

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

Requirements for inclusion

The minimum requirements for data to be included in the SpREAD 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)

Desirable:

1. Indication of trapping method (e.g. grid area/number of traps/type of trap)
2. Indication of trapping effort (e.g. trap nights)

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 Puumala Orthohantavirus, all belonging to the family *hantaviridae* (fig. 3).

References

Tables and Figures

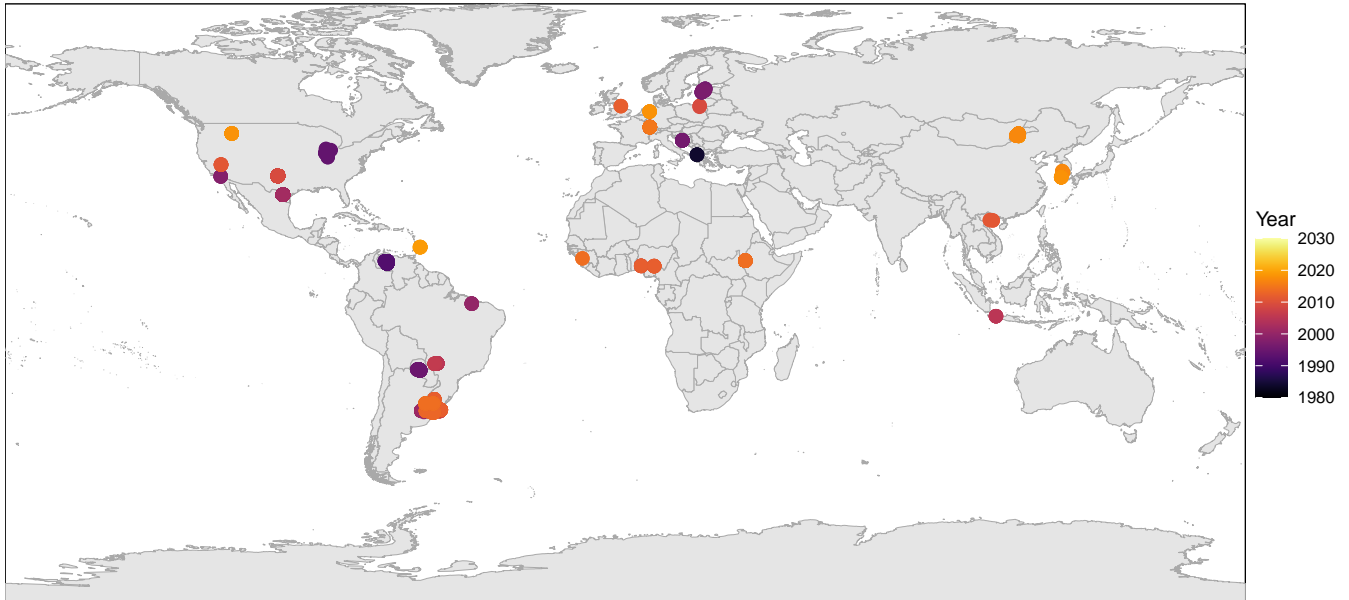


Figure 1: The geographic locations of trapped rodents included in our study. The colour of points denotes the year sampled.

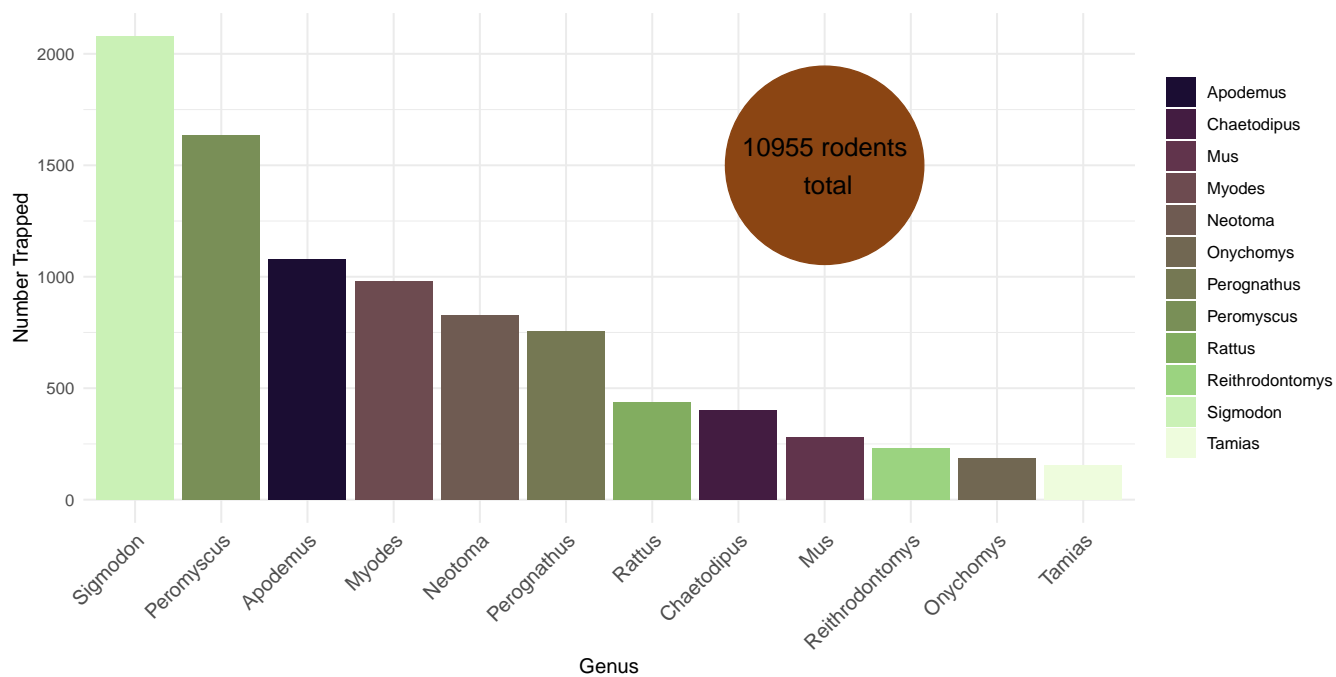


Figure 2: The number of hosts trapped for each genus

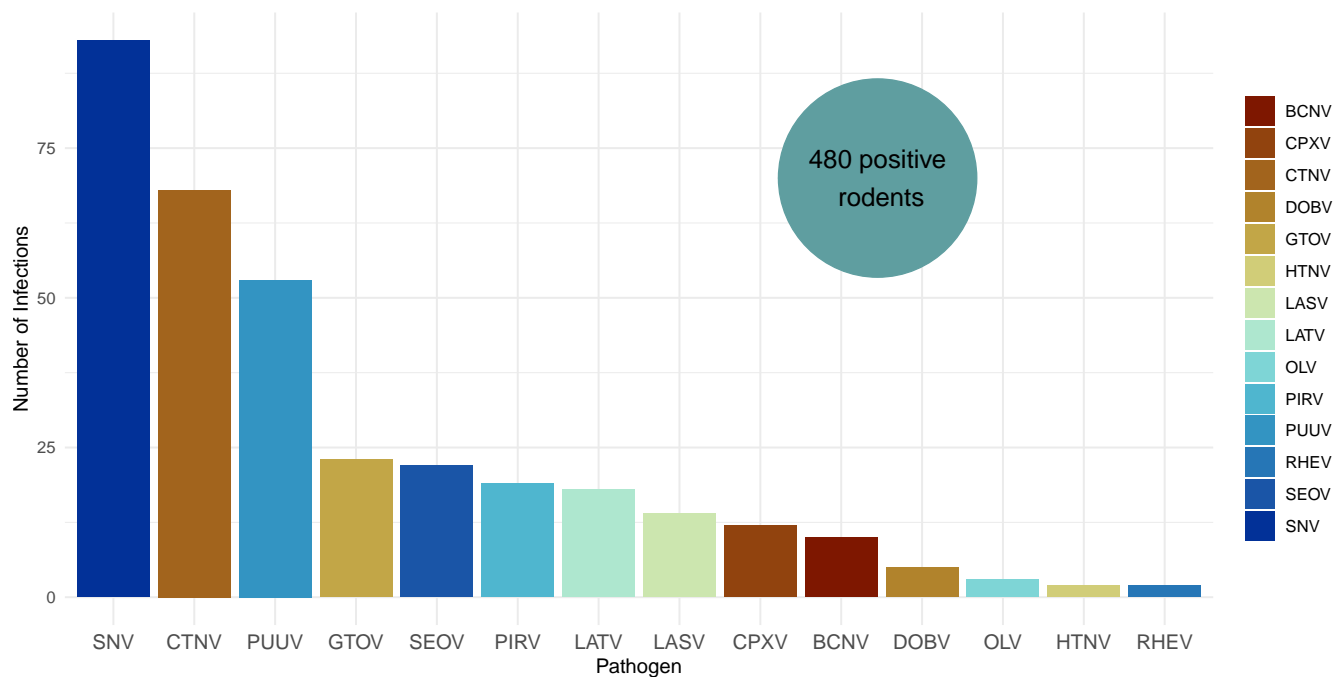


Figure 3: The number of infections for each virus tested