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# Nontyphoidal Salmonella transmission reservoirs in sub-Saharan Africa: a genomic assessment from a One Health Perspective

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Background: Nontyphoidal Salmonella causes more than 1.2 million annual deaths worldwide, the majority in resource-limited countries such as sub-Saharan Africa. Nontyphoidal Salmonella have also become increasingly resistant to antibiotics and are the most frequent cause of bacteraemia in sub-Saharan Africa. Recent data suggests that this typically livestock- associated pathogen has genetically developed and adapted to different hosts and environments, proposing anthroponotic transmission.
Methods: Within this study, we collected Salmonella from humans (stool and blood), animals and the environment (dust and soil), in Tanzania and in Ghana. Strains were identified by biochemical methods and confirmed using the VITEK 2 System. Serotyping and antibiotic susceptibility testing was performed. Further, isolates were subjected to sequencing using a NextSeq 500 Illumina sequencer.
Results: 9,099 samples were collected. From these, 222 Nontyphoidal Salmonella were identified comprising 58 serovars. The highest level of resistance was in humans with fluroquinolone resistance on the increase and multidrug resistance highest in isolates from blood cultures (24%, n/N=11/46). Of the invasive strains, MLST analysis confirmed the serovars and sequence types S. Typhimurium (ST313/ST19) being most common followed by S. Enteritidis (ST11/ST1479) and S. Dublin (ST10). A sequence type overlap amongst humans and livestock or environmental strains was detected for ST19.
Conclusions: Our study demonstrates a broad serovar distribution of Salmonella from livestock and the environment not typically associated with human infections. The substantially high level of multidrug resistance and emerging fluoroquinolone resistance seen in the invasive nontyphoidal Salmonella poses a challenge to current treatment strategies. Interestingly, we found ST19 more common in invasive human disease but also prevalent in samples from livestock compared to ST313, only seen in human samples. These findings strongly support the hypothesis of anthroponotic transmission of ST313 but not of ST19 in sub-Saharan Africa.

## Keywords

sub-Saharan Africa, transmission reservoirs, Whole genome, sequencing, Salmonella enterica, One Health approach

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## Professional Status of the Speaker

Senior Scientist

## Junior Scientist Status

No, I am not a Junior Scientist.

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