Rodent trapping studies to understand the prevalence of zoonotic disease in West Africa: A scoping review.

2021-07-30

# Introduction

* The role of zoonotic infectious diseases in human health and society have been dramatically highlighted through the ongoing SARS-CoV-2 pandemic and recent Ebola virus outbreaks in the Democratic Republic of Congo and Guinea.
* The number and intensity of zoonotic spillover events is projected to increase under anthropogenic pressure (e.g. increased human populations and increasing urbanisation) and global climate change.
* Rodents are important hosts of zoonotic disease. Of 2,220 extant rodent species, 244 (10.7%) are described as being reservoirs of 85 zoonotic pathogens (Han, 2016).
* Rodents typically demonstrate “fast” life histories (Dobson, 2007) and within rodents, these traits are associated with a species being a reservoir of zoonotic diseases (Han, 2015). Further, these traits are prevalent in species that thrive in human dominated landscapes, displacing species that are less likely to be reservoirs of zoonotic disease (Gibb, 2020).
* Paired with investigations of potential zoonotic pathogens within individual rodent species the prevalence and burden of pathogens within rodent hosts can be investigated, e.g. for Lassa fever (Fichet-Calvet, 2009) and Schistosomiasis (Catalano, 2018).
* Our undertanding of the associations between rodents and their pathogens are typically based on global datasets (e.g. PREDICTS, GIDEON and GBIF) that consolidate information obtained from multiple studies. These datasets may lack the contextually rich information on the presence, absence and abundance of individual species and the habitats in which they were trapped that is potentially provided by individual rodent trapping studies (Bovendorp, 2017).
* These datasets have been used to identify potential geographic hotspots where virus and host species diversity may be expected to be at its greatest and therefore quantitate the risk of a zoonotic disease spillover event occuring at a defined location. However, there remains the potential for important confounding introduced to these associations through bias generated by study design or through selection of sampling sites.
* For example systematically increased sampling (e.g. more intensive studies over longer time periods) or over-representation of certain habitats (e.g. periurban landscapes) could lead to an apparent association between locations and risk that is driven by these factors rather than an underlying host and virus association.
* Conversely some regions may not be sampled adequately and therefore under-represented in these datasets due to sparse human populations or inaccessible habitats which may lead to erroneously identifying regions as low risk of zoonotic disease spillover events.
* West Africa has previously been identified to be at relatively high risk of emerging zoonotic infectious disease events from wildlife populations (Jones, 2008). Ongoing changes in land use and increasing population may lead to an increasing burden from zoonotic diseases.
* Here, we identify rodent trapping studies performed across West Africa and identify the location and habitat types in which they’ve been conducted, the pathogens assessed and the host-pathogen associations that have been reported to quantitate the potential bias and identify areas requiring further focus.

# Methods

## Literature search

* The following terms were searched for as keywords 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:
  1. Rodent OR Rodent trap\*
  2. West Africa (or the individual countries)
     1. AND 2.
* Other resources including the UN Official Documents System, Open Grey, AGRIS FAO and Google Scholar were searched using combinations of the above terms.
* One reviewer screened titles, abstracts and full texts against the inclusion and exclusion criteria. At each stage, a random subset (10%) was reviewed by a second reviewer. \*Data extracted included i) study identifiers; ii) study aims; iii) trapping methodology; iv) geolocation data; v) method of speciation; vi) trapping locations and dates; vii) trapped species; viii) number of trap-nights and ix) microorganisms/pathogens of interest.

## Data extraction

### Location of rodent trapping studies

* GPS locations were extracted for the most precise location presented (i.e. trap, trap-line, study site or study region). Coordinates were extracted in the format reported and converted to decimal degrees.

### Habitats investigated

* The habitat classification scheme a study used was recorded (e.g. IUCN Habitat Classification Scheme (Version 3.1)). For studies not using standardised recording, the explicit description from of the habitat in which the trap was placed was extracted. For studies reporting multiple habitat types (e.g. rice field, corn field and vegetable garden) for a single trap, trap-line or trapping grid, a higher order classification of habitat type was recorded (e.g. agricultural land).

### Rodent presence, absence, abundance

* The presence, absence and number of trapped individuals and their genus/species was extracted. For studies reporting on all trapped individuals (i.e. not those only reporting on the presence of a specific species of interest), the pseudo-absence of a species reported as present elsewhere in the study was explicitly recorded as an absence at that trap location.

### Pathogen presence and absence

* In studies investigating rodents for potential zoonoses, data on all pathogens assayed for were extracted. The number of rodents tested and the number of positive or negative samples were extracted alongside the type of assay used (e.g. Polymerase Chain Reaction (PCR), Enzyme Linked ImmunoSorbent Assay (ELISA) or viral culture). If studies reported indeterminate results this was noted. Where possible, pathogens were identified to species level. However, where an assay only allowed for attribution to a family of viruses or bacteria, the higher order grouping was used (i.e. PCR using a non-specific arenavirus primer).

## Analysis

### Location and habitats of rodent trapping to investigate potential biases

* The number of studies, the year in which trapping occurred and the country in which they were conducted was summarised.
* GPS coordinates of single trap, trapping grid or line or study site were used to calculate the trap site density of level 2 administrative areas in West Africa.
* The habitat types of trap sites were summarised based on information reported in the study.
* For the subset of studies investigating rodent zoonoses the location of trapping sites was compared to SEDAC Global Population Density estimates (1970-2000 (10 year) and 2000-2020 (5 year)) and to land cover classifications (1975, 2000 and 2013).
* The presence and absence of rodent species will be mapped and compared to the presence and absence reported by both GBIF and IUCN to give a measure of the extent of each species range in which they have been sampled.

### Rodent pathogen associations

* The presence and absence of pathogens, the assays used, their host species and the locations from where the samples were obtained were summarised.
* The association between rodent species and the detection of potential pathogens were identified. The proportion of positive and negative tests for each species and pathogen pair were reported.

# Results

## Included studies

* 4,282 records were identified, with 124 studies included.
* The earliest studies included studies were from 1974 with increasing numbers of studies being performed since 2000.

## Location and habitats of rodent trapping studies to investigate potential biases

* Rodent trapping took place across 1,193 study sites with at least one trap site recorded from 14 West African countries. No rodent trapping studies were identified from Gambia or Togo.
* Thirty-one (25%) studies reported trapping at a single study site, 45 (37%) studies trapped at between two and five study sites, the remaining 48 studies trapped at between six and 93 study sites. The areas with highest trapping activity included the capital cities of Niger (Niamey), Sierra Leone (Freetown), Senegal (Dakar), Mali (Bamako) and Ghana (Accra) and the largest cities of Ivory Coast (Abidjan) and Benin (Cotonou). Outside of these cities, Northern Senegal (Fatique, Thies, Saint-Louis and Kedougou), Southern Guinea (Kindia and Nzerejore), Edo and Osun States in Nigeria and Eastern Sierra Leone were the most intensively studied regions.
* No studies reported trap habitats with reference to a standardised habitat classification scheme.
* Extracted habitat types were grouped into 30 categories (see Supplementary table 2 for the habitat dictionary). At least one habitat was recorded for 17,122 trap sites (95%), with two or more habitats for a single trap site recorded for 4,403 (24%) sites. Single trap sites could span multiple habitat types resulting in 22,202 distinct habitat and trap sites.
* The most commonly trapped sites were in or around buildings (29%), in areas described as the rodents “natural habitat” (24%), in agricultural areas (13%) (e.g. rice fields, palm plantations), forests (8%) and in the area surrounding buildings (4%).
* Explore whether trap sites are more likely to have been conducted within high population regions or whether there is an association with trap location and habitat as obtained from remote sensing data (Need to do this. The remote sensing data will be matched to the trap dates there will be several years between the trapping and data this is compared to it seems impractical to try and get annual population estimates or land classification so this will be chosen pragmatically)

Figure 1 - Panel A - location of traps, Panel B - The distribution of population density at trap sites, Panel C - The distribution of habitat types at trap sites compared to all habitat types in West Africa

Rodent presence, absence, abundance 73,164 small mammals were trapped (592 were trapped outside of West African countries), 2,830 (4%) trapped individuals were identified to order level (Rodentia), 7,760 (11%) were identified to genus level, the remaining 62,574 (85%) were identified to species level. Of the 147 distinct identified species trapped (see Supplementary table 3) the majority were from the order Rodentia (112). Muridae (82) represented the largest family of rodents, followed by, Sciuridae (10), Gliridae and Nesomyidae (both 6), Ctenodactylidae and Anomaluridae (2) and Dipodidae, Hystricidae and Thryonomidae (all 1). The remaining 34 species came from the orders of the Soricomorpha (30), Erinaceomorpha (2) and Afrosoricida (1). The most commonly trapped genera of rodents were Mastomys sp. (27,072, 38.5%), Rattus sp. (10,191, 14.5%), Mus sp. (8,624, 12.3%), Arvicanthis sp. (5,821, 8.3%) and Praomys sp. (5,409, 7.7%). At species level Mastomys natalensis (11,221, 17.9%), Rattus rattus (8,578, 13.7%), Mastomys erythroleucus (7,379, 11.8%), Mus musculus (6,245, 10%), Arvicanthis niloticus (5,497, 8.8%) and Mastomys huberti (4,699, 7.5%) were the most commonly trapped. Presence and absence maps for the six most commonly trapped species are compared to GBIF and IUCN data. (Need to do this) The number of individuals trapped provides a measure of abundance, the interpretation of this is limited by incomplete reporting on the trapping effort (i.e. number of trap nights) within a study. The most abundant species at presence locations were … (Need to do this. I will explore the number of individuals trapped by species, I imagine it will show that if a species is detected at a site the most abundant ones will be the synanthropic species such as mus, rattus etc. while the more specialised species will be less abundant in areas where they are detected)

Figure 2 - Three plots side by side with 6 rows, one each for the most commonly trapped species L - presence/absence from this review, C - presence/absence from GBIF, R - Species range from IUCN

Pathogen presence and absence Sixty-two studies presented data on microorganisms that infect or are carried by small mammal species in West Africa. Seven studies solely investigated pathogens of rodents, including Hydatigera species (previously Taenia species) and Trichuris species. Fifty-five studies investigated organisms that were potentially zoonotic pathogens. Thirty-two microorganisms were tested for, 8 of these were defined at species level, with the remaining 24 at levels of higher taxonomic classification. Thirty-two studies used Polymerase Chain Reaction (PCR) to detect the presence of 22 different species or families of microorganisms in 21,953 rodent samples. Eleven studies used antibody or antigen based molecular tests to detect the presence of 9 different species or families of microorganisms in 11,430 samples. Eight studies conducted histological or direct visualisation assays of samples for 11 parasitic or bacterial species in 11,229 samples. Three studies performed direct culture of Lassa mammarenavirus or Leishmania species to detect the presence of the pathogen in 643 samples. The most common pathogens assessed for using PCR were Lassa mammarenavirus or other Arenaviridae (31%) the bacteria Borrelia sp. (11.3%) and Bartonella sp. (6.5%) followed by Usutu virus (6.4%) and Hantaviridae (5.6%). The most common pathogens assessed for with serology were Lassa mammarenavirus or other Arenaviridae (78%), Toxoplasma gondii (10.6%), Borrelia sp. (6.3%) and Leptospirosis sp. (2.2%). The most common pathogens assessed for with histology or direct visualisation were Borrelia sp. (48.7%), Schistosoma sp. (20.4%) and other parasites. All studies using direct culture were investigating either Lassa mammarenavirus (81%) or Leishmania sp. (19%). Most studies tested for a single pathogen (39), with 16 studies testing for two or more pathogens. The most frequently tested for pathogens were Lassa mammarenavirus (28%) or members of the Arenaviridae family (16%), the spirochete bacteria Borrelia sp. was investigated in 8 studies, Bartonella sp. and Toxoplasma gondii were investigated in 4 each, the remaining 25 pathogens were reported in three or fewer studies. Define presence and absence of pathogens by country (Need to do)

Figure 3 - Presence/absence plots for the following pathogens Arenaviruses with LASV highlighted, Bartonella, Borrelia and Toxoplasma.

Host-pathogen associations Ninety-seven rodent species were investigated for the presence of a zoonotic pathogen. 42,940 assays were performed on 32,014 individual rodents. The rodent species most commonly assayed for zoonotic pathogens were, Rattus rattus (n = 2,977) assessed for 24 pathogens, Mus musculus (n = 3,402) for 23, Mastomys natalensis (n = 7,189) and Mastomys erythroleucus (n = 3,013) both 19 and Arvicanthis niloticus (n = 3,840) for 18. All remaining species were investigated for 10 or fewer pathogens. Lassa mammarenavirus was detected in 414 Mastomys natalensis, 9 Mastomys erythroleucus, 5 Hylomyscus pamfi and 3 Mus baoulei through PCR. In serological assays, evidence of prior infection or acquisition of maternal antibodies to Lassa mammarenavirus was found in 465 Mastomys natalensis, 361 Mastomys sp., 6 Mus musculus and 4 Rattus rattus. From direct viral culture 19 Mastomys natalensis, 2 Rattus rattus and 1 Mus minutoides were found to be infected with Lassa mammarenavirus. Bartonella sp. were detected in; 113 Mastomys natalensis, 50 Mastomys erythroleucus, 39 Rattus norvegicus, 16 Rattus rattus and 13 individuals of 7 further species through PCR. Borrelia sp. infections were identified through PCR in 110 individuals; 37 Mastomys erythroleucus, 12 Mus musculus, 11 Mastomys huberti and Praomys daltoni., tThe remaining 39 positive results were from 9 further species. In serological assays, 47 Mastomys natalensis, 12 Mastomys erythroleucus and 8 Praomys daltoni were found to be positive, the remaining 11 positive individuals came from three further species. Most Borrelia sp. infections were identified through histology or direct visualisation with, 243 Arvicanthis niloticus, 102 Mastomys natalensis, and 78 Mastomys huberti along with a further 64 individuals from 8 species infected. Finally, Toxoplasma gondii was detected via PCR in 89 Mus musculus, 13 Cricetomys gambianus, 5 Crocidura olivieri and 3 Rattus rattus. From serological assays evidence of infection was found in 25 Mus musculus, 46 Mastomys erythroleucus, 4 Rattus rattus, and Mastomys natalensis, using histology and direct visualisation 1 Mus musculus and 1 Rattus rattus were also found to be infected. Thirty-eight species of Rodentia, 3 species of Soricomorpha and 2 species of Erinaceomorpha that were tested for potential pathogens had entirely negative results.

Figure 4 - Matrix heat plot Y - rodent species/genera, X - pathogen species/genera. Colour relates to proportion positive (Perhaps use bivariate colour to also highlight the number of test performed in that species).

Discussion 124 trapping studies were identified across 14 West African countries. 54 studies provided additional information about potential zoonotic pathogens of trapped rodents.