## Antimicrobial Resistance of Acinetobacter baumannii in Veterinary Settings: A One Health Perspective from Punjab, Pakistan

Authors : Minhas Alam, Muhammad Hidayat Rasool, Mohsin Khurshid, Bilal Aslam

Abstract: The genus Acinetobacter has emerged as a significant concern in hospital-acquired infections, particularly due to the versatility of Acinetobacter baumannii in causing nosocomial infections. The organism's remarkable metabolic adaptability allows it to thrive in various environments, including the environment, animals, and humans. However, the extent of antimicrobial resistance in Acinetobacter species from veterinary settings, especially in developing countries like Pakistan, remains unclear. This study aimed to isolate and characterize Acinetobacter spp. from veterinary settings in Punjab, Pakistan. A total of 2,230 specimens were collected, including 1,960 samples from veterinary settings (nasal and rectal swabs from dairy and beef cattle), 200 from the environment, and 70 from human clinical settings. Isolates were identified using routine microbiological procedures and confirmed by polymerase chain reaction (PCR). Antimicrobial susceptibility was determined by the disc diffusion method, and minimum inhibitory concentration (MIC) was measured by the micro broth dilution method. Molecular techniques, such as PCR and DNA sequencing, were used to screen for antimicrobial-resistant determinants. Genetic diversity was assessed using standard techniques. The results showed that the overall prevalence of A. baumannii in cattle was 6.63% (65/980). However, among cattle, a higher prevalence of A. baumannii was observed in dairy cattle, 7.38% (54/731), followed by beef cattle, 4.41% (11/249). Out of 65 A. baumannii isolates, the carbapenem resistance was found in 18 strains, i.e. 27.7%. The prevalence of A. baumannii in nasopharyngeal swabs was higher, i.e., 87.7% (57/65), as compared to rectal swabs, 12.3% (8/65). Class D β-lactamases genes blaOXA-23 and blaOXA-51 were present in all the CRAB from cattle. Among carbapenem-resistant isolates, 94.4% (17/18) were positive for class B β-lactamases gene blaIMP, whereas the blaNDM-1 gene was detected in only one isolate of A. baumannii. Among 70 clinical isolates of A. baumannii, 58/70 (82.9%) were positive for the blaOXA-23-like gene, and 87.1% (61/70) were CRAB isolates. Among all clinical isolates of A. baumannii, blaOXA-51-like gene was present. Hence, the co-existence of blaOXA-23 and blaOXA-51 was found in 82.85% of clinical isolates. From the environmental settings, a total of 18 A. baumannii isolates were recovered; among these, 38.88% (7/18) strains showed carbapenem resistance. All environmental isolates of A. baumannii harbored class D β-lactamases genes, i.e., blaOXA-51 and blaOXA-23 were detected in 38.9% (7/18) isolates. Hence, the co-existence of blaOXA-23 and blaOXA-51 was found in 38.88% of isolates. From environmental settings, 18 A. baumannii isolates were recovered, with 38.88% showing carbapenem resistance. All environmental isolates harbored blaOXA-51 and blaOXA-23 genes, with co-existence in 38.88% of isolates. MLST results showed ten different sequence types (ST) in clinical isolates, with ST 589 being the most common in carbapenemresistant isolates. In veterinary isolates, ST2 was most common in CRAB isolates from cattle. Immediate control measures are needed to prevent the transmission of CRAB isolates among animals, the environment, and humans. Further studies are warranted to understand the mechanisms of antibiotic resistance spread and implement effective disease control programs. Keywords : Acinetobacter baumannii, carbapenemases, drug resistance, MSLT

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