Cataloguing zoonotic tick-borne bacterial pathogen strain diversity in wild rodent species in rural South Africa

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Rodents are widespread and abundant and considered important reservoir hosts for many pathogens. They can act as both intermediate infected hosts or as hosts for arthropod vectors such as ticks, mites and fleas; consequently playing a key role in the natural circulation of vector-borne viral, bacterial and parasitic infections.

As in the rest of Africa, undifferentiated febrile illness is among the most common presenting signs in patients seeking medical care at the community health clinics in the Mnisi community, Mpumalanga, South Africa; an area of high rural poverty. Fever is often misclassified as malaria; and understanding of aetiologies is very limited. Recent research suggested that rodent-borne zoonoses may be common aetiologies for febrile illness in Mnisi. It is evident that 76% of households has reported seeing rodents in and/or around their homes; of those, 62% saw them on a daily basis. The potential contribution of rodent pathogen transmission to human febrile illnesses in the Mnisi community, as well as in Africa, is thus of concern, and the active surveillance for potential pathogens is of utmost importance in order to predict and combat emerging tick-borne diseases. The aim of the study is, therefore, to catalogue the tick-borne bacterial pathogen strain diversity present in wild rodent species in the Mnisi community that could impact human health by using a metagenomics approach. We will also characterize A. phagocytophilum strains at the molecular level to elucidate the degree of phylogenetic relationship with known human pathogenic strains. This project will provide information about zoonotic tick-borne (and possible emerging) pathogens in South Africa, and will generate a wealth of genomic data that will form the basis for the development of diagnostic tests that can be implemented in rural communities ensuring appropriate interventions and benefiting human health and well-being.