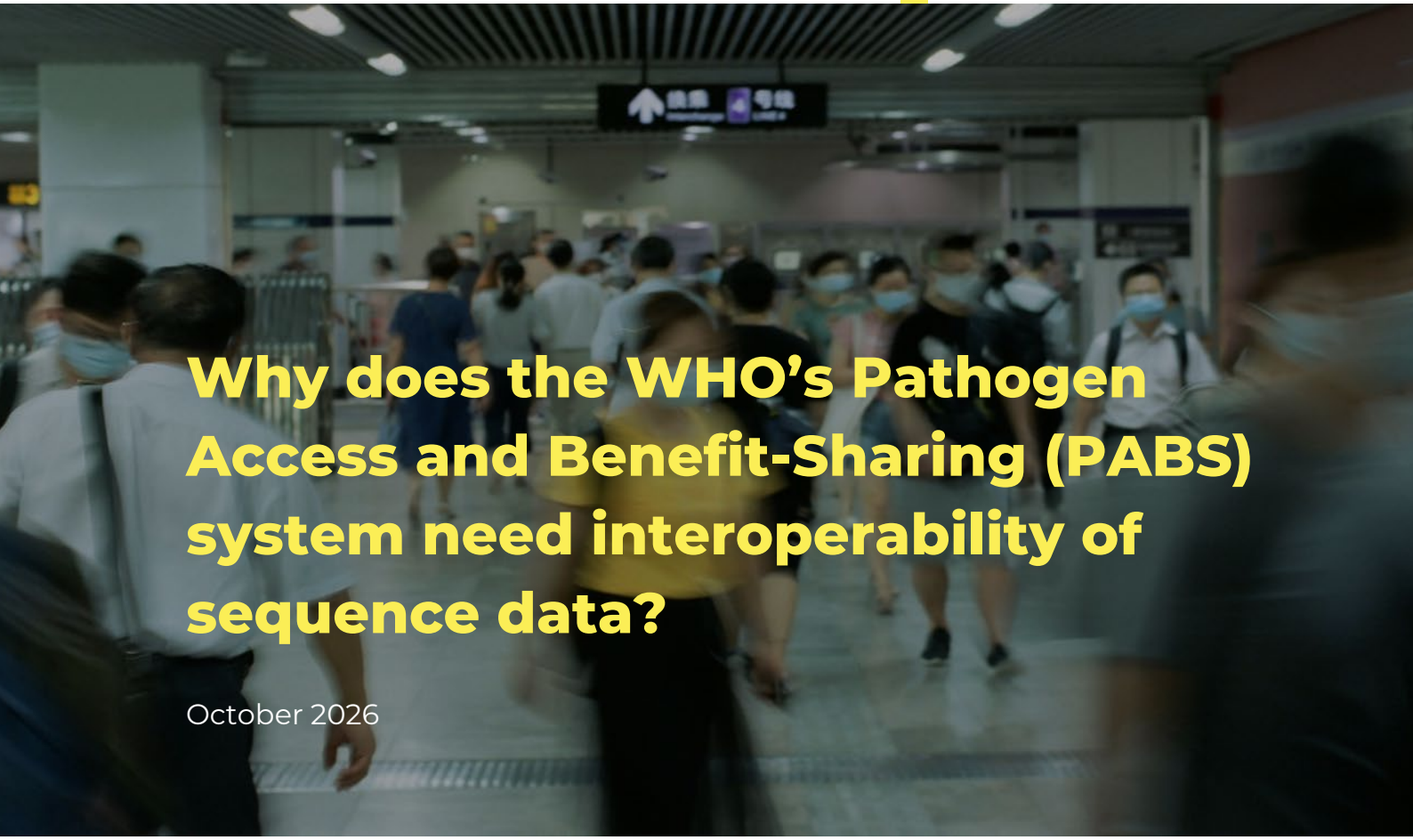

Why does the WHO's Pathogen Access and Benefit-Sharing (PABS) system need interoperability of sequence data?

October 2026

The WHO Pathogen Access and Benefit-Sharing (PABS) system can only meet its goals if companies sign PABS contracts. Some proposals under discussion see restricting access to sequence data as the most efficient way to secure these contracts – and ensure that vaccines, therapeutics and diagnostics (VTDs) are shared. We argue that WHO Member States should use targeted, complementary measures with other tools and levers to encourage PABS contract signature and not rely exclusively on approaches that restrict access to data and limit interoperability, such as user registration requirements. A multi-pronged approach coupled with addressing scientific inequities and database governance is more fit-for-purpose, because it supports the sharing of benefits without compromising the timely and seamless integration of pathogen data from multiple sources that is essential for research and development, and public health emergency response. **We recommend that WHO Member States consider these measures:**

- Addressing scientific inequities in pathogen education and research
- Building policy tools that target VTD manufacturers and companies directly
- Using downstream monitoring of publications, patents and products
- Establishing standardized global PABS Terms of Use for databases that host pathogen data

The recommendations above would represent a significant shift from entrenched negotiating positions across economies and global regions. But without flexibility, the PABS Annex will not move forward, and the Pandemic Agreement may remain unable to enter into force, to the detriment of global health. Despite the enabling scientific environment created by open access to data, there are legitimate equity questions around who profits and who shares benefits. PABS can improve this without sacrificing openness. The architecture of the PABS system will greatly impact scientific research, therefore we strongly urge WHO Member States to seek a science-compatible compromise and consider the crucial role of interoperability and open data. Policymakers should focus on creating an effective and workable system that establishes rules for benefit-sharing that can truly contribute to global health equity.

This policy brief is a short version of the forthcoming manuscript "Align the WHO's Pathogen Access and Benefit Sharing System with scientific reality to support research and global health equity" by the DSI Scientific Network PABS working group. The document explores 1) how sequence data interoperability works across the existing database ecosystem and how data moves across databases; 2) how registration requirements intended to control access and enforce benefit-sharing would negatively affect our collective ability to prepare for and respond to public health threats; and 3) which alternative measures can be taken to ensure and enhance benefit-sharing.

Introduction

In May 2025, World Health Organization (WHO) Member States adopted the WHO Pandemic Agreement (PA). However, this will not open for signature until the Pathogen Access and Benefit-Sharing (PABS) system Annex to the PA, established under Article 12, is agreed upon[1,2]. This system is being negotiated by an Intergovernmental Working Group (IGWG) with an outcome expected by May 2027.

Given the challenges faced in vaccines, therapeutics and diagnostics (VTD) distribution during the COVID-19 pandemic – particularly in low- and middle-income countries (LMICs), despite initiatives designed to help such as COVAX – the PABS system must ensure that benefits derived from commercial use are shared equitably[3]. One central tension is how to ensure benefits – including VTDs, capacity-building, research collaboration and potentially monetary contributions – are shared. As already agreed in the PA, the policy mechanism for requiring benefit-sharing is the signing of a "PABS contract" by participating manufacturers

[1] World Health Organization. World Health Assembly adopts historic Pandemic Agreement to make the world more equitable and safer from future pandemics. (2025). https://www.who.int/news/item/20-05-2025-world-health-assembly-adopts-historic-pandemic-agreement-to-make-the-world-more-equitable-and-safer-from-future-pandemics
[2] Kai Kupferschmidt. Global pandemic treaty finalized, without U.S., in 'a victory for multilateralism'. Science. (2025). https://www.science.org/content/article/global-pandemic-treaty-finalized-without-us-victory-multilateralism
[3] Hampton A-R, Eccleston-Turner, M., Rourke, M. et al. Equity in the Pandemic Treaty: Access and Benefit-Sharing as a Policy Device or a Rhetorical Device? Journal of Law, Medicine & Ethics. (2023). https://doi.org/10.1017/jme.2023.59

with the WHO. **The most important policy design question is therefore how to ensure companies sign PABS contracts.**

Because it is an *access* and benefit-sharing system, attention has turned to restricting access to pathogen materials and sequence data ("PABS Materials and Sequence Information (SI)") to identify companies. Various access control options have been proposed, including building a stand-alone WHO-run database only for pathogen sequence information from pathogens with pandemic potential (hereafter pathogen SI) or a closed federated set of national PABS databases. While federated approaches are under active research in how they can be helpful in enabling cross-border collaboration and integrating distributed genomic and clinical data, these are still too untested to build a global PABS system upon. Moreover, duplicated or fragmented systems – with limited interoperability, inconsistent standards and infrastructure barriers – will delay pandemic prevention, preparedness and response (PPPR)[4]. Prohibiting pathogen SI download and creating a pathogen SI silo as proposed in controlled access approaches would be catastrophic for research and the development of vital VTDs. A third option would be to allow pathogen SI to enter the mainstream biological databases, but to require databases that host pathogen SI to register users before allowing access to data. This "user registration barrier" is thought to serve both to identify persons or entities accessing pathogen SI and compel companies to sign PABS contracts.

Although this option is seen by many as the most "harmless", conditioning access to pathogen SI in this way risks thwarting the research process and public health response. It would have three negative scientific and public health consequences: a) severely affect the speed of response by limiting computer-to-computer interaction between databases; b) progressively "de-pathogenize" the global sequence dataset; and c) affect millions of researchers and not just VDT manufacturers. This focus on access is not required *de facto*. Access does not need to be the trigger for sharing benefits, but, rather, can be seen as one element of a package where access is granted and specific mechanisms ensure that benefits must be shared.

1. What is interoperability? How does open access allow data to move across databases?

Open access underpins the current sequence database landscape[5], enabling data to be interoperable, be shared, reused, and integrated rapidly, free of charge, without friction and in machine-readable formats[6]. Rapid sharing and interoperability are especially important in early phases of outbreaks. Interoperability can be understood as the ability of databases to automatically exchange, link, and build upon each other's data, allowing information deposited in one database to flow seamlessly into other databases, tools or models without restrictions such as manual re-entry or separate negotiations at each transfer step (see

[4] Khurana, M.P., Tsui, J.LH., Gutierrez, B. et al. Global approaches to infectious disease surveillance and modeling. Nature Medicine. (2026). https://doi.org/10.1038/s41591-026-04351-4

[5] Haas, A. S. Ventouratou, M., Gatti, S. et al. Today's pathogen database landscape. DSI Scientific Network. (2026). https://www.dsiscientificnetwork.org/wp-content/uploads/2026/02/DSI-Scientific-Network-Todays-pathogen-database-landscape-2026.pdf

[6] DSI Scientific Network. What does Open Access mean to researchers? (2024). https://www.dsiscientificnetwork.org/wp-content/uploads/2024/12/DSI-Open-Access-ENG-WEB.pdf

Figure 1). Computer-to-computer interactions enable the rapid daily exchange of large amounts of nucleotide sequence data and other biological data.

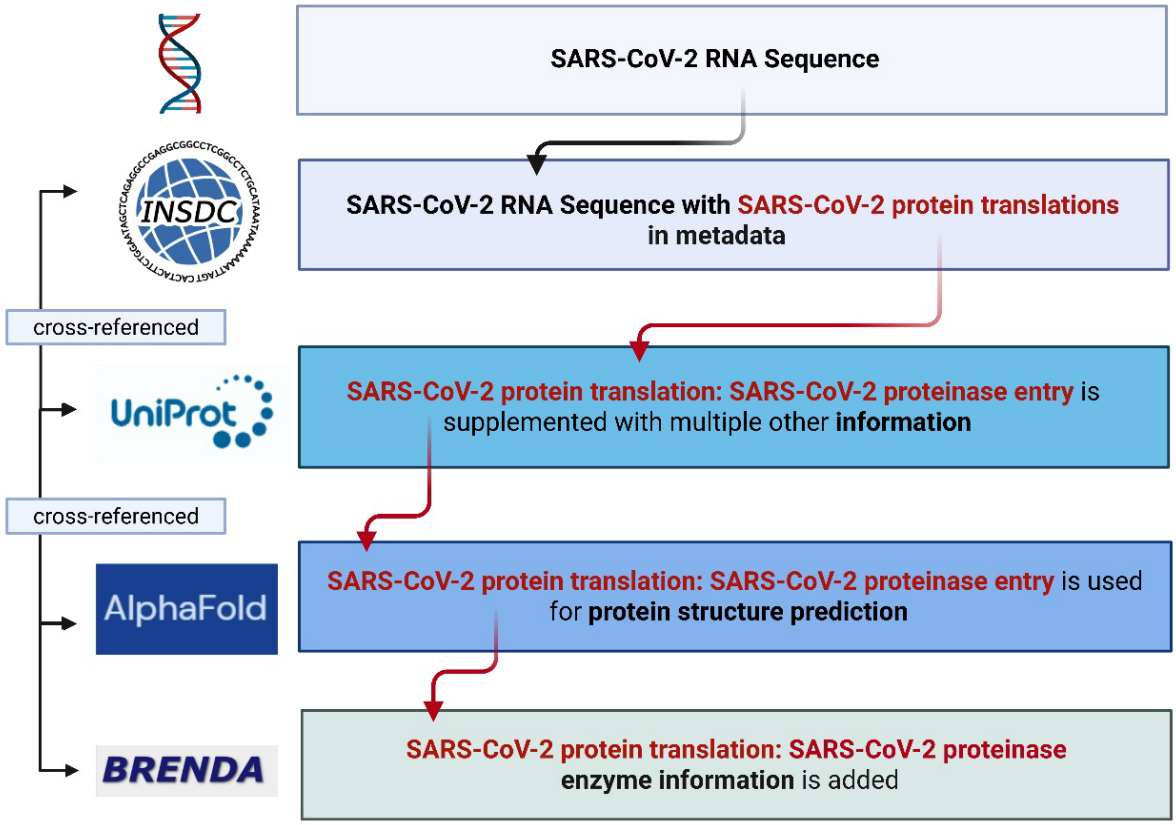

***Figure 1**: Simplified description of how SARS-CoV-2 nucleotide sequence data is a starting point for data interoperability enabled through computer-to-computer interactions: The SARS-CoV-2 genome sequence is uploaded to INSDC (International Nucleotide Sequence Database Collaboration). It contains several protein sequence translations in its metadata under the "Coding Sequence (CDS)" field. These protein sequences are each automatically ingested by the protein database UniProt, forming distinct protein entries. These records are then used to predict the 3-D structure of the proteins in AlphaFoldDB. Protein data also is used and complemented by other databases, such as the enzyme database BRENDA. All of this is automatic and happens across thousands of databases.*

During pandemics, rapid data access and transmission are essential for timely response, faster research, and the development of life-saving interventions[7]. Efficient and open sharing of pathogen SI, supported by instantaneous computer-to-computer data exchanges, is what enables scientists to quickly identify pathogens and inform public health officials and the scientific community through dedicated services like the COVID19 Data Portal[8] or Nextstrain[9]. All these data flows are necessary to answer diverse biological questions, such as understanding the metabolic potential of a new virus for example – a task which is impossible with "just" nucleotide (DNA/RNA) sequence data.

[7] Watson, C. Rise of the preprint: how rapid data sharing during COVID-19 has changed science forever. Nature Medicine. (2022). https://doi.org/10.1038/s41591-021-01654-6
[8] COVID-19 Data Portal. https://www.covid19dataportal.org/
[9] Nextstrain. Ongoing 2026 Bundibugyo ebolavirus outbreak in DRC & Uganda. https://nextstrain.org/ebola/bdbv-drc-uganda-2026

2. How will access restrictions through a "user registration barrier" negatively affect our collective ability to prepare for and respond to public health threats?

Setting up access restrictions through a "user registration barrier" would mean:

- **Slowing down response by limiting computer-to-computer interaction between databases:** User registration creates a barrier because it applies not only to human interactions with a database, but also to any other database accessing the pathogen SI. By numbers, the largest "users" of pathogen SI are not people, but rather servers of other databases. Registration requirements by PABS would undermine these critical automated data exchanges because data would not be permitted to be shared across the thousands of existing biological databases[10] and tools. Although, in theory, machine-to-machine registration (and registration at the human interface of all other database tools) would be technologically possible, this would require a technological overhaul of thousands of publicly-funded databases, and this would still not solve the issue that restricted access data is very likely subject to data sharing restrictions. Given that public sequence databases generally stem from research endeavors with limited funding, it is difficult to imagine that these databases would be incentivized to join such a PABS system (especially since pathogens with pandemic potential only represent around 3% of the biological dataset)[11]. Furthermore, the estimated 7% of pathogen databases that

[10] DSI Scientific Network. Mapping the landscape of DSI databases: A large, interconnected, and ever evolving DSI data ecosystem. (2024). https://www.dsiscientificnetwork.org/wp-content/uploads/2024/12/DSI-Database-landscape_WEB.pdf
[11] Sett, S., Kress, W. J., Halewood, M. et al. Harmonize rules for digital sequence information benefit-sharing across UN frameworks. Nature Communication. (2024). https://doi.org/10.1038/s41467-024-52994-z

currently require user registration mechanisms[12] do not use it as an enforcement mechanism, and usernames are not shared with either the WHO or countries. Databases do not have the legal competency nor mandate to capture user identities, report them to supranational authorities and potentially sanction users.

- **Progressively "de-pathogenizing" the global sequence dataset:** Because pathogens with pandemic potential only account for around 3% of the global dataset, databases might begin to remove pathogens with pandemic potential from their datasets, rather than implementing a narrow solution for a small proportion of the data. If most or all databases were to implement these practices, then our scientific ecosystem will be progressively deprived of certain pathogen data. Databases that do implement PABS registration requirements would become siloed from the global dataset due to the data-sharing restrictions. Our understanding of pathogens that pose a pandemic threat would become increasingly patchy and generally poorer, which would severely limit effective research and future PPPR.

- **Affecting millions of academic researchers and not just VDT manufacturers and companies:** There are millions of users[13] of biological databases but there are (at most) around several hundred VTD manufacturers[14, 15, 16]. Data access restrictions that are used as leverage for companies to sign PABS contracts would disproportionately impact non-commercial users. Compared with total global research activity, only a fraction of the scientific activities that use pathogen SI are commercial in nature. Many scientific breakthroughs in basic research are required before products can reach the market, for example, discovering how and where a virus binds to a human cell and how viruses are transmitted. This crucial work will not directly result in commercial benefits to be shared but would be negatively (irreparably) impacted by a user registration barrier.

3. What can be done instead of user registration that will truly enhance benefit-sharing?

PABS should address scientific inequities in pathogen education and research: The capacity of researchers to take advantage of the open access system and contribute to science and public health remains uneven. The PABS system should build scientific capacity in LMICs linked to Article 9 of the PA and be sustained between emergencies. Investments in scientific infrastructures such as biobanks, sequencing centers, sequence databases and bioinformatics capacity are needed to improve global disease surveillance

[12] Haas, A. S. Ventouratou, M., Gatti, S. et al. Today's pathogen database landscape. DSI Scientific Network. (2026). https://www.dsiscientificnetwork.org/wp-content/uploads/2026/02/DSI-Scientific-Network-Todays-pathogen-database-landscape-2026.pdf

[13] Rhoden F., Huang, S., Dröge, G. et al. Combined study on Digital Sequence Information (DSI) in public and private databases and traceability. Secretariat of the Convention on Biological Diversity. (2020). https://www.cbd.int/doc/c/1f8f/d793/57cb114ca40cb6468f479584/dsi-ahteg-2020-01-04-en.pdf

[14] Coalition for Epidemic Preparedness Innovations (CEPI). CEPI'21 vaccine manufacturing survey results. https://static.cepi.net/downloads/2024-04/Regional%20Vx%20MfG%20survey%20and%20workshop%20comms%20MRD%20DM%20210913.pdf

[15] World Health Organization. Global market landscape of vaccine manufacturing and procurement. (2025). https://iris.who.int/server/api/core/bitstreams/ecc663a7-cc11-4d3c-9b1a-1463bce61044/content

[16] World Health Organization. 2025 WHO Global Vaccine Market Report. (2025). https://www.who.int/publications/m/item/2025-who-global-vaccine-market-report

efforts and enhance the in-country use of open SI in research and development. Underrepresentation in global datasets due to sequencing costs, or lack of infrastructure and sustainable funding can limit the visibility of regional pathogen diversity[17]. This may have practical consequences for pathogen surveillance, risk assessment and public-health decision-making by providing an incomplete picture of pathogen diversity and evolution. The PABS system should therefore also address inequities in the representation of LMICs in global pathogen sequence databases, by supporting countries to generate, curate, share and derive scientific value from their own pathogen sequence data. All PABS investments should strengthen and expand existing infrastructure.

PABS should take a multi-pronged approach to secure PABS contracts: It is essential to identify companies and ensure they sign PABS contracts. Used in combination, the following measures could create pressure and leverage to this effect:

- **Treat PABS Material differently than PABS SI:** Currently, negotiators have treated materials and SI in the same way. Creating differentiated requirements for materials could enable more trust with open access to pathogen SI. Taking into account the differences in the use of PABS Materials and SI, PABS contracts could be signed when PABS Materials (biological samples or DNA) are accessed in the PABS system through the WHO Coordinated Lab Network.
- **Target the "big fish" companies that use PABS SI:** The PABS system should pursue policy tools that target VTD-manufacturing companies directly, incentivizing and enforcing PABS contracts both nationally and internationally. For example, the WHO could make a signed PABS contract a prerequisite for companies that seek WHO pre-qualification or emergency use listing and any WHO procurement, partnership or co-distribution arrangements could also be dependent on the presence of a PABS contract. At the national level, governments could offer research funding, procurement and

[17] Molina-Mora JA., Rojas-Varela, Á., Martínez-Arana, C. et al. Finding the Missing *IMP* Gene: Overcoming the Imipenemase *IMP* Gene Drop-Out in Automated Molecular Testing for Carbapenem-Resistant Bacteria Circulating in Latin America. Antibiotics. (2025). https://www.mdpi.com/2079-6382/14/8/772

stockpiling agreements, subsidies and tax incentives for companies with a PABS contract in place.

- **Downstream monitoring of patents and products:** PABS could have an "assumption mechanism" that assumes that PABS-relevant material or SI was used for all patents and products for pandemic countermeasures. Patents and many VTD products contain publicly available information that can be used to determine who should be a PABS participant. And, importantly, this information is already public and could be collated and publicly displayed without the need for new legislation. This also enables "name and shame" which can create a high-level of corporate social-responsibility pressure, which has been extremely effective, for example, in the environmental conservation space[18].
- **Downstream monitoring of publications:** Similar to patents, scientific publications that cite and use pathogen SI and materials, can be monitored to quantify non-monetary benefits, international collaboration, and capacity-building. While most publications already cite pathogen SI, more work can be done to improve attribution of data generators and citation practices[19]. Community standards, including those governing databases, preprints, and scientific journals, can more explicitly address the issues of equity and power imbalances and provide concrete guidance. PABS rules or future working groups, for example, with WHO International Pathogen Surveillance Network (IPSN)[20], would play a useful role here to increase awareness and action on these key issues.

Databases would align their governance to PABS if compatible with openness and interoperability: The PABS system should allow biological databases that align with key governance principles, to become designated by WHO. Governance principles could include:

- **PABS Terms of Use:** To ensure that PABS SI use respects potential benefit-sharing obligations, the PABS system should provide standardized global Terms of Use that will establish a minimum common policy standard across all designated databases. Terms of Use are supportive of open data and interoperability because they can be applied as an overarching governance principle across the entire database and relevant SI without any technological disruption. This approach was pursued under the Convention on Biological Diversity Multilateral Mechanism for Digital SI (CBD DSI MLM), which instructs users about benefit-sharing requirements but does not inhibit data interoperability and automated scientific analysis[21,22]. Moreover, coherence between the benefit-sharing architecture in PABS and the CBD DSI MLM is important for scientists to be able to use data across ABS regimes.

[18] Such as the Investment Tracker of the Tropical Forest Forever Facility (TFFF): https://tfffwatch.org/investment-tracker/Others
[19] Haas, A. S., Strobeyko, A., dos Santos Ribeiro, C. et al. Threading the needle on Traceability within the PABS System – Promoting Equity and Science. DSI Scientific Network. (2026). https://www.dsiscientificnetwork.org/wp-content/uploads/2026/02/DSI-Scientific-Network-Threading-the-needle-on-traceability-within-the-PABS-System-Promoting-equity-and-science-2026.pdf
[20] World Health Organization. International Pathogen Surveillance Network (IPSN). https://www.who.int/initiatives/international-pathogen-surveillance-network
[21] DSI Scientific Network. The role of databases under the CBD multilateral mechanism for sharing benefits from Digital Sequence Information (DSI). (2026). https://www.dsiscientificnetwork.org/wp-content/uploads/2026/09/The-role-of-databases-under-the-CBD-multilateral-mechanism-for-sharing-benefits-from-Digital-Sequence-Information-DSI.pdf
[22] European Nucleotide Archive. ENA and INSDC Policies. https://www.ebi.ac.uk/ena/browser/about/policies

- **Interoperability**: All designated databases should have a minimal standard of interoperability to ensure that exchange of pathogen SI is a two-way and not a one-way street: databases should be able to both receive pathogen SI and share it with other databases. As described above, the ability to exchange data with the wider biological database ecosystem is essential for PPPR. Interoperability will also be crucial for artificial intelligence tools that will accelerate VTD development and scientific research.
- **PABS database services:** Databases can support WHO and Member States by providing information on where PABS-related data is stored and what scientific outcomes are achieved. Databases can also provide information on the non-monetary benefits enabled through PABS SI and be key actors in capacity-building, training and amplification of the needs of the PABS community through new bioinformatics tools, services and analyses.

Thank you to the members of the DSI Scientific Network PABS working group who contributed to and reviewed both the forthcoming manuscript “Align the WHO’s Pathogen Access and Benefit Sharing System with scientific reality to support research and global health equity” and this policy brief.

This work was supported by the European Viral Outbreak Response Alliance (EVORA) project that has received funding from the Horizon Europe Program under Grant Agreement No. 101131959 as well as the DFG project PABS-SOS under Grant Agreement No. 582941979.

This brief can also be accessed on Zenodo at the following link: https://zenodo.org/records/23361173