistance to ciprofloxacin, rifampin and erythromycin were 76.2%, 66.7%, and 19%, respectively [21]. According to a study conducted by Wareth et al., the *Brucella* isolates were susceptible to most antibiotics, including doxycycline, tetracycline, ciprofloxacin, gentamicin, tigecycline, and trimethoprim/sulfamethoxazole [22],. Consequently, our study is the first to report the resistance of *Brucella spp.* to doxycycline, tetracycline, and trimethoprim-sulphamethoxazole in Egypt.

The resistance of these antibiotics may be attributed to the selection pressure of resistant strains due to their improper use in human and veterinary practices over the years [51, 52]. Moreover, the unregulated trade of animals across borders can disseminate resistant strains and increase the antimicrobial resistance burden [53]. In addition, the intracellular sequestration of this pathogen is the other reason for the emergence of resistant strains.

The emergence of resistance to doxycycline and trimethoprim-sulphamethoxazole may impact the treatment of human patients. One report detected a high relapse rate in 59.3% of cases with osteoarticular brucellosis who were cured with double therapy (rifampin and doxycycline or cotrimoxazole). However, no relapse occurred in patients who received triple therapy (rifampicin, doxycycline, and streptomycin) [54].

The emergence of antibiotic resistance is alarming as it is uncommon for *Brucella* isolates. Moreover, the World Health Organization recommends multiple antibiotic therapy instead of single therapy to avoid relapse, which is common in human brucellosis. The World Health Organization recommends doxycycline with other antibiotics, such as rifampin. Another regimen recommends trimethoprim-sulfamethoxazole, erythromycin, or gentamicin. In our study, the emergence of resistance to multiple antibiotics recommended as the first and second treatment choices is a menacing public health concern [17]. Antimicrobial resistance in *Brucellae* limits the treatment choices, which may lead to more complicated infections. Uncontrolled antibiotic usage is causing widespread resistance in these bacteria, which will likely worsen in the future. The emergence of drug-resistant *Brucella spp.* in camel species poses a severe hazard to human beings [20, 21, 55].

The epidemiological elucidation of brucellosis has been a challenging task as the fastidious nature of

Brucella limits the success of phenotypic markers, such as cultural description, metabolic, characteristic traits, and phage sensitivity in the study of bacterial outbreaks [28].

Fortunately, ERIC-PCR is a comparatively rapid and cost-effective method for the traceability of *Brucella* species, especially in developing nations that cannot afford sequence-based genotyping methods such as Multiple Locus Variable-number Tandem Repeat Analysis (MLVA) or Whole Genome Sequencing-Single Nucleotide Polymorphism (WGS-SNP) [35]. Despite the term ERIC means Enterobacterial repetitive intergenic consensus as the assay was initially developed for enterobacteria, the assay has been proven convenient with other genera and species, including *Brucellae* [26, 27].

In the current study, animals were selected from border areas such as Aswan and the Red Sea governorates, representing the entry portals of camels from Sudan and Somaliland to Egypt, respectively [10]. Other camels were sampled randomly from distant governorates such as Giza, Assiut, and Beni Suef. *Brucella melitensis* strains isolated from small ruminants (one from sheep and five from goats) were used to determine the genetic similarities and relatedness with those isolated from camels. The small ruminants were from El-Wadi-El-Gedid, Menoufia, and Assiut governorates. Different localities were chosen to investigate the effect of animal movement on the spread of this bacterium between different governorates in Egypt.

In this study, ERIC-PCR revealed a satisfactory discrimination index of 0.87 [56]. The phylogenetic tree of *Brucella* strains revealed three identical strains (ID 11, 20, 21) represented by the M13 genotype and two identical strains (ID 6, 17) represented by the M14 genotype. The reference *Brucella* Ether strain was nearest to strains M16 and M17 with 86% genotypic similarity. The most circulating *Brucella* genotypes were M13-M14. The M13 strains were found to be shared between isolates from camels and goats at Assiut and Aswan, while the M14 genotype was shared among isolates recovered from camels and goats at Giza and Menoufia governorates. This finding confirms the possible transmission of brucellosis between camels and goats of different governorates, The detection of identical strains, M13 (shared between a camel and two goats) and M14 (shared between a camel and a goat), indicates interspecies transmission of the pathogen. Furthermore, the presence of these identical strains in animals from different governorates (Fig. 4) suggests that the infection may be spreading across regions. This transmission could be linked to the unregulated trade of animals between localities, the lack of proper border quarantines, and inadequate veterinary inspections of animals before movement.

Moreover, the impact of unrestricted movement of different animal species on the epidemiology of brucellosis and brucellosis spread between different animal species and different localities is evident from our results [57, 58]. In addition, the mixed husbandry system of the animals is a significant risk factor for disease transmission from diseased to healthy livestock species [45, 59].

Besides the risk of the infection of humans from contacting infected camels, another significant risk is through the unregulated trade of apparently healthy animals and the transfer of the disease to non-infected regions [2, 3, 7, 38].

The mixed household breeding of camels and small ruminants plays a vital role in the spillover infection between different animal species. The spillover infection is evident as all *Brucella spp.* and biovars are the same in all ruminants. This may explain the comparatively high prevalence of camel brucellosis in certain regions familiar with mixed rearing of ruminants [5, 60].

Conclusion

Camel brucellosis constitutes a potential threat livestock in Egypt (4% isolation). The emergence of resistance in the first and second line of treatment of brucellosis restricts antibiotic choices. Moreover, it elevates the risk of relapse and serious complications. Therefore, it is highly recommended that the antibiotic sensitivity test precedes the treatment in clinical practices and that the breakpoints of *Brucella spp*. should be updated against the recommended antibiotics. These practices are of utmost importance to overcome the increasing rate of antibiotic resistance against *Brucella* isolates. We are looking forward to conducting future studies that include more isolates from a greater variety of animals across Egypt to determine the epidemiological significance of brucellosis. Our findings are considered an alarm to the Egyptian veterinary authorities to implement a broad brucellosis control plan and include camels in the national surveillance program.

Further advanced molecular studies with more *Brucella strains* are mandatory and highly recommended to determine the epidemiology of camel brucellosis in Egypt and the potential source of *Brucella* infection.

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Declaration of Conflict of Interest

The authors declare that there is no conflict of interest.

TABLE 1. Sequences of oligonucleotides utilized in the AMOS PCR for differentiation of Brucella isolates at the species level

PCR assays	Primer	5'-3' nucleotide sequence	Target gene	Amplicon size	Reference
AMOS-PCR	*B. abortus*-specific primer	GACGAACGGAATTTTTCCAATCCC	IS711	498 bp	Bricker and Halling, 1994
	IS711 primer	TGCCGATCACTTAAGGGCCTTCAT			
	B. melitensis -specific primer	AAATCGCGTCCTTGCTGGTCTGA		731 bp	
	IS711 primer	TGCCGATCACTTAAGGGCCTTCAT			

TABLE 2. Results of the Disc Diffusion method of 14 Brucella isolates

Antibiotic	Abbreviation	Concentration µg /disk	Sensitive	Intermediate	Resistant
Doxycycline	DO	30	10 (71.4%)	0 (0%)	4 (28.6%)
Tetracycline	TE	30	10 (71.4%)	0 (0%)	4 (28.6%)
Erythromycin	E	30	13 (92.9%)	0 (0%)	1(7.1%)
Trimethoprim/ sulfamethoxazole	COT	1.25/23.7	11 (78.6%)	0 (0%)	3 (21.4%)
Ciprofloxacin	CIP	5	14(100%)	0 (0%)	0 (0%)
Tigecycline	TGC	15	14 (100%)	0 (0%)	0 (0%)
Rifampin	RIF	5	14 (100%)	0 (0%)	0 (0%)
Gentamicin	GEN	10	14 (100%)	0 (0%)	0 (0%)

Fig. 1. A google map of Egypt showing the places of sample collection from slaughtered camels.

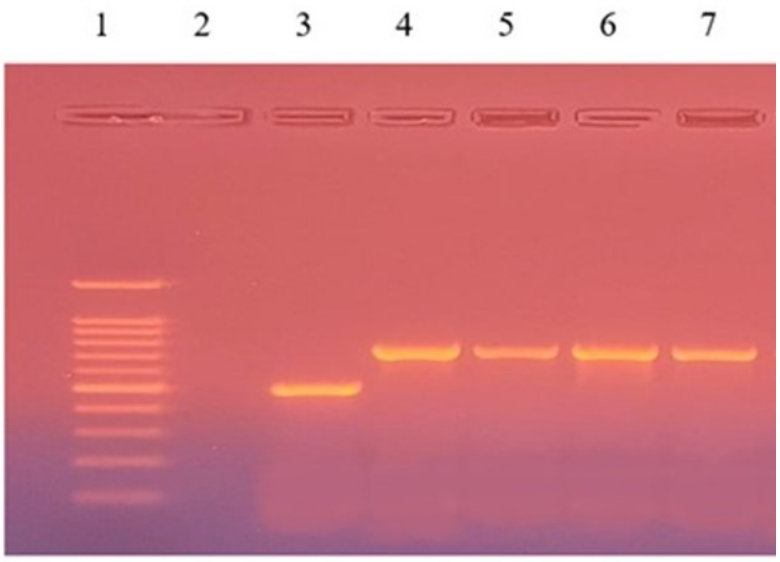

Fig. 2. AMOS PCR products of *B. abortus* and *B. melitensis* (a standardization setup) Lane 1: 100 bp DNA ladder, Lane 2: negative control (no template), Lane 3: *B. abortus* 498 bp specific product, lane 4: 731 bp *B. melitensis* specific product (Ether strain) and Lnes 5-7: 731 bp products of 3 *B. melitensis isolates* from camels.

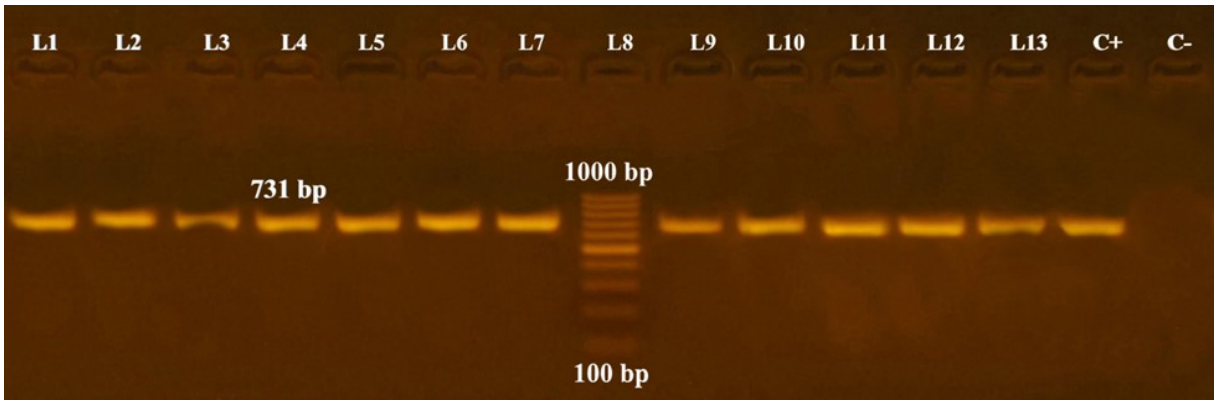

Fig. 3. AMOS PCR of Brucella isolates revealing DNA bands specific for *B. melitensis* (731 bp). Lanes 1-7 and Lanes 9-13: *Brucella melitensis* field strains, Lane 8:100 bp DNA ladder, Lane 14 (C+): *B. melitensis* reference strain Ether, and Lane 15 (C-): Negative control.

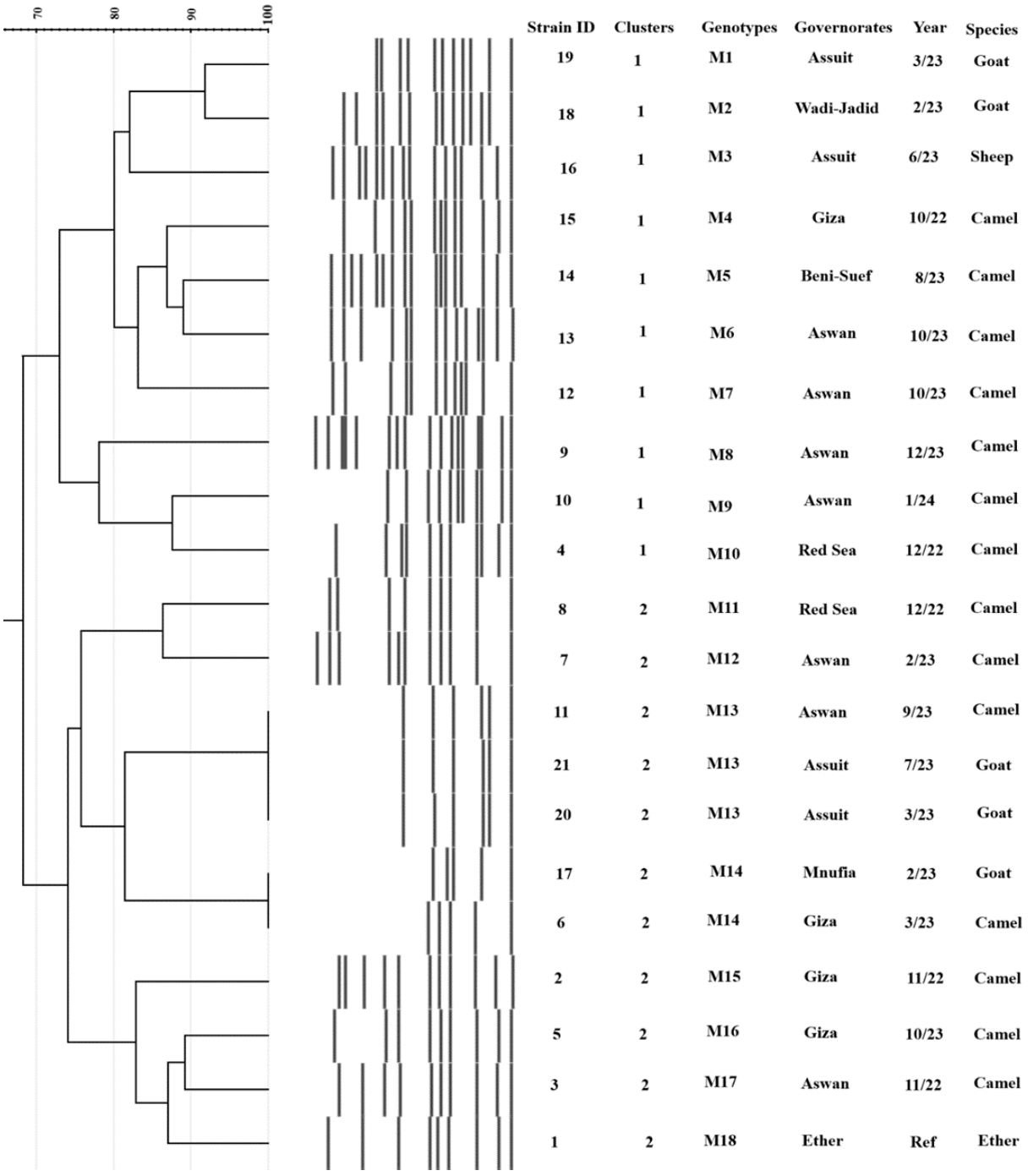

Fig. 4. Dendrogram generated from the amplified ERIC primers in fourteen *Brucella melitensis* strains isolated from camels, sheep and goats.

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التوصيف الجيني على أساس اختيار ERIC-PCR والحساسية للمضادات الميكروبية لعزلات بروسيلا ميلتنزس من إبل مذبوحة في مصر

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الملخص

داء البروسيلا هو مرض مشترك يصيب الحيوانات المختلفة شاملة الإبل. وقد إستهدفت هذه الدراسة عزل وتعريف أنواع البروسيلا المنتشرة بين الجمال و حساسيتها أمام ثماني عقاقير علاجية والتي توصف غالباً لعلاج البروسيلا في الإنسان. وتمت الدراسة على 350 عقدة ليمفاوية مجمعة من إبل مذبوحة بمحافظات مصرية مختلفة. وبناءاً على التعريف بالطرق البكتيريولوجية واختبار AMOS-PCR تم تعريف 14 عزلة بروسيلا على أنها بروسيلا ميلتنزس نوع 3 وبنسبة 4%. وقد أشارت نتائج اختبار الحساسية إلى أنه 28,6% من العزلات كانت مقاومة للتتراسيكلين والدوكسي سايكلين. وكان 21,4% و 7,1% من العزلات مقاومة لكل من الترايميثوبريم/سلفاميثوكسازول و الإريثرومايسين، على التوالي. وقد دلت الشجرة الوراثية باستخدام تقنية ERIC-PCR أن عزلات بروسيلا ميلتنزس التي تحصلنا عليها من الإبل في هذه الدراسة تشبه لحد كبير عترات بروسيلا تم عزلها من الماعز. وخلاصة القول أن البروسيلا المعزولة في هذه الدراسة كانت جميعها حساسة للسيبروفلوكساسين والتيجاسيكلين والجنتاميسين والريفامبسين. ويعتبرنشوء عترات بروسيلا مقاومة للمضادات الحيوية التي توصف كخط أول وثاني لعلاج البروسيلا في الإنسان يمثل عائقا عند اختيار العلاجات. وعليه فإننا نوصي إجراء اختبار حساسية لوصف العلاج الأمثل للآدميين.

الكلمات الدالة: المضادات الحيوية، البروسيلا، الإبل، ERIC-PCR، الوبائية، المقاومة، الأمراض المشتركة.