ISSN: 2356-7767

Bovine mastitis associated with *Pseudomonas aeruginosa* and their molecular characterization Abdelgawad, M.H. and Bkheet, A.A.

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Received in 04/10/2019 Accepted in 11/11/2019

Abstract

Bovine mastitis associated with *Pseudomonas aeruginosa* has been increased in recent years causing large economic losses and significant problems to dairy farms and small farmers as *P. aeruginosa* is naturally resistant to wide spectrum of antibiotics in addition to its possession to a variety of virulence factors that may related to its pathogenicity. This study was carried out on bovine mastitis accompanied with *P. aeruginosa* in which 170 milk samples from mastitic cows and buffalos (100 cow and 70 buffalo) were collected from different localities in El-Behera governorate. Molecular characterization (PCR) were developed to identify *P. aeruginosa*, detect some virulence genes that associated with pathogen city (toxA, exoS and oprl genes) and detect bla TEM gene (beta lactamase)which responsible for antibiotic resistance. The obtained results showed that 7 samples (5 cow and 2 buffalo) were confirmed as *P. aeruginosa*, oprl gene was detected in all isolates, toxA and exo S genes were detected in 5 isolates. while bla TEM gene was detected in all isolates which indicate that *P. aeruginosa* is naturally resistant to beta lactam antibiotics.

Key words: Pseudomonas aeruginosa, Bovine mastitis, PCR, virulence factors - bla TEM gene

Introduction

Pseudomonas aeruginosa is an aerobic, motile, Gram-negative rod, widely present in the environment, water and in humid settings, but it is also an important opportunistic pathogen for humans, plants and animals (**Bergonier** *et al.*, **2003**).

P. aeruginosa is an environmental pathogen that can cause severe clinical mastitis with systemic signs as well as subclinical chronic mastitis. The organism is considered an opportunistic pathogen causing disease when the environment is contaminated and when the host defenses are decreased by stress, concomitant disease, or by nutritional imbalances (**Kirk and Bartlett, 1984**).

Drug resistance and severe toxemia due to Pseudomonas infections are supposed to produce high case fatality rate in immunesuppressed host. There are many factors are responsible for *P. aeruginosa* infection in cattle and buffaloes, particularly exposure of open wounds with contaminated soils and water (Geyik et al., 2003).

Clinical mastitis resulting from herd infection of *P.aeruginosa* has been reported to be caused by a variety of factors, including contaminated dry-off preparations (**Osborne** *et al.*, 1981), teat wipes (**Daly** *et al.*, 1999; **Power**, 2003)and wash water used to clean udders prior to milking (**Erskine** *et al.*, 1987).

Virulence of *P. aeruginosa* is multifactorial and has been attributed to cell-associated factors such as lipopolysaccharide (LPS), flagellum, and pilus and non-pilus adhesins, as well as to exoenzymes or secretory virulence factors, including protease, elastase, phospholipase, pyocyanin, exotoxin A, exoenzyme S, hemolysins, and siderophores (Hentzer *et al.*, 2003).

P. aeruginosa possess several pathogenic fac-

tors respon-sible for their pathogenicity, among which exotoxin A (*toxA*) and exoenzyme S (*exoS*) are two major fatal weapons which remain associated with subclinical mastitis infection in bovines (Narayanan, 2013).

L and I lipoproteins are two outer membrane proteins of *P. aeruginosa* responsible for inherent resistance of *P. aeruginosa* to antibiotics and antiseptics. As these proteins are found only in this organism, they could be a reliable factor for rapid identification of P. aeruginosa in clinical samples (Nikaido, 1994) and (de Vos D et al., 1997).

P. aeruginosa has the ability of causing mastitis in dairy cow, this bacterium presents a difficult challenge, as it tends to protect itself from antibiotics and white blood cells in layers of slim (Monett *et al.*, 2004). It is highly resistant to many antibiotics and such phenomenon might be due to R-factor (El- Jakee *et al.*, 1995).

Polymerase chain reaction (PCR) has been developed to identify various mastitis pathogens (**Meiri-Bendek** *et al.*, 2002). The development of PCR-based methods provides a promising option for the rapid identification of bacteria. With this method, identification of bacterial pathogens can be made in hours, rather than the days required for the conventional culture methods. Molecular methods have been reported to be superior to the phenotypic methods for identification of *P. aeruginosa* (Qin *et al.*, 2003).

Therefore, this study was aimed for isolation and identification of *Pseudomonas aeruginosa* from milk samples collected from mastitic cow and buffalo in addition to application of PCR to confirm *P. aeruginosa* isolates, detect of some virulence genes that associated with pathogenicity (*toxA*, *exoS* and *oprl* genes) and for detection of *bla TEM* gene (beta lactamase) which responsible for resistance to beta lactam antibiotics.

Materials and Methods

Collection of samples: A total of 170 milk samples were collected from mastitic cow and buffalo (100 cow and 70 buffalo) from differ-

ent localities at El-Behera governorate. The samples were collected, labeled and transported with a minimum of delay in ice box to the laboratory for bacteriological examination.

Isolation and Identification of *Pseudomonas aeruginosa*: The milk samples were plated onto *Pseudomonas* agar medium supplied with Cetrinix Supplement (Cetrimide and nalidixic acid) obtained from Hi Media (India) after overnight enrichment on nutrient broth followed byincubation aerobically at 37°C for 24 hrs. The suspected colonies were subjected to further morphological and biochemical identification according to **Kreig and Holt (1984).**

Molecular characterization of *Pseudomonas aeruginosa:* PCR was carried out using (16SrDNA of *P. aeruginosa*) to identify *P. aeruginosa*, detect of some virulence genes using specific primers to *toxA*, *exoS* and *oprl* genes (Spilker *et al.*, 2004 and Nikbin *et al.*, 2012) and detect of *bla TEM* gene (beta lactamase) by using of specific primer to*bla TEM* gene.

DNA extraction. DNA extraction from isolates was performed using the QIAamp DNA Mini kit (Qiagen, Germany, GmbH) with modifications from the manufacturer's recommendations. Briefly, 200 μ l of the sample suspension was incubated with 10 μ l of proteinase K and 200 μ l of lysis buffer at 56°C for 10 min. After incubation, 200 μ l of 100% ethanol was added to the lysate. The sample was then washed and centrifuged following the manufacturer's recommendations. Nucleic acid was eluted with 100 μ l of elution buffer provided in the kit.

Oligonucleotide Primers:. Primers used were supplied from Metabion (Germany) are listed in table (1).

PCR amplification. For PCR, primers were utilized in a 25- μ l reaction containing 12.5 μ l of EmeraldAmp Max PCR Master Mix (Takara, Japan), 1 μ l of each primer of 20 pmol concentration, 4.5 μ l of water, and 6 μ l of DNA template. The reaction was performed in an Applied biosystem 2720 thermal cycler.

Analysis of the PCR Products.

The products of PCR were separated by elec-

trophoresis on 1.5% agarose gel (Applichem, Germany, GmbH) in 1x TBE buffer at room temperature using gradients of 5V/cm. For gel analysis, 20 μ l of the PCR products were loaded in each gel slot. Gelpilot 100 bp DNA ladder (qiagen, gmbh, Germany) and Generuler 100 bp ladder (Fermentas, Thermo Scientific, Germany) were used to determine the fragment

sizes. The gel was photographed by a gel documentation system (Alpha Innotech, Biometra) and the data was analyzed through computer software **Nikbin** *et al.*, (2012) PCR was carried out in the Reference lab. For veterinary quality control on poultry production (Egypt).

Table (1). Primers sequences, target genes	, amplicon sizes and	cycling conditions for a	conventional PCR.
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Tar- get gene	Primers sequences	Ampli- fied seg- ment (bp)	Prima- ry dena- turatio n	Amplification (35 cycles)				
				Second- ary de- naturati on	Anneal- ing	Exten- sion	Final exten- sion	Reference
ToxA	GACAAC- GCCCTCAGCATCAC CAGC	396	94°C 5 min.	94°C 30 sec.	55°C 40 sec.	72°C 45 sec.	72°C 10 min.	Matar <i>et</i> <i>al.</i> , (2002)
	CGCTGGCCCATTCG CTCCAGCGCT							
oprL	ATG GAA ATG CTG AAA TTC GGC	504	94°C 5 min.	94°C 30 sec.	55°C 40 sec.	72°C 45 sec.	72°C 10 min.	Xu <i>et al.</i> ,
	CTT CTT CAG CTC GAC GCG ACG							(2004)
exoS	GCGAGGTCAG- CAGAGTATCG	118	94°C 5 min.	94°C 30 sec.	55°C 30 sec.	72°C 30 sec.	72°C 7 min.	Winstanley <i>et al.</i> , (2005)
	TTCGGCGTCAC- TGTGGATGC							
blaTE M	ATCAGCAATAAAC- CAGC	516	94°C 5 min.	94°C 30 sec.	54°C 72° 40 sec. 45 s	72°C	72°C	Colom <i>et</i> <i>al.</i> , (2003)
	CCCCGAAGAACGTT TTC					45 sec.	10 min.	
P. aeru- ginosa 16S rDNA	GGGGGGATCTTCG- GACCTCA	056	94°C 5 min.	94°C	52°C 40 sec.	72°C 50 sec.	72°C 10 min.	Spilker <i>et</i>
	TCCTTAGAG- TGCCCACCCG	930		30 sec.				al., (2004)

Results

1-Isolation of *Pseudomonas aeruginosa* from milk samples:

Seven milk samples (5 cows and 2 buffalo) were positive for *P. aeruginosa* with percentage of 4.1 % (7 isolates out of 170 samples) as in table (2).*P. aeruginosa* isolates showed fluorescent green color colonies on *Pseudomonas*

agar platesphoto (1). The isolates were found to be Gram negative bacilli with Gram staining.

Type of animal	No of examined samples	Positive samples	Percentage (%)
Cow	100	5	5%
Buffalo	70	2	2.8%
Total	170	7	4.1%

Table (2). Prevalence of Pseudomonas aeruginosa among the examined samples



Photo. (1): Fluorescent green color colonies of *Pseudomonas aeruginosa* on *Pseudomonas* agar plates2-Biochemical identification: The isolates showed positive to catalase, oxidese, nitrate reduction and citrate utilization test and were found negative to indole test, methyl red test and voges-Proskauer (VP) test.

3-Molecular characterization of *Pseudomonas aeruginosa:* The suspected seven isolates that biochemically characterized were subjected to PCR. The results are illustrated as in table (3) and photo (2-6).

isolate No	Source of isolates	Tested genes				
-	-	P. aeruginosa 16S rDNA	toxA	exoS	oprL	blaTEM
1	Cow	+	+	+	+	+
2	Cow	+	+	+	+	+
3	Cow	+	+	+	+	+
4	Cow	+	+	+	+	+
5	Buffalo	+	-	-	+	+
6	Buffalo	+	-	-	+	+
7	Cow	+	+	+	+	+

Table (3). Molecular characterization of *P. aeruginosa* and different detected genes.



Photo. (2): Agarose gel electrophoresis of PCR products showing amplification of *P. aeruginosa* 16SrDNA gene products at 956 bp, lane L: molecular weight marker MWM (100 - 1000 bp DNA ladder), lane positive: Positive control, lane negative: negative control, lanes (1, 2, 3, 4 and 7): *P. aeruginosa* isolated from cows, lanes (5, 6): *P. aeruginosa* isolated from buffalo. All isolates were positive to *P. aeruginosa*.



Photo (3) Agarose gel electrophoresis of PCR products after amplification of *oprL* gene products at 504 bp. lane L: molecular weight marker MWM (100 - 600 bp DNA ladder), lane positive: Positive control, lane negative: negative control, lanes (1, 2, 3, 4 and 7): *P. aeruginosa* isolated from cows, lanes (5, 6): *P. aeruginosa* isolated from buffalo. All isolates were positive for *oprL* gene



Photo. (4): Agarose gel electrophoresis of PCR products after amplification of *toxA* gene products at 396 bp. lane L: molecular weight marker MWM (100 - 600 bp DNA ladder), lane positive: Positive control, lane negative: negative control, lanes (1, 2, 3, 4 and 7): *P. aeruginosa* isolated from cows, lanes (5, 6): *P. aeruginosa* isolated from buffalo. The isolates (1, 2, 3, 4 and 7) were positive for *toxA* gene while (5, 6) were negative.



Photo. (5): Agarose gel electrophoresis of PCR products after amplification of *exoS* gene products at 118 bp. lane L: molecular weight marker MWM (100 - 600 bp DNA ladder), lane positive: Positive control, lane negative: negative control, lanes (1, 2, 3, 4 and 7): *P. aeruginosa* isolated from cows, lanes (5, 6): *P. aeruginosa* isolated from buffalo. The isolates (1, 2, 3, 4 and 7) were positive for *exoS* gene while (5, 6) were negative.



Photo. (6): Agarose gel electrophoresis of PCR products after amplification of *bla TEM* gene products at 516 bp. lane L: molecular weight marker MWM (100 - 1000 bp DNA ladder), lane positive: Positive control, lane negative: negative control, lanes (1, 2, 3, 4 and 7): *P. aeruginosa* isolated from cows, lanes (5, 6): *P. aeruginosa* isolated from buffalo. All isolates were positive to *bla TEM* gene

Discussion

The incidence of clinical mastitis due to *P. ae-ruginosa* has been increased in large dairy herds in recent years, causing large economic losses and significant problems for the affect edfarms. The origin of mastitis due to *P. aeru-ginosa* has been traced to contaminated water sources, with hoses and nozzles in milking parlors, and the pipes and tanks in cattle sheds, being the primary sources of infection (Erskine *et al.*, 1987; Hicks *et al.*, 1991).

P. aeruginosa has been reported to be among the three most prevalent cultured from bovine milk samples and the three most frequently associated with clinical mastitis (Barkema et al., 1998). P. aeruginosa produces two different toxins ETA (exotoxin A) and exoenzyme S (Bodey et al., 1983). The highly toxic ETA is produced by the majority of P. aeruginosa strains and can inhibit eukaryotic protein biosynthesis at the level of polypeptide chain elongation factor 2, similarly to diphtheria toxin. ETA consists of two subunits; fragment A is catalytic, and fragment B is responsible for interaction with eukaryotic cell receptors. ETA is cytotoxic to numerous mammalian cells (Matthew, 1983). Exoenzyme S causes significant tissue damage in lung, burn and wound infections (Wolfgang et al., 2003).

Table (2) showed that percentage of *P. aeru*ginosa isolated from examined milk sampleswas 4.1% (7 out of 170). These results were nearly similar to those obtained by Al Dabbagh (2012) who isolated P. aeruginosa4.4 % from clinical and subclinical mastitis in Mosul city. Lower incidence was recorded by Sori et al., (2005) who isolated P. aeruginosa from clinical bovine mastitis with percentage of 2.13 % and Sumathi et al., (2008) who isolated Pseudomonas spp. from clinical bovine mastitis with percentage of 1.33%. Moreover, Atyabi et al., (2006) isolated P. aeruginosa from bovine mastitis with a percentage of ,21 %in Tehran. Higher isolation rate was be detected by Younis et al., (2015) who isolated P. aeruginosa from mastitic milk samples with percentage of 25%, Ghazy et al., (2015) isolated P. aeruginosa from bovine mastitis with percentage of 10 % and Saleh et al., (2016) who isolated P. aeruginosa with percentage of 11.4 % from milk of mastitic cattle.

The percentage of *P. aeruginosa* isolated from buffalo milk samples was 2.8% as in table (2), that approach to **Heleili** *et al.*, (2012)whofound that the prevalence of *Pseudomonas* spp. in sub -clinical mastitis cases of bovines and buffaloes was (3.0%). Moreover, **Baloch** *et al.*, (2011) found thatthe incidence of *P. aeruginosa* from clinical mastitis in buffalo was 1.42%. Higher incidence detected by **Vishwakarma** (2008) who reported that the prevalence of *Pseudomonas* spp. in sub-clinical mastitis cases of bovines and buffaloes was 6.9%. The variation in incidences among authors could be attributed to the variation of hygienic conditions, managmental parameters and variations among the animal holders as well as sample volume.

Molecular characterizations of the isolates were done using (16SrDNA of *P. aeruginosa*) by conventional PCR. The results revealed that all seven isolates were confirmed as P. aeruginosa table (3) and photo (2).P. aeruginosa possesses a variety of virulence factors that may contribute to its pathogenicity. PCR was used for detection of P. aeruginosa exotoxin A (toxA), exoenzyme S (exo S) and oprL gene. The obtained results demonstrated that oprL gene was detected in all seven isolates of P. aeruginosa photo (3), this agree with Mohammed et al., (2015) who detected oprL gene in all examined isolates from raw milk (100 %) and Nikbin et al., (2012) who detected oprL gene (L- lipoprotein) among all examined P. aeruginosa isolates from different infectious origins while Neamah (2017) detected oprL gene in examined milk samples with a percentage of 50%.

ToxA gene was detected in 5 isolates (1, 2, 3, 4, 7) photo (4). This matching with **Banerjee** et al., (2017) who found that the percentage of toxA gene in examined isolates from bovine subclinical mastitis was 63.2% while **Lanotte** et al., (2004) and **Mohammed** et al., (2015) detectedtoxA gene in all examined isolates with percentage of 100%. On the other hand Younis et al., (2015) could not detect toxA gene (0.00%) from examined milk samples but could detected toxA gene with percentage of 8.57% from other samples(nasal swabs and wound).

ExoS genes was detected in 5 isolates (1, 2,3, 4, 7) photo (5), this agree with Sharma *et al.*, (2004), Badr *et al.*, (2008) and Nikbin *et al.*, (2012) who reported that the presence of *exoS* genes in examined isolates was 50-84% and Neamah (2017) who detected *exoS* genes with percentage of 75% from examined milk sam-

ples. While greater than Younis *et al.*, (2015) who detected *exoS* genes with percentage of 16% from examined milk samples and **Banerjee** *et al.*, (2017) who detected *exoS* genes with percentage of 36.8% while lower than Lanotte *et al*., (2004) who detected *exoS* genes with percentage of 84.5%.

ToxA and exoS genes could not detected in isolates no (5, 6) which isolated from buffalo this may be matching with **Younis** et al., (2015) as theycould not detect toxA gene from examined milk samples and this may be due to absence of expression enhancer gene of toxA (PtxR gene) from some isolates of P. aeruginosa as observed by **Vasil** et al., (1986) who reported that the PtxR gene expression enhancer gene of toxA was only detected in P. aeruginosa isolates, whereas other species of Pseudomonas did not yield any positive results. Low sensitivity with toxA PCR screening is due to the fact that some isolates of P. aeruginosa do not carry this gene naturally.

Several mechanisms are involved in P. aeruginosa resistance to antimicrobial agents, such as chromosomal expression of resistance encoding genes, β -lactamase production, efflux pumps and decrease inmembrane permeability Rodrigues et al., (2011). PCR assays were developed with specific primers for the detection of *bla TEM* gene (beta lactamase). The results showed that *bla TEM* gene were detected in all seven isolates of P. aeruginosa photo (6), this indicate that all isolates resist to ßlactamantibiotic. This agree with Saleh et al., (2016) who detected beta lactamase (bla - OX-Agene) in all *P. aeruginosa* isolates from milk of mastitic cattle. While Das et al., (2017) detected *bla TEM* gene with percentage of (12%) from examined isolates of Gram negative bacteria including pseudomonas causing subclinical mastitis. The differences in prevalence of P. aeruginosa and distribution of its genes observed among different studies may be due to variation in hygienic standards of the dairy environment and milking conditions, management practices, different environmental and geographical cause, breeds of the animals, immune responses, climatic conditions as well as genetic variation in disease resistance amongst the breeds of animals.

Conclusion

Bovine mastitis associated with Pseudomonas aeruginosa has been increased in recent years. P. aeruginosa could beisolated from mastitic cow and buffalo. Virulence genes (toxA, exoS and oprl gene) and antibiotic resistance gene (bla TEM gene) were detected in P. aeruginosa isolates and this suggested that they are associated with different levels of intrinsic virulence and antibiotic resistance of P. aeruginosa isolates. From this study we recommended that hygienic measures and good management in dairy herds should be applicated, application of pre and post milking treatments, routine examination to water source in the farm for any pathogen especially pseudomonas and rapid dealing with immunologically depressed animals especially after viral infection to prevent P. aeruginosa infection causing large economic losses as it is an opportunistic pathogen and naturally resistant to wide spectrum of antibiotics.

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