

Introduction

- Recent studies indicate that change of landscape, correlating with microclimatic properties, can greatly influence tick populations
- Ecosystem engineers, species which play a significant role in the active change of habitat they inhabit, can be the agents of such change
- We are studying the impact of some of the ecosystem engineer species (semi-wild reintroduced large mammals and exotic, farm mammals) on tick populations co-inhabiting the same areas

Highlights

- Significant differences in tick abundance on areas pastured by ecosystem engineer species vs. non-pastured areas
- High overall prevalence of *Borrelia* DNA in serum samples of all of the tested ecosystem engineer species
- Possible case of non-vector transmission of the *Borrelia* bacterium via sexual or maternal route in Common eland (*Taurotragus oryx*) antelopes

Preliminary results

- 634 live ticks collected overall on all sampling sites
 - 83 found on **pastured** area
 - 551 found on **non-pastured** or transitioning areas
- Paired sample T-test comprising all samplings confirmed that there is a statistically significant difference between the means of these two sample set
- 68 animals of various species sampled for serum
- High prevalences of *Borrelia* pathogen but small sample sizes

Methods

Flagging

Semi-feral enclosures: selected transects of approx. 300 m² on both pastured and unpastured/transitioning areas

Farms: on active pasture and surrounding areas of the farm

Collection of animal sera from whole blood

Farm: *Taurotragus oryx*, *Camelus dromedarius*, *C. bactrianus*, *Lama glama*, *Bubalus bubalis* european breeds, *Struthio camelus*

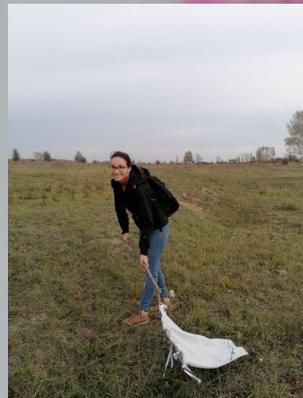
Semi-feral: *Bison bonasus*, *Equus ferus* f. *Caballus*

Molecular diagnostics

Nested-PCR: primers focusing on flagellin genes of *Borrelia burgdorferi* s.l. complex sp.

Sanger sequencing of positive samples – outsourced

Cultivations for *Borrelia* spp.



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