**Title:** Navigating the antibiotic resistance conundrum: Insights into gene distribution and transfer in livestock

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**Abstract**

The rise of multidrug-resistant (MDR) bacteria in livestock production presents a growing challenge to both animal and human health. This seminar will explore the prevalence, distribution, and transfer potential of antibiotic resistance genes (ARGs) in food-producing animals, with a focus on mobile genetic elements as drivers of resistance dissemination. Our studies reveal a widespread occurrence of ARGs in Enterobacteriaceae isolated from livestock feces, soil, and wastewater, with resistance determinants frequently associated with tetracyclines, β-lactams, colistin, and aminoglycosides. Comparative genomic analyses and *in vitro* experiments demonstrate that ARGs, including *bla\_CTX-M*, *mcr-1*, and *tet(W)*, are often carried on plasmids and integrative conjugative elements, facilitating horizontal gene transfer (HGT) between commensal and pathogenic bacteria. Conjugation assays confirm the mobilization of critical resistance genes, which highlights the potential for cross-species transmission within production systems. Additionally, our findings indicate that in-feed antibiotic use contributes to the selection of MDR bacteria, but environmental reservoirs also play a role in maintaining and spreading resistance. In ruminants, metagenomic and metatranscriptomic analyses further highlight the active expression of ARGs in the rumen microbiome, with evidence of positive selective pressure acting on key resistance determinants. These results emphasize the complexity of the antibiotic resistance conundrum in livestock systems and the need for a comprehensive approach to mitigate its impact on animal and public health.