Contribution ID: **200** Type: **Oral presentation**

Linking immunogenetics to tuberculosis susceptibility and progression in wild meerkats

Wednesday, 11 October 2023 10:45 (15 minutes)

Tuberculosis (TB) remains a major cause of morbidity and mortality in humans and livestock, with high zoonotic and epizootic potential based on the high transmissibility between species. Host-Mycobacterium interactions are complex, and despite highly infectious clinical stages, only a fraction of infected hosts contribute to TB transmission. In wildlife, general predictors of TB progression and disease dynamics are poorly understood. Over the last two decades, wildlife TB has been on the rise in Southern Africa, affecting also the wild meerkats (Suricata suricatta) intensely studied within the Kalahari Meerkat Project. Infection prevalence with M. suricattae has increased since the late 1990s, contributing to meerkat mortality. Despite high exposure levels, there is marked variation in TB progression, with many individuals never displaying overt signs of TB. Here, we capitalize on the exceptional long-term dataset of life-history and health records to investigate the immune-genetic basis of variation in TB progression. More than 1500 individuals alive between 1999 and 2023 were genotyped at the major histocompatibility complex class II DRB-exon 2 locus to investigate whether MHC composition and/ or functional diversity contribute to TB susceptibility, progression and survival. This project advances our understanding of the role of genetics in TB epidemiology, potentially allowing for extrapolation of the findings to other, less well studied mammal species affected by TB.

Keywords

Tuberculosis, Major histocompatibility complex, long-term study, meerkats (Suricata suricatta), disease transmission

Registration-ID code

ZOO23-492

Professional Status of the Speaker

Postdoc

Junior Scientist Status

No, I am not a Junior Scientist.

Primary author: MÜLLER-KLEIN, Nadine

Co-authors: Dr SCHMID, Dominik (Institute for Evolutionary Ecology and Conservation Genomics, Ulm University); Dr RISELY, Alice (School of Science, Engineering and Environment, Salford University); Dr SANTOS, Pablo (Institute of Medical Epidemiology, Biostatistics and Informatics, Martin-Luther-University, Halle); WILHELM, Kerstin (Conservation Genomics and EcoHealth, Institute for Evolutionary Ecology and Conservation Genomics, Ulm University); Prof. CLUTTON-BROCK, Tim (Large Animal Research Group, Department of Zoology, University of Cambridge); Prof. MANSER, Marta (Department of Evolutionary Biology and Environmental Studies, University of Zurich); Prof. SOMMER, Simone (Conservation Genomics and EcoHealth, Institute for Evolutionary Ecology and Conservation Genomics, Ulm University)

Presenter: MÜLLER-KLEIN, Nadine

Session Classification: Session 9: Zoonoses & Wildlife I

Track Classification: Zoonoses & Wildlife