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How are rodent species assemblages structured in a Lassa fever endemic region?

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Lassa fever has been reported across much of West Africa



https://www.who.int/health-topics/lassa-fever

The distribution of the known and potential reservoirs of Lassa fever is complex

- > Mastomys natalensis
- > Mus baoulei
- > Hylomyscus pamfi
- Mastomys erythroleucus
- > Mus minutoides
- > Rattus rattus
- > Lemniscomys striatus
- > Praomys daltoni
- > Lophuromys sikapus
- > Mus musculus

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> Praomys rostratus

Colangelo et al. (2013) Biological Journal of the Linnean Society



Lassa fever outbreaks demonstrate epidemic dynamics



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Nigerian Centre for Disease Control. 2022. https://www.ncdc.gov.ng/diseases/sitreps

Understanding Lassa fever distribution is complicated by host and viral occurrence spatial heterogeneity

(a)



Changing land use is predicted to increase the endemic range of Lassa fever



Redding, et al. (2016). Methods in Ecology and Evolution

Lassa fever is endemic in Sierra Leone, the impact of ongoing land use change on disease risk is unknown.





Do we need to understand the composition of species assemblages to better understand heterogenous risk across space and time?



Trap success varied within and between study villages



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Lambayama



Seilama







Lalehun

We have conducted 26,665 trap nights







The most commonly trapped Muridae are members of *Mastomys* and *Praomys* – potential hosts of Lassa fever

Village	Number of rodents	Number of trapnights	TS
Baiama	63	4,900	1.29%
Bambawo	14	784	1.79%
Lalehun	96	8,036	1.19%
Lambayama	81	4,900	1.65%
Seilama	209	8,036	2.6%

Species	Total	
Mastomys spp	79	
Mus musculus	57	
Rattus rattus	49	
Lophuromys sikapusi	44	
Praomys spp	42	
Crocidura crossei	30	
Crocidura poensis	24	
Mus setulosus	19	
Crocidura lamottei	14	
Praomys rostratus	12	
Crocidura spp	10	
Praomys daltoni	10	
Praomys tullbergi	10	
Crocidura olivieri	7	
Malacomys edwardsi	6	
Mus minutoides	5	
Hylomyscus spp	5	

We found that *Mastomys spp.* and *Mus musculus* were not typically found in the same habitat sites within villages. This was not the case for *Rattus rattus*.



The locations of *Mastomys, Mus, Rattus* and *Praomys* species show a degree of segregation across our village sites





Lambayam:



Co-location of rodent genera during the same visit

We observed that in these settings *Mastomys natalensis* was commonly colocated with *Rattus rattus*



Habitat specific contact networks may be important for maintenance of viral transmission directly modifying risk of pathogen spillover into human populations.



Next steps

- Further analysis to understand occupancy and species richness across the land use gradient and derive species distributions across the studied region.
- Laboratory work to understand pathogen prevalence in species across habitats and time.
- These data will then be combined to model the risk of pathogen spillover into human populations.



