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Identification of multi-drug resistant *Pseudomonas aeruginosa* from otitis

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Abstract
The sample was taken from the goat that was receiving treatment at the TVCC in Mannuthy, Thrissur, for an ear infection. The sample was collected from the otitis region by using a sterile cotton swab. *Pseudomonas aeruginosa* (*P aeruginosa*) was isolated from the sample by streaking it over culture media. Using morphological, cultural, and biochemical methods, the pure colonies were identified. Using the disc diffusion method, the results from multiple antibiotics were found to be resistant. Aminoglycosides was the most powerful one since it is also show resistance. Polymyxin B, Quinolones, Cephalosporins, Sulfonamides, Penicillin and Tetracycline antibiotics groups also showed 100% resistance to this *P. aeruginosa*.

Keywords: *Antibiotic resistance*, *P. aeruginosa*, otitis infection, goat

Introduction
Pseudomonas spp. is the most significant pathogenic agent in the infections (Van Eldere, 2003; Xia and Tang, 2016) [13, 14]. Antibiotics become resistant to various medical professionals, such as aminoglycosides, fluoroquinolones, and beta-lactams against *P. aeruginosa*. The most common critical issue associated with *P. aeruginosa* inhalations is the frequently observed multiple-drug resistance mechanism (Burdon and Whitby, 1967) [3].
P. aeruginosa a more virulent pathogen that increases the average infection and mortality rate in hospitalised individuals with compromised immune systems. (Burdon and Whitby, 1967; Cornelis *et al*., 1989) [3, 5]. This specific bacteria has been the source of most hospital infections in recent times, leading to high mortality rates ranging from 18 to 61%. (Grundmann *et al*., 1993) [6]. In this study deals with isolation, identification and antibiotic susceptibility tests for *P. aeruginosa* from goat clinical sample.

Materials and Methods
A 2-year old goat with otitis infection was presented to TVCC in Mannuthy, Thrissur during December 2022. The swab was collected from the otitis region. The sample was cultured on brain-heart Infusion agar (BHIA), blood agar (BA) and MacConkey's agar (MAC), then incubated at 37°C for 24-48 hrs. The colonies were identified by morphological, staining and biochemical techniques (Koneman *et al*., 1983; Quinn *et al*., 1994) [8, 9].
Antibiogram was performed with 14 antibiotics by disc diffusion method as per Bauer *et al*., (1966) [2]. The following antibiotics were used: Gentamycin (30 µg), Polymyxin B (10 µg), Ciprofloxacin (10 µg), Norfloxacin (30 µg), Enrofloxacin, (10 µg) Tetracycline (25 µg), Cephalexin (10 µg), Cefotaxime (10 µg), Cefotaxime clavulanic acid (10 µg), Ceftriazone sulbatum (10 µg), Ceftriazone taxobatum (10 µg), Co-trimazole (25 µg), Amoxicillin clavulanic acid (10 µg), Amoxcillin Sulbactam (10 µg). The zones of inhibition were measured in mm and compared with CLSI (2020) [4].

Results and Discussion
In BHIA the organism showed smooth colonies with a strong bluish-green colour and colourless on MAC. On Gram staining the organism appearance as Gram-negative short rod. In the biochemical test, the organism gave a positive result in the oxidase test and Voges proskauer, indole, and methyl red tests. The organism showed results in positive on catalase testing. The bacteria was identified as *P. aeruginosa* according to the morphology of the colonies and biochemical tests.

Aminoglycosides are widely used in clinics, mainly for the treatment of highly infectious diseases caused by Gram-negative microorganisms (Spilker *et al*., 2004; Tijet *et al*., 2011; Hasso and Al-Janabi, 2019) [10, 11, 7]. Antimicrobial resistance is highly prevalent and has various reasons. One of the most prevalent pathogens in hospitals is *Pseudomonas aeruginosa* and its infections (Akama et al., 2004) [1] indicated that isolates had very high percentages of resistance to aminoglycoside antibiotics. However, in this present study, the antibiotics ciprofloxacin, norfloxacin, enrofloxacin, tetracycline, cephalexin, co-trimoxazole, amoxicillin clavulanic acid, amoxicillin sulbactam did not exhibited the sensitive pattern. *P. aeruginosa* exhibits resistant to the antibiotic classes gentamicin, polymyxin-B, cefotaxime, cefotaxime clavulanic, ceftriaxone tazobactam, ceftriaxone sulbactam. These variables could result from inappropriate antibiotic use, which might cause genes to mutate into highly resistant variants, and transfer resistant genes from one person to another (Turnidge, 2003) [12].

Conclusion

In this study, *P. aeruginosa* was isolated from goat otitis infection. Identification was carried out by colony morphology and biochemical tests. The organism showed multiple antibiotic resistance. The spread of resistant genes from one individual to another and inappropriate use of antibiotics could lead to gene mutation and high variant resistance.

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