

Global Mammal Parasite Database version 2.0

Patrick R Stephens^{1,2*}, Paula Pappalardo^{2*}, Shan Huang³, James E. Byers², Maxwell J. Farrell⁴,
Alyssa Gehman⁵, Ria R. Ghai⁶, Sarah E. Haas⁷, Barbara Han⁸, Andrew W. Park², John P.
Schmidt², Sonia Altizer², Vanessa O. Ezenwa², Charles L. Nunn⁹

*equal authorship

¹ Corresponding author: prsteph@uga.edu

² Odum School of Ecology, University of Georgia, Athens GA

³ Senckenberg Biodiversity and Climate Research Center (BiK-F), Senckenberganlage 25 D-
60325 Frankfurt (Main), Germany

⁴ Department of Biology, McGill University, Montreal, Quebec Canada H3A1B1

⁵ Department of Zoology, University of British Columbia, Vancouver, British Columbia Canada
V6T1Z4

⁶ Department of Environmental Sciences, Emory University, Atlanta, Georgia 30322

⁷ Inland Fisheries Division, Texas Parks and Wildlife Department, Austin, Texas 78744

⁸ Cary Institute of Ecosystem Ecology, Millbrook, New York 12545

⁹ Biological Sciences, Duke University, Durham North Carolina 27708

Abstract

Illuminating the ecological and evolutionary dynamics of parasites is one of the most pressing issues facing modern science, and is critical for basic science, the global economy and human health. Extremely important to this effort are data on the disease-causing organisms of wild animal hosts (including viruses, bacteria, protozoa, helminths, arthropods and fungi). Here we present an updated version of the Global Mammal Parasite Database, a database of the parasites of wild ungulates (artiodactyls and perissodactyls) , carnivores, and primates, and make it available for download as complete flat files. The updated database has more than 24,000 entries in the main data file alone, representing data from over 2,700 literature sources. We include data on sampling method and sample sizes when reported, as well as both “reported” and “corrected” (i.e., standardized) binomials for each host and parasite species. Also included are current higher taxonomies and data on transmission modes used by the majority of species of parasites in the database. In the associated metadata we describe the methods used to identify sources and extract data from the primary literature, how entries were checked for errors, methods used to georeference entries, and how host and parasite taxonomies were standardized across the database. We also provide definitions of the data fields in each of the four files that users can download.

Key Words: parasites, infectious disease, wild mammals, transmission modes, Carnivora, Primates, ungulate, Artiodactyla, Perissodactyla

METADATA

INTRODUCTION

Understanding the diversity, spread, and evolution of disease-causing organisms is a critical area of scientific inquiry, and is important for topics as diverse as human health, wildlife conservation and agriculture. Key to this effort are large databases of the micro and macroparasites (including viruses, bacteria, protozoa, helminths, arthropods and fungi) that occur in the wild. Studies using data on wild mammal parasites have provided key insights into understanding the traits that explain variation in parasite species richness among host species (Nunn et al. 2003, Ezenwa et al. 2006, Huang et al. 2015), the factors that make it likely for hosts to share parasite species (Cooper et al. 2012, Huang et al. 2014), and geographic areas from which novel human zoonoses are likely to emerge (Pedersen and Davies 2009). The challenge of collecting the data needed for such studies is enormous both in terms of logistics and personnel hours. For years several research groups have been compiling data on the naturally occurring parasites of wild primate, carnivore and ungulate hosts: the Global Mammal Parasite Database (GMPD, <http://www.mammalparasites.org/>). Nunn and Altizer (2005) previously provided a description of the primate portion of this database. No detailed description of the ungulate and carnivore sections of the GMPD has yet been published (but see Ezenwa et al. 2006, Lindenfors et al. 2007, Huang et al. 2014). Even within the primates, the methods used have continued to evolve and coverage has continued to expand with ongoing development of the database.

For the first time we provide a description of the full GMPD. We also describe new data not previously available that have been developed as part of a number of recent and ongoing studies. This version of the GMPD stands at more than 24,000 lines of data and includes data quality improvements, such as a unified parasite taxonomy, that will allow data from all three host

groups to be used as a single global dataset. An array of supporting data, such as parasite transmission modes and higher level taxonomy, are also included. Finally, the majority of entries are now georeferenced, most for the first time. In the associated metadata, we describe the contents and organization of this updated GMPD version including definitions for all variables and how data were derived.

CLASS I. Data set descriptors

A. Data set identity: Global Mammal Parasite Database v. 2.0: a compilation of parasite occurrence data for wild primates, carnivores and ungulates

B. Data Identification Code:

1. Main data file
2. Full citations
3. Parasite transmission modes
4. Parasite taxonomy

C. Data set description

1. Originators: Patrick R Stephens, Paula Pappalardo, Shan Huang, James E. Byers, Maxwell J. Farrell, Alyssa Gehman, Ria R. Ghai, Sarah E. Haas, Barbara Han, Andrew W. Park, John P. Schmidt, Sonia Altizer, Vanessa O. Ezenwa, Charles L. Nunn.

2. Abstract

Illuminating the ecological and evolutionary dynamics of parasites is one of the most pressing issues facing modern science, and is critical for basic science, the global economy, and human

health. Extremely important to this effort are data on the disease-causing organisms of wild animal hosts (including viruses, bacteria, protozoa, helminths, arthropods and fungi). Here we present an updated version of the Global Mammal Parasite Database, a database of the parasites of wild mammals, available for download as complete flat files. The updated database has more than 24,000 entries in the main data file alone, representing data from over 2,700 literature sources. We include data on sampling method and sample sizes when reported, as well as both “reported” and “corrected” (i.e., standardized) binomials for each host and parasite species. Also included are current taxonomies and data on transmission modes used by the majority of species of parasites in the database. We describe the methods used to identify sources and extract data from the primary literature, how entries were checked for errors, methods used to georeference entries, and how host and parasite taxonomies were standardized across the database. We also provide definitions of the data fields in each of the four files that users can download.

D. Key Words: parasites, infectious disease, wild mammals, transmission modes, Carnivora, Primates, ungulate, Artiodactyla, Perissodactyla

Class II. Research origin descriptors

A. Overall project description

1. Identity: Understanding the diversity and distribution of the parasites of wild mammals.

2. Originators: Patrick R Stephens, Paula Pappalardo, Shan Huang, James E. Byers, Maxwell J. Farrell, Alyssa Gehman, Ria R. Ghai, Sarah E. Haas, Barbara Han, Andrew W. Park, John P. Schmidt, Sonia Altizer, Vanessa O. Ezenwa, Charles L. Nunn.

1 **3. Period of Study:** 2002 – continuing.

2 **4. Objectives:** Provide data necessary to investigate the drivers of parasite transmission among
3 host species, the factors that influence host parasite species richness, and the global patterns of
4 parasite species richness in wild mammals. As a necessary prerequisite to these studies, data on
5 the parasites naturally contracted by free-ranging populations of carnivores, ungulates, and
6 primates, the three best studied groups of mammals, were collected from the primary literature.

7 **5. Abstract:** Key to understanding the factors that influence the diversity, spread, and evolution
8 of diseases are baseline data on host-parasite associations and distributions of disease-causing
9 organisms. We collected data on parasites, defined broadly as disease-causing organisms ranging
10 from viruses and bacteria to helminths, arthropods, and fungi, reported to occur in wild mammals
11 in four orders: Primates, Carnivora, Artiodactyla, and Perissodactyla. This work was supported
12 primarily by grants NSF DEB 0212096 to Nunn and Altizer and NSF/ NIH/ USDA DEB
13 1316223 to Stephens et al., as well as two additional working group grants. The data have been
14 used for a number of studies including (but not limited to) studies of parasite species richness
15 and parasite sharing in ungulates, carnivores and primates and studies of zoonotic disease
16 emergence risk to humans from primates hosts. Ongoing studies as of this writing using the data
17 include studies of the factors that determine the host and geographic breadth of parasites, studies
18 of the structure of host parasite association network, and a study predicting novel host parasite
19 associations in response to climate change.

20 **6. Sources of funding:**

a. Stephens, P. R., S. Altizer, S., K. Smith, R. Poulin, A. Aguirre. National Science Foundation Research Coordination Network Proposal: Macroecology of Infectious Disease. September 2012 to August 2018 (NSF/ NIH/ USDA DEB 1316223).

b. Altizer, S., C. Nunn, A. Dobson, and J. L. Gittleman. The role of pathogens in mammalian conservation. January 2006 to April 2008 (Conservation International Working Group Grant).

c. Nunn, C. and S. Altizer. Understanding the ecology and evolution of infectious diseases in three mammal orders. July 2002 to July 2005 (NSF DEB 0212096).

d. Altizer, S. and C. Nunn. Ecology and evolution of infectious diseases in mammalian mating and social systems. February 2001 to June 2003 (National Center for Ecological Analysis and Synthesis Working Group Grant).

B. “Specific subproject” description

1. Site description: Data collection focused on literature reports of parasites in wild carnivores, ungulates and primates globally.

2. Experimental design: Data collection attempted to identify all relevant studies published in the primary literature through 2010 for carnivores and ungulates and through early 2015 for primates.

3. Research methods:

a. Main data sources: Starting in 1999, literature searches of online reference databases were used to identify papers that contained reports of parasites in wild ungulates, carnivores and primates. Data for ungulates and carnivores includes that from nearly all relevant published studies through 2010, when data collection on those portions of the GMPD concluded. Data

collection in primates is ongoing, data through 2015 are presented here (that portion of the data that had been verified as of August 2016). Searches were primarily conducted using Biological Abstracts and Web of Science, but also AGRICOLA, Medline and PrimateLit in the case of primates. Searches were conducted using all primate, ungulate, and carnivore species binomials found in Wilson and Reeder (2005), Wilson and Reeder (1993), and for primates, Corbet and Hill (1991), as key words. Data were compiled across different time periods with somewhat different approaches, but as a general search strategy, we searched databases with species binomials and the additional keywords “pathogen”, “parasite” and “disease.” Searches excluded domestic species (e.g., *Felis catus*) and species in which it would have been difficult to distinguish between wild and managed populations (e.g, *Bubalis bubalis*), and these species do not occur in the database. Reports from species that are partially domesticated (e.g., *Rangifer tarandus*) were included only in cases where it could be verified that they were from unmanaged or mostly unmanaged populations.

b. Main data collection: Once valid sources of data were identified, data for a range of variables (see below) were collected using a custom web entry form that stored the results in a relational database. MySQL was generally used as the relational database management system. Initial data collection involved dozens of data miners employed by project personnel, most over the period of 2002 to 2010. Data collection for primates is ongoing. Data collection for ungulates and carnivores has ceased pending further funding. The database is focused on only a subset of data in the underlying papers that is most consistently available across the wide range of parasites and pathogens included therein. For researchers interested in obtaining information on the stage of the parasite, details on lab procedures, or taxonomic conflicts can refer to the paper via the full

references that we provide. We further note details that may help in such investigations, such as whether the organ from which a parasite was collected was recorded.

c. Main data verification: Once initial data entry was completed, senior personnel would check each entry against the original paper it was derived from to verify accuracy and make corrections where necessary. Senior personnel that conducted data verification were S. Altizer, V. O. Ezenwa, S. Huang, C. Nunn and P. R. Stephens.

d. Sources of data on parasite transmission modes: To characterize trait variation among parasite species, we compiled data on parasite transmission modes because it is universal to all parasites. We chose this over traits that would have only applied to particular parasite groups such as developmental stage (which would have primarily applied to helminths) or presence or absence of a capsule (which would have mainly applied to bacteria). Parasite transmission modes were initially populated based on reports in standard veterinary references (Granoff and Webster 1999, Samuel et al. 2001, Williams and Barker 2001). For parasites that were not found in these references, searches were conducted on Web of Science and Google Scholar using parasite binomials to find primary literature that identified parasite transmission modes. These parasites were only scored in cases where at least two literature sources on transmission modes could be found. These searches were conducted circa 2006-2009 and separately for each of the main host groups. Transmission mode data from all three host groups were later combined for several ongoing projects. No attempt was made to double check the entire 1640 line database of transmission modes. However, species that exhibited more than two transmission modes did seem to constitute outliers in that there were relatively few of them. Therefore, in cases where parasites were reported to have more than two transmission modes in the combined data additional research was conducted in the primary literature to verify the transmission modes that

a given parasite species utilized. Corrections were made if necessary, and literature sources for corrected entries are recorded in the transmission mode table.

The goal was to include all transmission modes that could reasonably describe transmission of a given parasite in wild populations, where detailed data on transmission mode is almost always lacking. We only report parasite traits for entries in which the parasite was identified to a corrected binomial name and information was found on transmission modes. In total, we were able to obtain transmission mode data for 81% of the parasites identified to species. A. Gehman was responsible for double-checking transmission mode entries that exhibited more than two transmission modes.

e. Host and parasite taxonomy: The final database includes 462 unique hosts of which 448 are identified to species; and 2412 parasites of which 2031 are identified to species level. Host taxonomy was standardized to follow Wilson and Reeder (2005). We followed this taxonomy to allow data in the GMPD to be used in analyses with a previously published supertree of all mammals (Bininda-Emonds et al. 2007) and a publicly available database of mammalian trait, life history, ecological and geographic data (Jones et al. 2009). Nomenclature for non-virus parasites followed those published by the National Center for Biotechnology Information (NCBI) in their “Taxonomy” section whenever possible. However, in many cases parasite species reported in papers were not found in the NCBI database. In these cases, we checked the Global Biodiversity Information Facility (GBIF: <http://www.gbif.org/>) or the World Register of Marine Species for the parasites (WoRMS: <http://www.marinespecies.org/>) of aquatic carnivores. Species not found in NCBI, GBIF, WoRMS or other recognized online database were verified by searching the primary literature for references other than the ones used to construct the GMPD that refer to a given species. For such species, one reference supporting the validity

the species binomial is listed in the parasite taxonomy table. Finally, nomenclature for viruses was standardized to follow that of the International Committee on the Taxonomy of Viruses online database (<http://www.ictvonline.org/>; 2015 release). If the reported name is currently abolished, or the reported name was split in different virus names, the corrected parasite name will indicate “abolished” or “splitted by ICTV”. To allow users to easily filter out parasites not identified to the species level, we include a column in the main datafile indicating if the parasite has a binomial name. The primary goal was to ensure that lists of parasite binomials contained no synonyms. Subspecies and serovars were assigned to the corresponding species name. P. Pappalardo, M. Farrell and P. Stephens double-checked viral nomenclature to standardize it among mammal orders. P. Pappalardo, P. R. Stephens, M. Farrell, C. Nunn, R. R. Ghai, A. W. Park and S. Haas verified and identified synonyms in the remaining parasites and in the host names. We also include the most detailed higher-level taxonomic information that we could find for each entry based on ICTV, NCBI and other sources mentioned above.

f. Georeferencing: Geo-coordinates directly reported for study sites in an original reference were converted to decimal degree latitude-longitude coordinates when necessary. When the original reference reported a region and not an individual point, we approximated the centroid of the area (when possible) or looked for a locality within that region that could be georeferenced. Only entries from primary sources and that reported parasites to the species level were georeferenced. In cases where no geographic coordinates were reported but a study locality was listed, entries were georeferenced using 1) the “geocode” function in the package ggmap (Kahle and Wickham 2013) in the R computing environment (R Core Team 2013), 2) geonames (<http://www.geonames.org/>), 3) GoogleEarth (<https://www.google.com/earth/>), 4) GoogleMaps (<https://www.google.com/maps>), or 5) the geoHack option from Wikipedia. Using the primary

source, location names were expanded to include the region or country when necessary to attain accurate geocoding results. In cases where many locations are listed in the main data file, the georeferenced point location represents either a central locality or the centroid of an area or country that includes all localities. Given that our data spans the globe, we georeferenced most entries at and below the level of country but did not georeference broad regions such as “South America”, “Western Asia” or “Africa”, or study areas that span more than one country.

Georeferenced localities were verified both by projecting latitude-longitude coordinates onto a map of the globe to check for outliers, and by double checking that points occurred in the general vicinity that would be expected based on the locality reported in each study. P. Pappalardo and S. Haas performed georeferencing of study localities that lacked coordinate data with assistance from P. Stephens, J. Byers, J. P. Schmidt.

4. Project personnel: Patrick R. Stephens, Paula Pappalardo, Shan Huang, James Byers, Maxwell J. Farrell, Alyssa Gehman, Ria R. Ghai, Sarah Haas, Barbara Han, Andrew W. Park, John P. Schmidt, Sonia Altizer, Vanessa O. Ezenwa, Charles L. Nunn.

Class III. Data set status and availability.

A. Status

Latest Update: February 3, 2017.

Latest archive date: N/A

Data Verification: Data have been checked by senior personnel after initial entry. See description of procedures in Class II Section B above.

B. Accessibility

Storage location and medium: All four checked tables are provided here. Raw data are stored on servers in Odum School of Ecology at the University of Georgia and in Evolutionary Anthropology at Duke University.

Contact persons: Patrick R. Stephens (prsteph@uga.edu) and Sonia Altizer (saltizer@uga.edu), Odum School of Ecology, University of Georgia, Athens GA 30602; Charles L. Nunn (clnunn@duke.edu) Biological Sciences, Duke University, Durham NC 27708.

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Proprietary Restrictions: None

Costs: None as these data were collected using public funds. We do ask that authors using these data cite this paper, along with Nunn and Altizer (2005) if using the primate data.

Class IV: Data structural descriptors

A. Data set files

1. Identity: GMPD_main.csv, GMPD_parasite_traits.csv, GMPD_citations.csv, GMPD_parasite_taxonomy.csv.

1 **2. Size:** GMPD_main: 24323 lines of data, 6556 kilobytes; GMPD_parasite_taxonomy.txt: 3849
 2 lines of data, 829 kilobytes; GMPD_citations.txt: 2772 lines of data, 655 kilobytes;
 3 GMPD_parasite_traits.txt: 1640 lines of data, 121 kilobytes

4 **2. Format:** Comma-separated values text files, not compressed.

5 **B. Variable definitions**

6 Variables for the three data files were collected and verified using the procedures described
 7 above under Class II. Section B, Subsection 3.

8 **Table 1:** Variable definitions for GMPD_main.

Variable	Definition
Group	Ungulate (artiodactyl, perissodactyl), carnivore or primate.
HostReportedName	Host name as reported in original source.
HostCorrectedName	Host name from Wilson & Reeder 2005.
HostOrder	Host order from Wilson Reeder 2005.
HostFamily	Host family from Wilson Reeder 2005.
HostEnvironment	Terrestrial or marine. Species that only use terrestrial shorelines (e.g., pinnipeds) are listed as marine. Purely freshwater species (e.g., river otters) are listed as terrestrial.
ParasiteReportedName	Parasite name as reported in original source.
ParasiteCorrectedName	Updated name, see procedures in metadata Class II.

Section B, Subsection 3, Paragraph e.

HasBinomialName	If yes, indicates that the ParasiteCorrectedName is a full binomial (i.e., is identified to species).
ParType	Virus, bacteria, protozoa, helminth, fungus or arthropod.
ParPhylum	Parasite phylum. In the case of viruses, either RNA virus or DNA virus.
ParClass	Parasite class. In the case of viruses, ds (double stranded), ss+ (single stranded positive-sense), ss- (single stranded negative sense) or ssRT (retrovirus).
Citation	Short form of citation. See GMPD_citations.txt for full citation that these refer to.
LocationName	Location or region name of study as stated in the original source.
Longitude	Decimal degree longitude where study occurred. In cases where many localities are reported, a central location is provided.
Latitude	Decimal degree latitude where study occurred. In cases where many localities are reported is a central location.
PopulationType	WN (wild, non-managed), WO (managed in some way but mostly wild), or O (other).

SamplingBasis	Was infection status determined based on one sample per animal (animal) or multiple (samples). For example, fecal samples from an unknown number of hosts would be considered “samples”.
SampleNotes	Further notes on sampling (for example, how many ML of blood were sampled or what organs were sampled).
Prevalence	Proportion of samples found to be infected. NA indicates a study that reported that a parasite species infects a given host, but did not report prevalence.
HostsSampled	Number of individual animals of listed host type, age and sex that were sampled for the listed parasite.
HostSex	Sex of host all (i.e., both sexes), male or female.
HostAge	Age of hosts, all (i.e., both adults and juveniles), adult or juvenile (i.e., less than age of sexual maturity).
Intensity	Average number of parasites per infected animal.
IntensityMeasure	Type of sample used to quantify intensity (e.g., fecal egg count).
NativeRange	Was the host sampled within its native range, no or yes.
NumSamples	Number of samples used to estimate prevalence; either number of animals or number of samples.
SamplingType	The type of samples used to detect parasite presence;

either serology (host antibodies), direct isolation of parasites from blood, fecal, or other host tissues using microscopy or PCR.

1

2 **Table 2:** Variable definitions for GMPD_citations.

Variable	Definition
Citation	Short form of citation found in main file.
PubData	Complete reference. Note that we did ensure that references contain complete information (e.g., authors, year, title, journal, issue and pages for journal articles), but did not attempt to completely standardize the formatting of all 2772 references.

3

4 **Table 3:** Variable definitions for GMPD_parasite_traits.

Variable	Definition
ParasiteCorrectedName	Updated name, see procedures in metadata Class II. Section B, Subsection 3, Paragraph e.
Close	Parasite transmissible via close non-sexual contact such as grooming, biting, scratching, aerosols.
Nonclose	Parasite transmissible via non-close contact such as by fomites or ingestion of food or water contaminated with feces or urine.

Vector	Parasite transmissible by biting arthropod vectors.
Intermediate	Parasite transmitted by intermediate hosts such as snails or crustaceans (complex life cycles).
ParasiteTraitsCitations	Other citations consulted for parasite transmissions traits that were not mentioned in metadata Class II. Section B, Subsection 3, Paragraph d.

1

2 **Table 4:** Variable definitions for GMPD_parasite_taxonomy

Variable	Definition
ParasiteReportedName	Parasite name as reported in original source.
ParasiteCorrectedName	Updated name, see procedures in metadata Class II. Section B, Subsection 3, Paragraph e.
HasBinomialName	If yes, indicates that the ParasiteCorrectedName is a full binomial (i.e., is identified to species).
NameObservations	Notes on how the ParasiteCheckedBinomial was assessed. Observations were done until November 2016.
FLAG	If yes, indicates some doubts regarding the validity of the ParasiteCorrectedName.
NameID	This column contains an ID to a database when possible. Mostly NCBI, but also GBIF,

	WoRMS, etc. When the decision was made on a paper, this column contains the paper short citation format.
NameCitation	Complete citation, when the parasite name was checked using a paper/book.
ParType	Virus, bacteria, protozoa, helminth, fungus or arthropod.
ParPhylum	Parasite phylum. In the case of viruses, either RNA virus or DNA virus.
ParClass	Parasite class. In the case of viruses, ds (double stranded), ss+ (single stranded positive-sense), ss- (single stranded negative sense) or ssRT (retrovirus).
ParOrder	Parasite Order.
ParFamily	Parasite Family.
StrainorSubs	Strain or subspecies name if that information was available.

1

2 **Further Acknowledgments:** We would like to thank the many assistants that helped with data
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4 Halle, C. Nix, and J. Shapiro. We also acknowledge Patrik Lindenfors for his work collecting
5 pre-2006 data in carnivores.

6

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