 Archives of Razi Institute, Vol. 77, No. 2 (2022) 525-532 DOI: 10.22092/ARI.2022.357802.2099

1. Introduction

Original Article

Molecular Detection and Phylogenetic Analysis of Pseudomonas aeruginosa Isolated from Some Infected and Healthy Ruminants in Basrah, Iraq

Al-Tememe, T. M. K[1], Abbas, B. A[1] *

1. College of Veterinary Medicine, University of Basrah, Basrah, Iraq

Received 12 February 2022; Accepted 6 March 2022

Corresponding Author: basil.abbas@uobasrah.edu.iq

Abstract

Although *P. aeruginosa* is an environmental organism, it is infrequently found on the skin, mucous membranes, and in the feces of some healthy animals (wild, companion, or farm animals). *P. aeruginosa* produces a variety of toxins and enzymes which promote tissue invasion and damage. *P. aeruginosa* demonstrated resistance to several antimicrobial agents. It is of significant importance in both animal and human medicine. The present study aimed to isolate and diagnose *P. aeruginosa* isolates from some ruminants, cow and sheep, from different regions of Basrah, Iraq. A total of 200 samples were taken from infected and healthy ruminants, as well as the environment surrounding the animal in Basrah, Iraq. The identification of *Pseudomonas aeruginosa* was performed by conventional and molecular methods using the 16SrRNA gene and aroE gene by polymerase chain reaction (PCR). The recorded data pointed out that *P. aeruginosa* was successfully isolated from infected animals (cows and sheep) with total percentages of 46% and 22%, respectively. These percentages were obtained at 8% and 4% from healthy cows and sheep, respectively. The percentages of isolation of the environment surrounding cows and sheep were 40% and 32%, respectively. A higher percentage of infection was observed in the eye, skin, and wound swabs of cows. Healthy cows and sheep gave only three isolates of *P. aeruginosa*, while the environmental swabs recorded 18 isolates. Bacterial isolates were identified by culture methods and Vitek- 2. To confirm the diagnosis more accurately at the level of the species, the molecular confirmation was performed by PCR amplification of genus and species with 16S rRNA gene sequences. The results pointed out that all 10 selected isolates gave positive results, and the gene size was ≈ 1500 bp. New strains were recorded in GenBank/NCBI, and the phylogenetic tree was constructed. The isolates fall in three clads. Molecular confirmation of other isolates in this study (42 isolates) was carried out by PCR amplification of aroE gene. All PCR products of these isolates were amplified≈ 495 pb on agarose gel electrophoresis.

Keywords: a*roE*gene, Cow, *Pseudomonas aerugenosa*, Sheep, 16SrDNA

Although *P. aeruginosa* is an environmental organism, it is also infrequently found on the skin, mucous membranes, and in the feces of some healthy animals (wild, companion, or farm animals) (1). *P. aeruginosa* is an opportunistic pathogen and infection is preceded by a breach in host defenses, such as breaks in the skin. This organism produces a variety of toxins and enzymes which promote tissue invasion and damage. *P. aeruginosa* demonstrates resistance to several antimicrobial agents. It is usually susceptible to the aminoglycosides, semisynthetic penicillins, such as piperacillin and ticarcillin, third- and fourth-generation cephalosporins (ceftazidime and cefepime, respectively), carbapenems (except ertapenem), and the fluoroquinolones (1). *P. aeruginosa* has significant