



# Epidemiological Characteristics of Human-infective RNA Viruses





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**Aim of the study**


To create an open-source database of human-infective RNA viruses and their characteristics to inform research on their public health burden and pandemic potential.

## Introduction


**RNA viruses ...**  
cause infectious diseases responsible for a significant global health burden (influenza, measles, AIDS).

have potential to cause epidemics and pandemics (Ebola virus, SARS-CoV-2).


**239** human-infective RNA virus species are currently known. These are catalogued in our database alongside extensive metadata, all updated from a previous 2018 version.

This database will benefit future studies of human virus diversity and the identification of virus characteristics linked to potential for emergence as a public health threat.


## Methods




- Searches every 1-3 years (Jan 1999 - Jun 2024) across databases (Web of Science, Google Scholar, PubMed, Scopus) and secondary sources (e.g. WHO and NCBI websites)
- Search strategies: [virus name] AND human AND (case\* OR patient\* OR infection\* OR disease\* OR outbreak\* OR zoono\*). Searches for newly reported viruses additionally had (new OR novel).

**Virus species accepted as human-infective based on:**

- virus recognition by ICTV; number of reported infections; number of independent reports; diagnostic(s) used to distinguish human infection; author confidence in virus identity and infectivity

**Metadata gathered:**

- envelope status; genome type; location of first reported human infection; transmission level and route; host range

**Methodology for creating the database closely adheres to that detailed in our 2018 publication (1)**

## Results

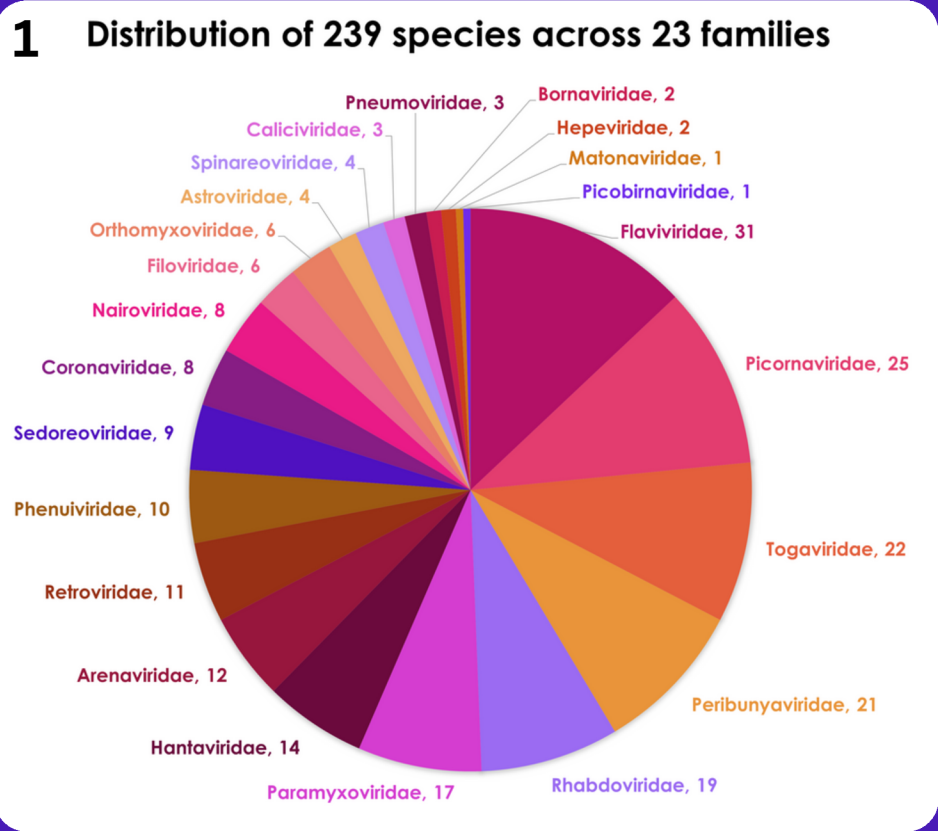


Figure 1. Distribution of the 239 human-infective RNA virus species across 23 virus families.



Figure 3. Map of locations of first reported human cases of all currently recognised human-infective RNA viruses.

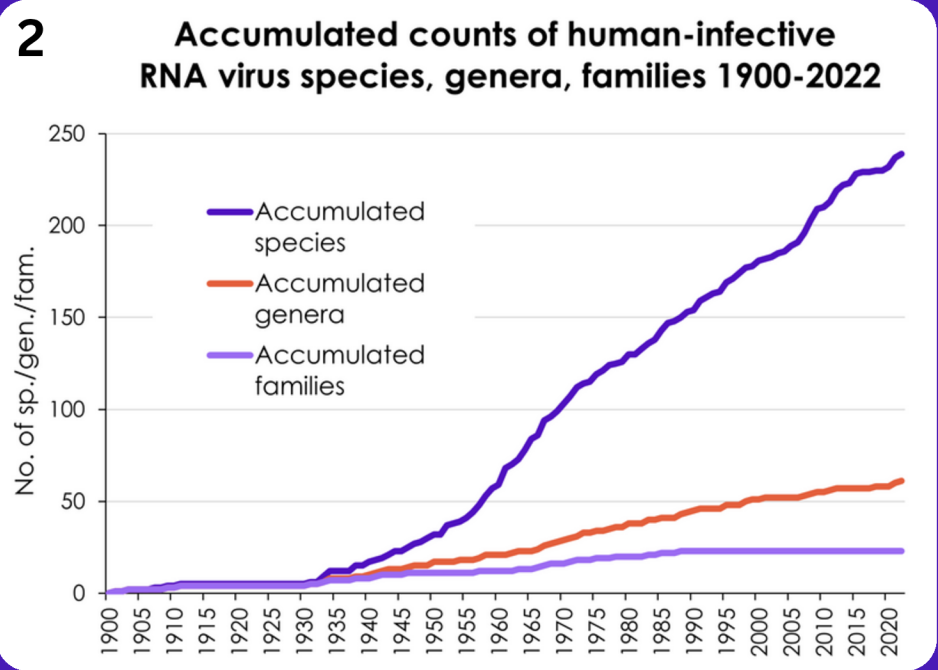


Figure 2. Accumulated counts over time of human-infective RNA virus species and of genera and families with  $\geq 1$  human-infective RNA virus species.

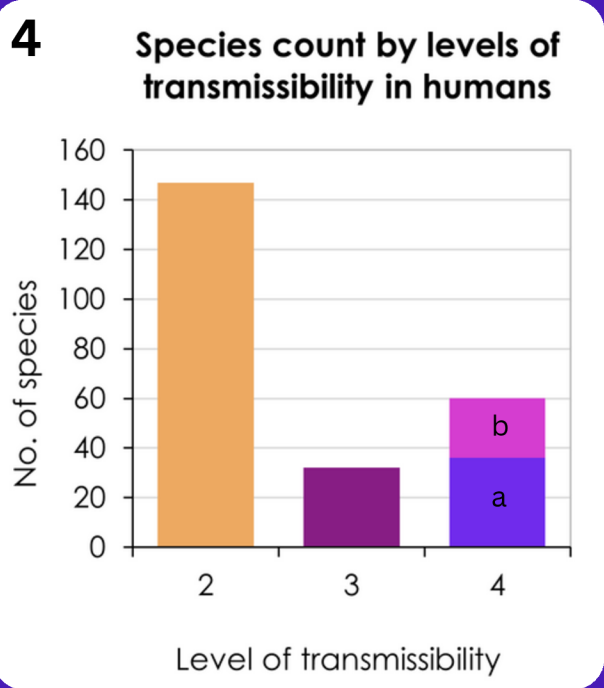


Figure 4. Human-infective RNA virus species count by transmissibility level in humans. Levels: 2 (strictly zoonotic); 3 (self-limiting outbreaks); 4 (epidemic or endemic in humans). Level 4 consists of 4a (species also infect non-human hosts) and 4b (species only infecting humans).

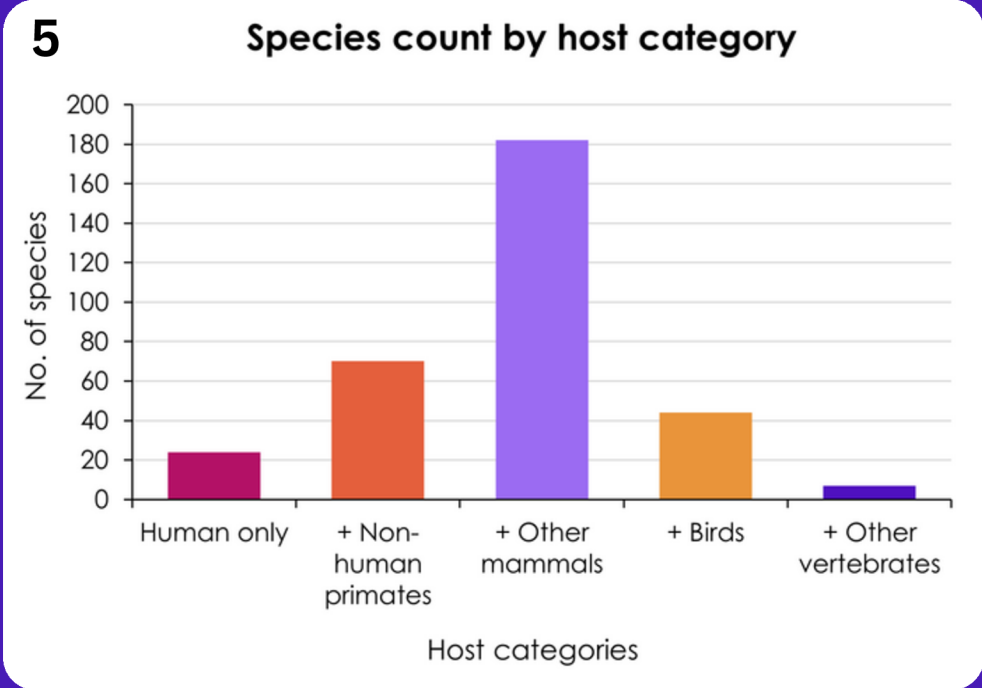




Figure 5. Human-infective RNA virus species count by host category. Five broad categories: natural infections only in humans; also naturally infects non-human primates, or other mammals, or birds, or other vertebrates (mainly reptiles). Some species infect  $\geq 1$  category of non-human host.


## Discussion




- By extrapolating the species accumulation curve, it is possible to predict future rates of human-infective RNA virus discovery and estimate their total diversity.




- The deceleration in discovery of new families and genera may indicate approaching limits to human RNA virus diversity.




- Nonetheless, the pool of viruses is not static (2); over 20 species have been added since 2018, but 40 have not been reported in humans since 1999.




- There are hot-spots for the discovery of human-infective RNA viruses, consistent with previous work (3).




- Statistical modelling has shown that high GDP, rapid urbanization, warm and wet climates, and mammalian species richness are predictors of virus discovery (3).




- More efforts are required for virus discovery in resource-limited regions (3).



- Human-to-human transmissibility is critical for a virus's epidemic potential. Monitoring transmissibility levels is central to assessing risk of outbreaks (4).



- Surveying animal reservoirs to identify high-risk pathogens prior to their spill over into humans would help predict and track emerging infectious diseases (5).



- Such large-scale surveys would be arduous, requiring substantial investment of time and resources (5).

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