Investigating the contribution of food animals to human non-typhoidal *Salmonella* disease in East Africa

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Background: Invasive non-typhoidal *Salmonella* (NTS) is estimated to cause 680,000 deaths annually, mostly in Africa. NTS is an important cause of diarrhoea and bacteraemia in Tanzania. We are investigating the potential contribution of the ruminant and poultry meat pathway to human NTS disease in northern Tanzania.

Methods: Using an interdisiplinary team consisting of social, biological and quantitative scientists, we are applying supply and value chain analysis, microbiological, epidemiological and mathematical modelling methods to integrate the information supply in a One Health approach to assess the contribution of food animals to NTS disease. Data and sample collection was performed in the Kilimanjaro and Arusha Regions in Tanzania. Faeces, carcass swabs, and meat from cattle and goats were obtained at slaughter and from butchers. Cloacal swabs were obtained from live chickens on farms. Environmental samples were taken from the slaughter and butcher sites. Modified FDA-BAM methods were used for NTS isolation. The genetic relatedness of Tanzanian NTS isolates from animals and East African NTS isolates from human stool and bloodstream will be compared using ribosomal Multilocus Sequence Typing and core genome sequence typing.

Results: To date, our analysis has supply chains of varying lengths and complexity, including formal and informal slaughter locations and eateries. NTS have been recovered from 4 (2.2%) of 185 chicken cloacal swab samples, 2 (1.2%) of 166 cattle faecal samples, 6 (3.6%) of 165 goat faecal samples, 26 (11.8%) of 220 beef samples, 7 (4.9%) of 143 goat meat samples, 0 (0.0%) of 116 cattle carcass swabs, 1 (0.8%) of 129 goat carcass swabs and 14 (12.2%) of 115 of environmental samples.

Conclusions: We have isolated NTS from cattle, goat, and chicken samples. Further isolate characterisation and modelling will indicate if and how livestock contributes to human NTS disease.