Effects of land use on ectoparasite communities in Kenyan rodents

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Introduction

Recent research suggests that human alteration of natural landscapes (e.g. removal of large wildlife, land conversion) can amplify disease risk. For example, Lyme disease (*Borellia* spp.) in the Northeastern US has increased as forests have fragmented because a primary rodent host (*Peromyscus leucopus*) increases in abundance under such conditions (Keesing et al 2010). These types of observations indicate that conservation initiatives may act synergistically to promote public health and safeguard the environment. Since the majority of emerging infectious diseases are zoonotic (transmitted from animals to humans) and vector-borne, this could have large implications for human health. However, the mechanisms and effects of land use change on disease risk are understood for few diseases, and could be strongly affected by changes in abundance, diversity, and host specificity of ectoparasites across land use types. As part of a larger project examining these links between rodent borne disease and land use change, **this project aimed to understand diversity, host specificity, and effects of land use change on rodent ectoparasite communities, a major potential vector of disease, in the Laikipia district of Kenya.** Kenya is currently a zone of interest because 1) it is a hotspot of emerging infectious zoonotic diseases (Jones et al 2008), 2) land use is changing rapidly (Hartley et al 2007), and 3) multiple vector borne diseases are present in the relevant regional populations.

Specifically this project aimed to answer three main questions:

- **Q_1: How many ectoparasites are present? What are they? Do they transmit diseases?**
- **Q_2: How host specific are ectoparasite communities?**
- **Q_3: How does land use change affect ectoparasite communities, on both the host and landscape levels?**

Fig. 1. Map of Africa with Kenya highlighted in black. Inset is a picture taken at Mpala Research Center, the primary site at which samples were collected.

Fig. 2. Using data from the phylogenetic trees, we were able to identify host specificity among ectoparasites. In one example shown above, ectoparasite communities could actually confirm host species identities of somewhat cryptic gerbil species.

Materials and Methods

•The project was designed with a real world and an experimental component, the latter of which involves the long-term exclosure of ungulates from an otherwise conserved habitat.
•The sampling design for both experimental and real world aspects of this study was paired (converted/ exclosure landscapes paired with conserved areas) and rodent sampling at each site (n=6 for experimental manipulations, n=8 for real world land uses) was conducted using 4 nights of live trapping in 10x10 m grids over 1 ha plots. All captured rodents were thoroughly combed for ectoparasites, permanently marked, and released. Ectoparasites removed from rodents were stored in ethanol for subsequent analysis.
•At Smithsonian, ticks and fleas were initially sorted into numbered groups based on morphological differences; mites and lice were merely counted and neither sorted nor analyzed.
•A subset of parasites were sent to the University of Guelph for genetic barcoding to supplement the morphological categorizations – these were selected with the goal to have five of each morphospecies barcoded from each host type.
•From barcoding information ,we built a phylogenetic tree (Fig. 3) and used this data in conjunction with our original morphological classifications, as well as information from expert taxonomists and literature review, to create a revised understanding of ectoparasite community characteristics.
•Data analysis was conducted in EstimateS and JMP. Shannon indices were used to estimate diversity; the Mao Tau estimator was used to calculate asymptotic estimates of species richness (Colwell 2009); and ANOVAs or student t-tests were used to compare abundance and density of ectoparasites across land use types. Prior to these analyses, data sets were log transformed and then tested for normality. Following significant ANOVAs, Tukey-Kramer post hoc pairwise comparisons were performed.

Results

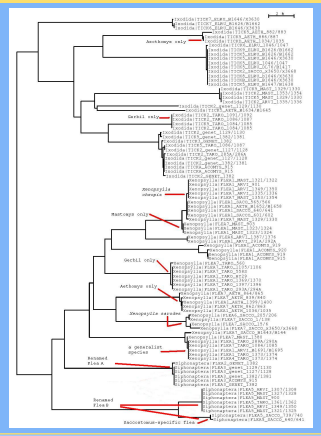

Fig. 3. Annotated phylogenetic tree with notes on host specificity and hypothesized species when supported by expert identifications and literature review. On the right are representative specimens of three common morphotypes (top to bottom): Tick Morph 2 (putative *Haemaphysalis)*, a flea of genus *Xenopsylla*, and Flea B (originally called Flea Morph 5).

Host species	# animals sampled	Total # mites	Total # ticks	Total # lice	Total # fleas	Xenopsylla spp.	Flea A	Flea B
Acomys wilsoni	32	0	2	0	7	7	0	0
Aethomys hindei	30	192	18	2	70	69	0	1
Arvicanthis niloticus	46	71	1	2	74	57	0	17
Elephantulus rufescens	12	20	224	0	2	0	1	1
Gerbillus pusillus	15	9	0	0	22	22	0	0
Mastomys natalensis	25	191	3	2	37	20	1	16
Rattus rattus	7	0	0	0	1	0	0	0
Saccostomus mearnsi	343	3021	7	18	1170	1112	2	56
Taterillus harringtoni	38	110	3	0	150	150	0	0
Gerbilliscus robustus	122	2431	59	5	658	656	0	2

Table 1. Raw counts of ectoparasites collected and sorted according to the new definitions of the morphospecies, listed for each rodent species sampled. Ticks occur almost exclusively on *Elephantulus rufescens, Aethomys hindei,* and *Gerbilliscus robustus*, with a few other individuals containing a handful of parasites each. Fleas occur nearly across the board, with the highest counts on *Saccostomus mearnsi, Taterillus harringtoni,* and *Gerbilliscus robustus*. Original classifications (visible in Fig. 3) were revised upon receipt of genetic information: all Xenopsylla have been grouped until backsorting can be done, ticks have been likewise grouped until backsorting can be done, although we have identified individuals from two genera: *Rhipicephalus* and *Haemaphysalis*.

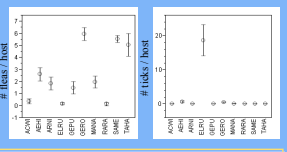

Fig 4. We observed strong host specific variation in ectoparasite communities for three of the four ectoparasite groups examined: fleas (A;), ticks (B), mites (data not shown), $P < 0.001$ for all. Only lice showed no host specificity, but sample size was small for this group (n= 29). Abbreviations for host species are as follows: ACWI= *A. wilsoni,* AEHI= *A. hindei,* ARNI= *A. niloticus,* ELRU= *E. rufescens,* GEPU= *G. pusillus,* MANA = *M. natalensis,* RARA = *R. rattus,* SAME= *S. mearnsi,* TAHA= *T. harringtoni*

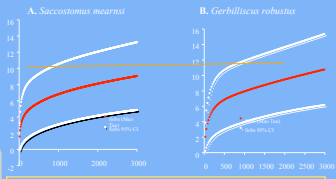

Fig 5. Mao Tau species accumulation curves for the two most-sampled rodent species: *Saccostomus mearnsi* and *Gerbilliscus robustus*. While the curves appear to be leveling off, they do not yet reach an asymptote, and the 95% confidence interval for the two species shows strong overlap. Further sampling would be necessary in order to accurately assess any differences in species richness per host species.

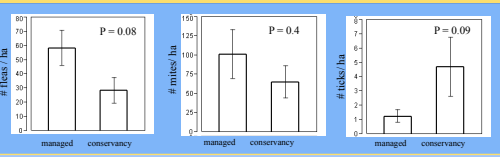

Fig. 6 Effects of land use change on ectoparasite abundance appear to vary by type of ectoparasite. Flea abundance on a landscape scale increases in managed areas, but tick abundance decreases. Results above are from real world land use change, but landscape level patterns (data not shown) are similar from exclosure experiments. Density per host shows more idiosyncratic affects (variable by species and treatment; data not shown)

Discussion and Conclusions

Q1: observable presence of ectoparasites and disease

- •Ectoparasites are abundant, but numbers vary by host and ectoparasite type. Ticks are present in low density on all species except for *E. rufescens,* where they are abundant (18.7 ticks/host). Fleas are found on all species, often in concentrations above 2-3 fleas/host.
- •*Bartonella* spp, a fever-causing bacteria, was detected in sampled fleas. It has been documented in two species of ectoparasites found in this study: *Xenopsylla cheopis* and *Rhipicephalus* spp. (Billeter et al 2008).
- •Bacteria in the genus *Rickettsia,* which causes murine typhus and is transmissable by ticks of the genus *Rhipicephalus,* was also found (Parola et al 2009).

Q2: host specificity varies, but is prevalent

- •Fleas are highly host specific, which our phylogenetic tree confirms. This will facilitate future sorting of *Xenopsylla* species mostly based on host information, assuming the generalist species *X. cheopis* can be easily identified.
- •Ticks are usually generalists, but here show an unexpected degree of host specificity. Five ticks have near-exclusive host specificity. This is surprising, but should ease the mapping and prediction of disease spread.

Q3: land use and disease risk likely connected

- •As expected, fleas occur in greater densities in managed landscapes as compared to conserved ones, as rodent abundance and/or flea density increases in these managed habitats.
- •Likewise, the higher observed concentrations of ticks in conserved areas is anticipated as ticks are more common on the larger ungulates that are less abundant in managed landscapes.
- •As habitats become more disturbed, our data suggest that flea populations will increase. *Bartonella* incidence may do likewise, as may incidence of plague (*Y. pestis,* transmitted by *X. cheopis*), which likely occurs in slightly wetter climates (Ewing and Fox 1938).
- •It appears that land use change and the risk for human disease are connected. However, a larger sample size is needed to verify these conclusions and link it to specific vectors.

Further Research Needed

•Substantial back-sorting of ectoparasites is needed, especially once more genetic information is returned. Ticks in particular pose a problem: they initially appeared to be sorted in accordance with genetic information, but information from the second barcoded tray indicates that the morphospecies are often confused. Further expert identifications will aid this process.
•We do not currently possess a sample of ample size (Fig 5) to truly analyze diversity results. In order to have an accurately sampled population, we need further collection and sorting. A large additional set of ectoparasites was recently collected from Kenya but has yet to be analyzed.

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Acknowledgments

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