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

Content

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

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