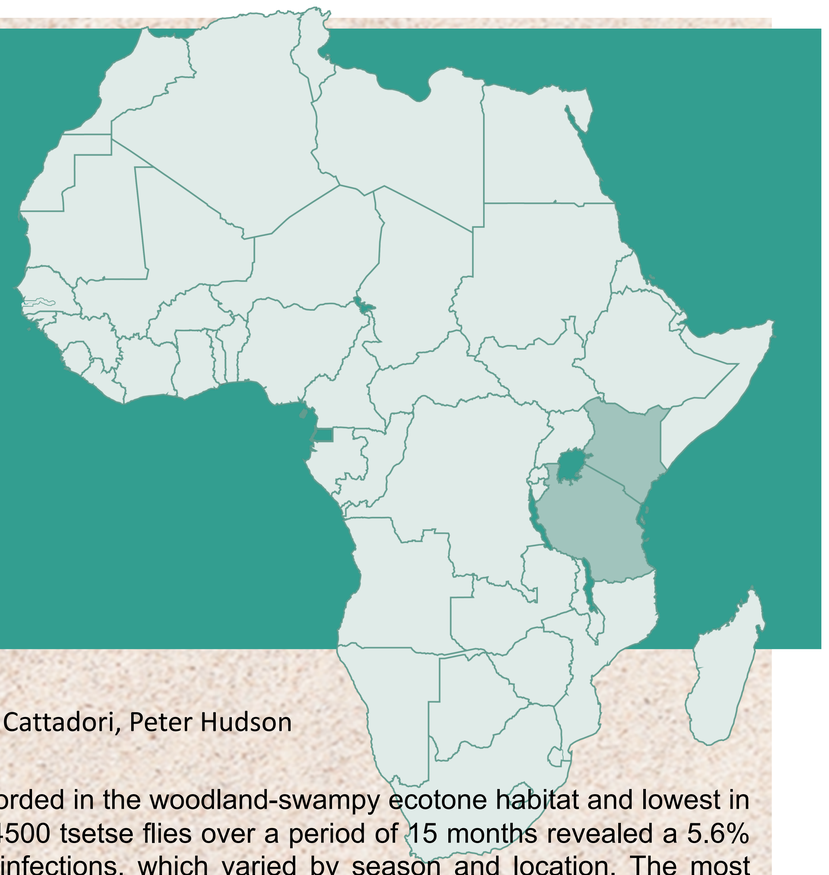
PREDICTING VULNERABILITY AND IMPROVING RESILIENCE OF THE MAASAI COMMUNITIES TO VECTOR-BORNE INFECTIONS:

AN ECOHEALTH APPROACH IN THE MAASAI STEPPE ECOSYSTEM



AUTHORS LIST:

Paul S. Gwakisa, Mary Simwango, Happiness Nnko, Anibariki Ngonyoka, Linda P. Salekwa, Moses Ole-Neselle, Anna Estes, Isabella Cattadori, Peter Hudson

The Nelson Mandela African Institution of Science and Technology, PO Box 447, Arusha, Tanzania; correspondence: psgwakisa@gmail.com

ABSTRACT

Distribution of tsetse flies is affected by changes in climate and land cover. We show that tsetse fly abundance varies with season and temperature. The generalised linear mixed (GLMM) effect model indicated significant negative relationship between maximum temperature and vector abundance across habitats.

The highest tsetse catches were recorded in the woodland-swampy ecotone habitat and lowest in riverine. Molecular analysis of over 4500 tsetse flies over a period of 15 months revealed a 5.6% overall prevalence of trypanosome infections, which varied by season and location. The most prevalent trypanosome species was *T. vivax* while *T. congolense* and *T. brucei* were least abundant. DNA sequencing of blood meals from caught tsetse flies revealed a diversity of hosts including ostrich, buffalo and humans. Further analysis of 1002 cattle DNA samples revealed an infection prevalence of 17.2% with 5% of these being *T. brucei*. These results are being used to develop an ecohealth approach for disease control.

AIMS AND OBJECTIVES

Aim: To develop an ecohealth partnership for enhancing community resilience to vector borne diseases.

Objectives

1. To downscale global climate models to the Maasai Steppe and predict current and future localised hotspots of trypanosome transmission;
2a. To use land cover models to describe recent and predict future changes influencing spatial variation in vector abundance, incorporate host availability and compare spatial overlap with climate models;
2b. To determine prevalence of trypanosome infections in tsetse flies and cattle in Maasai villages;
3. To identify opinion leaders and technology adopters in the Maasai community and work with them to develop an ecohealth partnership on disease control.

METHODOLOGY

We sampled tsetse flies monthly for a period of 15 months in Emboreet village for temporal and spatial distribution. The relationship between months, temperature and abundance of tsetse fly species were analyzed using GLMM in R 3.24. Traps were set in four habitat types (woodland-swampy ecotone, open woodland, swampy and riverine) in order to study land use/cover correlates of tsetse distribution.

Data on ground cover, vegetation cover and host availability were recorded. Tsetse flies were screened for trypanosome infections using a specific polymerase chain reaction (PCR). 1002 cattle blood samples collected from the study area were also screened for trypanosome infections using PCR. Additionally, DNA from blood meals in caught tsetse flies was analysed using mitochondrial cytochrome oxidase 1 (CO1) as well as the Cytochrome b (Cyt b) genes and sequenced to identify hosts.

RESULTS

Tsetse fly abundance varied with season and temperature, with *G. swynertonni* and *G. m. morsitan* abundance peaks differing from *G. pallidipes* peaks. Further, there was limited relationship between tsetse fly species abundance and temperature variation (fig. 1). The generalised linear mixed (GLMM) effect model indicated siginificant negative elationship between maximum temperature and abundance of G. m. morsitan and G. pallidipes. The months with high catches corresponded to a dry period with the exception of March which is the start of the rainy season and presumably included remaining flies from the dry season. High tsetse flies catches were recorded between 25-280C maximum temperatures which also reflects the high activity of tsetse fly.

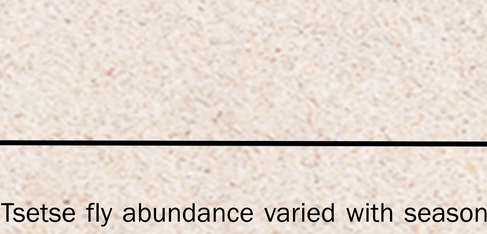


Fig 1: Seasonal variation in the abundance of tsetse fly species over multiple months and the concomitant change in temperature observed during the study period at Emboreet village.

The highest tsetse catches were recorded in the woodland-swampy ecotone habitat and lowest in riverine, where G. pallidipes was significantly abundant (Fig. 2).

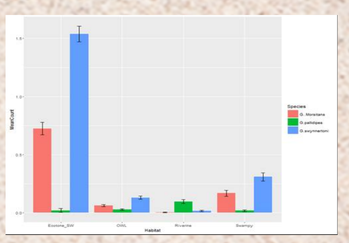


Fig 2: Variation in the mean catches of tsetse fly species in different habitats in the Maasai steppe. Abundance is expressed as geometric mean Log (x+1) and shows *G. mortisans* and *G. swyennertoni* active in Ecotone with *G. pallidipes* inhabiting riverine habitat.

Tsetse fly abundance varied in time and space, and this may be associated with proximity to wildlife. Overall, highest abundance of tsetse flies was found in Loiborsiret village. A 5.6% prevalence of trypanosome infections was found in tsetse flies and this was highest in Loiborsiret and Emboreet villages. Prevalence of trypanosomes in cattle was 17.2% with variations between the 4 villages. Three species of trypanosomes, *T. vivax, T. congolense* and *T. brucei* were detected, whereas *T. vivax* was the most predominant species in both cattle and tsetse flies (Fig. 3).

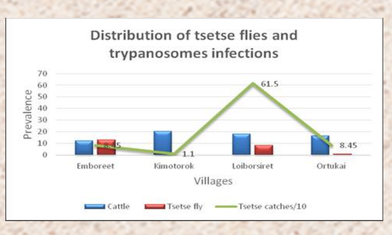


Fig 3: Tsetse fly abundance and Spatial distribution of trypanosome infections in cattle and tsetse flies

CONCLUSIONS

1. Temporal and spatial variations of tsetse flies and trypanosomes allows simulation of these parameters for future prediction of disease dynamics;
2. Correlates of land use / cover with tsetse fly distribution will help to designate hotpots of transmission and target vector control;
3. Although no human-infective trypanosomes were detected in tsetse flies, but anthropo-zoonotic feeding behaviour of tsetse flies suggests vulnerability of Maasai communities to African Trypanosomiasis

TEAM MEMBERS

Paul S. Gwakisa, Mary Simwango, Happiness Nnko, Anibariki Ngonyoka, Linda P. Salekwa, Moses Ole-Neselle, Anna Estes, Isabella Cattadori, Peter Hudson

PROJECT PARTNERS

The Nelson Mandela African Institute of Science and Technology (NMAIST), Tanzania; Penn State University (PSU), Pennsylvania, USA; Climate Systems Analysis Group, University of Cape Town (UCT), South Africa; National Institute for Medical Research (NIMR), Tanzania; Sokoine University of Agriculture (SUA), Morogoro, Tanzania

ACKNOWLEDGEMENTS

1. The Maasai communities in Simanjiro district, Tanzania
2. WHO/TDR Special Programme for Research and Training in Tropical Diseases
3. IDRC