Using high-throughput amplicon sequencing to uncover cryptic variation in African buffalo piroplasm communities

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Introduction

- Piroplasms (*Theileria* spp. and *Babesia* spp.) are globally distributed, intracellular blood borne parasites [1,2].
- *Theileria parva* is highly pathogenic in cattle resulting in large economic losses in southern and eastern Africa[3].
- African buffalo (*Syncerus caffer*) are considered reservoir hosts for *T. parva*[3] .
- African buffalo are infected with complex communities of pirpolasm species[4]; species interactions may contribute to lack of pathogenicity observed in *T. parva* infections.
- Previous studies were unable to obtain the resolution of data needed to tease apart community dynamics.

Here, we ask: Can novel molecular methods uncover the resolution of data needed to understand important community dynamics within the African buffalo - piroplasm system?

Methods

- A semi-wild herd of ~65 buffalo from a 900 hectare enclosure in central Kruger National Park was studied for 2 years.
- Blood samples were taken every 2-3 months for high-throughput amplicon sequencing of the 18S rRNA gene.
- Sequence data was filtered and relative abundance of each unique sequence was calculated using SeekDeep[4].
- Unique sequences were identified to taxa using Neighbor Joining and Bayesian Inference phylogenetic analyses.

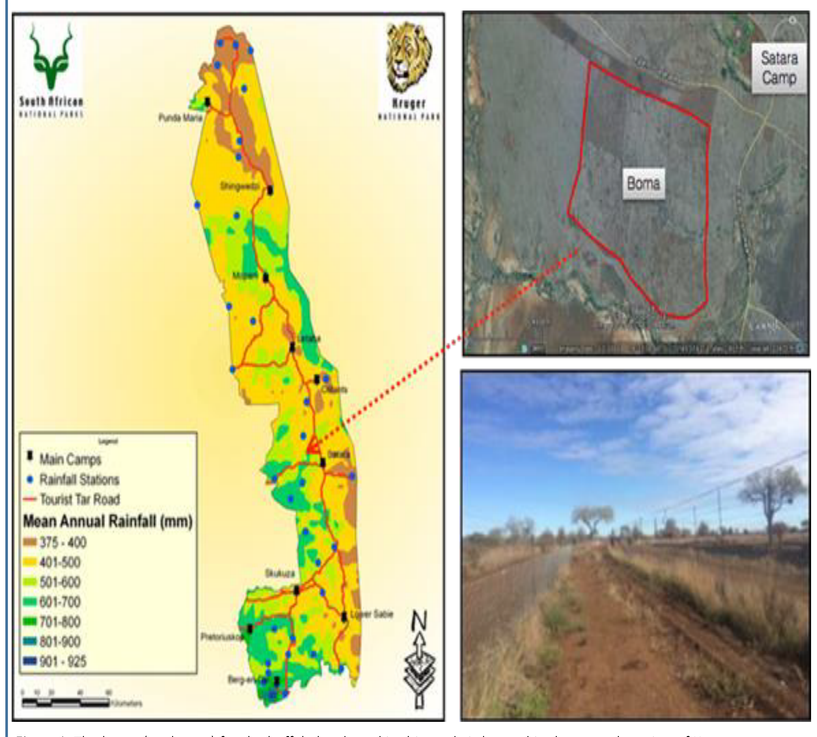

Figure 1: The boma (enclosure) for the buffalo herd used in this study is located in the central portion of Kruger National park. Total size of the enclosure is 900 hectares, and a double fence was constructed to exclude predators.

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Results

- Our samples contained 28 unique sequences; Neighbor – joining and Bayesian inference phylogenetic analyses show that each sequence groups into previously defined species clades and subtypes.
- Presence / absence data of species clade (previously reported results) indicate no variation in the system.
- Presence / absence data of subtypes and relative abundance of each taxa indicate interesting variation in community composition between animals and over time.
- *T. parva* occurs at low relative abundance.

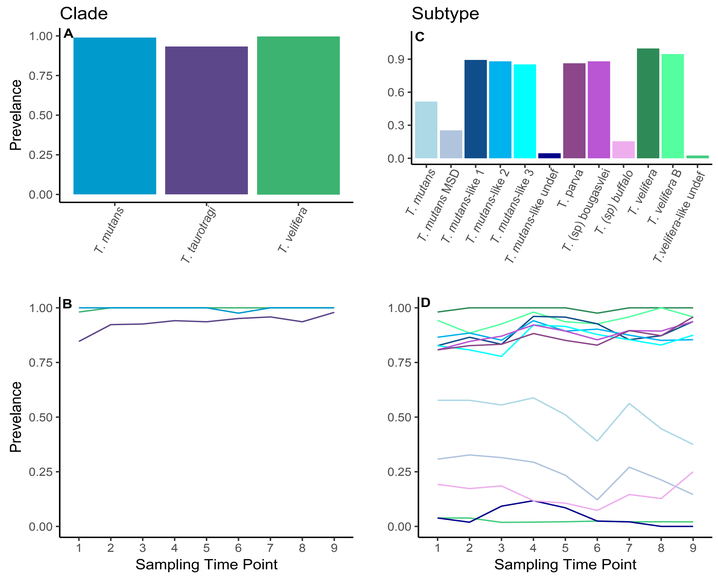


Figure 2: Prevalence over the entire study for clade (A) subtype (C) as well as prevalence of clade (B) and subtype (D) at each sampling time point. Importantly, previous studies have only reported data displayed in panel (A).

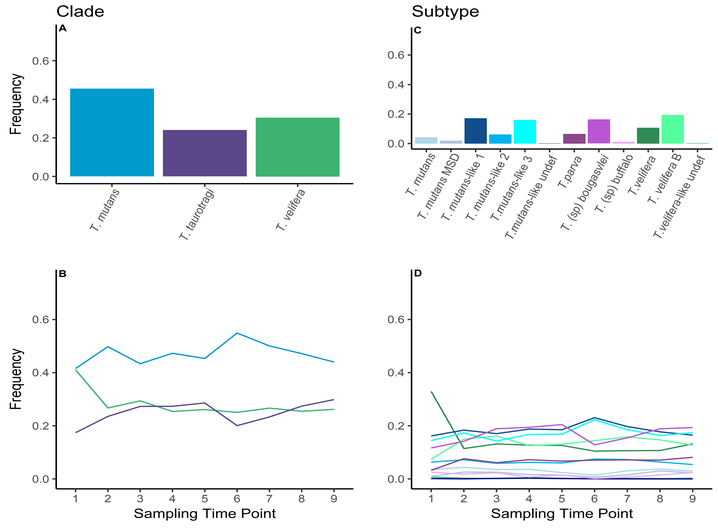
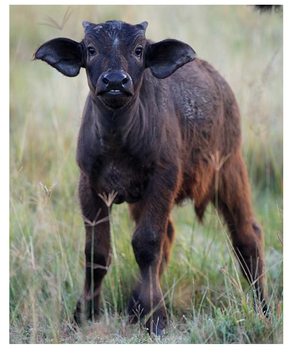


Figure 3: Frequency (relative abundance) over the entire study for clade (A) and subtype (C) as well as frequency (relative abundance) of clade (B) and subtype (D) at each sampling time point

Future Directions

- Identify sources of variation within the system (e.g. age, sex, season)
- Tease apart species interactions
- Tie community composition and species interactions to host health (i.e. How may community composition and species interactions reduce pathology of *T. parva*?)



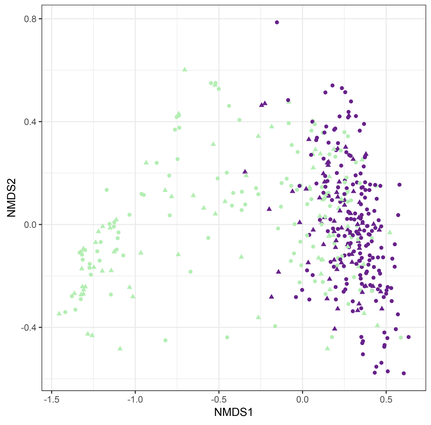


Figure 4: An ordination (NMDS, bray-curtis distance measures) displaying variation in community composition.

References:
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