



# MERS-CoV & Mpox:

## Using DSI to understand and fight infectious disease outbreaks

### Infectious disease outbreaks are a growing threat to global health

Infectious diseases represent a significant global health threat, with recent outbreaks highlighting the need for a more robust and coordinated international response.<sup>1</sup> Zoonoses, which are diseases that can spread from animals to humans, are particularly concerning, accounting for up to 75% of emerging infectious diseases worldwide.<sup>2</sup>

The threat posed by emerging infectious diseases is growing, with over 30 new human pathogens detected in the last three decades alone.<sup>3</sup> This trend is driven by various factors, including climate change, rapid urbanization and increased global trade and travel, which are creating more opportunities for viruses to jump species and spread rapidly across borders.<sup>4</sup>

The COVID-19 pandemic, and its devastating global impact, recently brought attention to the dangers of animal-to-human virus transmission. Alongside COVID-19, other emerging zoonoses have demonstrated their potential to cause significant global health crises.

In 2003, SARS (Severe Acute Respiratory Syndrome) – an infectious disease thought to have originated in bats – spread worldwide following an outbreak in China, causing nearly 800 deaths before being successfully contained.<sup>5</sup> MERS (Middle East Respiratory Syndrome) – an acute respiratory infection first identified in Saudi Arabia and Jordan – has been reported in at least 27 countries since 2012.<sup>6</sup>

<sup>1</sup> Bloom DE, and Cadarette D. Infectious Disease Threats in the Twenty-First Century: Strengthening the Global Response. *Frontiers in Immunology* (2019). <https://doi.org/10.3389/fimmu.2019.00549>

<sup>2</sup> Taylor LH, Latham SM, and Woolhouse ME. Risk factors for human disease emergence. *Philosophical Transactions of the Royal Society B: Biological Sciences* (2001). <https://doi.org/10.1098/rstb.2001.0888>

<sup>3</sup> WHO. Zoonotic disease: emerging public health threats in the Region. <https://www.emro.who.int/about-who/rc61/zoonotic-diseases.html>. Accessed September 2025.

<sup>4</sup> Baker, R.E., Mahmud, A.S., Miller, I.F. et al. Infectious disease in an era of global change. *Nature Reviews Microbiology* (2022). <https://doi.org/10.1038/s41579-021-00639-z>

<sup>5</sup> WHO. SARS: how a global epidemic was stopped. <https://www.who.int/publications/i/item/sars-how-a-global-epidemic-was-stopped>. Accessed September 2025.

<sup>6</sup> WHO Regional Office for the Eastern Mediterranean (EMRO). MERS situation update, August 2025. <https://www.emro.who.int/health-topics/mers-cov/mers-outbreaks.html>. Accessed September 2025.

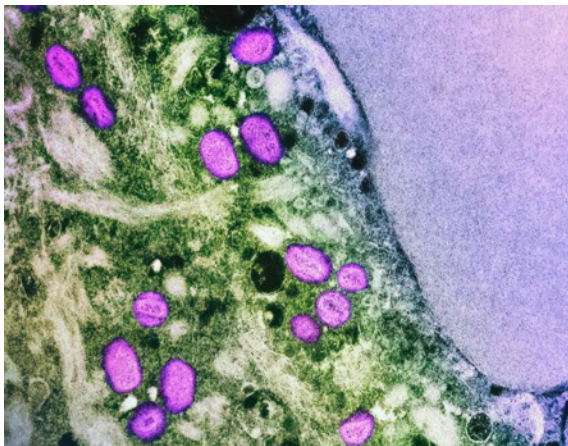


Also likely to have originated in bats, dromedary camels were found to be the main source of spillover to humans.<sup>7</sup>

Mpox, caused by the mpox virus (MPXV), is another example of a zoonotic disease with global impact. First reported in humans in 1970

in the Democratic Republic of Congo, the disease is now endemic in Western and Central Africa. In 2022, the World Health Organization declared the Mpox outbreak a Public Health Emergency of International Concern (PHEIC) following its spread through more than 75 non-endemic countries.<sup>8</sup>

## The Open Science infrastructure of linked databases is key to effective outbreak response



There are many ways in which the current Open Science infrastructure supports effective response to disease outbreaks. These all rely on the ability to access and share data across many databases, and to leverage many different types of data, beyond the pathogen of concern.

### Sequencing and sharing pathogen genetic material to pool knowledge

The sequencing of pathogens' genetic material is a crucial step in understanding and combating infectious disease outbreaks. Once the genetic material is extracted and sequenced, it can be uploaded to online data repositories as Digital Sequence Information (DSI) in the form of text

files. Ensuring open access to this DSI is essential for researchers worldwide to advance research on infectious diseases and develop timely countermeasures to fight them, such as vaccines, therapeutics and diagnostics.

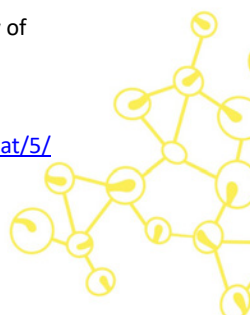
There are many viral genome databases,<sup>9</sup> each serving a specific function and providing different information.<sup>10</sup> The European Nucleotide Archive ([ENA](#)) – a member of the International Nucleotide Sequence Database Collaboration ([INSDC](#)) – hosts data on various pathogens, allowing researchers to query and analyze DSI relevant to Mpox. Data repositories such as [Nextstrain](#) enable researchers to visualize the evolution of viruses like Mpox across different regions, offering insights into virus outbreaks. Databases like [ViralZone](#) provide detailed overviews of specific viral genomes, such as the Mpox virus genome, helping researchers study these in depth. Local research also plays a key role. German researchers, for example, sequenced the genomes of Mpox viruses circulating in their country and made these available on the [NCBI](#)

<sup>7</sup> Azhar EI, El-Kafrawy SA, Farraj SA, et al. Evidence for Camel-to-Human Transmission of MERS Coronavirus. *The New England Journal of Medicine* (2014). <https://doi.org/10.1056/NEJMoa1401505>

<sup>8</sup> Institut Pasteur. Mpox (formerly monkeypox). <https://www.pasteur.fr/en/medical-center/disease-sheets/mpox-formerly-monkeypox>. Accessed September 2025.

<sup>9</sup> Ritsch M, Cassman NA, Saghaei S, and Marz M. Navigating the Landscape: A Comprehensive Review of Current Virus Databases. *Viruses* (2023). <https://doi.org/10.3390/v15091834>

<sup>10</sup> Oxford Academic. Journals. <https://www.oxfordjournals.org/nar/database/subcat/5/18>. Accessed September 2025.





[GenBank](#) and ENA databases.<sup>11</sup> Finally, the [Pathogens Portal](#) – based on an initiative created in response to COVID-19 – composes information from primary databases like ENA to make data on the World Health Organization (WHO) priority pathogens available. The portal has national or regional nodes, like Sweden, who also try to gather data and make it more accessible.

Researchers' ability to access information from a variety of different sources enhances global collaboration and preparedness, enabling to track pathogen evolution, monitor outbreaks, and develop effective responses to emerging infectious diseases.

### **Comparing and analyzing data from many sources to understand diseases before and during outbreaks**

DSI is crucial to monitor and understand how disease outbreaks evolve over time and across regions. As viruses spread, they replicate their genetic material, but mistakes in the copying

process lead to changes in genetic sequences, called mutations. These mutations allow researchers to analyze the relationship between different virus samples, providing insights into spillovers, transmission routes, and emerging variants. By extracting, sequencing, and digitizing viral genomes, scientists can compare them to determine whether outbreaks stem from a single zoonotic event or multiple events in different locations. This analysis is crucial for assessing disease outbreaks and implementing targeted measures to prevent diseases from spreading further.

Many pathogens will also circulate and evolve for a long time without necessarily causing major health threats despite their potential to do so. Because of this, continuous monitoring and information-sharing between researchers worldwide before outbreaks occur is crucial to track transmission routes, detect emerging threats and eventually enable a swift response to outbreaks.<sup>12</sup>

In 2013, researchers investigated a MERS outbreak in Saudi Arabia by sequencing virus samples from affected patients in hospitals and comparing them with existing MERS-CoV genome sequences available in the NCBI GenBank database.<sup>13</sup> Their study showed that the hospital outbreak resulted from multiple introductions of the virus and significantly expanded the genome data available for MERS-CoV.

Similarly, to better understand Mpox outbreaks, researchers analyzed the 2017 West African Mpox outbreak, which led to the first exported Mpox cases outside of the African continent. The DSI produced in this study was also made available on NCBI GenBank, including protein translations, which are made automatically accessible on UniProtKB, a DSI protein database that provides detailed metadata, including information on original source databases and related publications with links to the literature databases PubMed and Europe PMC.<sup>14</sup>

<sup>11</sup> Brinkmann A, Kohl C, Pape K, et al. Extensive ITR expansion of the 2022 Mpox virus genome through gene duplication and gene loss. *Virus Genes* (2023). <https://doi.org/10.1007/s11262-023-02002-1>

<sup>12</sup> Dos S Ribeiro C, van Roode M, Farag E, et al. A framework for measuring timeliness in the outbreak response path: lessons learned from the Middle East respiratory syndrome (MERS) epidemic, September 2012 to January 2019. *Euro Surveill* (2022). <https://doi.org/10.2807/1560-7917.ES.2022.27.48.2101064>

<sup>13</sup> Cotten M, Watson SJ, Kellam P, et al. Transmission and evolution of the Middle East respiratory syndrome coronavirus in Saudi Arabia: a descriptive genomic study. *Lancet* (2013). [https://doi.org/10.1016/S0140-6736\(13\)61887-5](https://doi.org/10.1016/S0140-6736(13)61887-5)

<sup>14</sup> Mauldin MR, McCollum AM, Nakazawa YJ, et al. Exportation of Monkeypox Virus From the African Continent. *The Journal of infectious diseases* (2022). <https://doi.org/10.1093/infdis/jiaa559>





To understand diseases that affect humans, researchers often need to look at data sourced from other organisms, such as animals, in the case of zoonotic diseases like MERS, Mpox, Ebola and others. Open access databases are crucial to this process. Currently, several UN bodies, such as the Convention on Biological Diversity (CBD) and the World Health Organization (WHO), either already have or are in the process of creating new rules governing the sharing of benefits stemming from the use of this data. CBD's rules mean to apply broadly to genetic data, unless already covered by another ABS regime, while WHO is focused on a subset of pathogens with "pandemic potential".

Because zoonoses, such as MERS and Mpox, involve animal pathogens which affect human health, research on these diseases would use data relevant to both the CBD and the WHO. If rules regarding access and benefit-sharing from the use of these datasets are widely different or require researchers to sort through different documents and procedures to understand which rules apply to which data, this will make research more complicated, require a considerable time investment, and possibly lead to avoidance of specific data or research areas.

Currently, MERS-CoV is listed as a WHO priority disease that poses great public health risk.<sup>15</sup> It does not fall under the scope of the Pandemic Influenza Preparedness (PIP) framework as it is not an influenza strain. MERS-CoV samples would thus be considered genetic resources under the framework of the CBD Nagoya Protocol and associated DSI under the CBD's Multilateral Mechanism (MLM), but biological material and respective DSI of pathogens known to infect humans could potentially fall into the Pathogen Access and Benefit Sharing (PABS) system being negotiated under the WHO Pandemic Agreement, depending on which pathogens end up being included in its scope.

<sup>15</sup> WHO. Prioritizing diseases for research and development in emergency contexts. <https://www.who.int/activities/prioritizing-diseases-for-research-and-development-in-emergency-contexts>. Accessed September 2025.





### Providing curated, consolidated data to speed up research

The ability to quickly and easily access pathogen DSI is critical to develop timely responses to disease outbreaks. Databases that consolidate and integrate data relevant to a specific pathogen can help researchers develop countermeasures more efficiently. If the WHO Pathogen Access and Benefit Sharing system (PABS) were to lead to a mechanism whereby pathogen data were to be siloed and kept under limited access for an indefinite period of time, it would hinder research, as this data could not be combined with information from other sources and be continuously updated.

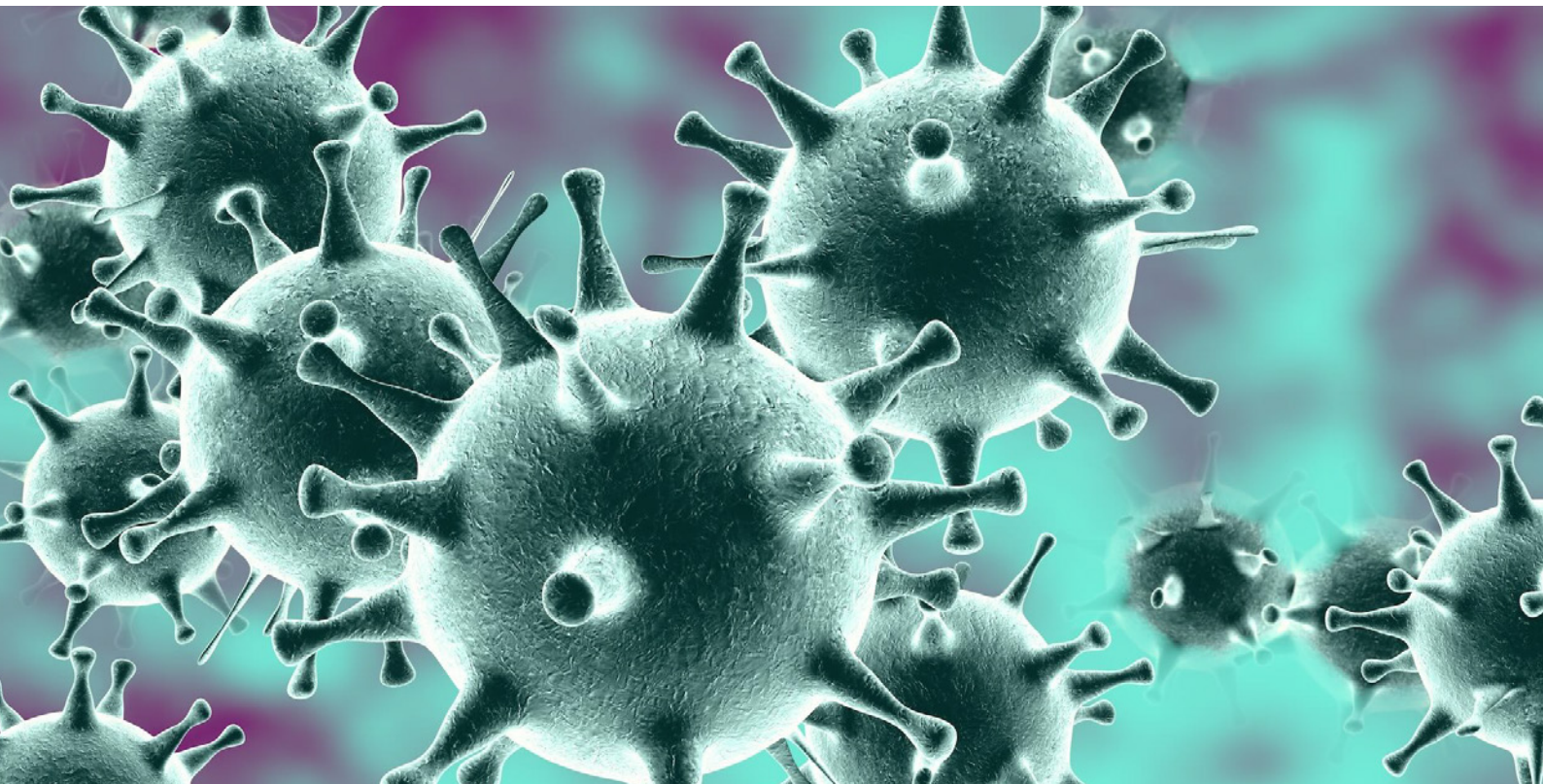
An example of the value of combining diverse pathogen data is the Bacterial and Viral Bioinformatics Resource Center ([BV-BRC](#))<sup>16</sup> – a specialized database for bacterial and viral infectious disease research which brings

together data from the NCBI database (including nucleotide and protein sequences), with, for example, epitope and protein structural data as well as bioinformatic analysis tools. The BV-BRC also includes an [Mpox outbreak tracker](#), which allows scientists and public health officials to monitor the global spread of the disease, the strains involved and related publicly available genome data.

Resources like this are vital as they provide easy access to all available data and allow researchers to carry out large-scale analyses of different types of information. The BV-BRC highlights the importance of open access data in strengthening global health security. Making DSI on pathogens publicly available prevents the loss of crucial data while also allowing researchers to reuse available information, saving time, costs, and labor.

<sup>16</sup> Olson RD, Assaf R, Bretin T, et al. Introducing the Bacterial and Viral Bioinformatics Resource Center (BV-BRC): a resource combining PATRIC, IRD and ViPR. *Nucleic Acids Research* (2023). <https://doi.org/10.1093/nar/gkac1003>





## **The WHO PABS system should leverage the international database ecosystem to support monitoring and response**

The Open Science infrastructure of databases is critical to strengthen pandemic prevention, preparedness and response. It should be leveraged to support a system for fair and equitable sharing of diagnostics, vaccines and therapeutics. For researchers to effectively track, understand, and respond to emerging disease threats from zoonoses, they need seamless access to diverse datasets.

The access and benefit-sharing systems put in place in different UN fora, such as WHO and CBD, should be designed to support monitoring activities before health emergencies occur and to facilitate data-sharing and response efforts

when outbreaks arise. Restrictive or incompatible access and benefit-sharing frameworks can limit researchers' ability to share and analyze critical data, leading to siloed data and to slowed global response efforts, including the ability to develop treatments and drugs.

Ensuring that policies across different UN instruments are mutually compatible and support responsible and effective data-sharing will enable rapid response, and in turn support the sharing of benefits that stem from that response, such as vaccines, diagnostics and therapeutics.

