

Study of ecpA prevalence with biofilm formation ability in *Klebsiella pneumoniae* isolated from Respiratory Tract of Cattle in Certain area of Iraq

¹Rand T. Yaseen, ²Mohammed J. Alwan

Pathology and Poultry Diseases Department
Veterinary Medicine College, Baghdad University, Baghdad / Iraq

Abstract: In order to determine the percentage of *Klebsiella pneumoniae* which isolated from the upper and lower bovine respiratory tract, to determine a biofilm formation ability of these isolates, in addition to detection the presence of ecpA gene in these strains using conventional PCR assay. One hundred nasal swabs and same number of lung tissue samples were taken randomly from apparently healthy and diseased cattle that expressed respiratory clinical signs of different ages and gender and they were processed in laboratory of Veterinary Medicine College. The *K. pneumoniae* biofilm formation ability was detected by spectrophotometric method. Results of bacterial isolation showed that unhealthy animals exposed 7 (3.18%) of *K. pneumoniae* in lung samples and 4(1.8%) from nasal passages while apparently healthy animals revealed 1 (0.45%) and 3 (1.4%) *K. pneumoniae* isolates from lung and nasal passages respectively. The biofilm formation result showed that 10 (66.7%) were positive formers while negative formers composed 5(33.3%). Results of PCR assay revealed that 14(93.3%) of *K. pneumoniae* isolates had ecpA gene while 1(6.7%) of these isolates were lacked this gene.

Keywords: Respiratory tract, *Klebsiella pneumoniae*, biofilm formation, PCR, ecpA gene.

I. INTRODUCTION

Bovine respiratory disease took into consideration as main economical disease resulted in comprehensive losses in the dairy and beef industries [1]. [2] mentioned that the infection has diversified etiology such as biological, nutritional and environmental factors that resulted in important economic problems among livestock leading to significant morbidity and mortality. There were microbiota situated as the bovine upper respiratory tract ubiquitous flora but they are turn into opportunistic pathogens when immune system impairment such *Staphylococcus*, *Streptococcus* spp., *K. pneumoniae* and etc. which can reach lung by inhalation then colonized in lung tissue and encouraged pulmonary tract infections such as bronchopneumonia [3]. However, *K. pneumoniae* was widespread opportunistic microbiota of human and animal that can infect large and small ruminant, horse, wild and companion animals [4].

[5] and [6] illustrated that the *K. pneumoniae* belongs to Enterobacteriaceae family and hypermuroid strains of this species induced invasive infections in human and animals species mainly mastitis in dairy cattle and bovine respiratory diseases. *K. pneumoniae* was important respiratory tract microbiota of all domestic animal species as well as cow milk and dry udder secretions and it was highly significant in dairy cattle due to remediation difficulties [7]. [8] reported that there were a wide spread of multidrug resistant *K. pneumoniae* among animals and human including third generation Cephalosporin (3GCs) and antibiotic resistance transmission between human and animal resulted in the important public health and economic troubles. [5] explained that *K. pneumoniae* virulence and resistance factors explicit by capsular polysaccharides, adhesins, siderophores and antimicrobial determinants which responsible for *K. pneumoniae* infections.

Moreover, host immune response resisted by a biofilm via restraint phagocytosis, opsonization process and mechanical host barrier such as organism removal by mucocillary system [9].

In Iraq, there is little study about the features and percentage of *K. pneumoniae*, therefore, the aims of current study were to isolate and identify *K. pneumoniae* and determining their owning of *ecpA* gene with biofilm formation ability.

II. MATERIALS AND METHODS

1. Sampling:

Total of (200) Slaughtered cattle's lung tissue and nasal swabs specimens were collected from pneumonic and apparently healthy cattle. Each sample was placed in separate sterile containers and tubes which were fully labeled with the date, tissue and animal identification.

These containers and swabs tubes were transported under cooled condition as soon as possible to laboratory for bacteriological examination.

2. Isolation and identification of *K. pneumoniae*:

The isolation of *K. pneumoniae* was accomplished according to [7] and the purified colonies were identify according to [13];[10], while [11] was confirmed diagnosis of purified *K. pneumoniae* colonies by detection presence of *ecpA* gene using conventional PCR assay.

3. Biofilm assay:

Quantitative biofilm formation assay (Spectrophotometric method) was performed according to [12] which include: Briefly, a colony from each isolated *K. pneumoniae* was grown in BHIB at 37°C for 18hrs. 20µl of a bacterial suspension from broth culture of 0.5 McFarland standard (1.5×10^8 CFU/ml) was used to inoculate 96-well polystyrene plates containing 180 µl of BHIB, then the plates were incubated at 37 °C for 24 h. Thereafter, the wells were evacuated from the medium, then were rinsed thrice with 1X PBS and fixed with 2% formalin at 4 °C for 1 hr. Instantly, the wells were stained with 200 µl of 1% crystal violet for 20 min. Excess dye was eliminated, and 200 µl of absolute methanol was added to the wells. Determined color intensity using a Multiskan or Elisa reader at a wavelength of 620 nm. The ranking of biofilm-producing strains was established based on the absorbance readings as following: non biofilm producer, low, medium and high biofilm formers.

4. PCR assay:

The PCR assay was accomplished according to [14].

III. RESULTS

1) Bacterial isolates:

A total percentage of *K. pneumoniae* from lung tissue of diseased animals were 7(3.18%) while from nasal swabs were 4(1.8%) and total percentage of *K. pneumoniae* from lung tissue of healthy animals were 1(0.45%) while from nasal swabs were 3(1.4%).

2) Bacterial identification:

The fifteen bacterial isolates are Gram negative rods, straight, arranged singly or in pairs, their colonies on the MacConkey agar are pink, lactose fermenter and mucoid. They are non-motile and gave negative reaction for oxidase and a positive result for catalase. These features may indicate that the isolates are *K. pneumoniae*.

3) Biofilm assay:

Biofilm forming isolates categorization depending on absorbance readings obtained from ratio of blank (0.069) and positive control (0.744). If absorbance readings of isolates (<0.138) were considered non - biofilm producers; low biofilm -formers values ranked between (0.139 -0.276); absorbance reading value between (0.277-0.414) were deemed as medium biofilm-producer isolates, whereas isolates were classified as high biofilm formers with absorbance greater than (>0.415). Our analysis showed that 10/15 (66.7 %) of *K. pneumoniae* strains were able to form biofilm. Furthermore, 1/10(10%) of

strains were high biofilm formers, 5/10(50%) were medium biofilm formers and 4/10 (40%) were low biofilm former whereas 5/ 15(33.3%) were non biofilm formers.

4) Prevalence of *ecpA* gene:

The result of PCR assay revealed that 14 (93.3 %) of *K. pneumoniae* isolates were owned *ecpA* gene while 1(6.7%) of these isolates were lacked this gene as mentioned in the appendix.

IV. DISCUSSION

K. pneumoniae is the main opportunistic pathogen responsible for worldwide nosocomial and acquired community infections as meningitis, pneumonia and urinary tract infection [15] with tremendous range of reservoir sources as organic and inorganic bedding materials, soil, water, plants, dairy herds and their utensils and bovine skin, mucosae and feces[16]. *K. pneumoniae* infection controlling was depended on infected cases diagnosis and treatment, in current study, endeavors to isolate and identify *K. pneumoniae* from upper and lower respiratory tract of apparently healthy and unhealthy cattle were achieved.

The present findings disclosed that the unhealthy animals exposed high percentage of isolates as compared with the apparently healthy ones which may indicated that *K. pneumoniae* associated with respiratory tract infections of cattle, this result was in conformity with [7] in Egypt, who registered that high incidence of the *Klebsiella* spp. 62 (25.2 %) which isolated from (246) ailing animals from cattle predominantly with isolation percentage form (25.6 %) followed by sheep which consisted (24.2 %) and they detected that 44 (17.9 %) of inspected animals were revealed *K. pneumoniae*, also [17] found that *K. pneumoniae* occupied about 11 (64.7%) of 17 mastitic animals.

The actual finding elucidated that the isolated *K. pneumoniae* proportion from lung tissue 7 (3.18 %) was higher than nasal cavity isolates 4(1.8%) of animals expressed respiratory signs ,this result may indicated that animals may exposed to exertion factors that facilitate *K. pneumoniae* reaching, a normal flora to alveolar spaces ,this proof was concurrent with results of isolated bacteria from apparently healthy animals that exhibited high percentage of nasal cavity bacterial isolates 3(1.4%) as compared with proportion of lung isolates 1(0.45%).

The present result was in agreement with [7], who stated that (28.7 %) of the nasopharyngeal swabs from cattle were positive for *K. pneumoniae* isolates which followed the fecal samples isolates percentage, also [18] reported that the nasal and bronchial mucosa swabs of mammals and human suffered from respiratory sign such as severe pneumonia expressed positive *K. pneumoniae* isolates.

K. pneumoniae proportion isolated from lung tissue in present study was agreed with the finding of [19], who proved that this pathogen was isolated from (15.9 %) of sheep lung tissue suffering from pneumonia and pulmonary abscesses. isolated *K. pneumoniae* from nasal cavity of seemingly healthy animals may corroborate some authors statements which stipulated that *K. pneumoniae* is a nasopharyngeal as well as intestine normal flora of humans and animals [20]. However, environment may consider as important cattle infection source by *K. pneumoniae* in which this pathogen are present in soil, drinking water and plants.

Our result reported that 10 (66.7%) of *K. pneumoniae* isolates had biofilm creation ability which indicated that these local isolates were responsible for the cattle respiratory infection as long as *K. pneumoniae* can using biofilm in early infection stage [21].

The biofilm considered prime *K. pneumoniae* virulence factor responsible for infection, act as bacterial assistant to overcome antibiotic treatment along various biofilm formation stages (planktonic cells at mid-log and stationary phase, adherent monolayers and mature biofilms) and prevention C3b and IgG activity resulted in bacterial infection permanency [22]; [23].

The actual result showed that among (15)bacterial isolates 10(66.7%)were biofilm producers, this result may referred to their survival ability in cattle flock environment and this was consent with [24], who mentioned that miscellaneous bacterial biofilm formers had survival ability in hospital circumference, surgical wound and medical implant, nevertheless the present result was inconsistent with [11], who proved that the *K. pneumoniae* was (100 %) biofilm inducers while our result correlated with [24], who reported that (76%)*K. pneumoniae* isolates were biofilm creators.

K. pneumoniae possessed certain genes such as the fimbrial *ecpA* gene that had biofilm production and drug resistant responsibilities, thus, our PCR assay results confirmed the result of biofilm formation screening and also supported idea of our isolates had variable virulence degree.

Our result found that 14 (93.3 %) among (15) *K. pneumoniae* isolates owned (*ecpA*) gene which corresponded with [14], who found that (66/69) clinical strains of *K. pneumoniae* had *ecpA* gene (96%) whilst [11], found that 50/ 50 (100%) of *K. pneumoniae* isolates possessed *ecpA* gene.

The changeful percentage of *ecpA* existence relied on nature of *K. pneumoniae* fimbriae that played a role in bacterial adherence to epithelial cells, biofilm formation on abiotic and biotic surfaces and considered as substantial virulent agent correlated with *K. pneumoniae* pathogenesis [25]. *E. coli* common pilus (ECP) is extracellular adhesive fiber disseminated in outer bacterial membrane, encoded by the chromosomal *ecpRABCDE* operon which substantiated firstly in association with *E. coli* strains, thereafter found in many other serious pathogenic Enterobacteria as *Citrobacter rodentium*, *Shigella boydii*, *Enterobacter* and *K. pneumoniae* which appear in (90 %) in the latter.

There was suggestion that (ECP) plays a dual role in early biofilm developmental phase and host cells discrimination [26]; [14]. It was recorded that (90 %) of *K. pneumoniae* strains isolated from hospital acquired infections produced ECP and biofilm formation that mediated chronic infections and resistant immune response [14].

V. CONCLUSIONS

The local *K. pneumoniae* isolates were biofilm producer strains as well as they expressed *ecpA* gene which responsible for biofilm formation and antibiotic resistance.

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