Rodent trapping studies as an overlooked information source for understanding endemic and novel zoonotic spillover.

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# Abstract

Rodents are important globally distributed reservoirs of known and novel zoonotic pathogens. Ongoing anthropogenic land use change is altering the composition of host species assemblages and modifying the risk of zoonoses spillover events. These changes mean that an understanding of the current distribution of rodent species is vital for accurately describing disease hazard and managing risk. However, available species distribution and host-pathogen association datasets (e.g. IUCN, GBIF, CLOVER) are often taxonomically and spatially biased. Here, we synthesise data from West Africa from 127 rodent trapping studies, published between 1964-2022, as an additional source of information to characterise the range and presence of important zoonotic pathogen host species in this region. We identify that these rodent trapping studies, although biased towards human dominated landscapes across West Africa, can usefully complement current rodent species distribution datasets and we calculate the discrepancies between these datasets. For five regionally important zoonotic pathogens (Arenaviridae spp., Borrelia spp., *Lassa mammarenavirus*, Leptospira spp. and *Toxoplasma gondii*), we identify host-pathogen associations that have not been previously reported in host-association datasets. These omissions have the potential for biasing estimates of current risk and drivers of zoonoses. Finally, for these five pathogen groups, we find that the proportion of a rodent hosts range that has been sampled remains small. A priority of future rodent trapping studies should be to sample rodent hosts across a greater geographic range to better characterise current and future risk. In the interim, future studies of spatial pathogen risk informed by rodent distributions must incorporate a measure of the current sampling biases. The current synthesis of contextually rich rodent trapping data enriches available information from IUCN, GBIF and CLOVER which can support a more complete understanding of the hazard of zoonotic spillover events.

# Introduction

There is increasing awareness of the global health and economic impacts of novel zoonotic pathogen spillover, evidenced by the ongoing SARS-CoV-2 pandemic and previous HIV/AIDs and Spanish Influenza pandemics (Bernstein *et al.*, 2022). The number of zoonotic disease spillover events and the frequency of the emergence of novel zoonotic pathogens from rodents are predicted to increase under intensifying anthropogenic pressure driven by increased human populations, urbanisation, intensification of agriculture, climate change and wildlife defaunation (Allen *et al.*, 2017; Hassell *et al.*, 2017; McMahon, Morand and Gray, 2018; García-Peña *et al.*, 2021). The impact of endemic zoonoses meanwhile remains underestimated (Maudlin, Eisler and Welburn, 2009). Endemic zoonoses disproportionally affect those in the poorest sections of society, those living in close contact with their animals and those with limited access to healthcare (Molyneux *et al.*, 2011; Halliday *et al.*, 2015; Judson and Rabinowitz, 2021).

Rodents along with bats contribute the greatest number of predicted novel zoonotic pathogens and known zoonoses (Han *et al.*, 2015; Gibb *et al.*, 2021). Of 2,220 extant rodent species, 244 (10.7%) are described as reservoirs of 85 zoonotic pathogens (Han *et al.*, 2015), although many species provide important and beneficial ecosystem services including pest regulation and seed dispersal (Fischer *et al.*, 2018). Rodents typically demonstrate “fast” life histories (Dobson and Oli, 2007) with traits such as early maturation and short gestation times (<4 days) further associated with being zoonotic reservoirs (Han *et al.*, 2015; Albery and Becker, 2021). Rodent species with “fast” life histories thrive in human dominated landscapes, displacing species less likely to be reservoirs of zoonotic pathogens (Gibb, Redding, *et al.*, 2020). The widespread occurrence of reservoir species and their proximity to human activity make the description of rodent species assemblages and host-pathogen associations vitally important to understanding the hazard of zoonotic disease spillover and novel zoonotic pathogen emergence (Han, Kramer and Drake, 2016).

Despite the importance of understanding these complex systems, current evidence on host-pathogen associations is considerably affected by taxonomic and geographical sampling biases (Gibb, Franklinos, *et al.*, 2020; Gibb *et al.*, 2021). Curated biodiversity datasets such as the Global Biodiversity Information Facility (GBIF) and resources produced by the International Union for Conservation of Nature suffer from well described spatial and temporal sampling biases (Boakes *et al.*, 2010; Bowler *et al.*, 2022). These sampling biases can importantly distort produced species distribution models (Beck *et al.*, 2014). Datasets on host-pathogen associations also can suffer from biases introduced from literature selection criteria and taxanomic discrepancies. These biases are important because identification of potential geographic hotspots of zoonotic disease spillover and novel pathogen emergence are often based on these types of host species distributions and host-pathogen associations (Plowright *et al.*, 2019; Carlson *et al.*, 2021). For example, systematically increased sampling, over-representation of certain habitats and clustering around areas of high human population could lead to an apparent association between locations and hazard that is driven by these factors rather than underlying host-pathogen associations (Redding *et al.*, 2017; Wille, Geoghegan and Holmes, 2021; Gibb *et al.*, 2021). Predictions of zoonotic disease spillover and novel zoonotic pathogen emergence must account for these biases to understand the future hazard of zoonotic diseases (Carlson *et al.*, 2021).

West Africa has been identified as a region at increased risk for rodent-borne zoonotic disease spillover events, the probability of these events are predicted to increase under different projected future land-use change scenarios (Grace *et al.*, 2012; García-Peña *et al.*, 2021). Currently within West Africa, rodents are involved in the transmission of multiple endemic zoonoses with large burdens on human health, these pathogens include, Lassa fever, Schistosomiasis, Leptospirosis and Toxoplasmosis (Meerburg, Singleton and Kijlstra, 2009; Galeh *et al.*, 2020). Understanding of the distribution of these zoonoses are limited by biases in consolidated datasets. Rodent trapping studies provide contextually rich information on when, where and under what conditions rodents were trapped, potentially enriching consolidated datasets (Bovendorp, MCCleery and Galetti, 2017). Studies have been conducted in West Africa to investigate the distribution of rodent species, their species assemblages, the prevalence of endemic zoonoses within rodent hosts (e.g., Lassa fever, Schistosomiasis) and to identify emerging and novel zoonotic pathogens (Fichet-Calvet *et al.*, 2009; Catalano *et al.*, 2020; USAID, 2021). However, individual level data from these studies have not previously been synthesised for inclusion in assessments of zoonotic disease spillover and novel zoonotic pathogen emergence.

Here, we synthesise rodent trapping studies conducted across West Africa published between 1964-2022. First, we use this dataset to investigate the geographic sampling biases in relation to human population density and land use classification. Second, we compare this to curated host datasets (IUCN and GBIF) to understand differences in reported host geographic distributions. Third, we compare identified host-pathogen associations with a consolidated dataset (CLOVER) to explore discrepancies in rodent host-pathogen associations and report the proportion of positive assays for pathogens of interest. Finally, within our dataset we investigate the spatial extent of current host-pathogen sampling to identify areas of sparse sampling of pathogens within their host ranges. We expect that rodent trapping studies provide an important additional source of high-resolution data that can be used to enrich available consolidated datasets to better understand the hazard of zoonotic disease spillover and novel zoonotic pathogen emergence across West Africa.

# Methods

## Data sources

### Host and pathogen trapping data

To identify relevant literature, we conducted a search in Ovid MEDLINE, Web of Science (Core collection and Zoological Record), JSTOR, BioOne, African Journals Online, Global Health and the pre-print servers, BioRxiv and EcoEvoRxiv for the following terms as exploded keywords: (1) Rodent OR Rodent trap\* AND (2) West Africa, no date limits were set. We also searched other resources including the UN Official Documents System, Open Grey, AGRIS FAO and Google Scholar using combinations of the above terms. Searches were run on 2022-05-01, and returned studies conducted between 1964-2021.

We included studies for further analysis if they met all of the following inclusion criteria; i) reported findings from trapping studies where the target was a small mammal, ii) described the type of trap used or the length of trapping activity or the location of the trapping activity, iii) included trapping activity from at least one West African country, iv) recorded the genus or species of trapped individuals, and v) were published in a peer-reviewed journal or as a pre-print on a digital platform or as a report by a credible organisation. We excluded studies if they met any of the following exclusion criteria: i) reported data that were duplicated from a previously included study, ii) no full text available, iii) not available in English. One author screened titles, abstracts and full texts against the inclusion and exclusion criteria. At each stage; title screening, abstract screening and full text review, a random subset (10%) was reviewed by a second author.

We extracted data from eligible studies using a standardised tool that was piloted on 5 studies (Supplementary Table 1.). Data was abstracted into a Google Sheets document, which was archived on completion of data extraction [ref to zenodo on finalised]. We identified the aims of included studies, for example, whether it was conducted as a survey of small mammal species or specifically to assess the risk of zoonotic disease spillover. we extracted data on study methodology, such as, the number of trap nights, the type of traps used and whether the study attempted to estimate abundance. For studies not reporting number of trap nights we used imputation based on the number of trapped individuals, stratified by the habitat type from which they were obtained. This was performed by multiplying the total number of trapped individuals within that study site by the median trap success for study sites with the same reported habitat type. Stratification was used as trap success varied importantly between traps placed in or around buildings (13%, IQR 6-24%) compared with other habitats (3%, IQR 1-9%)

We also recorded how species were identified within a study and species identification was assumed to be accurate. The number of individuals of these species or genera was extracted with taxanomic names mapped to GBIF taxonomy (GBIF: The Global Biodiversity Information Facility, 2021). We expanded species detection and non-detection records by explicitly specifying non-detection at a trap site if a species was recorded as detected at other trapping locations within the same study.

Geographic locations of trapping studies were extracted using GPS locations for the most precise location presented. Missing locations were found using the National Geospatial-Intelligence Agency GEOnet Names Server (National Geospatial-Intelligence Agency, no date) based on place-names and maps presented in the study. All locations were converted to decimal degrees. The year of rodent trapping was extracted alongside the length of the trapping activity to understand seasonal representativeness of trapping activity. The habitats of trapping sites were mapped to the IUCN Habitat Classification Scheme (Version 3.1). For studies reporting multiple habitat types for a single trap, trap-line or trapping grid, a higher order classification of habitat type was recorded.

For relevant studies we extracted data on all microorganisms and zoonotic pathogens tested and the method used (e.g., molecular or serological diagnosis). Where assays were able to identify the microorganism to species level this was recorded, non-specific assays higher order attribution was used (e.g. to family level). We recorded the species of rodent host tested, the number of individuals tested and the number of positive and negative results. For studies reporting summary results all testing data were extracted, this may introduce double counting of individual rodents, for example, if a single rodent was tested using both molecular and serological assays. Where studies reported indeterminate results, these were also recorded.

Out of 4,692 relevant citations, we identified 127 rodent trapping studies (Supplementary Table 2.). The earliest trapping studies were conducted in 1964, with a trend of increasing numbers of studies being performed annually since 2000. The median year of first trapping activity was 2007, with the median length of trapping activity being 1 year (IQR 0-2 years) (Supplementary Fig 1.). Studies were conducted in 14 West African countries, with no studies reported from The Gambia or Togo, at 1,611 trap sites (Fig 1A.).

Included studies explicitly reported on 601,184 trap nights, a further 341,445 trap nights were imputed from studies with no recording of trapping effort based on trap success, leading to an estimate of 942,629 trap nights (Fig 1B.). A minority of studies trapped at a single study site (30, 24%), with 46 (36%) trapping at between two and five sites, the remaining 51 studies (40%) trapped at between six and 93 study sites.

In total 76,275 small mammals were trapped with 65,628 (90%) identified to species level and 7,439 (10%) identified to genus, with the remaining classified to higher taxonomic level. The majority of the 132 identified species were Rodentia (102, 78%), of which Muridae (73, 72%) were the most common family. Soricomorpha were the second most identified order of small mammals (28, 21%). 57 studies tested for 32 microorganisms, defined to species or genus level that are known or potential pathogens. Most studies tested for a single microorganism (48, 84%). The most frequently assayed microorganisms were *Lassa mammarenavirus* or Arenaviridae (21, 37%), *Borrelia sp.* (9, 16%), *Bartonella sp.* (4, 7%) and *Toxoplasma gondii* (4, 7%). Most studies used Polymerase Chain Reaction (PCR) to detect microorganisms (37, 65%), with fewer studies using serology-based tests (11, 19%) or histological or direct visualisation assays (11, 21%). From 32,920 individual rodent samples we produced 351 host-pathogen pairs. With *Rattus rattus*, *Mus musculus*, *Mastomys erythroleucus*, *Mastomys natalensis* and *Arvicanthis niloticus* being assayed for at least 18 microorganisms.

![Fig 1: A) The location of trapping sites in West Africa. No sites were recorded from Togo or The Gambia. Heterogeneity is observed in the coverage of each country by trap night (colour) and location of sites. For example, Senegal, Mali and Sierra Leone have generally good coverage compared to Guinea and Burkina Faso. B) Histogram of trap nights performed at each study site, a median of 248 trap nights (IQR 116-500) was performed at each site](data:application/pdf;base64,)

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