Title

A database of common vampire bat reports

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Abstract

The common vampire bat (*Desmodus rotundus*) is a sanguivorous (i.e., blood-eating) bat species distributed in the Americas from northern Mexico southwards to central Chile and Argentina. *Desmodus rotundus* is one of only three mammal species known to feed exclusively on blood, mainly from domestic mammals, although large wildlife and occasionally humans can also serve as a food source. Blood feeding makes *D. rotundus* an effective transmissor of pathogens to its prey. Consequently, this species is a common target of culling efforts by various individuals and organizations. Nevertheless, little is known about the historical distribution of *D. rotundus*. Detailed occurrence data are critical for the accurate assessment of past and current distributions of *D. rotundus* as part of ecological, biogeographical, and epidemiological research. This article presents a dataset of *D. rotundus* historical occurrence reports, including >39,000 locality reports across the Americas to facilitate the development of spatiotemporal studies of the species. Data are available at https://doi.org/10.6084/m9.figshare.15025296.

Background and Summary

The common vampire bat, *Desmodus rotundus* (É. Geoffroy, 1810) is a member of the family Phyllostomidae, subfamily Desmodontinae[1]. *Desmodus rotundus* is endemic to the Neotropics, where it occurs from northern Mexico, through all of Central America, and across most of South America[2,3]. D. rotundus is found over an elevational range from sea level up to 3600 m in the Andes mountains[4]. Two subspecies are recognized: *D. r. rotundus* (Trinidad, Tobago, Colombia, Venezuela, the Guianas, Ecuador, Peru, Brazil, Bolivia, Paraguay, Argentina, Uruguay, and central Chile) and *D. r. murinus* (Mexico, Central America, northern and western Colombia, and western Andean slopes in Ecuador and Peru)[2]. *Desmodus rotundus* is a strictly sanguivorous species that feeds mainly on the blood of medium to large-bodied terrestrial mammals and some birds[5]. While groups such as humans and cattle are not natural prey of *D. rotundus*, they have been documented as being fed upon by this species[6,7]. The most common prey species of *D. rotundus* are peccaries, deer, tapirs, horses, cattle, pigs, and goats, and to a lesser extent, species such as chickens, dogs, and sea lions[4,8–10].

Desmodus rotundus uses various landscapes throughout its broader geographic distribution, including open grasslands, savannas, tropical, subtropical, and dry forests, and even desert environments[2,8,11–15]. *Desmodus rotundus* can also adapt to different landcover types, and has been found not only in patches of old-growth or undisturbed forests, but also in disturbed areas such as agroforestry plots, silvopastoral systems, pastures, and secondary forests[13,16,17]. *Desmodus rotundus* usually roosts in small groups, from as few as 10 to a few hundred individuals, but can also be found roosting in groups of up to a few thousand individuals[2]. *Desmodus rotundus* also uses a variety of roosts, including tree holes, crevices, caves, and abandoned mines and houses[2]. The conservation status of *D. rotundus* was defined as of “Least Concern” in 2015 by the International Union for Conservation of Nature and Natural Resources (IUCN) Red List of Threatened Species, as it is presumed to be a common species with large and stable populations[18].

Desmodus rotundus can act as a natural reservoir for various microorganisms with zoonotic potential, such as bacteria, including *Bartonella* spp.[19], coronaviruses[20,21], and rabies virus[12,22]. *Bartonella* spp. bacteria are globally distributed and have been known to cause endocarditis in humans and other animals[19,23,24]. Endocarditis is an infection of the inner lining of the heart, and can potentially be lethal[23,24]. Furthermore, several variations of coronaviruses have been identified in *D. rotundus*[20,25]. In the Americas, bats are considered to be a key reservoir of the rabies virus[26,27], with *D. rotundus* being the main species responsible for transmitting rabies to livestock[28]. It has been estimated that bovine rabies transmitted by vampire bats causes the death of thousands of cattle annually, resulting in economic losses of hundreds of millions of dollars in Latin America[29,30]. Indirect costs associated with *D. rotundus* related rabies include the vaccination of millions of cattle as a preventative measure, and post-exposure treatments (rabies immunoglobulin serums and vaccination) for people exposed to *D. rotundus* bites[29,30]. The perpetuation of rabies in livestock may also be associated with the abundance and distribution of *D. rotundus*[28,31,32], as sex-related (male) dispersal may contribute to the expansion of rabies virus into new areas[33]. Thus, the addition of livestock to the landscape promotes suitable conditions for *D. rotundus* breeding and feeding[28,34–36].

Due to its reservoir status for potential pathogens*, D. rotundus* is considered to be a major public health problem in the tropical and subtropical regions of the Americas. Public health concerns are particularly prevalent in Amazonian regions, where many people live in vulnerable housing[37,38] and human diseases transmitted by *D. rotundus* remains high[39]. In fact, since 2020, rabies has been included in the World Health Organization (WHO) 2021-2030 road map as a zoonotic disease, and now requires coordination of mitigation strategies at the regional, national, and global levels[40,41]. Numerous outbreaks in rural human communities have been reported in Amazonian regions, including Peru[42], Brazil[6,43], and French Guiana[7,44].

Several Latin American countries have developed programs to reduce the number of *D. rotundus* bites to humans and livestock[45]. Culling campaigns to reduce *D. rotundus* populations; however, have not proven useful in reducing the seroprevalence of rabies within vampire bat colonies[46]. It has been suggested that *D. rotundus* geographic distributional expansion is linked to landscape heterogeneity, degradation, and agricultural aggregations[13,37,47]. Nevertheless, an increase of suitable areas under future climatic scenarios may contribute to the increased risk of rabies in some regions of the Americas[34]. The study and analysis of *D. rotundus* occurrence data are, therefore, critical for the development of preventive measures for vampire-transmitted rabies[48,49]. This article presents a comprehensive dataset of curated historical occurrence reports of *D. rotundus* across the Americas to facilitate spatiotemporal modeling and other relevant *D. rotundus* research. The dataset is available at https://doi.org/10.6084/m9.figshare.15025296 [Ref. [50]].

Methods

Data gathering for this dataset began in January 2020 and ended in December 2021. Occurrence reports of *D. rotundus* were collected from a variety of publicly available resources and databases, from a network of natural history museums across North, Central, and South America, from official repositories in ministries of agriculture and health, from published scientific literature across Latin America, and from privately held databases from individual contributors (**Figure 1**). The final dataset includes

39120 individual occurrence reports (i.e., recorded instances where one or more *D. rotundus* individuals were recorded or observed) (**Figure 2**) and 7576 unique geographic locations of *D. rotundus* existence. All data were collected in Darwin Core Archive format[51]. The Darwin Core Archive is a biodiversity and taxonomy based data definition format that makes use of standardized terms and file structures[51]. The use of the Darwin Core Archive allows for better data accessibility and mobilizations, as well as facilitates the data's compliance with intercommunity standars[51,52]. *Desmodus rotundus* occurrence reports were geo-referenced using the World Geodetic System 1984 coordinate system in decimal degree units. Inclusion criteria for this dataset were:

A) That the report consisted of the modern species *Desmodus rotundus*[1]

B) The report consisted of at least one individual

C) The report had a recorded geographic coordinate (e.g., latitude and longitude), or a detailed locality description from which the occurrence could be geolocated (i.e., at finer detail beyond municipality level)

D) The report was from a validatable database, museum record, published piece of literature, machine recording (e.g., acoustic monitor or camera), human observation, preserved specimen, or live specimen

Metadata such as individual count (i.e., number of individuals recorded at each occurrence location, which may vary based on how the original report was collected), specimen age or life stage, basis of record, and date of capture were collected for each report whenever possible (**Figure 3**). For occurrence reports where full metadata were not available or unable to be confirmed, the information was left blank in the final file (**Supplementary Materials**). Definitions for the database and metadata can be found in **Online-only Table 1.** After data gathering and technical validation the dataset was published in the Figshare data repository for public access (available at: https://doi.org/10.6084/m9.figshare.15025296)[50].

Data Records

To collect occurrence reports from published literature, a review was conducted of all publications available in the Web of Science literary repository on August 28, 2020 (Clarivate™, 2020. available from: https://apps.webofknowledge.com/Search). We conducted a keyword search of topics in journal manuscripts, proceedings papers, and official reports. Keywords included "*Desmodus rotundus*", "vampire bat", and "common vampire bat", and resulted in 315 manuscripts. The resulting manuscripts in Spanish, English, and Portuguese were then screened for associated *D. rotundus* occurrence data. A summary of these literature data sources can be found in **Online-only Table 2**. Additional reports were obtained from 37 institutions or researchers with privately held data. These contributors are summarized in **Online-only Table 3**. Data curation and validation followed the standardized protocol used for other data sources.

Occurrence reports were also collected from publicly available data repositories or databanks (i.e., web-based sources which centrally house data from other sources)[53]. These repositories included the Global Biodiversity Information Facility (GBIF)[54], Biodiversidata[55], and speciesLink[56]. Occurrence reports for *D. rotundus* were downloaded from the GBIF on October 30, 2020[54]. GBIF occurrence reports with coordinates which were located in the western hemisphere (n=12865) were downloaded from the database in Darwin Core Archive format[51]. Occurrence reports based on fossil specimens (n=3) were removed. After the cleaning and validation process (see Technical Validation), the final number of occurrences from GBIF was 12736. Originating datasets which contributed to the GBIF download are summarized in the Supplementary Materials. Occurrence reports from Biodiversidata (Uruguayan Consortium of Biodiversity Data Repository)[55] were downloaded in December of 2020 from the vertebrate mammal sub dataset (n=67)[55]. Occurrence reports from speciesLink (Centro de Referência em Informação Ambiental) were downloaded in August of 2021 (n=2578). Of these reports, 918 were found to be already present in the GBIF database. In total, 1660 occurrences from speciesLink were added to the final dataset. A total of 298 occurrence reports without recorded coordinates were also downloaded from the publicly available data repositories and 48 of these reports were able to be georeferenced based on their locality descriptions. The other 250 could not be located due to a lack of detail in their locality descriptions and were therefore excluded. Georeferencing was completed using the *tidygeocoder* package in R[57]. All data are stored in the finalized dataset in the Figshare data repository for public access[50].

Technical Validation

To validate the collected data, we identified "redundant" reports (i.e., unique reports present in more than one dataset repository). Occurrence reports were flagged as redundant when the occurrence geolocation information (i.e., latitude, longitude, locality, and elevation) and institutional information (e.g., institutional identification number, originating dataset, institutional code, etc.) were identical. Other metadata such as date of occurrence, individual count, sex, life stage, and basis of record were used to confirm or reject redundancy. Reports where these variables matched were flagged and manually investigated to confirm redundancy. When redundant reports were found and confirmed, the original source occurrence report was retained. This process was completed using the *dyplr* package and base functions such as duplicate and unique in R[58,59].

All occurrence reports were also investigated to eliminate occurrences with errors in geolocation using the *coordinateCleaner* package[60]. Using the functions cc_cap, cc_cen, cc_gbif, and cc_inst, we identified and removed occurrence reports which were erroneously assigned to country capitals, country centroids, or the GBIF/Biological Institution headquarters[60]. We also used cc_zero and cc_val functions to identify and remove reports with 0 latitude and 0 longitude as the geographic coordinates, or other invalid geographic coordinates (i.e., non-numeric or not possible coordinates such as Northern latitudes over 90°)[60]. The remaining occurrences were then visualized in geographic space. Occurrence reports which were located outside of the American continents (i.e., in the ocean) were identified and flagged. These occurrences were then investigated manually for errors. Coordinates that were identified as suspicious spatial outliers (>500 km from their nearest neighbor) were validated by contacting the publishing institution or individual (e.g., the natural history museum, collection, or author). Mapping was done using the package *ggplot2* in R and ArcGIS Pro software[59,61,62].

Usage Notes

This occurrence report dataset includes both geographic and temporal information on the presence of *D. rotundus*. This information could be used to assess the biogeography of the species retrospectively. Additionally, *D. rotundus* data could be coupled with environmental data to conduct ecological studies of the environmental tolerances of the species, landscape use, behavior, and prey availability. Future studies could also use this dataset to assess how *D. rotundus* distribution has changed over time and how distributional changes could be linked to climate and land cover change. Other potential applications of this dataset include the study of rabies reservoirs, which could aid in the understanding of rabies outbreaks. Epidemiological forecasting using *D. rotundus* data could serve to address gaps in current rabies prevention plans and could facilitate targeted social outreach to vulnerable communities.

Code Availability

Data, metadata descriptions, and R code are available in the Figshare data repository for public access (accessible from: https://doi.org/10.6084/m9.figshare.15025296)[50].

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Author Contributions

LEE: conceived and designed the study. PV: developed the data curation and designed the manuscript. MMD, ARSP, JLA, DG, HZ, SVdO, ECC, JRMB, LEE collected in-country data. PV, NB: collected electronic data. LEE, PV: conducted the technical validation process. All authors wrote and approved the final version of the manuscript.

Competing Interests

The authors declare that they have no competing interests.

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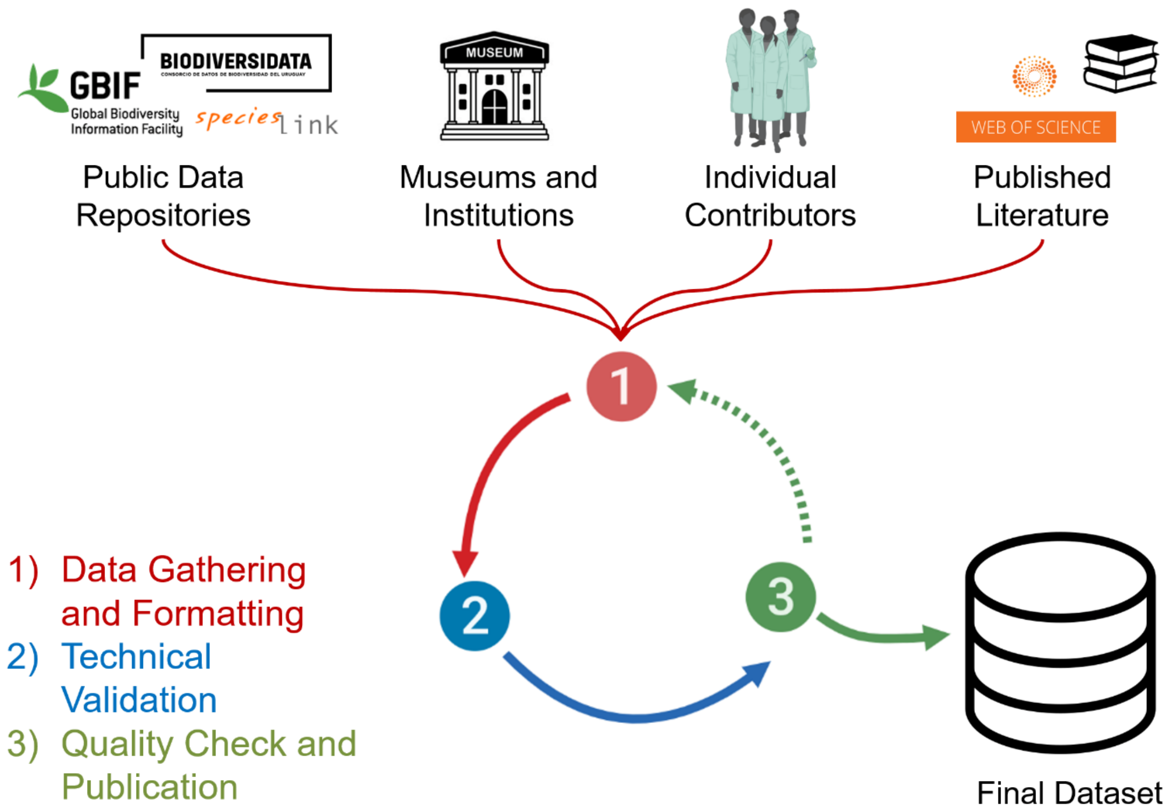

Figure 1: Dataset Workflow. Visual representation of the data curation, formatting, technical validation, and quality control process of this dataset of *Desmodus rotundus* occurrence reports. 1) **Red:** the data were first collected from various sources, including public data repositories, natural history museums and institutions, individual contributors, and published scientific literature. These data were formatting to meet Darwin Core archive standards. 2) **Blue:** the formatted data were then examined for error and underwent the technical validation process where reports which did not meet inclusion criteria were removed (see Technical Validation section). 3) **Green:** the data were examined again after the technical validation process for quality and for any remaining errors. This process was repeated as new *D. rotundus* occurrence reports were collected (dashed arrow). The final dataset was published at the

end of this repeated validation and quality check process and is accessible from: https://doi.org/10.6084/m9.figshare.15025296.

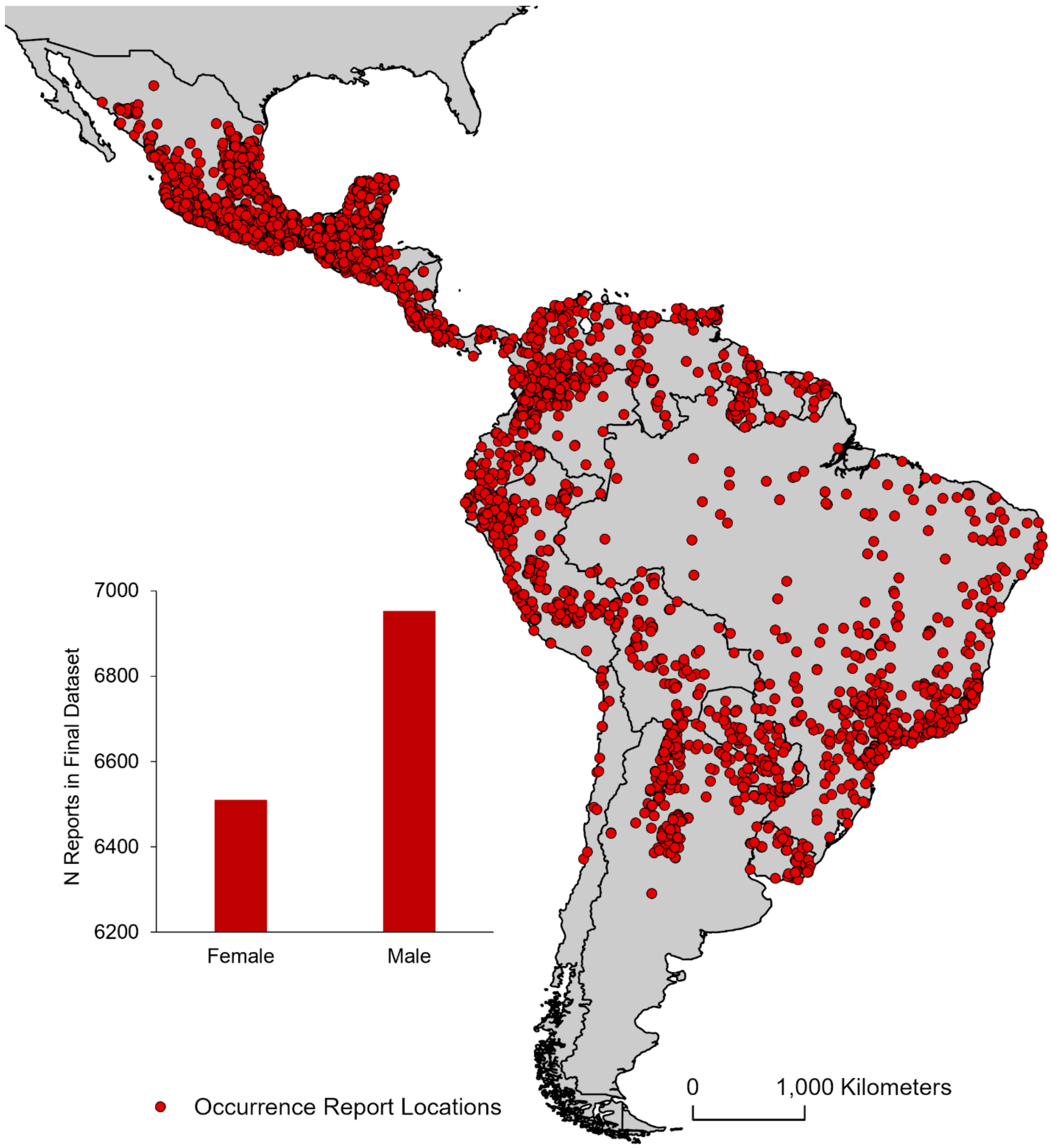

Figure 2: Map of occurrence report locations. Geographic locations of all occurrence reports in the final *Desmodus rotundus* report dataset (red points) representing 7576 unique geographic locations available from the 39120 original reports. Inset: number of reports by sex in the final dataset (red bars) showing more reports of male individuals than females.

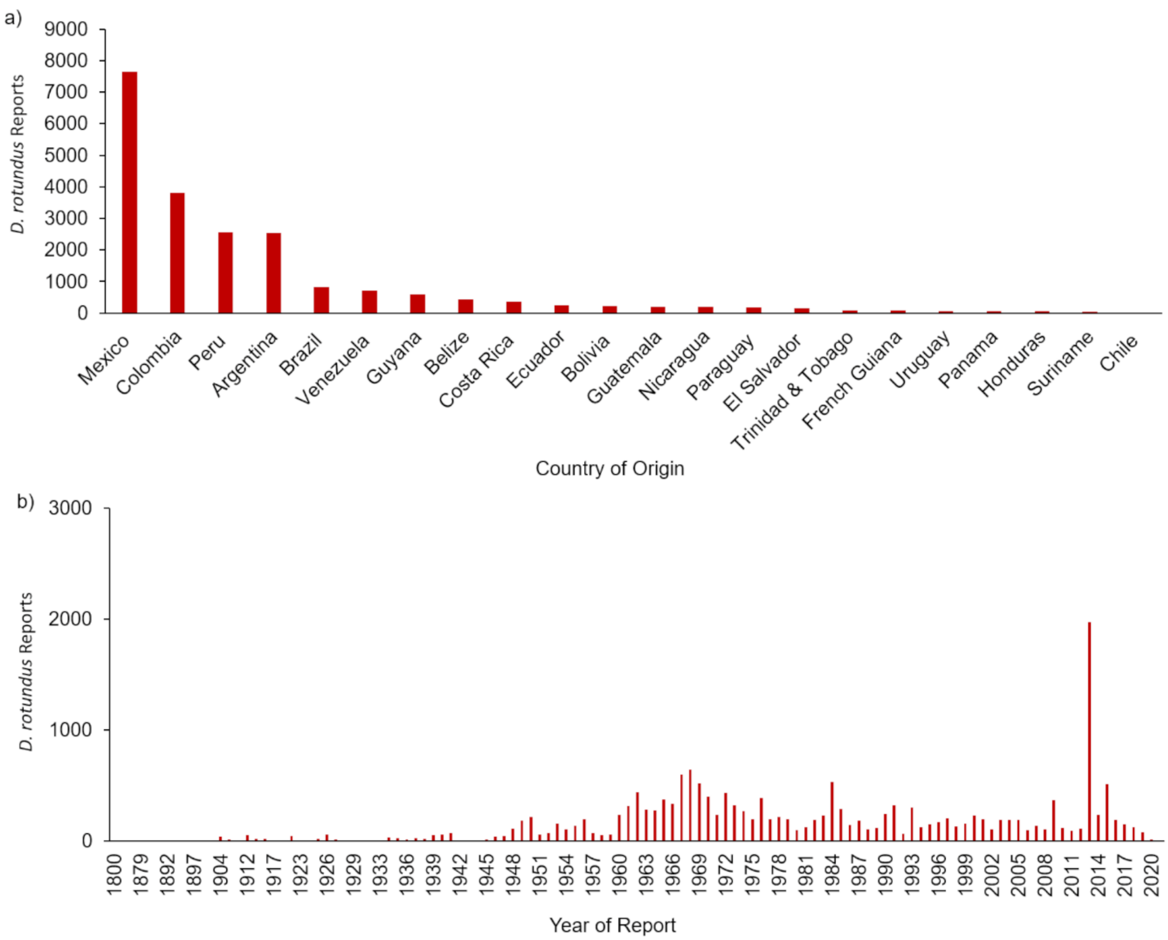

Figure 3: Data distribution by country and year. a) The number of occurrence reports in the final *Desmodus rotundus* dataset are reported based on the country in which the occurrence report occurred. The country with the most recorded occurrences was Mexico (n=7653), followed by Colombia, Peru, and Argentina, which contributed over 2000 *D. rotundus* occurrence reports each. b) Number of occurrence reports in the final *D. rotundus* dataset shown based on the year in which *D. rotundus* were recorded.