Linking zoonotic disease prevalence to human and livestock exposure risk across a gradient of anthropogenic land use in Madagascar

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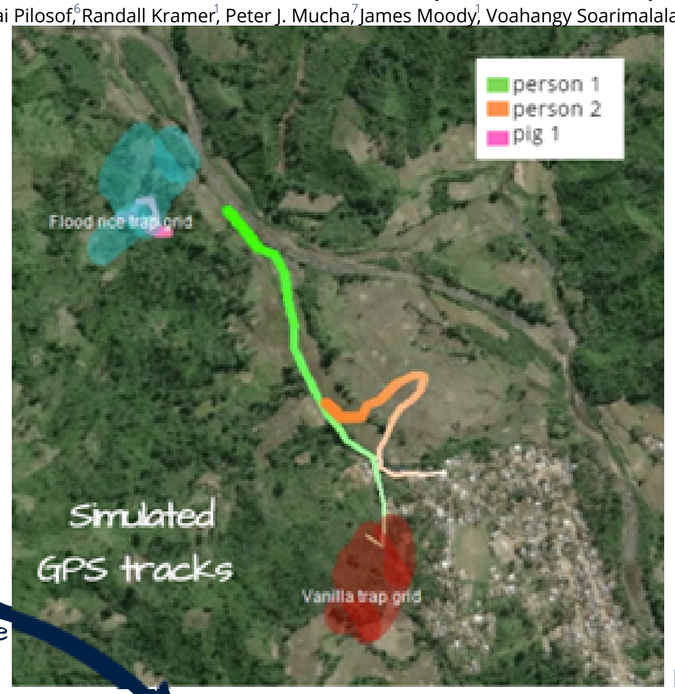
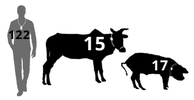
Introduction

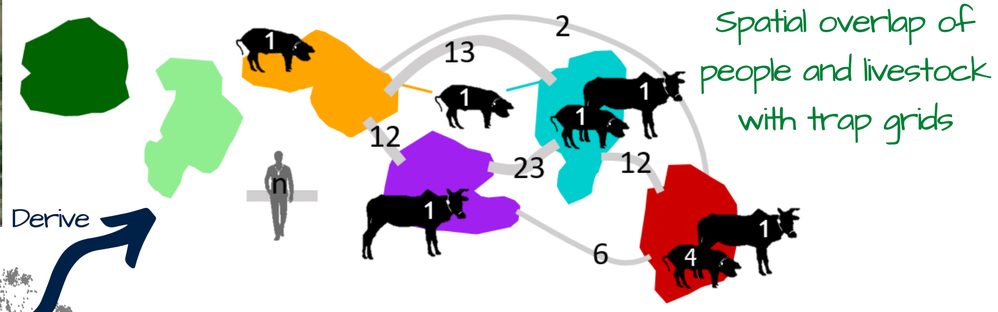
Habitat degradation alters host community structure, which can affect pathogen prevalence and influence the exposure of people and domestic animals to zoonotic diseases. The risk of exposure to zoonoses is especially high in rural areas of tropical countries, which have rich biodiversity and a high degree of habitat degradation. Investigating the links between habitat degradation, host diversity and human exposure requires data on disease prevalence combined with spatial data on human, native, and introduced wildlife and domestic animal hosts. **These data provide the means to test whether known exposures result in infections and to identify which individuals could spread a pathogen between areas.**





GPS Sample

Derive



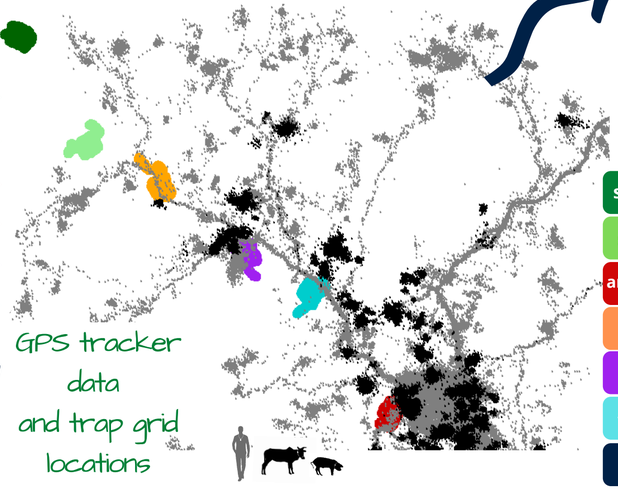
Degradation gradient

- 6 - 100m-sq grids
- 97 sherman traps
- 24 tomahawk traps
- 22 pitfall traps

Non-Native
Rattus, Mus, Suncus

Native
Tenrecidae, Nesomyidae

semi-intact forest
secondary forest
anthropogenic forest
brushy regrowth
crop fields
flooded rice fields



GPS tracker data and trap grid locations

Trap

Sample

Small mammals
All major organs, urine, feces, blood, serum, ectoparasites

Humans
Urine, feces, blood

Livestock
Urine, feces, blood, serum, ectoparasites

Test

PCR to test for:

- *Leptospira*
- Hantaviruses
- Paramyxoviruses
- Coronaviruses
- Astroviruses

Methods

- Trap native and non-native small mammals on grids following the degradation gradient in a rural area of northeastern Madagascar adjacent to Marojejy National park
- Conduct pathogen screening on all captured small mammals using molecular microbiology (DNA/RNA extraction, PCR, Sequencing)
- Distribute GPS trackers (iGotU-120) to people and their livestock in the adjacent village
- Overlay GPS data with the trap grid locations to build a bipartite network based on human and livestock overlap with trap grids

Results

- 60/122 people and 9/32 livestock overlapped with 4/6 trap grids (anthropogenic forest, brushy regrowth, crop field, flooded rice field)
  - The majority of people (n = 30) and livestock (n = 8) interacted with only 1 trap grid; 2 people interacted with all 4 trap grids
- Anthropogenic forest (vanilla) grid was accessed by the most people (n = 41), followed by the flooded rice field (n = 30), crop field (n = 24), and brushy regrowth (n = 13)
- Across all pathogen groups, prevalence was higher in non-native (0.11 +/- 0.10) than native species (0.04 +/- 0.06), but not significant (p = 0.16)

Pathogen prevalence

	Leptospira		Hantavirus		Astrovirus		Paramyxovirus		Coronavirus	
	Non-Native	Native	Non-Native	Native	Non-Native	Native	Non-Native	Native	Non-Native	Native
semi-intact forest	0 (0/2)	9 (1/11)	0 (0/2)	0 (0/11)	-	-	0 (0/2)	0 (0/11)	-	-
secondary forest	20 (13/65)	3 (1/29)	5 (3/65)	0 (0/29)	24 (13/55)	0 (0/13)	3 (2/65)	24 (7/29)	0 (0/55)	0 (0/13)
anthropogenic forest	5 (2/42)	-	0 (0/42)	-	8 (2/25)	-	5 (2/42)	-	0 (0/25)	-
brushy regrowth	14 (6/42)	10 (4/39)	5 (2/42)	0 (0/38)	-	-	2 (1/42)	10 (4/39)	-	-
crop field	34 (30/88)	4 (1/23)	6 (5/88)	0 (0/23)	-	-	6 (5/88)	4 (1/23)	-	-
flooded rice field	47 (17/36)	9 (1/11)	11 (4/36)	0 (0/11)	28 (10/36)	0 (0/11)	14 (5/36)	36 (4/11)	0 (0/36)	0 (0/11)
+ / n	25 (68/275)	7 (8/113)	5 (14/275)	0 (0/112)	22 (25/116)	0 (0/24)	5 (15/275)	14 (16/113)	0 (0/16)	0 (0/24)

Conclusions

The degree centralities of people, livestock, and trap grids suggest usage patterns, and thus exposure risk, varied by individual and location. Pathogen prevalence was highest in flooded rice fields. However, prevalence did not follow the degradation gradient as we had expected.
Our next steps are to test humans and livestock sera for exposure to the pathogens detected in small mammals.

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