Ticks and environmental change in the GLTFCA

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Outline

1. Introduction
2. Understanding tick ecology at broad spatial scales
3. Research questions for AHEAD

Introduction

Pathogens a good focus for a research program that links ideas about ecosystems and societies.

Human wellbeing, pathogens, and conservation are closely linked (interdependencies; ecosystem goods and services, quality of life, willingness to tolerate diversity).

Ticks are an important component of the food web that pathogens belong to.

Introduction

In the GLTFCA, particular interest in:

- Where ticks occur, how many, which species, what drives spatiotemporal variation.
- How changes in the environment (hosts, abiotic, human) will influence ticks.
- How changes in tick and host distributions will influence tick-host interactions and tick-borne pathogens.

Understanding tick distributions

Influences on tick occurrences:

1. Hosts: domestic and wild

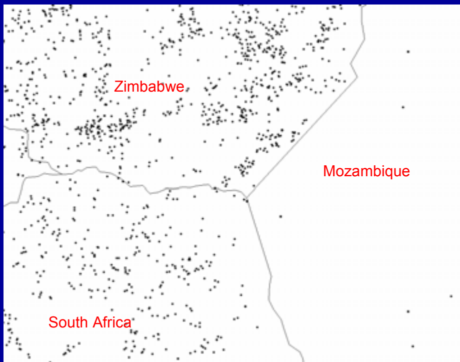
2. Habitat: vegetation, rainfall, temperature, elevation, soil type.

3. Alternative (less tenable): predation, disease, etc.

Broad-Scale Data

- Database of 43 615 individual collection records from published records
- 33 989 collections georeferenced (digitized or from a gazeteer)
- Data available on-line at http://wec.ufl.edu/cummingg/tickDIP.htm

GLTFCA Tick locality records

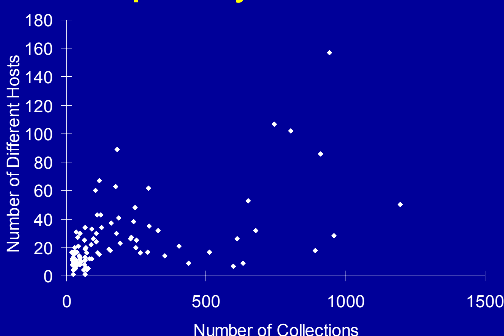


Host use: results

Of *c*.240 tick species in Africa,

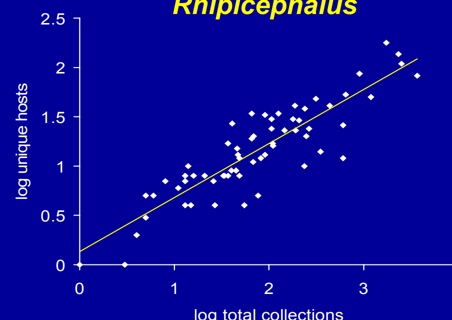
- 112 have been collected 20 times or more
- 14 are extreme generalists (collected from over 50 different host species)
- At least 39 have restricted host preferences
- Only four African ticks can be considered specialists to the host species level.

Host specificity and tick collections



N= 43 615 collections; 219 species; 8 generalists with collections > 1500 excluded

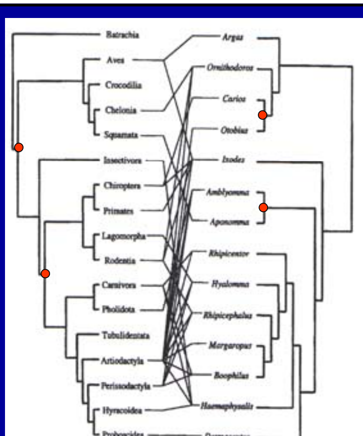
Host specificity and collections: *Rhipicephalus*



Log unique hosts vs log collection records for 64 *Rhipicephalus* species (least-squares Type I regression; $r^2 = 0.78$).

Evolutionary relationships

of ticks and their hosts: using ‘specialists’ only



Ticks and hosts

Cattle provide an informative example of lack of host regulation.

- 109 tick species collected from cattle
- 55 tick species collected from cattle at 10 or more localities
- Only 7 have distributions that match cattle.

Cattle and ticks in sub-Saharan Africa

Maps here showed cattle densities across Africa and the distribution of *R. appendiculatus*

Rhipicephalus appendiculatus

Rhipicephalus pulchellus

Map here showed the distribution of *R. pulchellus* (i.e., limited to the horn of Africa)

Amblyomma hebraeum

Map here showed the distribution of *A. hebraeum*

Summary – host analysis

- Few ticks are host specialists
- There is little evidence of cospeciation between ticks and their hosts
- Tick distributions (except for *Amblyomma rhinocerotis*, the rhinoceros tick) are not contiguous with those of their major hosts
- Tick distributions are not host-limited at broad scales

Habitat Hypotheses

Tick distributions might be limited by:

- Climate – rainfall, temperature, elevation
- Vegetation – type, structure, productivity

- both proposed as key limiting factors at smaller scales

- Also need to consider a null hypothesis (test for autocorrelation effects) and spatial biases in sampling

January NDVI

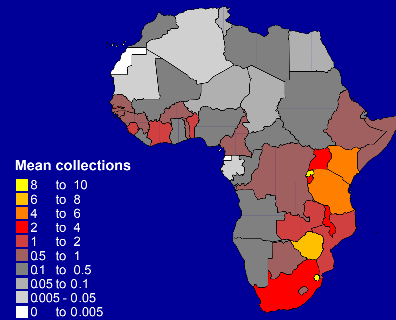
10-year mean

Map here showed AVHRR NDVI data at quarter-degree resolution across Africa.

White's Vegetation Map

Map here showed White's vegetation map of Africa

Collection localities are biased



Mean tick collections per quarter-degree square

Predicted distribution: *Amblyomma variegatum*

Maps here showed different ways of predicting *R. appendiculatus* distribution

Climate categories

Vegetation type

Predicted distribution: *Amblyomma variegatum*

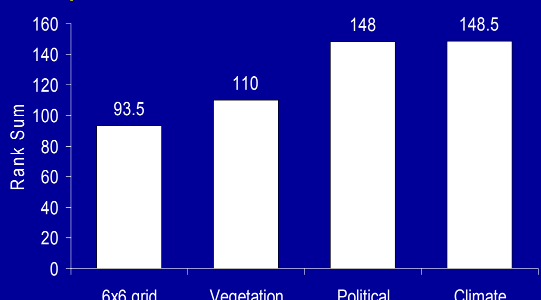
Maps here showed different ways of predicting *R. appendiculatus* distribution

Political boundaries

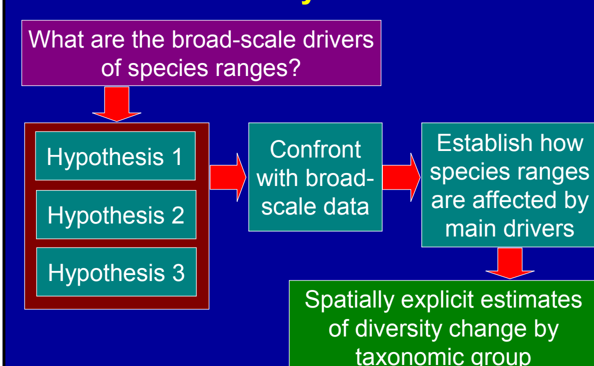
6x6-degree grid

Sum of model rank for each of 50 species

(Friedman 2-way ANOVA: F=60.72, p< 0.001)

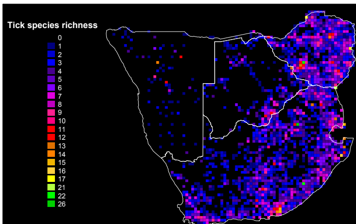


Biodiversity Estimation

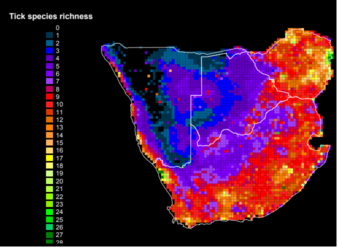


Map here showed known tick species richness across Africa at quarter-degree resolution

Map here showed predicted tick species richness across Africa at quarter-degree resolution, as improved using modelling.



Improved estimation



Current 'Invasion potential'

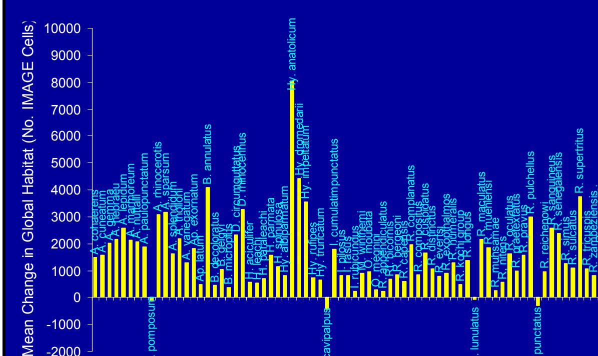
Map here showed global habitat suitability for African ticks at half-degree resolution

'Fortress World' scenario, 2100

Map here showed anticipated changes in global habitat suitability for African ticks under the Fortress World scenario

Mean change in global habitat suitability

Predicted from 8 climate scenarios



Spatial Pattern and Tick Collections

"Collection records from hosts give us a good idea of tick preferences".

Is this true?

Approach: simulate data that can be used to generate estimates of apparent and actual host preference, and see how they compare.

Assessing importance of spatial pattern

Actual Tick Tendencies
Varying between 0 and 1

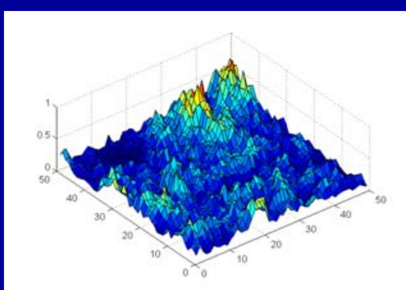
Host Abundance
Summed random walks from cellular automaton

Tick Occurrences
- random
- uniform
- clustered

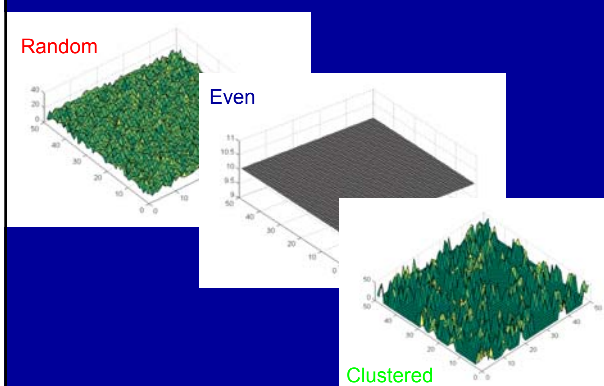
Attachment probability = $(1-(1-\textit{tendency})^{ticks})^{hosts}$

Apparent Tick Tendencies
Based on collection records

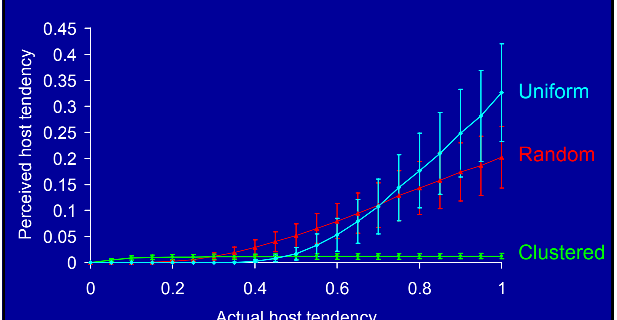
Example simulated host occurrence data



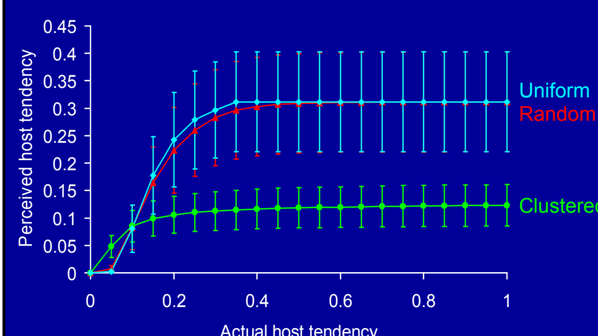
Simulated tick occurrences



Influence of spatial pattern: 2500 ticks



Influence of spatial pattern: 25,000 ticks



Summary: Interactions

- Ticks that have low population densities are more likely to be perceived as host specialists
- Ticks with clustered distributions are more likely to be perceived as host specialists
- Need to know spatial and temporal distribution of both tick and host to adequately characterize specificity

Questions for AHEAD

1. To what extent are broad-scale results for ticks applicable at smaller scales?
2. How does tick community composition influence pathogen community composition and emerging diseases?
3. How will the GLTFCA influence host, tick, and PID communities (and dynamic food web interactions)?
4. What impact will these changes have on human health?

Hypotheses

H1: Overall tick abundance will be of greater importance for the spread of disease than tick community composition, because 'problem' tick species are so generalist.

- Ticks of key species in the park are generalist enough that a single abundant vector can transmit pathogens effectively.
- Competing hypothesis: community composition matters, and the diversity of the pathogen community influences the rate of pathogen transmission.

Hypotheses

H2: Mammalian host community composition will be important for the transmission of disease, because host species will show different resistance to and transmission capability of different pathogens.

Numerous interesting study topics here. For example:

- Do predators, both of rodents and ungulates, reduce the incidence of the most important tick-borne diseases?
- Does higher ungulate diversity promote or reduce pathogen transmission?
- Does higher mammalian diversity support higher tick diversity and a higher diversity of pathogens, or not?

Hypotheses

H3: Disease transmission is more likely in 'disturbed' landscapes because simplified systems will permit ticks of opportunist species to multiply rapidly and reach high abundances in the absence of predation.

- Pathogens depend on ticks, which depend on hosts, which depend on habitat.
- Post-disturbance recolonization will occur in reverse order – i.e., plants, hosts, ticks, pathogens.
- Pathogens may be vulnerable in unexpected ways to source-sink dynamics, population fluctuations and trophic cascades lower in the food web.

Hypotheses

H4: Thresholds for transmission of tick-borne pathogens exist, and can be identified and managed, because pathogens are usually scarcer than their hosts.