

The bacterial microbiome of *Rhipicephalus sanguineus* ticks in the Mnisi community, South Africa

Ackermann R¹, Gall C², Brayton KA^{1,2}, Collins NE¹, van Wyk I³, Wentzel J³, Kolo AO¹, Oosthuizen MC¹

1 – Vectors and Vector-borne Diseases Research Programme, Department of Veterinary Tropical Diseases, Faculty of Veterinary Science, University of Pretoria, Pretoria, South Africa

2 - Department of Veterinary Microbiology and Pathology, Washington State University, Pullman, USA

3 – Hans Hoheisen Wildlife Research Station, Faculty of Veterinary Science, University of Pretoria, Pretoria, South Africa

Abstract

Rhipicephalus sanguineus is a three host tick that completes all its life stages on domestic dogs. It is, however, capable of parasitizing most vertebrates, including wildlife, cattle, dogs and humans. It is known to transmit various tick-borne diseases. In Mnisi, a rural community in Bushbuckridge, Mpumalanga, South Africa, *R. sanguineus* is one of the most prevalent ticks found on dogs. The community lies at the wildlife-livestock-human interface and the human population is at a risk of being infected with various tick-borne zoonotic diseases.

The aim of the study is to investigate the prevalence and diversity of tick-borne bacterial pathogens in *R. sanguineus* that may impact on human and animal health. To achieve this, we analyse the microbiome of ticks sampled from community dogs over a 12-month period to detect bacterial pathogens and symbionts. To date, *R. sanguineus* (n=582), *R. simus* (n=82), *Amblyomma hebraeum* (n=97), as well as 183 other ticks species have been collected from 51 dogs. Ticks are kept in a humidity and temperature controlled chamber for two days to allow them to digest their blood meal. Three *R. sanguineus* ticks from each dog are then pooled, surface sterilized, and dissected to remove their midguts and salivary glands. Genomic DNA is extracted and PCR amplified using universal 16S rDNA barcoded primers. Sequencing is done at the Washington State University's Genomics Sequencing Core using Pacific Bioscience's circular consensus sequencing. Environmental conditions and other factors that could influence the tick population or tick microbiome are also analysed. Preliminary data have shown that the microbiome is dominated by various *Coxiella* spp, including *C. burnettii*, the causative agent of Q-fever. The information gained about the bacterial

communities that abound in *R. sanguineus* will undoubtedly aid health care practitioners in the area with the diagnosis of important tick-borne diseases in animals and humans.