



Bacteriological and molecular detection of brucellosis with special reference to the effect of disinfectants on isolated strains.

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ABSTRACT

A total of 127 specimens (13 aborted foeti, 46 milk samples, 37 lymph nodes, 14 livers, 14 spleen and 6 vaginal discharges) were collected and examined for isolation and typing of *Brucella* microorganism. The results detected 15 strains (5 aborted foeti, 4 milk, 5 lymph nodes and 1 spleen) were detected and typed as *Br. melitensis* biovar 3. Application of PCR test for rapid identification of *Brucella* strains which isolated from lymph nodes five of naturally infected animals (two cattle, one buffaloes, one sheep and one goat) revealed that all samples were reacted positively with *Br. melitensis* specific DNA products with a molecular size of 731 pb. On sequencing, the Nucleotide sequence alignment of obtained sequences with other *Brucella* strain indicated that the obtained isolate have high identity with *Br. melitensis* biovar 3. The bacteriocidal activity of tested disinfectants against isolated *Br. melitensis* strain at variables concentration revealed that halogen showed highest bacteriocidal activity followed by QACs and phenolic while alkaline was the lowest effect.

Keywords: brucellosis, isolation, PCR, disinfectants sensitivity.

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1. INTRODUCTION

Brucellosis is a bacterial disease caused by members of the genus *Brucella* which is an important zoonosis that affects both humans and animals such as cattle, sheep, goats, dogs, and swine and the disease of economic significance in many developing countries (Al Dahouk *et al.*, 2009). Brucellosis is diagnosed in the laboratory by using various techniques like microbiological isolation and identification which are the most reliable methods. However, these procedures are cumbersome and represent a great risk of infection for laboratory personnel (George and Araj, 2010). AMOS-PCR (Abortus, Melitensis, Ovis, Suis PCR) is the most efficient technique for diagnosis of *Brucella* at the species level and these useful methods applied to DNA extracted from a positive culture (Wareth *et al.*, 2014). PCR-based genome sequence amplification method is a good alternative, as it allows for rapid identification of the bacteria. Differential identification of highly similar *Brucella* spp., however is only achievable with multiple gene sequence analyses (Tan *et al.*, 2015). Disinfectant is extremely effective measure for successful brucellosis control especially in endemic area (Al-Majali *et al.*, 2009). The present

study was conducted to detect *Brucella* microorganism strains using bacteriological and molecular methods in different tissue specimens collected from different seropositive animal species and to evaluate the effect of disinfectants (quaternary ammonium compounds, halogen, Phenolic and alkaline) on isolated strains.

2. MATERIAL AND METHODS:

2.1. Samples

2.1.1 Milk samples:

46 milk samples were collected from different animal species (16 from cattle, 13 from buffaloes, 7 from sheep and 10 from goats). Twenty ml of milk were collected from udder of reactors cattle and goat into a sterile vacuoner tube. Milk samples for bacteriological examination were stored at 4°C until used.

2.1.2 Aborted foeti:

The stomach contents of 13 aborted foeti (7cattle, 2buffaloes and 4 sheep) were collected according to Stableforth & Galloway (1959).

2.1.3 Lymph nodes:

37 lymph nodes (supramammary, internal iliac and retropharyngeal lymph nodes) were collected (9 from cattle, 4 from buffaloes, 12 from sheep and 12 from goats). The technique for isolation of *Brucella* microorganisms from lymph nodes was done as follows: - The fat which covers the lymph nodes was trimmed off using sterile scissors. Lymph nodes were immersed in 95% alcohol and put on to flame to allow alcohol to burn from the tissues. The lymph nodes were opened by scalpel and the internal surface was thoroughly minced. A piece of minced tissue was streaked over the surface of trypticase soy agar media. The inoculated plates were incubated at 37°C in CO₂ incubator, and then examined after 4 days for *Brucella* growth.

2.1.4 Liver and spleen samples:

14 liver samples were collected (6 from cattle, 5 from buffaloes and 3 from sheep) & 11 spleen samples (6 from cattle, 5 from buffaloes). Liver and spleen were trimmed carefully from the surrounding fat, were dipped in ethanol and burned with a flame to allow alcohol to burn the tissues then were placed in a sterile Petri-dish and cut longitudinally with a sterile sharp scalpel, and the internal surface was thoroughly minced and rubbed over the surface of the medium. Plates were incubated at 37°C in 5-10% carbon dioxide incubator.

2.1.5 Vaginal discharge:

Six vaginal swabs were collected four from cattle and two from buffaloes using sterile cotton swabs.

2.2 Bacteriological examination:

2.2.1 Isolation of *Brucella* micro-organisms:

It was carried out on milk samples and different tissue specimens according to the methods recommended by Alton *et al.*, (1988) on Trypticase soya agar media. The inoculated plates were incubated at 37°C in CO₂ incubator, and examined after four days for *Brucella* growth.

2.2.2 Identification and typing of *Brucella* isolates:

Suspected isolated *Brucella* strains were identified and typed according to Alton *et al.*, (1988).

2.3 Molecular identification and biotyping of *Brucella* isolates

PCR was carried out according to methods of Bricker and Halling (1994).

2.3.1 Preparation of killed bacteria for PCR.

When bacterial cells were used directly for PCR, All bacteria were killed by the addition of 67% methanol-33% saline. The killed bacteria were rinsed one time in distilled water to remove the methanol and were then resuspended in distilled water at an optical density of 0.15 to 0.20 at 600 nm (approximately 10⁹ cells per ml).

2.3.2 Preparation of genomic DNA according to (Promega), USA.

2.3.3 DNA amplification by PCR assay.

2.3.4 Visualization of extracted DNA:

Samples were electrophoresed on 1.5% agarose gel in 0.5 X TBE buffer containing 0.5 µg/ml ethidium bromide for about 30-50 minutes at 70 volts using a minigel electrophoresis unit. DNA Bands were visualized on ultraviolet transilluminator. The molecular size of the DNA bands was compared with those of the 100 bp DNA marker.

2.4 Sequence and phylogenetic analysis:

According to (Consumer protection Institute, Saxony Anhalt, Germany), the PCR products of *Brucella* samples were sequenced. Direct sequencing was carried out in both directions by termination cycle sequencing using the Big Dye Terminator Mix 1.1 (Applied Biosystems, Carlsbad, USA) with the same primers used for PCR product amplification. The assay was optimized by using a total reaction volume of 10 µl. Briefly, for one reaction 1 µl RNase-free water, 1 µl of 5x Sequencing Buffer, 2 µl Big Dye Terminator Mix 1.1 and 1 µl of the according primer (5 µM). The following thermal program was applied 1 cycle of 96°C for 1 min followed by 26 cycles of 95°C for 15 s, 53°C for 10 s, and 60°C for 4 min. After that, cycle sequencing products were purified with DyeEx 2.0 Spin Kit (QIAGEN GmbH, Hilden, Germany). The nucleotide sequences were resolved in an ABI 3130 Genetic Analyzer (Applied Biosystems, Carlsbad, USA).

2.5 Phylogenetic Analysis

Alignment of multiple nucleotide sequence *Br. melitensis* isolates based on *IS711a* gene nucleotide data were done by using BioEdit program.

2.6 Study the effect of disinfectants on isolated strains using minimum inhibition concentration (MIC).

Bacterial preparation: was carried out according to Chapin and Lauderdale (2003).

Preparation of used disinfectants: was carried out according to manufacturer's instructions.

Determination of MIC of used chemicals: it was carried out according Wang *et al.*, (2015)

3. RESULTS

The isolation of *Brucella* organisms from tissue specimens of different animals species revealed that (15 strains) were isolated (5 from aborted foeti, 4 from milk, 5 from lymph nodes and 1 from spleen) as in Table (1). Typing of 15 *brucella* isolates revealed that *Br. melitensis* biovar 3 is the only strain excited among the examined animals Table (1). Application of PCR test for rapid identification of *Brucella* species in lymph nodes of five naturally infected animals two cattle, one

buffaloes, one sheep and one goat revealed that five samples reacted positively to *Br. melitensis* specific DNA products with a molecular size of 731 pb, indicative of *Br. melitensis* DNA were obtained Figure (1). On sequencing, the Nucleotide sequence alignment of obtained sequences with other *Brucella* isolates Figure (2) indicated that the obtained isolate had higher identity with *Brucella melitensis* biovar 3 Figure (3). Concerning evaluation of the bactericidal activity of tested disinfectants against isolated *Br. melitensis* strains at different variables concentration revealed that halogen had the highest bactericidal activity followed by QACs and phenolic while Alkaline showed the lowest bactericidal effect.

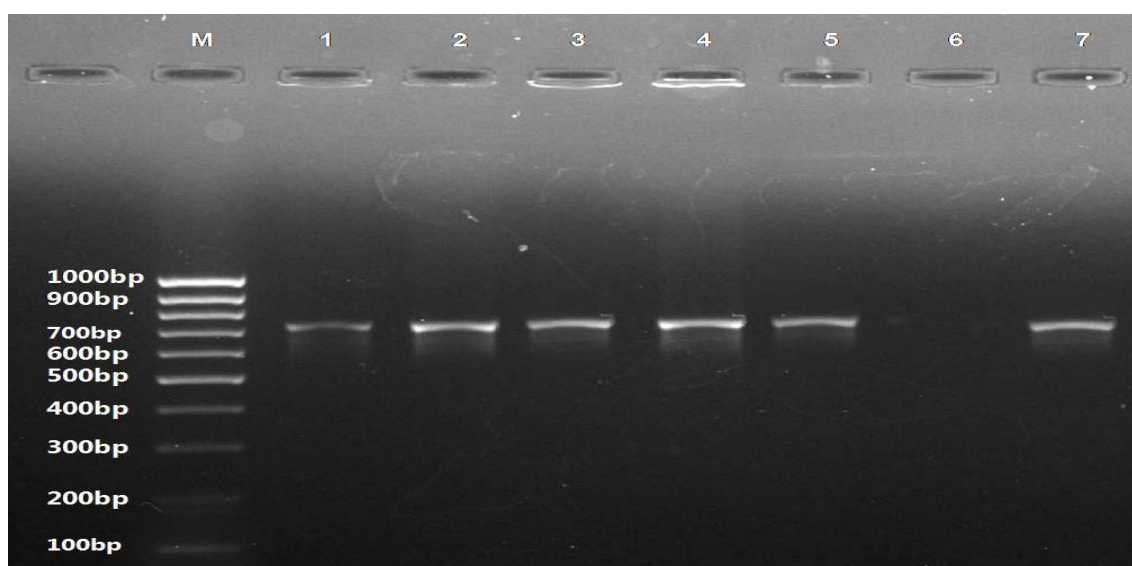


Figure (1): Amplified product of *Brucella melitensis* 731 bp stained with 2% ethidium bromide. (M) Represents a 100-bp DNA ladder as a size standard. (Lanes 1-2) +ve colony isolated from cattle. (Lane 3) from buffaloes, (Lane 4) from sheep. (Lane 5) from goats. (Lane 6) -ve control. (Lane 7) +ve control (*Br. melitensis*).

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TTCGGCTCAGAATAATCCACAGAAGGTAGAGCAGTAATATCCAATAGACGCCATTAACAATAG
CGAGATTGGAATAGCTTACCCGCCAATCTTCGCCCTGCCACCAGCCAATAACGGCAATTATCGC
TGTCAGTGTGCAAGTATGGCAGCGAGCGCTCTAGCGTGACGAAGCACTGTCTTTCTGACAATT
TCCAGATTCACCCCTAGGGCGTGTCTGCATTCAACGTAACCAGATCATAGCGCATGCGAGATGG
ACGAAGCCCATGAATGCGGTCAATGTTTTCTCGCATCGCAGCGCAATA.
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Figure (2). Nucleotide sequence of isolated *Brucella melitensis*.

Brucella melitensis this study	- - - - -	- - - - -	- - - - -	- - - - -	T C G G C T C A G A A T A A T C C A C A G A A G G T A G A G C A G T A A T A T C C A
Brucella melitensis IS711 partial sequence	A A A T C G C G T C C T T G C T G G	. T . A . T . A G T . T T . . A C . . A C . . C . T C G A T . T C G T A A .			
Brucella melitensis bv. 3 complete sequence	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
AJ271968.1 Brucella abortus	- - - - -	- - - - -	- - - - -	- - - - -	- A T A G G C . . C G G C T C A G . T C A . . G T . . A . C C A . C A . G
gb X081250.1 Brucella ovis IS711	- - - - -	T T T A C A C A G G C A A C A G C A . A G C C C G . A . G . C A G C . . C G C . A A . A C . C A G A T T .
Brucella melitensis this study	A A T A G C G A G A T T G G A A T A G C T T A C C G C C	- - A A T C T T C G C C C T G C C A C C A G C C A A T A A C G			
Brucella melitensis IS711 partial sequence	G G A T A T . . A T C . . A . C C T T T . T . T G . . C G . . T A . T A C C T . T . . G . T G C . C . C A A				
Brucella melitensis bv. 3 complete sequence	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
AJ271968.1 Brucella abortus	C G A C T G . . . G C . . T . C A . . G A A C G . . A T . A G . T . G A A T . . T T . T T T . A . . A G T T G A				
gb X081250.1 Brucella ovis IS711	. . A G A A T . A . A C A C . T - C C T . . T . G . G A . G C A G - . A . T G C . T . T G . C C A T T G A . . A A				
Brucella melitensis this study	G T C A C T G T T G C A A G T - A T G G C A G C G A G C G C - - - - - T C T A G C G T G A C - - - G A A G C - - A C T G				
Brucella melitensis IS711 partial sequence	. . . T T . . A C . T . . A . C G C . . T C A T A C . A . A . T . A G . - - - C . - - T . . G G . .				
Brucella melitensis bv. 3 complete sequence	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
AJ271968.1 Brucella abortus	. . C G . T G C G A . A . . A C A T . . A . C . . A T T . A T G G G - - . T . C . T C C A T . T C G C . T G . . A				
gb X081250.1 Brucella ovis IS711	A C A . T A A G . A G T . . A A . A A T . C . G A G . . T T T G G G T . T . C . T T . A G A A G A A . G T T T G G T . T				
Brucella melitensis this study	G A T T - - - - - C A C C C C - T A G G G C G T G T C T G C A T T C A A C G T A A C C A G A T C A T - - A G C G C A				
Brucella melitensis IS711 partial sequence	. T T T G T . G . G A A T . . C C . T A A . . A G . G G . A C C C . T . A . A A . . C A G . A . T G				
Brucella melitensis bv. 3 complete sequence	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
AJ271968.1 Brucella abortus	A T G C A G A - - - - - G . . C C A G . A T T . . C T T . T G C A T G A A - - - .				
gb X081250.1 Brucella ovis IS711	A C . . T A A G C A T T T T A . T A . . A A A T T A . . G . . A T G A A A . C . . . T C C . G C A C C A T C . G				
Brucella melitensis this study	C A T - G A A T G C G G T C A A T G T T T T C T C G C A T C G C A G C G C A A				
Brucella melitensis IS711 partial sequence	. . C A G . T A . A - - - - -				
Brucella melitensis bv. 3 complete sequence	- - - - -				
AJ271968.1 Brucella abortus	G . A G . . G A A . A . C . T T G A G - - - - -				
gb X081250.1 Brucella ovis IS711	- - - - -				

Figure (3) . Nucleotide sequence alignment of obtained sequences with other Brucella isolates from GenBank database.

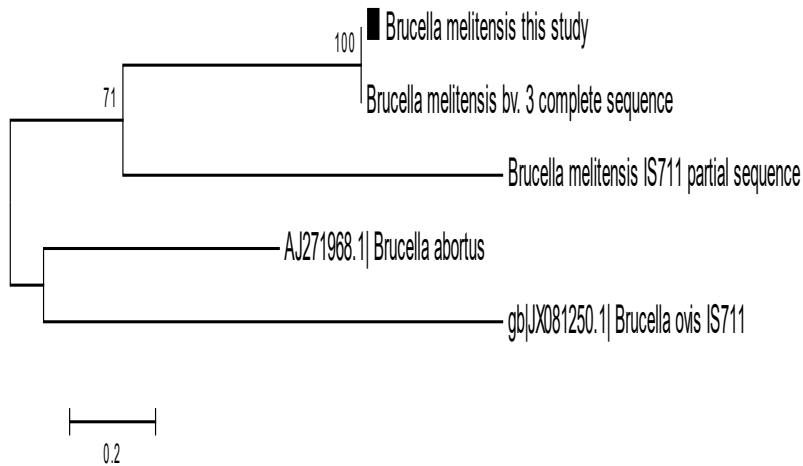


Figure (4): Phylogenetic tree of different Brucella strains based on the nucleotide sequences of the IS711 gene by using neighbour-joining methods in MEGA6 software

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Table (1) Isolated *Brucella* strains and their biotype from different animal species.

Animal species	Type of samples																					Isolated strains and biotyping
	Aborted foeti			Milk			Lymph nodes			Livers			Spleen			Vaginal discharges			Total			
	No.	+ve	%	No.	+ve	%	No.	+ve	%	No.	+ve	%	No.	+ve	%	No.	+ve	%	No.	+ve	%	
Cattle	7	3	42.9	16	1	6.3	9	2	22.2	6	0	0	6	1	16.7	4	0	0	48	7	14.6	<i>Br. melitensis</i> biovar 3
Buffaloes	2	1	50	13	1	7.7	4	1	25	5	0	0	5	0	0	2	0	0	31	3	9.7	
Sheep	4	1	25	7	1	14.3	12	1	8.3	3	0	0	0	0	0	0	0	0	26	3	11.5	
Goats	0	0	0	10	1	10	12	1	8.3	0	0	0	0	0	0	0	0	0	22	2	9.1	
Total	13	5	38.5	46	4	8.7	37	5	13.5	14	0	0	11	1	9.1	6	0	0	127	15	11.8	

Table (3): Oligonucleotide primers used for *Brucella* DNA amplification

Primer code	Primer sequences	Product size	Species specificity
IS711-SP	5'-TGCCGATCACTTAAGGGCCTCAT-3'	498 bp	<i>B. Abortus</i> (biotype 1, 2 & 3)
Ba-sp	5'-GACGAACGGAATTTTCCAATCCC-3'		
Bm-sp	5'-AAATCGCGTCCTTGCTGGTCTGA-3'	731 bp	<i>B. melitensis</i>

4. DISCUSSION

Animals of all ages are susceptible to brucellosis but the disease occurs most commonly in sexually mature animals particularly in dairy animals. The organism has marked predilection for ruminant placenta, fetal fluids, mammary glands and joints. Unknown factors in the gravid uterus, collectively called allantoic fluid factors, stimulate the growth of *Brucella*. Erythritol, a four carbon alcohol is considered to be one of these factors. High concentrations of erythritol are present in fetal tissues as well, which are the sites of infection establishment (Radostits *et al.*, 2007). In this study, 15 strains of *Brucella* were recovered from different samples collected from cattle, buffaloes, sheep and goats.

Typing of isolates according to Alton *et al.*, (1975) resulted in finding *Br. melitensis* Biovar (3) is the serotype existed in examined animals. Similar findings were reported by many authors as Ammar (2000), Montasser *et al.*, (2001), Lobna (2006), Abd El-Hamid (2007), Samaha *et al.*, (2008), Khoudair *et al.*, (2009), Afifi *et al.*, (2011), Manal (2011), Amin *et al.*, (2012) and El-Shymaa (2014) who were isolated *Brucella melitensis* biotype 3 from different animals species in Egypt. The reason of isolation of *Brucella melitensis* biovar 3 from cattle and buffaloes may be attributed to the nearly constant close contact during raising with infected sheep and goats. These findings have a great epidemiological importance as *Brucella melitensis* is more dangerous for human than other *brucella* species. PCR assay can simultaneously detect and differentiate of *Br. abortus* and *Br. melitensis* in the same time and one reaction (Mirnejad *et al.*, 2012).

The isolated *brucella* species from positive reactors animals were examined with multiplex conventional PCR for detection and identification of *Br. abortus* and *Br. melitensis*. The obtained results revealed amplification only with *Br. melitensis*. The results of application of (PCR) assay for rapid identification of *brucella* species in the lymph nodes of (5) naturally infected animals

(2cattle, 1buffaloes, 1sheep and 1 goats) showed that 5 samples reacted positively with *Br. melitensis* biovar (3) specific DNA products with a molecular size of 731 bp, indicative of *Br. melitensis* DNA were obtained as shown in Figure (1).

The obtained results were agreed with that reported previously by Ilhan *et al.* (2008) and El-Shymaa (2014) who recorded that PCR products with a molecular size of 731 bp indicative of *Br. melitensis* DNA. Also these results were similar to that obtained by Al-Bayatti and Al-Thwan (2009) who mentioned that is due to many advantages, like speed, safety, high sensitivity and specificity, PCR is recommended to use in diagnosis of animal brucellosis. In the same way, the obtained results were similar to that recorded by Simone *et al.* (2007) who reported that microbiological culture depends on organism viability, quality of the sample, contamination of the sample with other microorganisms and time between collection and analysis, also it is pathogenic to human while DNA detection by means of PCR does not depend on these factors. It can detect few number as 10^4 bacteria in sample.

Application of molecular assays may usefully provide high sensitivity and specificity as well as speed for genotyping. This Multiplex PCR in *Brucella* species was first used in USA. (Halling *et al.*, 1993). In this study, DNA sequence analysis of fragment OMP gene of *Br. melitensis* (PCR product) was performed by clone manager software. This program was used in matching in order to obtain the full length of nucleotide sequence data (Figure 2). Figure (3) showed Nucleotide sequence alignment of obtained sequences with other *Brucella* isolates from Gen Bank database and revealed that the sequence of the obtained isolate have high identity with *Br. melitensis* biovar 3 and showed heterogeneity with other *brucella* strains such as *Br. abortus* and *Br. ovis*. The result concluded that, the obtained isolate is *Br. melitensis* biovar 3. According to Dale *et al.*, (2003) the homology level of an isolate was called homolog if the homology level more than 60%. In

this work, Figure (4) revealed that there was a close relationship with *Br. melitensis* biovar 3 and *Brucella melitensis* IS711. In addition, *Br. melitensis* and *Br. melitensis* biovar 3 located together in separate clades. Furthermore, sequences belonging to the *brucella* clearly cluster together; while strains of other *Brucella* (*Br. abortus* and *Br. ovis*) are displayed by a separated outlier and this obviously showed the higher degree of similarity and genetic relationship among *Brucella* strains. Results in table (2) showed the bactericidal activity of tested disinfectants against isolated *Br.melitensis* strains at different variables concentration revealed to the highest bactericidal activity was recorded with halogen followed by QACs and phenolic while the lowest bactericidal effect was recorded in Alkaline. These results were similarly to previous results of (Wanke, 2004) and (Wang et al., 2015) which concluded that halogens, quaternary ammonium compound, phenolic, and alkaline could be selected for disinfection to control brucellosis.

It can be concluded that: The isolation and biotyping of *Br. melitensis* particularly biovar 3. PCR assay could be recommended as confirmatory methods and an alternative to culture for diagnosis of brucellosis as its speed, safety, high sensitivity, specificity and saving cost and time. Also Quaternary ammonium compound (QACs), Halogen (chlorine), phenolic and Alkaline (sodium hydroxide) are disinfectants of choice for the control of brucellosis.

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