

New Virus Catalogue Identifies Top Pathogen Threats to Human Health

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The persistent threat of emerging infectious diseases demands a clear understanding of which pathogens warrant the most urgent attention. Clinicians routinely face novel viral presentations, often with limited foresight into their broader public health implications. A new, extensive catalogue provides a much-needed framework for assessing viral risk, moving beyond reactive responses to proactive surveillance.

KEY TAKEAWAYS

- **The Pivot:** A new, comprehensive catalogue systematically ranks viral threats, shifting focus from reactive outbreak management to proactive risk assessment.
- **The Data:** The catalogue identifies specific viral families, including Coronaviridae and Flaviviridae, as consistently high-risk due to their zoonotic potential and transmission dynamics.
- **The Action:** Clinicians should be aware of the heightened surveillance for these identified high-threat pathogens, informing early diagnosis and public health reporting.

The global health community has long grappled with an incomplete understanding of the vast viral landscape, particularly regarding those pathogens with the potential to jump species and cause widespread human disease. Historically, attention often coalesced around viruses only after they initiated outbreaks, such as SARS-CoV-1, MERS-CoV, or Zika virus. This reactive approach, while necessary for containment, leaves significant gaps in preparedness for the next pandemic. The development of a comprehensive virus catalogue aims to systematically identify and characterise these threats before they escalate.

This catalogue, compiled through extensive data aggregation and expert consensus, moves beyond simply listing known human pathogens. It incorporates ecological data, host range, transmission routes, and genetic plasticity to assess the intrinsic pandemic potential of various viral families. The methodology involved a multi-criteria risk assessment model, evaluating factors such as zoonotic origin, human-to-human transmission efficiency, severity of disease, and existing countermeasures. The project synthesised information from virology databases, epidemiological reports, and phylogenetic studies, creating a dynamic resource for public health strategists and infectious disease specialists.

Prioritising the unseen threats

The catalogue identifies several viral families as consistently posing the greatest threat, notably Coronaviridae, Flaviviridae, and Filoviridae. Coronaviruses, exemplified by SARS-CoV-2, demonstrate a high propensity for zoonotic spillover and rapid adaptation to human hosts. The catalogue highlights specific bat-borne coronaviruses with genetic markers indicating a high likelihood of future human infection, even if they have not yet caused widespread disease.

This proactive identification allows for targeted surveillance in animal reservoirs, aiming to detect novel strains before they reach human populations.

Flaviviruses, including Dengue, Zika, and Yellow Fever viruses, present a different but equally potent threat due to their vector-borne transmission and expanding geographical ranges. The catalogue underscores the increasing risk posed by climate change, which extends the habitats of mosquito vectors, thereby increasing human exposure. It details specific serotypes and genotypes within the Flaviviridae family that exhibit higher virulence or greater transmissibility, guiding vaccine development and public health interventions. For instance, certain lineages of Dengue virus are flagged for their potential to cause severe haemorrhagic fever, necessitating enhanced clinical vigilance in endemic areas.

Filoviruses, such as Ebola and Marburg viruses, remain high-priority threats due to their extremely high case fatality rates (often exceeding 50%) and the severe public health disruption they cause, despite their typically localised outbreaks. The catalogue details the known animal reservoirs, primarily bats, and the specific ecological conditions that facilitate spillover events. It also provides a detailed analysis of the genetic diversity within these viruses, which informs the development of broad-spectrum antiviral therapies and vaccines. The focus here is on rapid response capabilities and robust contact tracing, given the explosive nature of filovirus outbreaks.

Beyond these prominent families, the catalogue also flags less commonly discussed but emerging threats, such as certain orthomyxoviruses (distinct from influenza) and paramyxoviruses. These viruses often circulate silently in animal populations, possessing genetic characteristics that suggest a high potential for host switching. The catalogue provides a granular breakdown of specific viral clades within these families, identifying those with receptor-binding domains compatible with human cell entry. This level of detail allows researchers to focus on specific viral proteins for drug and vaccine targets, rather than broadly targeting entire viral families.

The open-label nature of the data collection, drawing from diverse global sources, is an obvious strength, but also a caveat. Data completeness varies by region, and surveillance gaps in certain parts of the world mean some threats may be underestimated. The catalogue relies on current scientific understanding of viral evolution and zoonotic transmission, which is constantly evolving. Therefore, the risk assessments are dynamic and require continuous updating as new research emerges. The trial was not powered to detect differences in specific geographic regions, and that gap matters for local public health planning.

The catalogue also highlights the critical need for improved data sharing among international health organisations and research institutions. Without a unified, real-time reporting system for novel viral detections in both human and animal populations, the utility of such a catalogue remains somewhat constrained. The project's authors advocate for standardised genomic sequencing protocols and open-access databases to ensure that newly identified threats can be rapidly integrated into the risk assessment framework. This collaborative approach is essential for translating catalogue findings into actionable public health strategies.

CLINICAL IMPLICATIONS

This new virus catalogue offers a much-needed strategic shift in how we approach pandemic preparedness. For too long, clinicians and public health officials have been playing catch-up, reacting to outbreaks rather than anticipating them. Identifying specific viral families and even clades with high pandemic potential allows for targeted surveillance and resource allocation, rather than a scattergun approach.

The emphasis on Coronaviridae, Flaviviridae, and Filoviridae is not surprising, but the granular detail on specific lineages and their zoonotic origins provides actionable intelligence. This means clinicians in regions with known animal reservoirs for these viruses should maintain a higher index of suspicion for unusual febrile illnesses, even in the absence of a declared outbreak. Early detection in a single patient can prevent widespread transmission.

Pharmaceutical companies and academic researchers now have a clearer roadmap for vaccine and antiviral development. Instead of waiting for a novel pathogen to emerge, they can proactively develop platform technologies or broad-spectrum agents against the most threatening viral families. This catalogue effectively de-risks early-stage research by pointing to the most probable future targets, potentially shaving years off development timelines.

But the catalogue is only as good as the data feeding it. Without robust, real-time surveillance in animal populations and transparent international data sharing, its predictive power will diminish. Governments and international bodies must invest in strengthening global health infrastructure, particularly in regions identified as hotspots for zoonotic spillover, to ensure this valuable resource remains clinically relevant.

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