SpREAD: Spatio-temporal Rodent Community Ecology And Disease Database.

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Abstract

Rodents are reservoirs of zoonotic diseases, posing a significant threat to human health. Understanding rodent ecology and population dynamics is therefore important for mitigating human zoonotic hazards. Trapping studies have improved our understanding of zoonotic epidemiology, however, capturing known reservoirs to the exclusion of other rodent species limits inference on broader eco-epidemiological questions. Detailed information on rodent communities could be used to understand how global changes in habitat suitability and climate influence the dynamic ecosystems from which zoonotic diseases emerge and are maintained. Currently, there is no standard method for reporting rodent trapping data. This project aims to establish a high-resolution rodent community seroprevalence database by collating published data on rodent abundance and pathogen prevalence, and provide a standard for its reporting going forward. These data will facilitate robust inference on the eco-epidemiological predictors of rodent-borne disease, helping to shape our understanding of zoonotic disease risk in a changing world.

Introduction

Methods

The data included in this database are the result of three stages of data collection: initial literature search and data extraction from publications, subsequent data requests to corresponding authors, and final distribution of a general data request around rodent ecology spheres. The data request document used is provided in the supplementary materials (S1).

Literature Search and Data Extraction

The initial search and screening of studies was carried out as part of a separate project, Ar-Ha, the exact methods of which are available in the protocol paper for this project (citation). In short, searches were ran on PubMed and Web of Science that included search terms rodent*, shrew, arenavir* and hantavir* and combinations of these. The search carried out on 2023-10-16 yeilded 2,755 unique pubications, which were subsequently screened for relevance. This screening resulted in a final list of 917 publications where the methodology included rodent serosurveys, although the results were reported to varying degrees of resolution.

The minimum requirements for data to be included in this database are as follows:

1. **Date of trapping** (minimum resolution of a month)
2. **Duration of trapping** (or start and end date)
3. **Locality or coordinate location** of trapping site
4. **All captured rodents' abundances** are reported
5. **All individuals are tested** for at least one pathogen
6. **Type of test used and pathogen name** (at least family level e.g. hantavirus)

From these publications, we extracted data that met these criteria and collated them into a common format. Publications which were thought to have the desired resolution but did not report the data, or summarised the data, were contacted via the corresponding author's email. The email used is included in the supplementary material (S1). A breakdown of the data extracted, and provided via correspondence is given below. (sankey diagram x2, one for number of studies, one for number of individual rodents). (description of breakdown).

Filtering and Clearning of Data

Scientific names of host species and pathogens were harmonised.

Results

Through extraction of data from 27 published articles (so far), we have gathered data on 189 unique rodent communities across 5 continents (fig. 1). These are comprised of 10,955 rodents, of which 480 were positive for a pathogen of interest. The most common rodents found were of the *sigmodon* (cotton rats) and *peromyscus* (deer mice) genera (fig. 2). The most prevalent viruses were Sin Nombre Virus, Catarina Virus and Puumula Orthohantavirus, all belonging to the family *hantaviridae* (fig. 3).

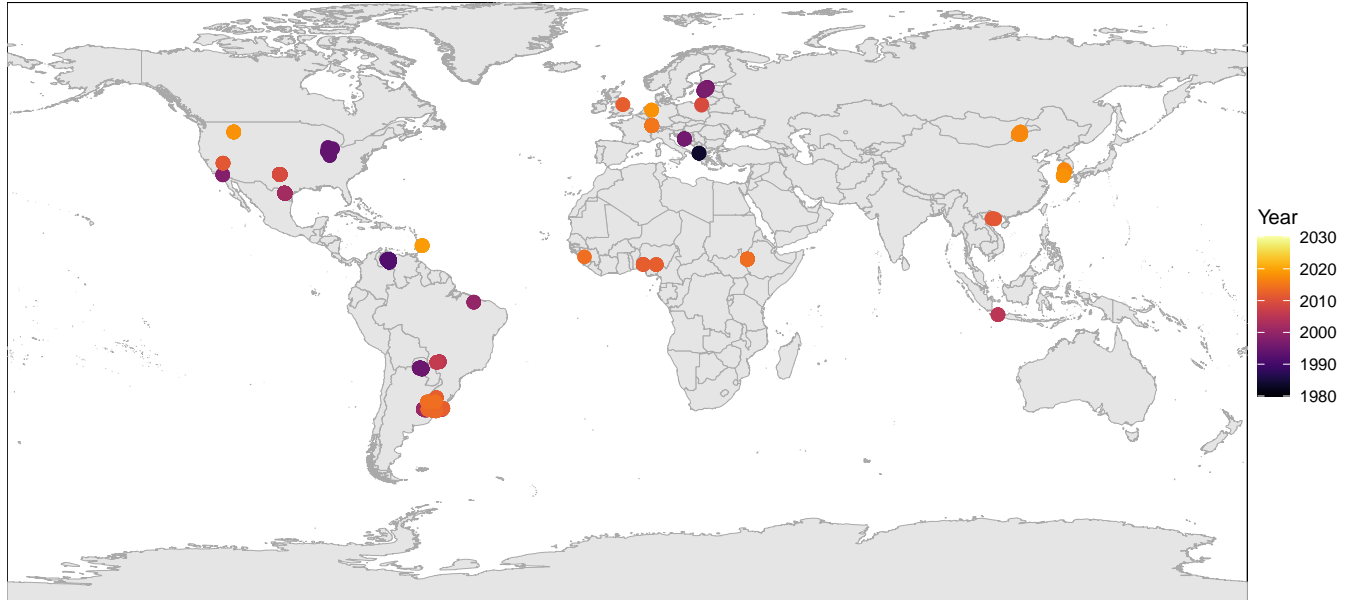## References

Tables and Figures

Figure 1: The geographic locations of trapped rodents included in our study. The colour of points denotes the year sampled.
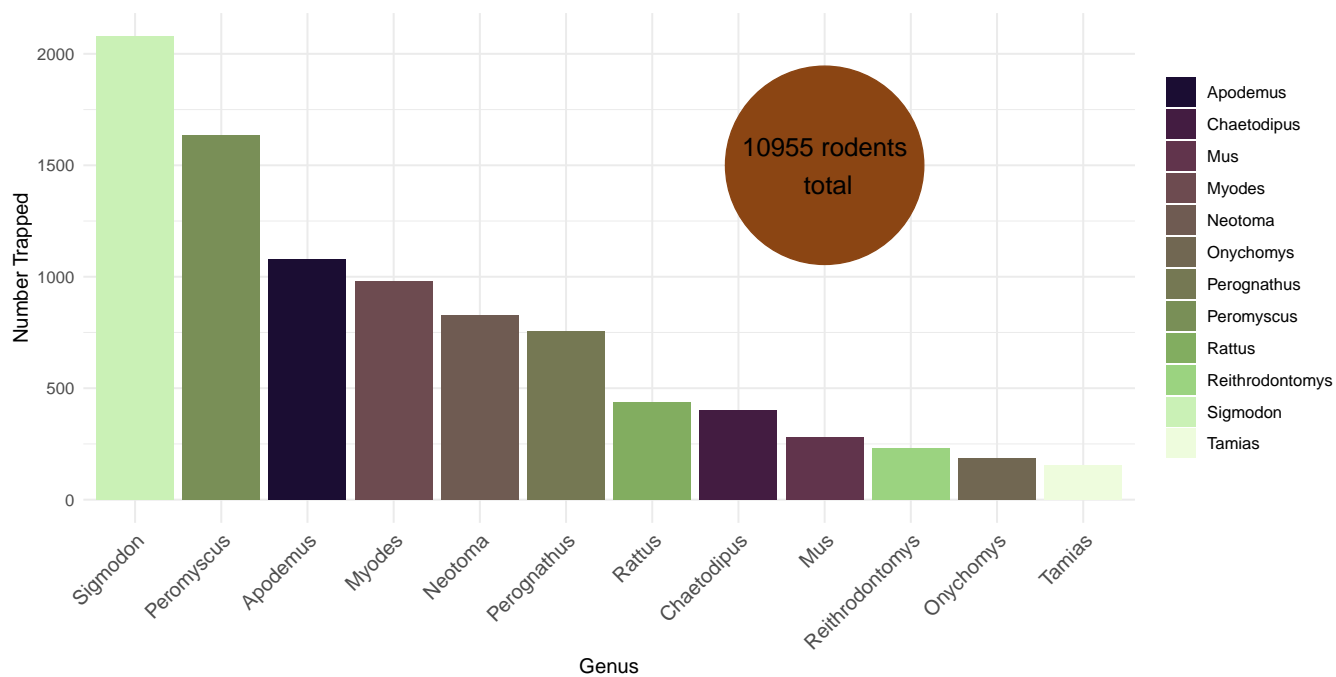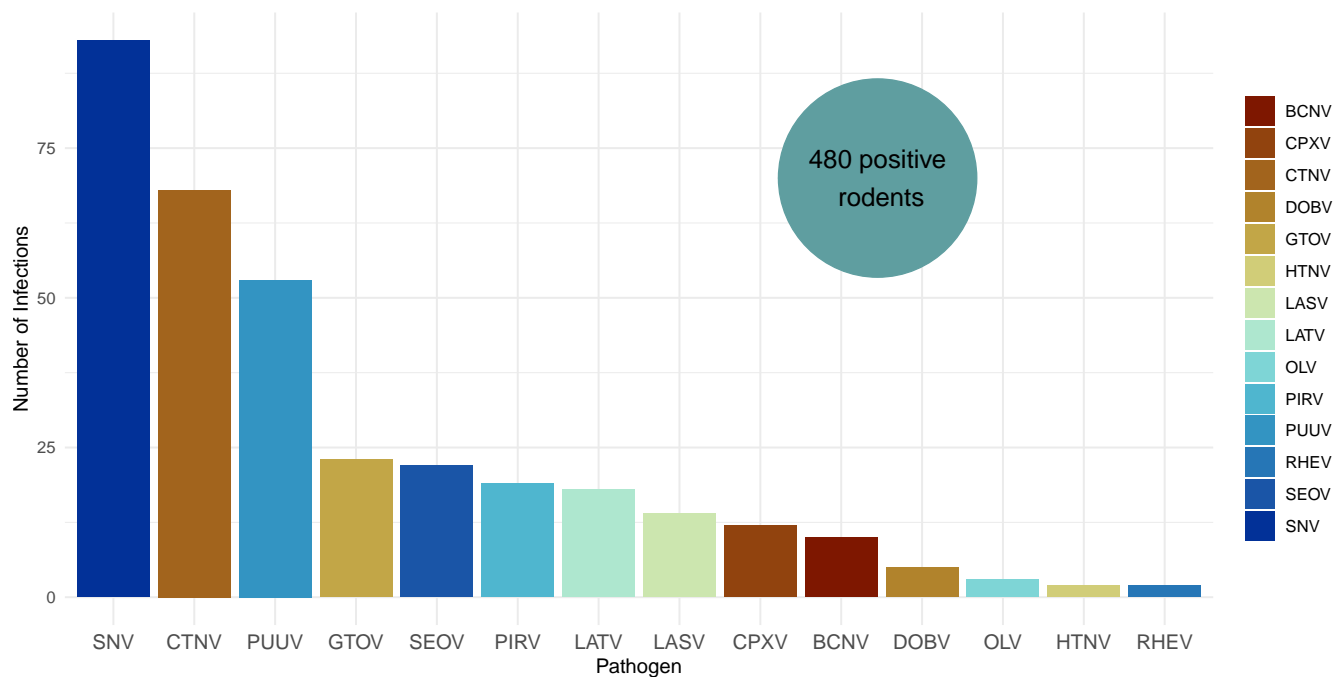
Figure 2: The number of hosts trapped for each genus

Figure 3: The number of infections for each virus tested