

INVESTIGATING AN *Acinetobacter baumannii* OUTBREAK IN A NEONATAL UNIT IN SOUTH AFRICA: IMPLICATIONS FOR IPC

Mulaudzi SI^{1,2}, Bolukaoto JY¹, Malemela KM¹, Motswiane MR¹, Moukangwe NF^{1,2}, Rashopole MS^{1,2}, Baloyi P³, Masote E³, Maphake J³, Musyoki AM^{1*}, Nchabeleng M^{1,2}

¹*Department of Microbiological Pathology, School of Medicine, Sefako Makgatho Health Sciences University, Pretoria, South Africa.*

²*Microbiology Department, National Health Laboratory Services, Dr George Mukhari Tertiary Laboratory, Pretoria, South Africa*

³*Department of Paediatric and Neonatal Units, Dr George Mukhari Academic Hospital, Pretoria, South Africa*

Introduction: *Acinetobacter baumannii* (*A. baumannii*) is an aerobic, Gram-negative coccobacillus that has emerged as an important human pathogen exhibiting increased antimicrobial resistance and causing most human infections. The laboratory, through ongoing passive surveillance for multidrug-resistant organisms, detected an increase in *A. baumannii* cases in the neonatal unit from the second week of June. These were from various samples such as blood cultures, tracheal aspirates and catheter tips. Typically, the unit sees between one and three cases per week. However, a noticeable rise in the number of cases prompted further investigation. Thus, this study aimed to assess the antimicrobial susceptibility patterns and genetic relatedness of the isolates to determine whether the increase in cases was indicative of a possible outbreak or transmission within the unit.

Methods: Patient samples were collected as per routine for microbial investigation. Environmental samples were taken by swabbing the surfaces of the equipment, which included the different parts of the mobile suction unit, the table used during ward rounds, the main door handle, and a stethoscope from one of the clinicians. These were processed according to laboratory standard procedures. The genetic relatedness of bacterial strains was also assessed using the rep-PCR assay.

Results: The patient's suction catheter had significant growth of both *A. baumannii* and *Klebsiella pneumoniae*. One environmental sample grew *Stenotrophomonas maltophilia*, while other environmental samples had no growth. The door handle and the stethoscope grew coagulase-negative *Staphylococcus*. Antibigrams of the *A. baumannii* isolates (n=19) from patient and environmental samples showed similar resistance patterns, while rep-PCR analysis revealed genetic clonality among the isolates. The isolates were extensively drug-resistant and remained susceptible to colistin and tigecycline.

Conclusion: Although the exact source of the infection could not be identified, the outbreak was successfully contained and managed through the reinforcement of multimodal IPC strategies.