

Linking immunogenetics to tuberculosis susceptibility and progression in wild meerkats

Inhalt

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-Myco**acterium** 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.

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

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No, I am not a Junior Scientist.

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