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Investigating the effects of *Mycobacterium suricattae* infection on the gut microbiome of wild meerkats (*Suricata suricatta*) applying High Throughput Sequencing technology

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Contents

Introduction

- Tuberculosis
- Meerkats
- Microbiome
- Study Aims

Materials & Methods

Results

Summary

https://www.jacadatravel.com/wp-content/uploads/2016/09/accor tion_photos__Meerkats_1-1200x800.jpg

https://bmcvetres.biomedcentral.com/articles/10.1186/s12917-016-0927-x

Meerkats (*Suricata suricatta*)

Carnivores of the mongoose family (Herpestidae)

Inhabit desert regions of southern Africa

First recorded outbreak of TB in 2002: *Mycobacterium suricattae*

Lots of variation in individual susceptibility and resistance

Three stages of TB infection: latent (undetectable), active infection but symptomless, active with symptoms (late-stage TB)

Is there an interaction between TB and the gut microbiome?

Microbiome: Entire community of microbiota, belonging to all three

domains of life, occupying the skin and all mucosal surfaces

of the body

Methods for measuring microbiome diversity:

Alpha diversity: within individual diversity

Beta diversity: between individual diversity

Functional benefits: nutrient breakdown

resource competition

immune system regulation

pathogen resistance
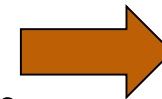
Disruption of microbiome can have negative effects on biological functions („dysbiosis)
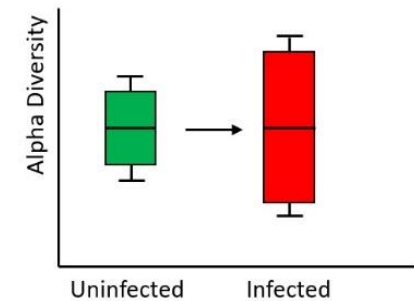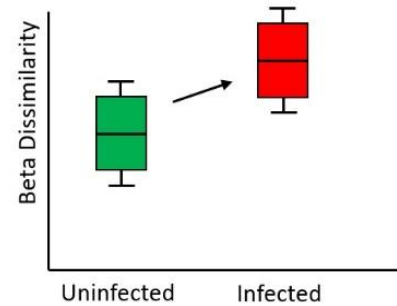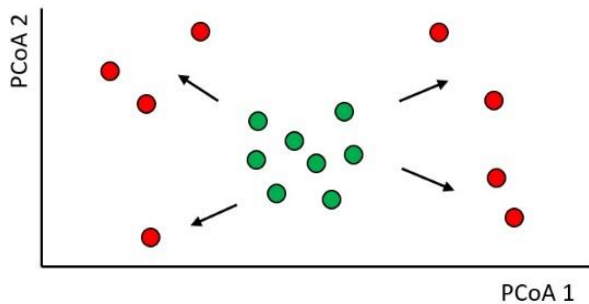
Study aims

- Does TB reduce physical condition?

- Relationship between TB infection and TB symptom status and alpha diversity?

- Relationship between TB infection and TB symptom status and beta diversity?

Major mechanisms by which TB infection causes dysbiosis

A) Deterministic change
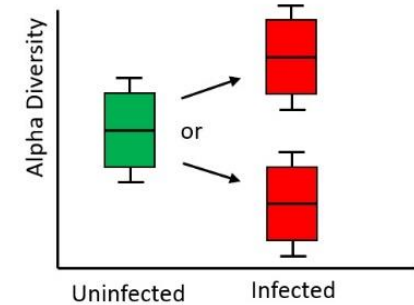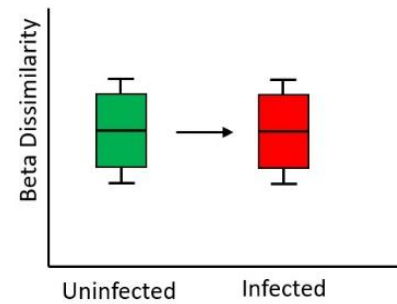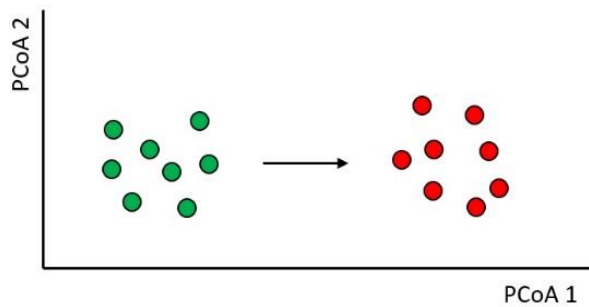
B) Stochastic change

Materials & Methods

Sample collection: Kalahari Meerkat Project in South Africa
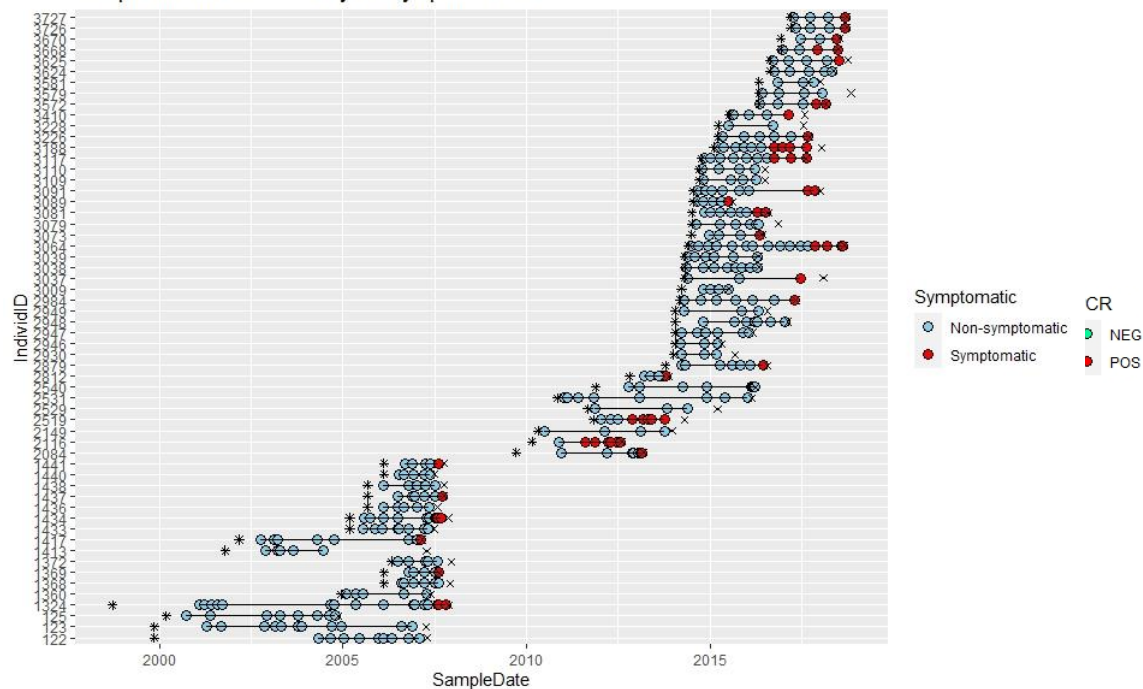
362 samples from 58 individuals
        203 PCR negative samples
        159 PCR positive samples → TB infection
        56 samples from symptomatic individuals

Sample timeline, coloured by TB symptom status

Materials & Methods

Alpha diversity:

- Observed number of ASVs
- Shannon's diversity index (abundance-weighted)
- Faith's phylogenetic diversity (phylogeny-weighted)

Beta diversity:

- Bray-Curtis dissimilarity (abundance-weighted)
- unweighted UniFrac (phylogeny-weighted)
- weighted UniFrac (abundance- and phylogeny-weighted)

Statistics:

- GLMMs for alpha diversity
- PERMANOVAs for beta diversity

Results

Hypothesis I: Uninfected meerkats are in better physical condition than infected meerkats
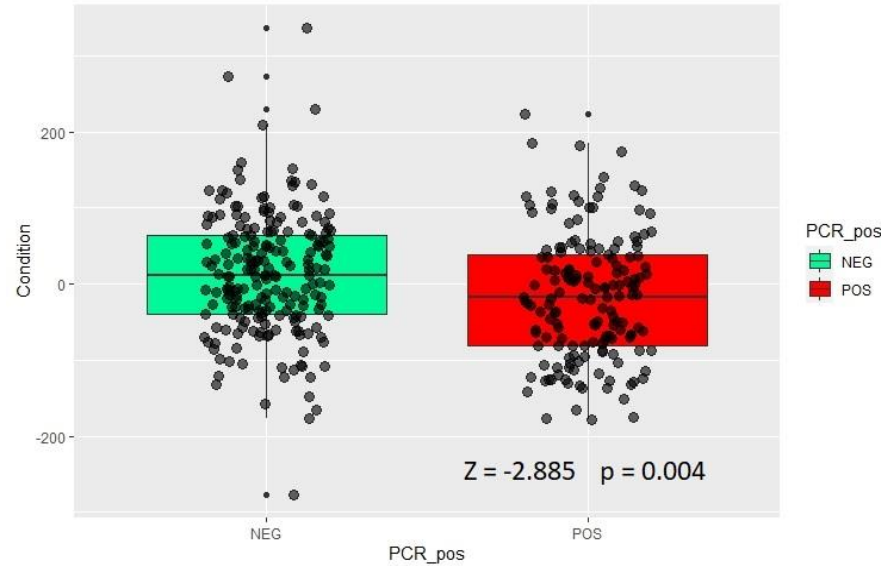
→ TB infection is associated with a lower physical condition, but effect size is small
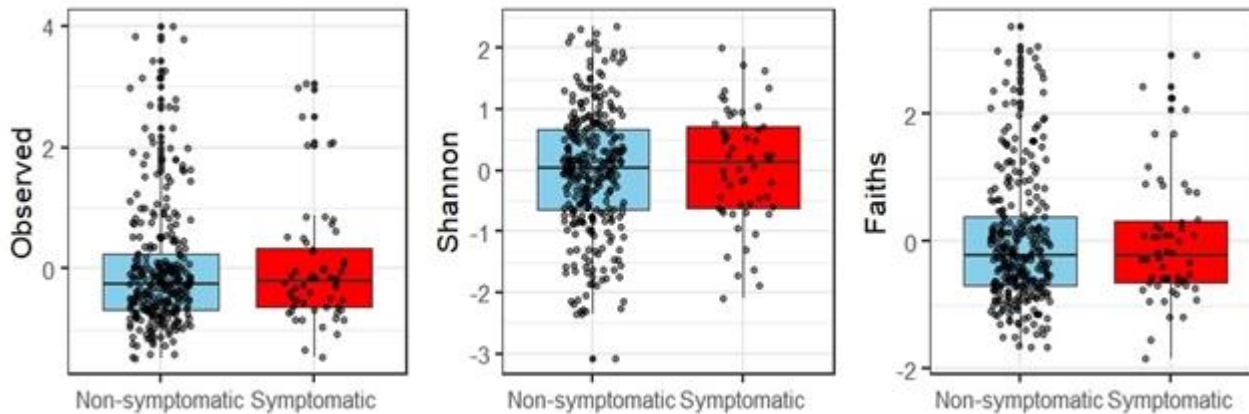
Alpha diversity

Hypothesis IIa: Variation in alpha diversity is higher in infected versus uninfected samples if effects of TB infection are stochastic
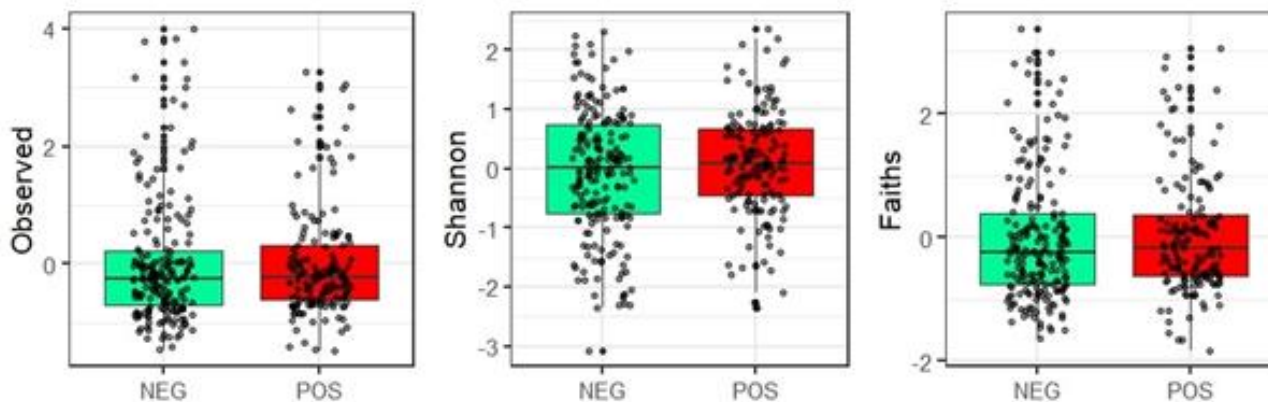
→ No difference in alpha diversity between uninfected and infected samples, nor in variation in alpha diversity

Hypothesis IIb: Because latent infections often do not affect host health, samples taken from TB symptomatic meerkats may therefore vary more in alpha diversity than those from non-symptomatic individuals

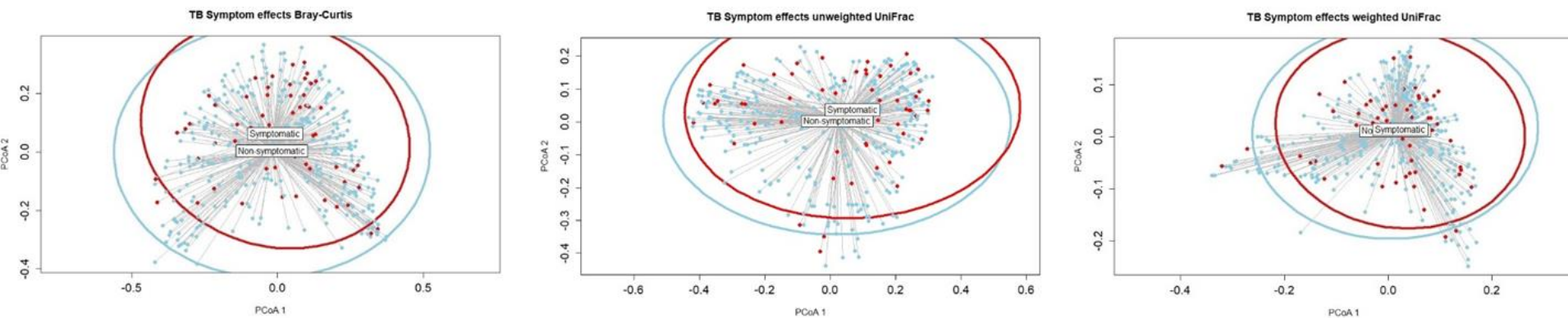→ No difference in alpha diversity between non-symptomatic and symptomatic meerkats

Beta diversity

Hypothesis IIIa: Dispersion in beta diversity is higher when meerkats are infected versus uninfected, according to the Anna Karenina principle
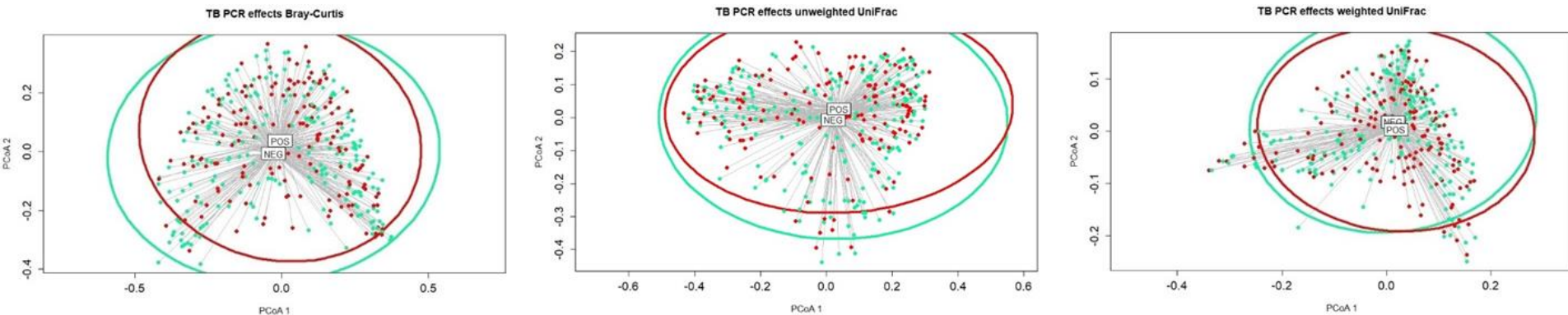
→ No difference in beta diversity and dispersion between uninfected and infected samples

Hypothesis IIIb: Samples taken when an individual is non-symptomatic may be more similar in their beta diversity to uninfected than infected states, since latent infections are often undetectable and with little effect on host health

→ No difference in beta diversity between non-symptomatic and symptomatic meerkats
→ Dispersion differed following unweighted UniFrac dissimilarity

Summary

TB infection is associated with a lower physical condition

No significant alterations of gut microbiome alpha or beta diversity induced by *M. suricattae* infection

No difference in alpha and beta diversity between non-symptomatic and symptomatic meerkats

No biological factors could be identified to influence microbiome dynamics

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Thanks for your attention!

Questions?