

## **Escherichia Coli Population Structure And Antibioresistance At A Buffalo/cattle Interface In Southern Africa**

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At a human/livestock/wildlife interface, *Escherichia coli* populations were used to assess the risk of bacteria and antibioresistance dissemination between hosts. We used phenotypic and genotypic characterization techniques to describe the structure and the level of antibioresistance of *E. coli* commensal populations and the resistant *Enterobacteriaceae* carriage of sympatric African buffalo (*Syncerus caffer*) and cattle populations characterized by their contact patterns in the southern part of Hwange ecosystem in Zimbabwe. Our results 1) confirmed our assumption that buffalo and cattle share similar phylogroup profiles, 2) identified a significant gradient of antibioresistance from isolated buffalo to buffalo in contact with cattle and cattle populations; 3) evidenced the dissemination of tetracycline, trimethoprim and amoxicillin resistance genes (*tet*, *dfrA*, *bla<sub>TEM-1</sub>*) in 26 isolated sub-dominant *E. coli* strains between nearby buffalo and cattle populations that led us 4) to hypothesize the role of the human/animal interface in the dissemination of genetic material from human to cattle and towards wildlife. The study of antibiotic resistance dissemination in multi-host systems and at anthropised/natural interface is necessary to better understand and mitigate its multiple threats. These results also contribute to attempts aiming at using *E. coli* as a tool for the identification of pathogen transmission pathway in multi-host systems.