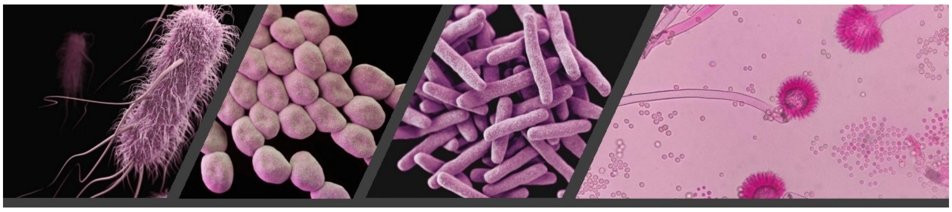
7th International Conference of the European College of Veterinary Microbiology (ECVM)



Contribution ID: **111** Type: **Oral presentation**

Antimicrobial resistance profile and mobilome of *Klebsiella pneumoniae* isolates from the reproductive tract of mares and stallions

Thursday 11 September 2025 16:30 (15 minutes)

Klebsiella pneumoniae is associated with reproductive infections in both mares and stallions, and has great potential for acquiring antimicrobial resistance genes.

Reproductive samples collected from thoroughbred horses in Australia were cultured (2020 and 2022 [inclusive]). Conventional laboratory methods (colony morphology, biochemical, motility tests) were used to presumptively identify *K. pneumoniae.* Antimicrobial susceptibility testing and whole genome sequencing were performed. Genetic diversity and phylogeny were evaluated by MLST and alignments/comparisons of complete sequences. Further analysis was performed to detect resistance genes and mobile genetic elements.

Of 91 *K. pneumoniae* isolates (mare: 76, stallion:15), multidrug-resistance (MDR) was identified in 59% and 33% of isolates from mares and stallions respectively. Thirty-one sequence types were identified, and phylogenetic analysis suggested a significant level of genetic diversity, with isolates grouped into 31 distinct subclades. A high frequency of IncFIB(K) plasmids and integrons was detected among MDR isolates and several novel configurations of resistance genes were identified.

This study revealed a concerning level of antimicrobial resistance and a diverse population of *K. pneumoniae* in the equine reproductive tract. These findings highlight the crucial need for ongoing monitoring and characterization of *K. pneumoniae* for effective disease control and management.

Keywords

Horse, Veterinary Microbiology, Whole Genome Sequencing, Phylogenetic Analysis, Mobile Genetic Elements

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Professional Status of the submitter, who is also the speaker

PhD Student

Author: Dr KAWARIZADEH, Amin (The Centre for Equine Infectious Disease, Melbourne Veterinary School, Faculty of Science, University of Melbourne)

Co-authors: Ms BLISHEN, Anna (Scone Equine Hospital); Dr CHICKEN, Catherine (Scone Equine Hospital); Prof. GILKERSON, James (The Centre for Equine Infectious Disease & National Centre for Antimicrobial Stewardship, Melbourne Veterinary School, Faculty of Science, University of Melbourne); Mr MITCHEL, Keith (Scone Equine Hospital); Dr BAILEY, Kirsten (The Centre for Equine Infectious Disease & National Centre for

Antimicrobial Stewardship, Melbourne Veterinary School, Faculty of Science, University of Melbourne); HARDEFELDT, Laura (The Centre for Equine Infectious Disease & National Centre for Antimicrobial Stewardship, Melbourne Veterinary School, Faculty of Science, University of Melbourne); Dr MARENDA, Marc (Asia-Pacific Centre for Animal Health, Melbourne Veterinary School, Faculty of Science, University of Melbourne); Mr BUSHELL, Rhys (Asia-Pacific Centre for Animal Health, Melbourne Veterinary School, Faculty of Science, University of Melbourne)

Presenter: Dr KAWARIZADEH, Amin (The Centre for Equine Infectious Disease, Melbourne Veterinary School, Faculty of Science, University of Melbourne)

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