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Mathematical modelling of human-domestic animals AMR spread: Exploring the use of colistin in livestock farming in rural areas

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Colistin, an antibiotic from the polymyxin group, targets gram-negative bacteria by destabilizing their outer membrane [1]. Despite its restricted use in Latin America due to toxicity concerns, colistin has re-emerged, even as a growth promoter for fattening animals, and is also an important option for the treatment of multidrug-resistant bacteria, which are considered a threat to global health [2]. Therefore, this resurgence has coincided with an alarming rise in resistance, particularly due to the mcr-1 and BLEE genes, which enable the horizontal transmission of resistance among bacteria [2, 3]. Intensive livestock farming in Latin America has exacerbated this issue by increasing the risk of resistance gene transmission between animals and humans [4].

Few mathematical models have been developed to analyze the impact of reducing antibiotic use in animals on AMR in humans, highlighting the need for more data on human-animal interactions in the spread of AMR [5]. We propose a mathematical model that incorporates the close contact of humans and domestic animals to study the spread of AMR to colistin. The model is validated using field-collected data, including the presence of BLEE and mcr-1 resistance genes in *Escherichia coli* and *Klebsiella pneumoniae* strains.

The model results suggest that the close contact between humans and domestic animals significantly influences colistin resistance levels, highlighting the need for strict measures to phase out colistin use and implement targeted interventions aimed at reducing its usage while limiting the environmental transmission of resistant strains.

Keywords: BLEE gene, mcr-1 gene, Escherichia coli, Klebsiella pneumoniae, model validation, stability

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