Phylogenetic analysis of *Klebsiella pneumoniae* isolates of respiratory tract infections in humans and sheep

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Abstract

Background: *Klebsiella pneumoniae* is an important opportunistic pathogen, which is capable of colonizing the respiratory system in both humans and animals causing mild to severe infections.
Aim: This study aims to isolate *K. pneumoniae* from the nasal discharges of human and sheep as well as identify the antibiotic resistance and molecular phylogeny of local isolates.
Methods: A total of 100; 50 humans and 50 sheep, positive nasal swab isolates were selected, and confirmed biochemically and by the VITEK-2 system. Molecular testing using the polymerase chain reaction (PCR) and phylogeny was conducted.
Results: On MacConkey agar, *Klebsiella* isolates appeared as large, pinkish, and mucoid colonies; while microscopically, it appeared as Gram-negative rods. Traditional biochemical tests revealed that 62% and 78% of human and sheep isolates were positive *Klebsiella* isolates, whereas respectively, 54.84% and 71.8% of these isolates were positive by VITEK-2. Antibiotic susceptibility tests showed that the human isolates were sensitive to aztreonam, piperacillin-tazobactam, ciprofloxacin, and cefuroxime. Subsequently, sheep isolates were sensitive to cefuroxime, ciprofloxacin, piperacillin-tazobactam, ampicillin, cefoxitin, and tetracycline. Targeting *16S rRNA* gene, a total of 17 human and 28 sheep isolates were molecularly positive *K. pneumoniae*. Phylogenetic analysis of study human and sheep isolates showed their identity to NCBI Indian (LC747146.1) and Iraqi (LC711141.1) isolates, respectively. Comparative analysis between the local human and sheep isolates revealed a significant identity that ranged from 99.82% to 99.88% with a percentage of mutation ranging from 0.008% to 0.002%.
Conclusion: *Klebsiella pneumoniae* is a highly prevalent bacterium in both human and sheep with an observable resistance to antibiotics. Molecular phylogeny of study isolates demonstrated their close relation, suggesting the possible direct or indirect transmission of the bacterium from sheep to human or *vice versa*. Moreover, studies are greatly important to estimate the routes of bacterial transmission. Also, extensive hygiene practices could be lowered the spreading of *K. pnuemoniae* to farm workers.
Keywords: *16S rRNA* gene, Antimicrobial susceptibility, Iraq, Polymerase chain reaction, Upper respiratory tract infections.

Introduction

Klebsiella genus is a group of non-motile, rod-shaped, Gram-negative bacteria that typically expresses two antigens on its cell surface: lipopolysaccharide (O antigen) and capsular polysaccharide (K antigen), (Choi *et al*., 2020; Gujarati *et al.*, 2020). In both human and animals, *K. pneumoniae* is the major pathogenic member of the *Klebsiella* genus, which colonized mainly in intestinal and respiratory tracts causing different diseases such as meningitis, arthritis, urinary tract illness, liver abscess, and bacteremia (Liao *et al.,* 2016; Wareth and Neubauer, 2021). In the respiratory system, asthma and pneumonia are the most common respiratory diseases which are complicated by other factors such as interactions with other infectious respiratory pathogens, low immunity of the host, poor environmental conditions, and stress (Trueba and Ritz, 2013; Lou *et al.,* 2018).

In many countries, sheep represent the most important growing animals in the livestock sector due to their ability to convert different types of forage into valuable