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Contact networks of small mammals highlight potential transmission foci of Lassa mammarenavirus

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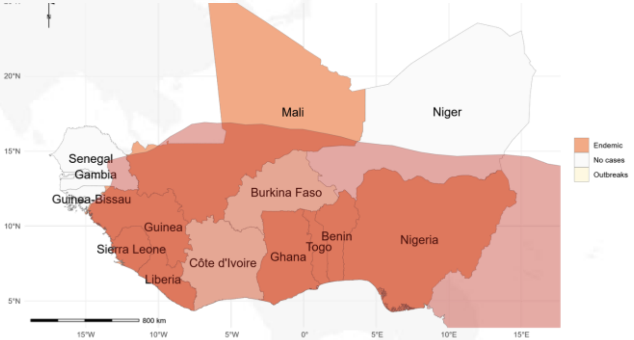
Lassa virus transmission is driven by its reservoir, but the role of habitat-specific community interactions is a key knowledge gap.

- *Mammarenavirus lassaense* (LASV) is a zoonosis of major public health importance in West Africa
- Transmission is maintained in and spills over from its primary reservoir, (*Mastomys natalensis*).
- Human land use alters small mammal communities, but how this affects the *contact patterns* relevant to transmission is poorly understood.



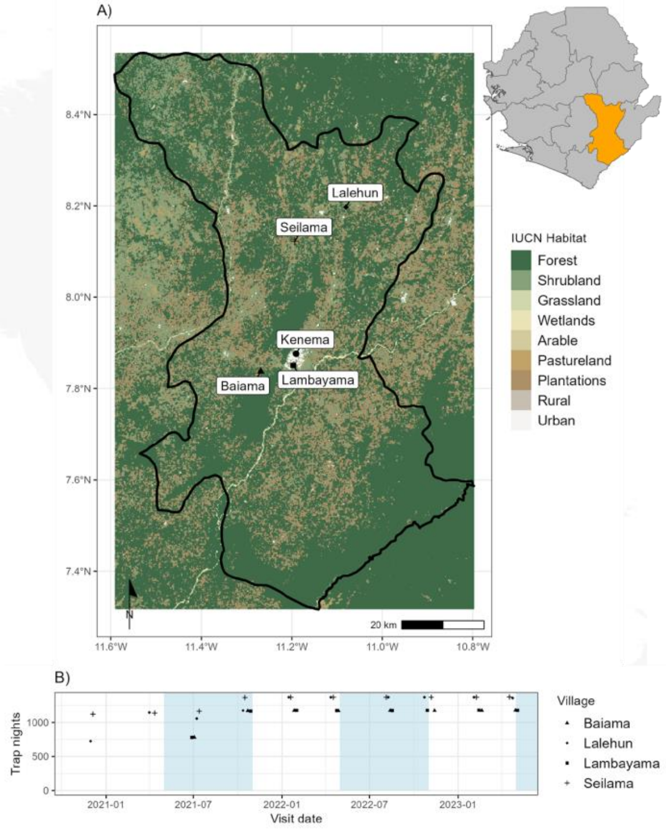
We used a network approach to quantify how land use shapes potential LASV transmission pathways.

We aimed to answer three questions:

1. How does small-mammal **contact network structure** differ across forest, agriculture, and village habitats?
2. What is the **LASV seroprevalence** and species distribution in this multi-host community?
3. Is an individual's **position within the network** associated with its LASV serostatus?

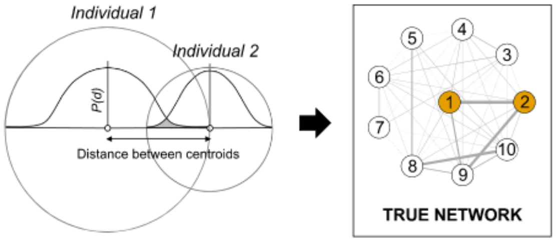
We conducted extensive trapping across an anthropogenic gradient in endemic Eastern Province, Sierra Leone.

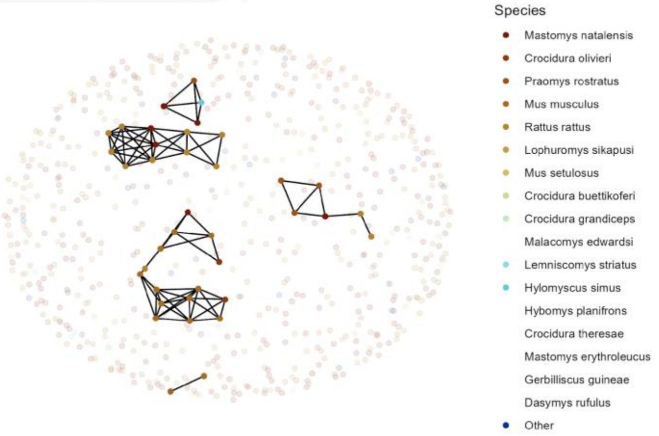
- **Location:** Four village sites in a known LASV-endemic zone.
- **Sampling Effort:** 43,266 trap-nights over three years (Oct 2020 - Apr 2023).
- **Habitats:** Trapping grids established in three distinct land-use types:
  - Villages (human dwellings)
  - Agriculture *(active and fallow farms)*
  - Forest *(less disturbed areas)*



We inferred contact networks from spatio-temporal co-occurrence within species-specific home ranges.

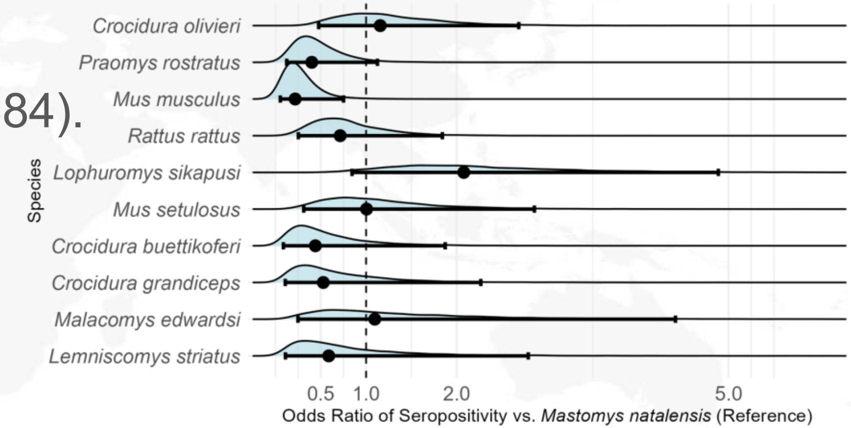
- **Contact Definition:** An "edge" was inferred between two individuals (nodes) if they were trapped:
    - During the same 4-night session...
    - ...within a species-specific home range radius (e.g., M. natalensis = 10.6 m).
- **Serology:** LASV IgG ELISA performed on blood samples to determine past exposure.
- **Analysis:**
    - Network structure metrics (degree, modularity).
    - Exponential-Family Random Graph Models (ERGMs) to model contact probability.





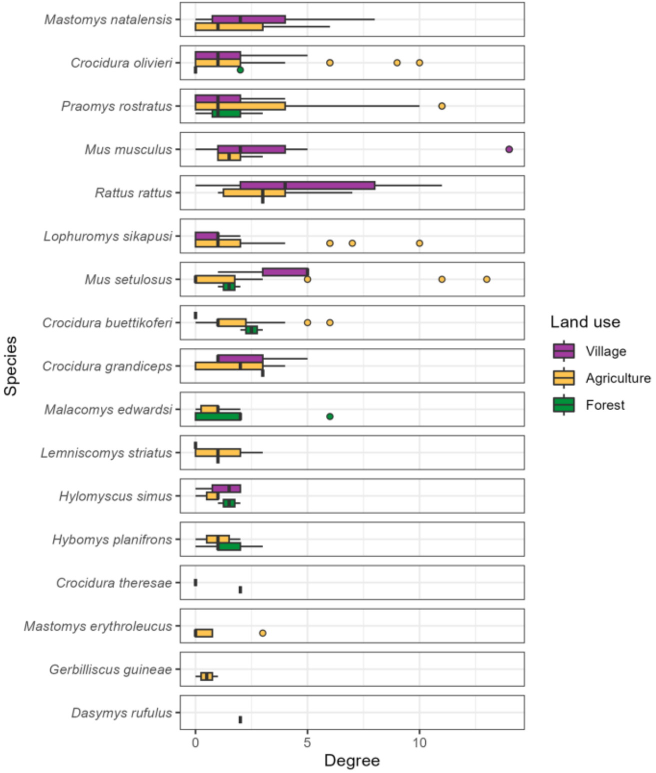
LASV exposure was found across a diverse, multi-host community, extending beyond the primary reservoir.

- 684 individuals captured, representing 17 species.
- Overall LASV seroprevalence: 5.7% (39/684).
- Antibodies were detected in 9 species.
- Major seropositive contributors:
  - *Mastomys natalensis* (28% of positives)
  - *Lophuromys sikapusi* (21%)
  - *Crocidura olivieri* (21%)



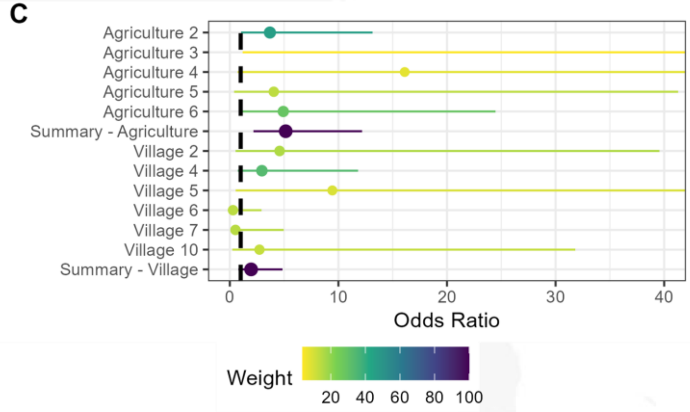
Contact network structure is fundamentally different across habitats, shaping interaction opportunities.

- Villages: Highest connectivity (mean degree = 3.4), dominated by commensals (*R. rattus, M. musculus*).
- Agriculture: High species mixing and network fragmentation (modularity). Hubs for inter-specific contact.
- Forest: Lowest overall connectivity (mean degree = 1.4).



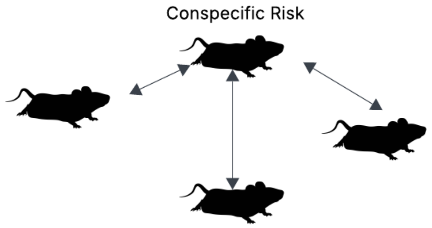
Agricultural landscapes, not villages, drive significant intra-specific clustering of the reservoir host, *M. natalensis*.

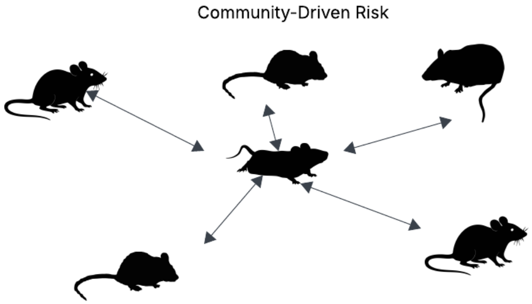
- ERGM results show the probability of *M. natalensis* contacting conspecifics:
    - **Agriculture:** Significantly more likely to form contacts with each other. *OR* = 5.14 (95% CI: 2.17–12.2)
    - **Villages:** No significant preference for conspecific contact. *OR* = 1.96 (95% CI: 0.79–4.82)
- **Implication:** Agricultural settings may be key foci for LASV amplification within the primary reservoir population.



The link between contact and infection is complex, with inter-specific contacts driving risk for highly-connected individuals.

- Counter-intuitively, seropositive individuals had a lower mean number of contacts (degree).
- However, modelling risk in *M. natalensis* reveals a crucial interaction:
  - Risk increases with total contacts (degree): OR = 1.25
  - Risk increases with conspecific contacts (homophily): OR = 2.02
  - Negative Interaction (Degree x Homophily): OR = 0.52
- **Interpretation:** For highly-connected individuals, risk is associated with volume of contacts, particularly with other species.





Habitat shapes a dual-transmission dynamic: intra-specific amplification in agriculture and community-driven risk at network hubs.

- Our findings point to agricultural landscapes as potential amplification sites, where high rates of contact within *M. natalensis* can sustain transmission.
- However, the broader multi-host community plays a clear role, with evidence of exposure in 9 species.
- The risk factor analysis suggests two pathways for *M. natalensis*:
  - Conspecific maintenance: Virus circulates among individuals with few, but targeted, contacts.
  - Interspecific spillover: "Hub" individuals with many diverse contacts are at risk from the wider community.
- Limitations: Inferred contacts, removal trapping.

Ecologically-informed, habitat-specific strategies are crucial for effective Lassa fever surveillance and control.

Conclusions:

- Small mammal contact networks are highly structured by anthropogenic land use.
- Agriculture is a key habitat for intra-specific transmission in the reservoir, *M. natalensis.*
- LASV circulates in a complex multi-host system where inter-species contact is an important, underappreciated risk factor.

Public Health Implications:

- "One-size-fits-all" control strategies are likely suboptimal.
- Targeting interventions in agricultural settings (e.g., rodent control) could be highly effective at disrupting LASV at its source.

Acknowledgements

Funding: Biotechnology and Biological Sciences Research Council and PANDORA-ID-NET

Institutions: Njala University, Royal Veterinary College, LSHTM, UCL, BNITM

Research Team: David Simons, Ravi Goyal, Umaru Bangura, Rory Gibb, Ben Rushton, Dianah Sondufu, Joyce Lamin, James Koninga, Momoh Jimmy, Mike Dawson, Joseph Lahai, Rashid Ansumana, Elisabeth Fichet-Calvet, Richard Kock, Deborah Watson-Jones, Kate E. Jones

Communities: Thank you to the communities of Baiama, Lalehun, Lambayama, and Seilama for their partnership.

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Thank you
Merci
Obrigado

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