GenomoBase: an integrated resource for *Genomoviridae* genomics and metagenomics

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Abstract

The family *Genomoviridae* (phylum Cressdnaviricota) comprises viruses with circular single-stranded DNA (ssDNA) genomes that typically encode a replication protein and a capsid protein. High-throughput sequencing has greatly expanded the number of known genomoviruses, but sequences and annotations remain dispersed across multiple repositories and publications, and no family-focused resource has been available. Here I present GenomoBase (https://www.genomobase.org), a curated web resource that integrates genomic, ecological and bibliographic data for all 237 *Genomoviridae* species currently recognized by the International Committee on Taxonomy of Viruses (ICTV). GenomoBase leverages a PostgreSQL backend to organize data according to standardized taxonomy, summarizing viral occurrences across ten genera, twelve host categories and nineteen countries. An "Explore Metagenomes" module incorporates more than 600 Sequence Read Archive (SRA) runs identified via Serratus, linking taxonomic records to metagenomic detections and highlighting the global distribution of genomovirus-related reads. To support research, the platform also provides automated literature updates via PubMed and local BLAST services for nucleotide and protein queries. GenomoBase offers a user-friendly entry point for exploring *Genomoviridae* diversity and is designed to facilitate taxonomic curation, ecological and evolutionary analyses, and the discovery of novel genomoviruses in both environmental and host-associated niches.

Keywords

Genomoviridae; CRESS-DNA viruses; metagenomics; viral database; Cressdnaviricota;

Introduction

Circular replication-associated protein encoding single-stranded (CRESS) DNA viruses are ubiquitous components of environmental and host-associated viromes and are currently classified within the phylum Cressdnaviricota. Members of this phylum possess small circular ssDNA genomes that replicate by rolling-circle replication mediated by a conserved replication-associated protein (Rep), a hallmark of all CRESS-DNA viruses, and they infect a broad range of eukaryotic hosts, including plants, fungi, invertebrates and vertebrates [1]. The best-known families include *Geminiviridae*, which infect mono- and dicotyledonous plants; *Circoviridae*, which infect pigs, poultry and other vertebrates; and *Nanoviridae*, which infect mainly crop plants [1]. More recently, within Cressdnaviricota, the family *Genomoviridae* was established following the discovery of *Sclerotinia sclerotiorum* hypovirulence-associated DNA virus 1 (SsHADV-1) [2], a circular ssDNA virus infecting the plant-pathogenic fungus *Sclerotinia sclerotiorum* [3]. Subsequent taxonomic work has expanded *Genomoviridae* to ten genera and more than two hundred species recognized by the International Committee on Taxonomy of Viruses (ICTV) [4]. Genomoviruses typically have compact genomes of approximately 1.9–3.9 kb that encode two major proteins in an ambisense arrangement: a rolling-circle replication initiation protein (Rep) and a capsid protein (CP). The Rep protein is homologous to the corresponding Rep of members of the family *Geminiviridae*, sharing conserved domains and sequence motifs required for viral replication [2]. The origin of replication is also similar in both families, consistent with replication via rolling-circle mechanisms [2]. In contrast, the CP forms a non-enveloped, isometric T=1 icosahedral capsid and shows no recognizable amino acid sequence similarity to capsid proteins of other known virus groups. Some members additionally encode small hypothetical open reading frames of unknown function. To date, no canonical movement protein has been identified in

genomoviruses, consistent with the etymology of the family name *Genomoviridae* (Ge- for "geminivirus-like", nomo- for "no movement protein") [2]. Although genomoviruses were initially described in fungi, subsequent metagenomic studies have detected them in a wide range of contexts, including plants, birds, mammals, invertebrates and diverse environmental matrices such as wastewater, sediments, soils and food-associated microbiomes. Experimental evidence of infection remains limited to *Sclerotinia sclerotiorum* [3] and successful replication in the sciarid fly *Lycoriella ingenua* [5], and the true host range of many lineages remains unclear.

The rapid expansion of genomovirus sequence data has been driven almost entirely by metagenomic studies of human, animal and environmental viromes and by large-scale surveillance projects. Gemykibiviruses and related taxa have now been reported in a variety of human clinical samples, including cerebrospinal fluid from acute encephalitis patients [6], vaginal secretions [7] and blood donors in the Brazilian Amazon [8]; the same virus has also been identified in bats [9], suggesting a possible zoonotic link. More recently, a human gemykibivirus was shown to actively replicate in HEK293T cells [10], further underscoring the need to better understand the biology and potential medical relevance of these viruses.

Despite the growing interest, genomovirus sequences and annotations remain dispersed across taxonomic resources, GenBank records and individual metagenomic studies, and no dedicated, curated database has been available for this rapidly expanding family. To address this gap, I developed GenomoBase (https://www.genomobase.org), an online resource focused specifically on the family *Genomoviridae*. GenomoBase integrates ICTV-based taxonomy with curated genome annotations, standardized host and geographic metadata, Serratus-filtered metagenomic detections from the Sequence Read Archive

97 (SRA), local BLAST services and a PubMed-derived literature catalogue. Here we describe
98 the construction, content and main features of GenomoBase and provide a concise
99 overview of the patterns that can be readily explored through the portal.

100 Materials and methods

101 Reference taxonomy and genome retrieval

102 ICTV-recognized genomovirus species were retrieved from the Virus Metadata Resource
103 (VMR) file VMR_MSL40.v2.20251013 (https://ictv.global/vmr), which lists all species
104 and genera formally assigned to the family *Genomoviridae*. From this file we extracted the
105 scientific name and the corresponding GenBank accession number for each species. The
106 curated table underlying GenomoBase contains 239 genome records: one representative
107 genome for each of the 237 species, plus the three genomic segments (A, B and C) of the
108 tripartite *Gemytripvirus fugra1*. Using a custom Python script (fetch_genomes.py) built on
109 Biopython v1.86 [11], we downloaded the corresponding GenBank records via NCBI E-
110 utilities and parsed the following information: accession, genus, species name, virus name,
111 sequence definition line, genome length, full genomic sequence and all annotated coding
112 sequences (CDSs). For each genome we identified the canonical Rep and CP ORFs based
113 on gene annotations and product descriptions, extracted their nucleotide and amino acid
114 sequences and stored them as separate fields. Any additional predicted CDS were
115 concatenated into "other proteins" fields (names, amino acid sequences and nucleotide
116 sequences).

117 The resulting dataset, including host and geographic information, was manually inspected
118 to ensure that all entries had complete circular genomes and coherent annotation of Rep and

119 CP. Where necessary, minor inconsistencies in the genus or species names were corrected
120 to match the latest ICTV taxonomy. The final curated table (**Supplementary Table 1**) was
121 used as the master source for populating the GenomoBase database.

122 Host, isolation source and country information were also extracted from the GenBank
123 records. For each genome we collected the host, isolation_source, country and
124 collection_date qualifiers when present. Host names were standardized and manually
125 grouped into 11 ecological categories, including mammals, birds, plants, insects, fungi,
126 molluscs, reptiles, arachnids, actinopterygian fishes, humans and environmental samples.
127 This manual curation step allowed us to separate human-associated records from other
128 mammalian hosts and to distinguish non-living matrices (e.g. wastewater or environmental
129 swabs) from host organisms.

130 Country strings were cleaned to remove subnational descriptors and harmonized to ISO-
131 like country names (e.g. "USA: California" to "USA"). When possible, additional locality
132 information (regions, cities or sampling sites) was kept as free-text descriptors in the
133 database. These standardized fields are used in the statistics and visualization pages of the
134 portal to summarize host and geographic patterns.

135 **Metagenomic survey and SRA/BioSample integration**

136 Because most genomoviruses have been discovered by metagenomics, we implemented an
137 "Explore Metagenomes" module to connect reference genomes with public high-
138 throughput sequencing projects. As a starting point we used Serratus, a large-scale
139 alignment platform for viral sequence discovery [12], to identify SRA runs with reads
140 matching genomovirus references. We queried the Serratus explorer for alignments against

141 genomovirus targets and retained runs whose best hits satisfied the specific filters on
142 alignment quality: genome alignment scores and percent identity between 75% and 100%
143 (query date November 2025). This range was chosen to capture both close relatives and
144 more divergent genomovirus-like sequences while excluding low-similarity matches that
145 are likely spurious.

146 We extracted the unique run identifiers and obtained 613 distinct SRA runs with putative
147 genomovirus signal. To enrich these with standardized metadata we developed a custom
148 Python script (fetch_sra_metadata.py) that queries the NCBI SRA and BioSample API for
149 NCBI-hosted runs and the ENA browser API for European accessions (e.g. SAMEA and
150 ERS identifiers). For each run, the script retrieves: SRA accession, BioSample accession,
151 release date, SRA "organism" or "environment" label, BioSample "host" and "isolation
152 source" attributes, when available location string and, when possible, latitude/longitude
153 coordinate. All retrieved fields are cleaned to remove control characters and harmonized
154 into a JSON structure with one dictionary per SRA run. For BioSamples hosted at ENA
155 (typically SAMEA, ERS or ERP accessions), the script parses XML records to extract host
156 and geographic information, including coordinates embedded in free-text fields. The final
157 JSON file (**Supplementary file 1**) is both downloadable from the portal and used internally
158 to populate the metagenomes table in PostgreSQL. A small fraction of runs lack either
159 explicit location names or coordinates; in these cases, only the available fields are stored.
160 The Explore Metagenomes web page uses these curated attributes to generate summary
161 plots and an interactive map of sampling locations.

162 **Literature retrieval and curation**

To provide an up-to-date overview of genomovirus research, we implemented a literature module driven by a dedicated PubMed query. A custom Python script (fetch_pubmed.py) uses NCBI E-utilities to search PubMed for articles containing the terms “Genomoviridae”, “genomovirus” and the names of each of the ten ICTV-recognized genera in titles, abstracts or Medical Subject Headings terms. The script retrieves the PubMed IDs of all matching records, then uses esummary to obtain titles, journal names, publication years and DOIs, and efetch to access additional metadata where necessary. Each record is annotated with one or more broad categories (e.g. “environmental metagenomics”, “animal viromes”, “human-associated viromes”, “fungal genomoviruses”, “reviews”) based on keyword matching in titles and abstracts. The output is stored in a JSON file, which is rendered on the Literature page as an interactive, searchable table with filters by category, year and journal.

BLAST services

To enable sequence similarity searches, GenomoBase provides local BLASTN and BLASTP services based on NCBI BLAST+ v2.17.0 [13]. From the curated genomovirus table we generated FASTA files for complete genomes, Rep proteins and CP proteins, which were converted into dedicated BLAST databases. User-submitted nucleotide or protein queries are run against these databases with a default parameters and E-value threshold of 1×10^{-3}, and the results are returned as sortable tables with basic alignment statistics and direct links from hit accessions to the corresponding GenomoBase virus detail pages.

Database implementation, BLAST services and web interface

185 GenomoBase is implemented using the Django web framework (Python v3.10+) with a
186 PostgreSQL backend. A primary database model stores curated genome-level information,
187 including accession, taxonomy, host and geographic metadata, as well as the nucleotide and
188 amino acid sequences of Rep, CP and additional CDS. Separate tables store metagenomic
189 run metadata and literature entries. The application is deployed on an Amazon Web
190 Services (AWS) EC2 instance, which provides a stable, scalable environment with regular
191 backups and straightforward future upgrades of both the database and the web front-end.
192 The web interface is styled using Bootstrap and custom CSS, with dedicated views for the
193 index page, master species list, species detail, statistics, BLAST search, metagenome
194 explorer, downloads, literature and external resources. Summary statistics (e.g. numbers of
195 species per genus, host category counts and country distributions) are computed
196 dynamically using Django's ORM and rendered as charts (bar plots and maps) using
197 JavaScript-based visualizations.

198 **Results**

199 **Resource content and example analyses**

200 GenomoBase organizes the currently ICTV-recognized *Genomoviridae* diversity into ten
201 genera, with *Gemycircularvirus* (126 species) and *Gemykibivirus* (50 species) clearly
202 dominating the dataset, and the remaining genera represented by between 1 and 16 species
203 each (Fig. 1a). Genome lengths range from ~1.99 to 3.9 kb (mean ≈ 2.19 kb), consistent
204 with compact CRESS-DNA genomes (Fig. 1b). The upper bound of ~3.9 kb corresponds to
205 the combined size of the three genomic segments of the tripartite *Gemytripvirus fugra1*.

Beyond taxonomic composition and genome size, host annotations reveal associations with 12 ecological categories, including mammals, birds, plants, insects, fungi, molluscs, reptiles, arachnids, actinopterygian fishes and non-living matrices. Mammals represent the largest category (37.66%, excluding humans) in terms of species–host combinations, followed by plants (14.64%), birds (13.39%) and insects (10.88%) (Fig. 1c). A discrete subset of seven genomoviruses belonging to *Gemykibivirus* (5 spp.), *Gemykrogvirus* and *Gemyvongvirus* genera has been recovered from human-associated samples, highlighting a small but potentially important group of lineages at the interface between environmental and medical virology. Geographic metadata indicate that genomoviruses have been reported from at least ~19 countries, with especially high counts from the USA (97 spp.), New Zealand (38 spp.), China (26 spp.) and Brazil (21), illustrating their broad global distribution (Fig. 1d).

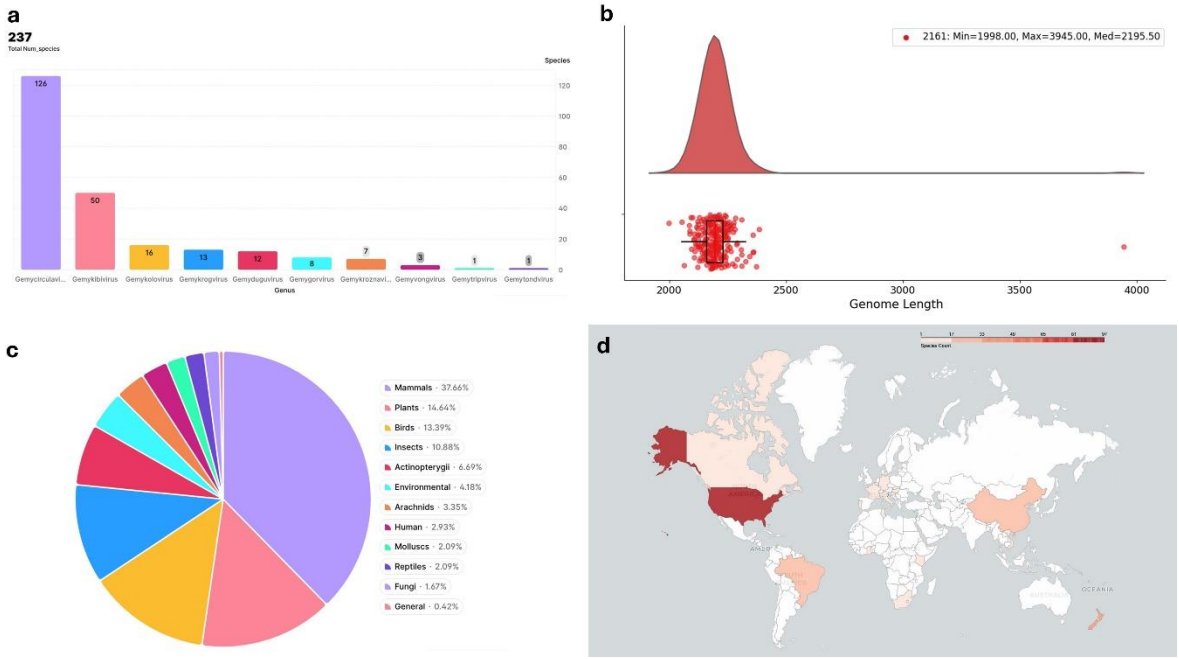

Figure 1. Overview of *Genomoviridae* species and associated metadata in GenomoBase. (a) Bar chart showing the distribution of currently classified species across ICTV-recognized genera. (b) Genome length distribution visualized as a raincloud plot combining a density curve, individual genomes plotted as points, and a boxplot. (c) Broad host categories for genomoviruses, summarized as a pie chart based on curated host metadata. (d) Global map indicating the number of genomovirus species reported per country according to available sampling location information.

Based on the harmonized host annotations for the 613 *Genomoviridae*-positive SRA runs, most detections fall into a set of recurrent host categories (Fig. 2a). The largest single class corresponds to "environmental samples", which account for 172/613 runs (28.1%) and encompass marine and freshwater systems, wastewater, air, soils and food-associated microbiomes. Among runs with biological hosts, human-associated samples (human gut, general human metagenomes, oral/skin/vaginal metagenomes) constitute the most frequent category, with 98 runs (16.0%), followed by metagenomes from birds (85 runs, 13.9%). Additional mammalian hosts include giant pandas (*Ailuropoda melanoleuca*; 27 runs, 4.4%), domestic pigs (*Sus scrofa*; 23 runs, 3.8%), mice (*Mus musculus*; 21 runs, 3.4%), bovines (*Bos* spp.; 17 runs, 2.8%) and *Macaca mulatta* (7 runs, 1.1%). There are also smaller contributions from *Xenopus laevis* (11 runs, 1.8%) and samples with unknown host information (50 runs, 8.2%). Beyond these dominant categories, the remaining runs form a long tail of individually represented wildlife and domestic animal hosts. Collectively, these patterns indicate that genomovirus-related reads are detected across a broad spectrum of vertebrate hosts and environmental matrices, while a substantial fraction of SRA runs still lacks precise host information.

Geographic metadata indicate that 462 of 613 runs (75.3%) include a textual location descriptor, corresponding to 180 distinct place names distributed across 47 countries or territories. In addition, 282 runs (46.0%) carry explicit latitude/longitude coordinates,

enabling map-based visualization of sampling sites. Within this set, the largest contributions come from projects in China (approximately 165 runs) and the USA (approximately 96 runs), followed by individual efforts in India, Ireland, Singapore, Norway, South Korea, Canada and several European and Latin American countries (Fig. 2b).

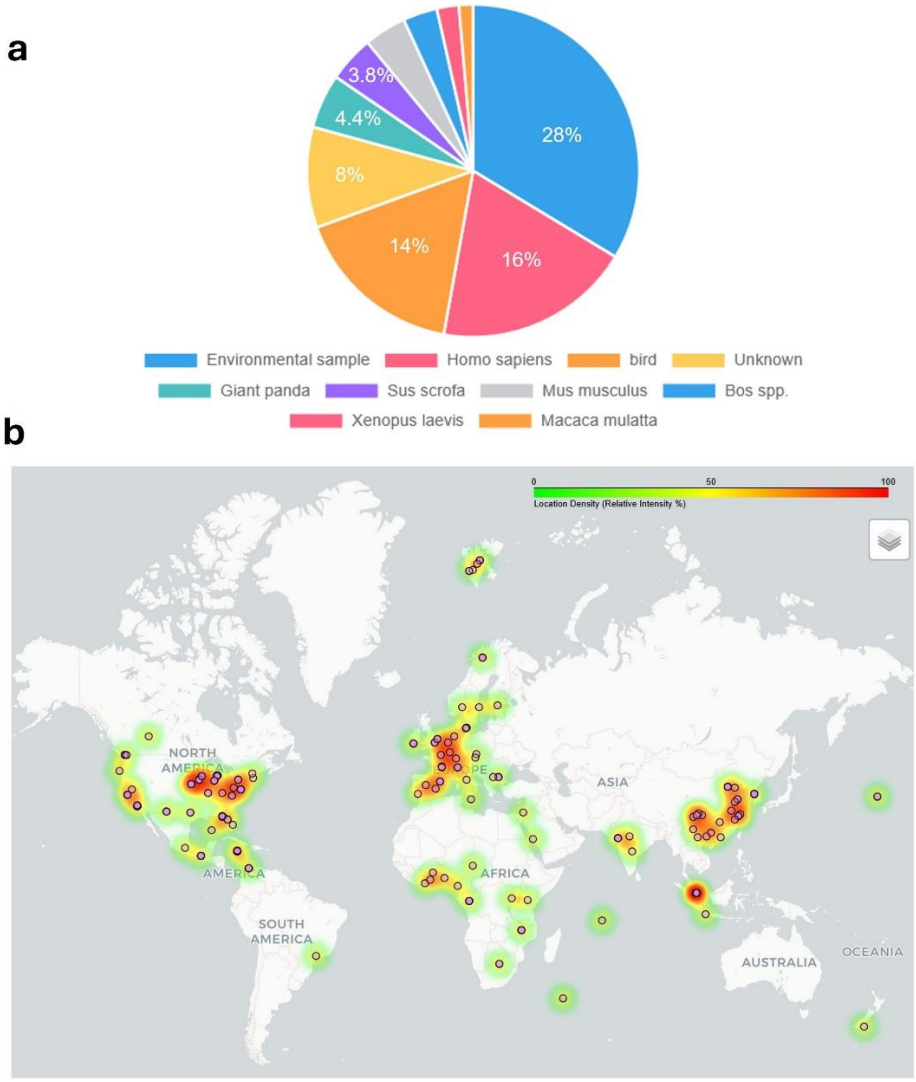

Figure 2. Overview of metagenomic runs with genomovirus detections in GenomoBase. (a) Pie chart summarizing SRA runs with genomovirus hits, grouped into broad host or sample categories (e.g. birds, humans, domestic pigs, environmental and others). (b) Global heat map of sampling locations for the 282 runs

253 with latitude/longitude metadata, illustrating the relative density of genomovirus-positive metagenomes.
254 Warmer colours indicate higher local density across countries and regions.

255 Discussion

256 The rapid expansion of genomovirus sequence data, largely driven by metagenomic studies,
257 has created a challenge for data integration and standardization. Until now, genomovirus
258 sequences and annotations have been scattered across general taxonomic resources,
259 GenBank (https://www.ncbi.nlm.nih.gov/datasets/taxonomy/1910928/), ViralZone
260 (https://viralzone.expasy.org/7382), ICTV (VMR_MSL40.v2.20251013) and individual
261 metagenomic surveys, without a family-focused curation framework. GenomoBase
262 addresses this gap by providing, to our knowledge, the first integrated resource that aligns
263 *Genomoviridae* genomes with the official ICTV taxonomy, harmonized host and
264 geographic metadata and systematically filtered metagenomic detections. By centralizing
265 these data within a dedicated web interface, the platform facilitates taxonomic curation and
266 enables ecological and evolutionary analyses that are difficult to perform from isolated
267 records.

268 The aggregated view provided by GenomoBase makes current sampling biases in
269 Genomoviridae immediately apparent. Geographic metadata for formally described species
270 indicate detections in 19 countries across all inhabited continents, while the metagenomic
271 module reveals SRA runs potentially containing genomoviruses from around 47 countries
272 worldwide. This pattern likely reflects sequencing effort rather than the true biogeography
273 of the family, even as it clearly indicates that members of the family *Genomoviridae* are
274 widespread across continents and environments. GenomoBase also highlights a broad
275 apparent host spectrum in both the species and metagenomic datasets, including mammals,

276 birds, invertebrates, plants and environmental samples; although infection has not been
277 experimentally confirmed for all of these hosts [4], many of these associations remain
278 plausible and merit further investigation. Of particular interest, seven formally recognized
279 species belonging to three genera have been reported in human clinical samples [6,8], and
280 genomoviruses are detected in at least ~90 human-associated metagenomes, including gut
281 [14], vaginal [7] and brain [15]. These observations suggest that genomovirus are recurrent
282 components of the human virome and underline the value of continued surveillance of this
283 family in a public-health context, especially in light of recent evidence that at least one
284 gemykibivirus can actively replicate in human cells [10].

285 A second key contribution of GenomoBase is that it does not merely summarize existing
286 detections, but explicitly links ICTV-aligned reference genomes with Serratus-derived
287 metagenomic reads and contigs. Connecting these "orphan" SRA sequences to curated
288 *Genomoviridae* genomes shows that members of this family are ubiquitous components of
289 environmental and host-associated viromes, often detected in studies that were not designed
290 to target them. Making such hidden detections visible and searchable within a family-
291 specific context allows researchers to identify under-sampled hosts and environments, and
292 to prioritize public SRA runs for targeted re-analysis or assembly of novel genomovirus
293 genomes. In this sense, GenomoBase functions not only as a static catalogue but also as a
294 hypothesis-generating platform for future work on genomovirus diversity, ecology and
295 evolution.

296 Conclusions and future directions

297 GenomoBase provides a focused, user-friendly platform for the *Genomoviridae* research
298 community and for researchers interested more broadly in circular ssDNA viruses. By

integrating ICTV-based reference genomes, harmonized host and geographic metadata, Serratus-filtered SRA detections, local BLAST services and an automatically updated literature catalogue, the resource enables users to (i) search and download curated genomovirus genomes and genes, (ii) explore host and geographic patterns of diversity, and (iii) investigate the occurrence of genomoviruses across public metagenomic datasets. At the same time, the current implementation makes explicit several limitations of the available data, such as incomplete host annotations and strong geographic sampling biases, which can guide future sequencing surveys. GenomoBase is freely available and will be periodically updated in line with ICTV releases and Serratus-based screenings, and its underlying framework can be readily extended to other CRESS-DNA virus families and related viral taxa.

Data and code availability

The online instance of GenomoBase is accessible at https://www.genomobase.org. All curated genomovirus genome metadata, host and geographic annotations, and the metagenomic summary used in this study are available for download through the GenomoBase portal and as archived files on Zenodo (DOI: 10.5281/zenodo.17860246). The complete species table and metagenome JSON, together with all custom scripts and the Django source code used to build and update GenomoBase, as well as sample input data and the corresponding output, are deposited on Zenodo and documented in detail in the accompanying README file, which provides additional implementation details.

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Author contributions

Y.C.-C. was responsible for conceptualization, data curation, software and web implementation (GenomoBase), formal analysis, visualization and writing of the manuscript.

Conflict of interest statement

The author declares no competing interests.

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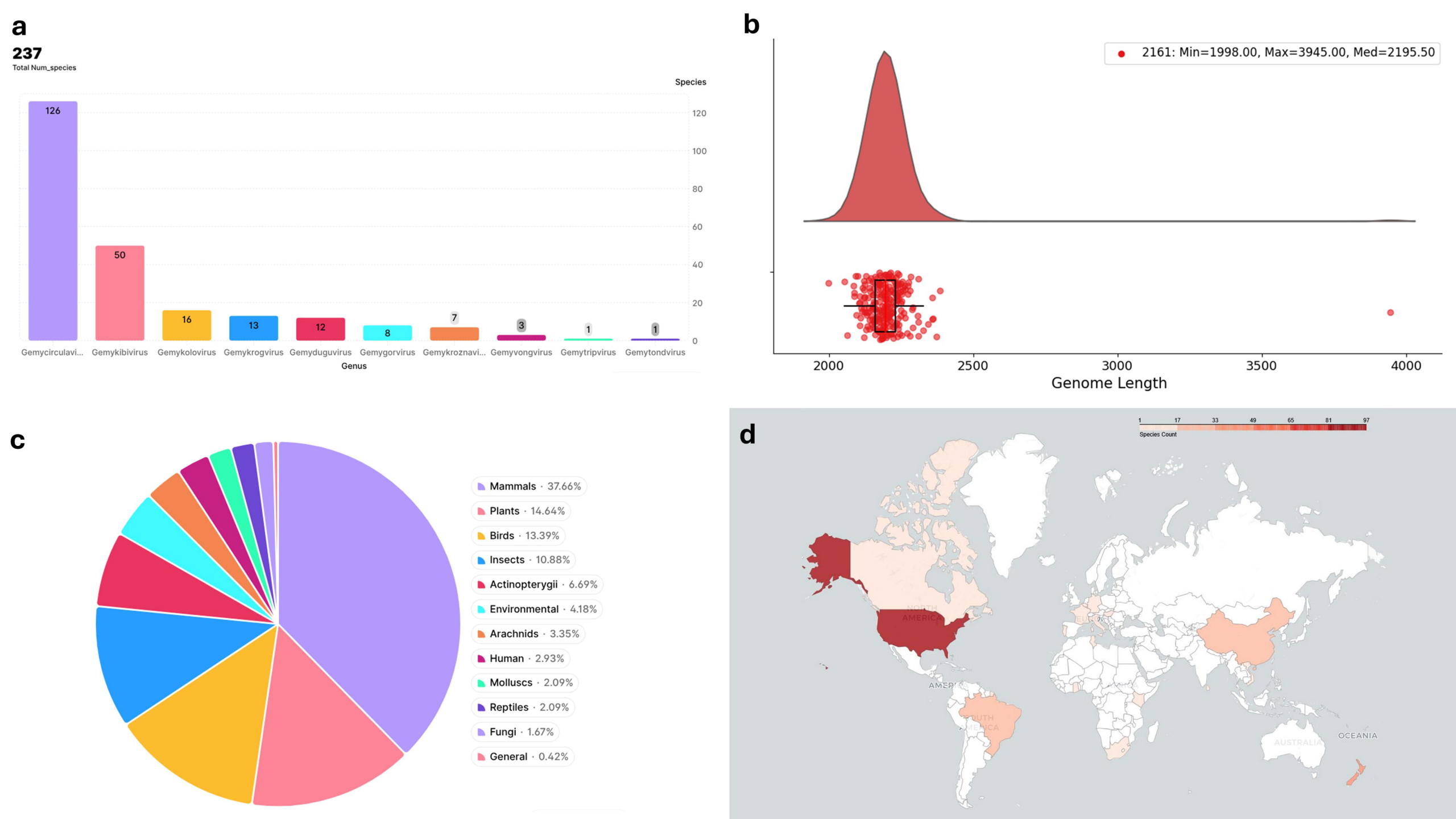
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237
Total Num_species
Species
126
50
16
13
12
8
7
3
1
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120
100
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20
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Gemycirculavi...
Gemykibivirus
Gemykolovirus
Gemykrogvirus
Gemyduguvirus
Gemygorvirus
Gemykroznavi...
Gemyvongvirus
Gemytripvirus
Gemytondvirus
Genus
b
2161: Min=1998.00, Max=3945.00, Med=2195.50
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Genome Length
c
Mammals · 37.66%
Plants · 14.64%
Birds · 13.39%
Insects · 10.88%
Actinopterygii · 6.69%
Environmental · 4.18%
Arachnids · 3.35%
Human · 2.93%
Molluscs · 2.09%
Reptiles · 2.09%
Fungi · 1.67%
General · 0.42%
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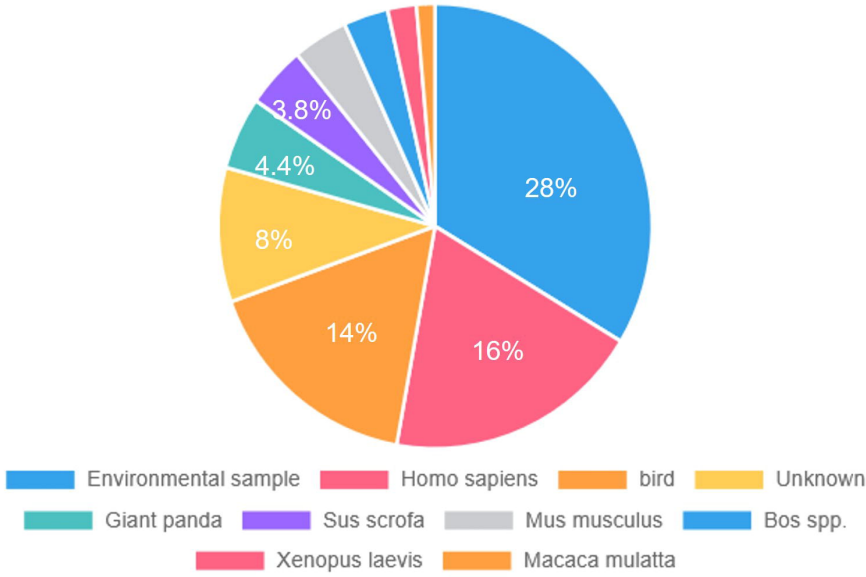
28%
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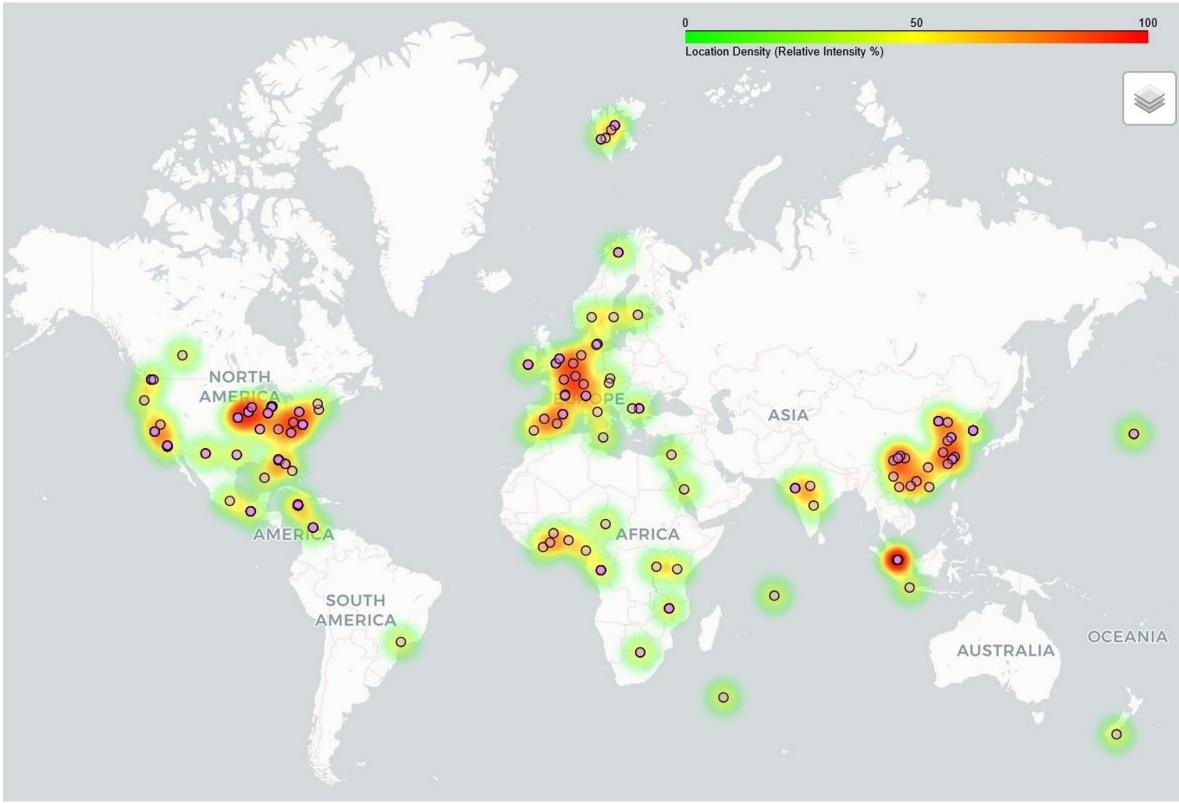
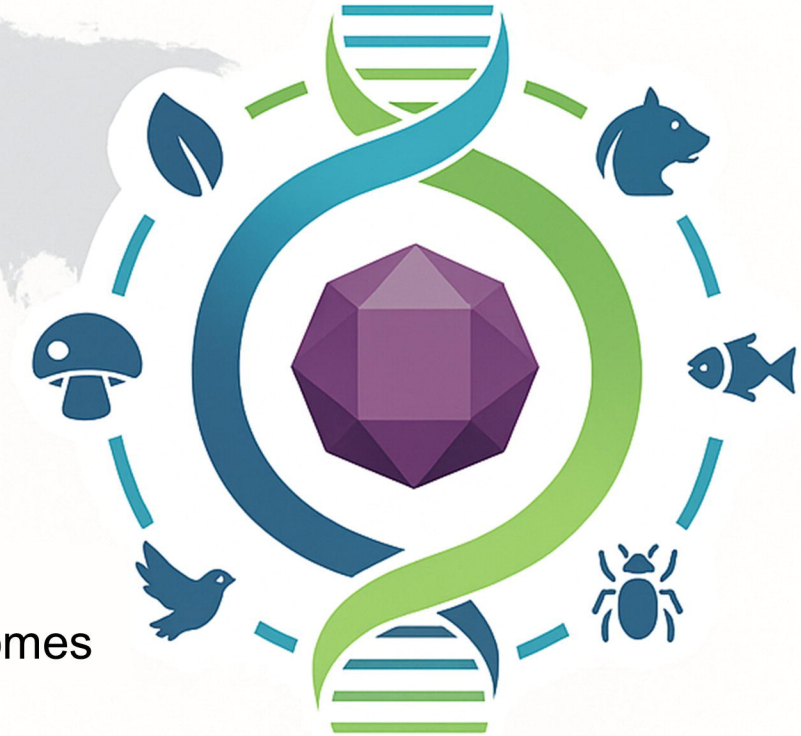
Homo sapiens
bird
Unknown
Giant panda
Sus scrofa
Mus musculus
Bos spp.
Xenopus laevis
Macaca mulatta

b

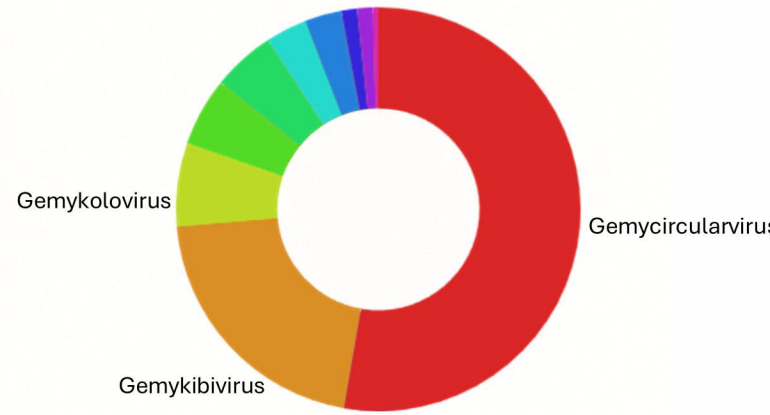

0
50
100
Location Density (Relative Intensity %)
NORTH AMERICA
AMERICA
SOUTH AMERICA
ASIA
AFRICA
AUSTRALIA
OCEANIA

GenomoBase: an integrated resource for Genomoviridae genomics and metagenomics

Global detections from
ICTV Species and metagenomes



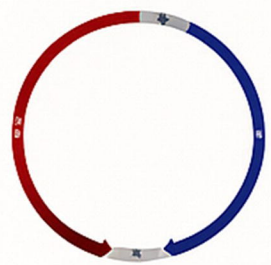
237 Genomoviridae spp.
from 10 genera



ICTV

NCBI

GenBank/SRA inputs



Curated genomovirus
genomes and SRA Runs

python

django

aws

GenomoBase
implementation