

Understanding the structure of rodent species assemblages and land use change on the occurrence of the rodent host of Lassa Fever.

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Abstract

Lassa mammarenavirus, the causative agent of Lassa fever is endemic to Eastern Sierra Leone. The principal reservoir species (*Mastomys natalensis*), is considered abundant in human dominated habitats, however, rodent species' assemblages in this context are not well described. We conducted three monthly small-mammal trapping to describe these rodent assemblages, their structure and associations with land use. We model the effect of land use on rodent species occurrence along a land use gradient and produce species distribution maps of the study region to understand current and potential *Lassa mammarenavirus* spillover hazard.

We found that *M. natalensis* were more likely to occur in areas of human habitation and agricultural settings although there was important variability between different study villages. *M. natalensis* co-occurred with other other small-mammals including the two invasive rodent species (*Rattus rattus* and *Mus musculus*). We found evidence that the presence of *M. musculus*, but not *R. rattus* reduced the probability of occurrence of *M. natalensis*, this finding potentially goes some way to explain the observation of lower than expected human cases of Lassa fever from urban settings in endemic regions. Other native rodent species' within these assemblages were found to diversify into distinct habitat niches. Species distribution maps identified areas of expected occurrence and non-occurrence of our species of interest *M. natalensis* and potential geographic isolation of populations.

We identify a complex system within rodent species assemblages co-located with human communities in Eastern Sierra Leone. We show the habitat occupancy patterns for each species of interest and use these observations to produce species distribution maps that explain the limited geographic radiation of outbreaks of Lassa fever. We anticipate that this data will help inform higher resolution models of rodent distributions across West Africa, which are of particular importance for rodent zoonotic diseases such as Lassa fever. These data highlight the spatially heterogeneous distribution of important rodent species with implications for public health interventions to reduce the impact of Lassa fever.

Introduction

Lassa fever, caused by *Lassa mammarenavirus* (LASV) is an endemic zoonotic infectious disease in West Africa, with an estimated 100,000-900,000 annual human infections (McCormick et al. 1987; Basinski et al. 2021). The majority of these remain undetected, up-to 80% of these are pauci- or asymptomatic infections (McCormick et al. 1987). However, outcomes in confirmed cases remains poor, with a reported case fatality rate of 18.5% among confirmed cases identified between 2017 and 2020 in Nigeria (Yaro et al. 2021). Changing land-use and climate are hypothesised to increase the suitable area for both the primary reservoir of LASV (*Mastomys natalensis*) and environmental suitability for the virus itself, together increasing opportunities for viral spillover into growing human populations (Redding et al. 2016, 2021; Klitting et al. 2021). Lassa fever is currently considered endemic in eight West African countries (Nigeria, Guinea, Sierra Leone, Liberia, Mali, Benin, Ghana and Togo) (World Health Organisation 2022). The suitability of both habitat type and climate for both the primary reservoir and the virus is likely heterogeneous across this region reflected by the spatial clustering of Lassa fever outbreaks within countries.

M. natalensis is found in 13 of 14 continental West African nations (not reported from Gambia) and all other sub-Saharan African nations (IUCN 2016). It is considered a commensal rodent species and is abundant in and around areas of human dominated landscapes where it is considered a pest species (Leirs, Verhagen, and Verheyen 1993). The introduction of non-native commensal rodent species (i.e. *Rattus rattus* and *Mus musculus*) has led to increased competition for resources and displacement of *M. natalensis* from locations within its natural range (Cuypers et al. 2017; Garba et al. 2014). Population dynamics within this reservoir species, correlated with resource availability and rainfall, are associated with outbreaks of Lassa fever in human populations (Redding et al. 2021). Few studies to date have used longitudinal, high intensity rodent trapping to characterise rodent species assemblages in Lassa fever endemic regions (**ideally reference scoping review manuscript**).

Understanding the true spatial distribution of *M. natalensis* and their population dynamics in the context of competing rodent species is vital to guide investigations of the epidemiology of Lassa fever (Basinski et al. 2021). Further, description of rodent abundance and diversity along land use gradients are required to better understand the spatio-temporal hazard of Lassa fever outbreaks under changing land use pressures (Klitting et al. 2021). Together, this information can be used to guide the implementation of contextually relevant public health responses, allocation of healthcare resources and the identification of suitable sites for future Lassa fever vaccine studies.

Here, we use data from a large, standardised, rodent trapping survey conducted in the Lassa fever endemic region of Eastern Sierra Leone along a land use gradient to provide novel evidence on the impact of land use on the occurrence of *M. natalensis* and rodent species assemblage structure. We first report the occurrence of rodent species at our trapping sites and describe these species assemblages, producing networks of co-located species. Second, we assess the association of land use with the probability of species occupancy at trapping sites and species richness. Third, we estimate the probability of co-occurrence between different species detected in our study. Finally, we produce species distribution maps for *M. natalensis* and the species with which it competes to investigate the potential alterations to these species assemblages based on projected climate and land use change to understand how future land use change may modify the hazard of Lassa fever outbreaks.

Methods

Study area

We conducted rodent trapping at 7 trapping sites within 4 villages in the Lassa fever endemic zone of the Eastern Province of Sierra Leone. We surveyed the rodent community in forested, fallow, agricultural and areas of human occupation (within and outside of homes) along an anthropogenic land use gradient. Eastern Sierra Leone has undergone significant deforestation and conversion to agricultural land, currently X% is designated as primary and secondary forest, Y% as agricultural land and Z% as areas of human occupation. The villages were enrolled based on accessibility to the sites during all seasons, discussions with the Lassa fever outreach team at Kenema Government Hospital and acceptability of the protocol to the village community. Villages and trapping sites were selected to be representative at the study level for land use in Eastern Sierra Leone.

Trap sites were geolocated for repeated trapping activities, with changes to land use at the trapping site were recorded at each visit. Within each study site 49 individual Sherman traps (**size and reference**) were baited with a locally produced mixture of oats, palm oil and dried fish for 4 consecutive nights. Each morning the traps were checked and closed for the day prior to re-baiting during the evening. The exact location of a trap was associated with a standardised 49m² (7m by 7m) grid square with the number of trap nights within each grid square aggregated.

Data collection

Morphological species classification

Trapped rodents were sedated with halothane and euthanised prior to obtaining morphological measurements and samples of blood and tissue (**reference to RVC and local ethics approval**) following published guidance (Fichet-Calvet 2014). Morphological speciation in the field was performed using a dichotomous key produced from two available resources to identify rodents to species or genus (**will place in supplementary**) (Happold and Kingdon 2013; Monadjem et al. 2015). Rodents were sexed based on external and internal genitalia. Age estimation was performed through, description of the rodents reproductive status (identification of perforate or imperforate vagina, scarring from prior embryo development, current pregnancy status or descent of testes and seminal vesicle development) and weighing of dried eye lenses. Carcasses were disposed and processed in the field to eliminate risk of pathogen transmission.

Molecular species classification

Molecular identification to species was performed on dried blood spots that were stored at -20°C until processing. Genomic DNA was extracted using QIAGEN DNAeasy kits as per the manufacturers instructions [ref]. DNA extracts were amplified using platinum *Taq* polymerase (Invitrogen) and cytochrome B primers. DNA amplification was assessed through gel electrophoresis with successful amplification products sent to Sanger sequencing. Obtained sequences were compared using BLAST against NCBI records for rodent cytochrome B.

Land use classification

Land use classification was obtained from a global map of IUCN matched habitat types using 2015 satellite images (Jung et al. 2020). We aggregated land use to forest, vegetation (including shrubland, savanna and grassland), agricultural (arable land, pastures and plantations) and urban areas (rural and urban built-up land). At the trapping sites habitat classifications were ground-truthed to observed land use. Using this composite layer, we calculated the proportion of land classifications in a 50m buffer (**or 100m**) to represent the landscape from which rodents may be sampled from based on their mobility [ref].

Statistical analysis

Rodent occurrence and species assemblage structure

We obtained 40,152 trap-nights over 10 trapping visits between 2020-11-30 and 2023-04-28. Trapping effort was assessed using species accumulation curves (Supplementary figure 1.), suggesting adequate effort to detect rodent species within each village site. We constructed detection/non-detection histories for all identified rodent species, assigning “1” when the species was detected and “0” otherwise, aggregated to standardised grid squares. We augmented data by creating all-zero detection histories of rodent species that have been previously described as occurring in the region and were never recorded in our study.

We describe species assemblages at multiple geographic scales. First, all species identified within a single trap site. Second, all species identified within a village. Third, all species identified within a single habitat type across multiple trapping sites and villages. We describe the age-sex population structure of each species trapped and variation in their abundance over the study period.

Rodent species networks

We produce rodent species networks at multiple temporal and geographic scales. These networks are weighted, uni-directional graphs, where the weights correspond to the number of individuals of each species trapped within the geographic scale of interest. First, the network of rodents trapped within 50m radius of each individual is generated within a study visit. Second, a network of species within the same habitat class is generated within a study visit. Third, a network of individuals trapped within 50m across all study visits is generated. Finally, a network of species within the same habitat class across all study visits is produced. These networks will be compared using ... (Tantardini et al. 2019)

Estimating the effect of land use on species occurrence and richness

First, we adopted a Bayesian multi-species occupancy framework to analyse rodent trapping data in the presence of incomplete detection. We implemented a model to estimate occupancy and species richness in each habitat type studied. Models were defined using the `spOccupancy` package in the R statistical computing language (Doser et al. 2022; R Core Team 2021). This approach models the true presence or absence (z) of a species (i), at site (j) as arising from a Bernoulli process (Equation 1.). Where ψ_j is the probability of occurrence of a species at a site during a given replicate. This is modelled using a logit link where β_i are the regression coefficients, including an intercept that describes the effects of covariates $\mathbf{x}_{i,j}$ with $^\top$ representing the transposition of column vector $\mathbf{x}_{i,j}$ (Equation 2.).

$$z_{i,j} \sim \text{Bernoulli}(\psi_{i,j}) \quad (1)$$

$$\text{logit}(\psi_{i,j}) = \mathbf{x}_{i,j}^\top \boldsymbol{\beta}_i \quad (2)$$

The regression coefficients in these multi-species occupancy models are described as random effects arising from a common community level distribution (Equation 3.). Where $\boldsymbol{\mu}_\beta$ represents the community level mean effect for each occurrence covariate effect and \mathbf{T}_β is a diagonal matrix representing the variability of these among species in the community.

$$\boldsymbol{\beta}_i \sim \text{Normal}(\boldsymbol{\mu}_\beta, \mathbf{T}_\beta) \quad (3)$$

The detection component estimates the unobserved $z_{i,j}$. Here, $y_{i,j,k}$ is the observed detection or non-detection of a species i , at site j , during replicate k (Equation 4.). This is approached as arising from a Bernoulli process conditional on the true latent occurrence process $p_{i,j,k}$. The probability of a species being detected at a site, during a replicate (given it is present at site j), is a function of site and replicate specific covariates V and a set of species-specific regression coefficients α_i (Equation 5.).

$$y_{i,j,k} \sim \text{Bernoulli}(p_{i,j,k} z_{i,j}) \quad (4)$$

$$\text{logit}(p_{i,j,k}) = \mathbf{v}_{i,j,k}^\top \boldsymbol{\alpha}_i \quad (5)$$

Similarly to Equation 3. these coefficients are described as random effects arising from a common community level distribution, where $\boldsymbol{\mu}_\alpha$ represents the community level mean effect for each detection covariate effect and \mathbf{T}_α is a diagonal matrix representing the variability of these among species in the community (Equation 6.).

$$\boldsymbol{\alpha}_i \sim \text{Normal}(\boldsymbol{\mu}_\alpha, \mathbf{T}_\alpha) \quad (6)$$

Minimally informative priors were specified for community and species level coefficients (α and β , a normal prior of mean = 0, variance = 2.72) and for community level occurrence and detection variance parameters (\mathbf{T}_α and \mathbf{T}_β , 0.1 for the scale and shape parameters of the inverse Gamma prior).

We included covariates in the model based on a pre-specified Directed Acyclic Graph and after assessing for co-linearity (defined as strong correlation >0.8) among variables (Supplementary Figure 2.). Continuous variables were standardised by scaling to values between 0-1. The fully specified model is defined in Equation 6 and 7.

$$\text{Probability of occurrence} \sim \text{Landuse} + \text{Village} + \text{scale}(\text{Distance to permanent structure}) + \text{scale}(\text{Distance to village centre}) + \text{scale}(\text{Distance to water body}) \quad (7)$$

$$\text{Probability of detection} \sim \text{scale}(\text{Monthly precipitation}) + \text{Moon fraction} + \text{scale}(\text{Number of trap nights}) \quad (8)$$

Using this model, we calculate the effect of landuse as the difference in occupancy probability for each species between each of the four land use classifications. Only estimates for species with at least X records to avoid inference from limited data. Occupancy is interpreted here as the species' probability of being detected through a successful trapping event during the study. We estimate species richness in each habitat type by obtaining the sum of species at a trapping site for each iteration of the Bayesian sampling process to compare rodent assemblage responses to land use classification.

Co-location of species

To investigate the presence of competitive exclusion by rodent species in this setting we adopted a Binomial joint likelihood model fit using Integrated Nested Laplace Approximation (INLA) in the R statistical computing language (Rue, Martino, and Chopin 2009; Martins et al. 2013). Here we set up co-occurrence models to estimate the probability of detection of two species Y_a and Y_b (Equation 8). Here, γ is the species specific intercept for species a and b respectively. $A.co.B$ and $B.co.A$ represent the co-occurrence of species a with species b and species b with species a respectively.

$$Y_a \sim \gamma_a + A.co.B \quad (9)$$

$$Y_b \sim \gamma_b + B.co.A \quad (10)$$

Minimally informative priors were set for the intercept and species co-occurrence variables with a mean of 0 and precision of 1.

Species distribution maps for current land use classifications and potential future change

We adopted a Bayesian additive regression tree (BART) approach to predict species distributions for each identified species of interest (*M. natalensis* and competing commensal rodents *R. rattus*, *M. musculus* and *Praomys rostratus*). Similar to other classification tree methods BART functions by producing a set of decision trees that explain different components of variance in the outcome variable (presence of the species of interest) with the additional benefit of capturing model uncertainty. Covariates will include, land use classification, mean temperature, isothermality, precipitation and human population density. Variable importance plots will be produced for the final models for each species. These species distribution models will be examined to investigate the spatial overlap between competing species' distribution and the impact this may have on potential expansion of the Lassa fever endemic region (i.e. mus or rattus displacing mastomys from suitable habitats).

Using projected land use change/climate change we will produce future potential species distribution models for these species to understand how future projected land use change and climate change may impact the distribution of these species and future hazard of Lassa fever outbreaks.

Results

During the study period 749 small mammals were obtained from 40,152 trap-nights across the four study villages (1.9% trap-success (TS)). The greatest number of small mammals were detected in agricultural settings, these communities also had the greatest species richness and Shannon diversity. However, the greatest TS was obtained from traps set within households, although in these settings species richness and diversity was lower (Table 1a). Seilama and Lalehun had the highest overall TS, species richness and Shannon diversity although the habitat types with the highest values of these metrics differed between the villages. Lambayama the most urbanised village had the lowest species richness and Shannon diversity with the majority of rodents trapped within households.

Table 1a. The number of individual small mammals (N), the number of trap nights (TN), trap-success (TS %), species richness and Shannon diversity are presented for each village and landuse type.

Village	Landuse	N	TN (TS %)	Species richness	Shannon diversity
All villages					
	Village (inside)	182	4168 (4.4%)	6	1.23
	Village (outside)	87	5176 (1.7%)	7	1.62
	Agriculture	420	23840 (1.8%)	10	1.82
	Fallow land	4	2344 (0.2%)	2	0.69
	Forest	62	4624 (1.3%)	8	1.66
Baiaama					
	Village (inside)	64	1152 (5.6%)	4	0.79
	Village (outside)	10	1176 (0.9%)	3	1.05
	Agriculture	44	3912 (1.1%)	5	1.31
	Fallow land	2	776 (0.3%)	1	0.00
	Forest	2	1568 (0.1%)	1	0.00
	Combined	122	8584 (1.4%)	7	1.44
Lalehun					
	Village (inside)	26	928 (2.8%)	3	1.01
	Village (outside)	21	944 (2.2%)	6	1.54
	Agriculture	111	7384 (1.5%)	9	1.68
	Forest	10	1568 (0.6%)	2	0.67
	Combined	168	10824 (1.6%)	9	1.77
Lambayama					
	Village (inside)	88	1160 (7.6%)	3	0.29
	Village (outside)	12	1160 (1%)	4	1.24
	Agriculture	20	4704 (0.4%)	3	0.80
	Fallow land	2	1568 (0.1%)	1	0.00
	Combined	122	8592 (1.4%)	4	0.89
Seilama					
	Village (inside)	4	928 (0.4%)	2	0.69
	Village (outside)	44	1896 (2.3%)	6	1.55
	Agriculture	245	7840 (3.1%)	10	1.82
	Forest	50	1488 (3.4%)	7	1.50
	Combined	343	12152 (2.8%)	12	1.96

The most commonly detected rodent species was *M. natalensis* (N = 144, 19.2%), followed by *R. rattus* (N =

90, 12%), *M. musculus* (N = 86, 11.5%) and *Lophuromys rostratus* (N = 74, 9.9%) (Table 1b.). There was large variation in the detection of these species between study villages, landuse and study period (Supplementary Table 1.). For example, *M. musculus* was the most commonly detected species within Lambayama and was rarely detected in any of the other village sites.

Rodent occurrence and species assemblage structure

Trapping effort was adequate across all four village sites, with saturation of species accumulation curves reached. Species diversity and richness was greatest in Seilama and lowest in Lambayama. The rodent assemblages in Seilama comprised the greatest number of species with relatively high prevalence of X, Y and Z and lower numbers of A, B and C. Similar patterns were observed in Lalehun and Baiama. The peri-urban site Lambayama had importantly different assemblage structure, dominated by a single species *M. musculus* with fewer detections of native small mammal species.

We found little variation in species richness by season, however, prevalence of species (measured by trap-success) fell for most species, except *M. natalensis* which was more commonly trapped (greater trap-success) during the wet season in indoor settings across the three village sites in which it was prevalent.

Rodent species networks

Rodent species networks varied by village and habitat type. The largest networks (greatest number of co-located species) were obtained from the villages Seilama and Lalehun.

Estimating the effect of land use on species occurrence and richness

- Model seasonal change in a) relative abundance of all rodents and b) number of species by seasonal indicators and proportions of different land use types as covariates
- Species distribution maps will be produced
- Difference between observed and expected will be investigated by comparing to observations of other species within these distributions

Species distribution maps for current land use classifications and potential future change

- Apply these species distribution models to expected future scenarios

Discussion

Conclusion

References

Supplementary figure 1.

- Basinski, Andrew J., Elisabeth Fichet-Calvet, Anna R. Sjodin, Tanner J. Varrelman, Christopher H. Remien, Nathan C. Layman, Brian H. Bird, et al. 2021. "Bridging the Gap: Using Reservoir Ecology and Human Serosurveys to Estimate Lassa Virus Spillover in West Africa." Edited by Amy Wesolowski. *PLOS Computational Biology* 17 (3): e1008811. <https://doi.org/10.1371/journal.pcbi.1008811>.
- Cuyppers, Laura N, Wim L Cuyppers, Amélie Gildemyn-Blomme, Laura Abraham, Senne Aertbeliën, Apia W Massawe, Benny Borremans, Sophie Gryseels, and Herwig Leirs. 2017. "No Evidence for Avoidance of Black Rat Scent by the Presumably Less Competitive Natal Multimammate Mouse in a Choice Experiment." *African Zoology* 52 (2): 119–23. <https://doi.org/10.1080/15627020.2017.1307139>.

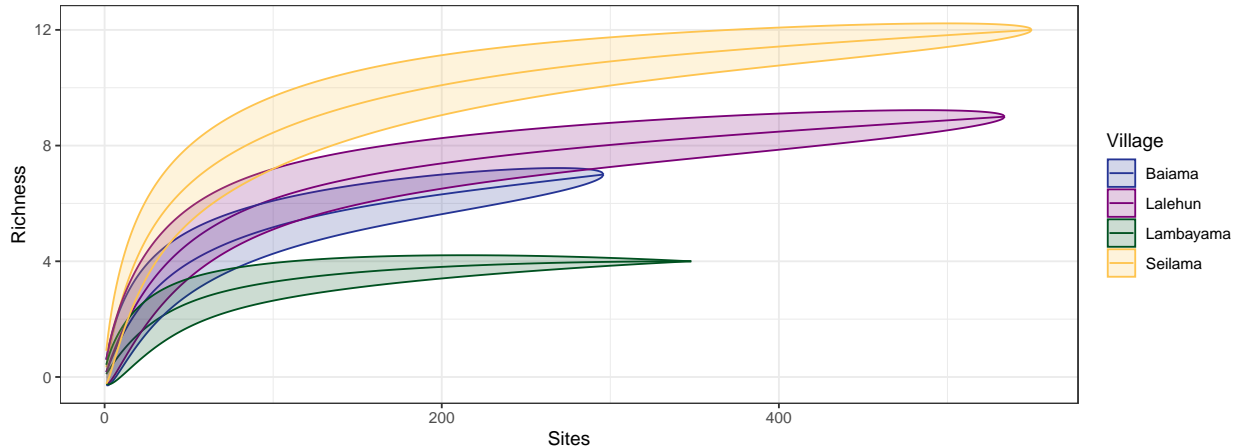


Figure 2: Supplementary figure 1. Species accumulation curves for each village site

- Doser, Jeffrey W., Andrew O. Finley, Marc Kéry, and Elise F. Zipkin. 2022. “spOccupancy: An r Package for Single-Species, Multi-Species, and Integrated Spatial Occupancy Models.” *Methods in Ecology and Evolution*. <https://doi.org/10.1111/2041-210X.13897>.
- Fichet-Calvet, Elisabeth. 2014. “Chapter 5 - Lassa Fever: A Rodent-Human Interaction.” In *The Role of Animals in Emerging Viral Diseases*, edited by Nicholas Johnson, 89–123. Boston: Academic Press. <https://doi.org/10.1016/B978-0-12-405191-1.00005-3>.
- Garba, Madougou, Ambroise Dalecky, Ibrahima Kadaoure, Mamadou Kane, Karmadine Hima, Sophie Veran, Sama Gagare, et al. 2014. “Spatial Segregation Between Invasive and Native Commensal Rodents in an Urban Environment: A Case Study in Niamey, Niger.” *PLOS ONE* 9 (11): e110666. <https://doi.org/10.1371/journal.pone.0110666>.
- Happold, David C. D., and Jonathan Kingdon, eds. 2013. *Mammals of Africa. Vol. 3: Rodents, Hares and Rabbits*. London: Bloomsbury.
- IUCN. 2016. “The IUCN Red List of Threatened Species 2016: *Mastomys Natalensis*.” International Union for Conservation of Nature. <https://doi.org/10.2305/IUCN.UK.2016-3.RLTS.T12868A22425266.en>.
- Jung, Martin, Prabhat Raj Dahal, Stuart H. M. Butchart, Paul F. Donald, Xavier De Lamo, Myroslava Lesiv, Valerie Kapos, Carlo Rondinini, and Piero Visconti. 2020. “A Global Map of Terrestrial Habitat Types.” *Scientific Data* 7 (1): 256. <https://doi.org/10.1038/s41597-020-00599-8>.
- Klitting, Raphaëlle, Liana E. Kafetzopoulou, Wim Thiery, Gytis Dudas, Sophie Gryseels, Anjali Kotamarthi, Bram Vrancken, et al. 2021. “Predicting the Evolution of Lassa Virus Endemic Area and Population at Risk over the Next Decades.” Preprint. Microbiology. <https://doi.org/10.1101/2021.09.22.461380>.
- Leirs, Herwig, Ron Verhagen, and Walter Verheyen. 1993. “Productivity of Different Generations in a Population of *Mastomys Natalensis* Rats in Tanzania.” *Oikos* 68 (1): 53–60. <https://doi.org/10.2307/3545308>.
- Martins, Thiago G., Daniel Simpson, Finn Lindgren, and Håvard Rue. 2013. “Bayesian Computing with INLA: New Features.” *Computational Statistics & Data Analysis* 67 (November): 68–83. <https://doi.org/10.1016/j.csda.2013.04.014>.
- McCormick, J B, P A Webb, J W Krebs, K M Johnson, and E S Smith. 1987. “A Prospective Study of the Epidemiology and Ecology of Lassa Fever.” *The Journal of Infectious Diseases* 155 (3): 437–44. <https://doi.org/10.1093/infdis/155.3.437>.
- Monadjem, Ara, Peter J. Taylor, Christiane Denys, and Fenton P. D. Cotterill. 2015. *Rodents of Sub-Saharan Africa: A Biogeographic and Taxonomic Synthesis*. Berlin, München, Boston: DE GRUYTER. <https://doi.org/10.1515/9783110301915>.
- R Core Team. 2021. *R: A Language and Environment for Statistical Computing*. Vienna, Austria: R Foundation for Statistical Computing. <https://www.R-project.org/>.
- Redding, David W., Rory Gibb, Chioma C. Dan-Nwafor, Elsie A. Ilori, Rimamdeyati Usman Yashe, Saliu H. Oladele, Michael O. Amedu, et al. 2021. “Geographical Drivers and Climate-Linked Dynamics of Lassa

- Fever in Nigeria.” *Nature Communications* 12 (1): 5759. <https://doi.org/10.1038/s41467-021-25910-y>.
- Redding, David W., Lina M. Moses, Andrew A. Cunningham, James Wood, and Kate E. Jones. 2016. “Environmental-Mechanistic Modelling of the Impact of Global Change on Human Zoonotic Disease Emergence: A Case Study of Lassa Fever.” *Methods in Ecology and Evolution* 7 (6): 646–55. <https://doi.org/10.1111/2041-210X.12549>.
- Rue, Håvard, Sara Martino, and Nicolas Chopin. 2009. “Approximate Bayesian Inference for Latent Gaussian Models by Using Integrated Nested Laplace Approximations.” *Journal of the Royal Statistical Society: Series b (Statistical Methodology)* 71 (2): 319–92.
- Tantardini, Mattia, Francesca Ieva, Lucia Tajoli, and Carlo Piccardi. 2019. “Comparing Methods for Comparing Networks.” *Scientific Reports* 9 (1): 17557. <https://doi.org/10.1038/s41598-019-53708-y>.
- World Health Organisation. 2022. “Lassa Fever.” 2022. <https://www.who.int/westernpacific/health-topics/lassa-fever>.
- Yaro, Clement Ameh, Ezekiel Kogi, Kenneth Nnamdi Opara, Gaber El-Saber Batiha, Roua S. Baty, Ashraf Albrakati, Farag M. A. Altalbawy, Innocent Utenwojo Etuh, and James Paul Oni. 2021. “Infection Pattern, Case Fatality Rate and Spread of Lassa Virus in Nigeria.” *BMC Infectious Diseases* 21 (1): 149. <https://doi.org/10.1186/s12879-021-05837-x>.