Open Letter on behalf of the
European Virus Archive (EVA) to the
Intergovernmental Negotiating Body (INB) of the WHO CA+

May 2023

The WHO CA+ vision of "aiming for a world where pandemics are effectively controlled" and "greater equity and effectiveness for pandemic prevention, preparedness and response through the fullest national and international cooperation" is a remarkable and desirable effort. Timely sharing of pathogen samples and data and the sharing of benefits thereof is integral to the policies and practices of the members of the European Virus Archive (EVA). EVA has distributed EU-subsidized (free of charge) viral resources throughout the COVID-19 pandemic and other epidemics (e.g. Ebola fever-2014 and Zika fever-2016, Monkeypox 2022) to users in 109 countries worldwide. EVA has also implemented access and benefit-sharing (ABS) compliance; raised ABS awareness among members and users; and provided non-monetary benefit sharing measures (Sett et al. *Lancet Microbe*).

As negotiations progress, we strongly recommend that the INB bureau and WHO's Member States consider three concerns from the perspective of academic biobanks in the current WHO CA+ Zero Draft:

Recommendations:

1. **Definitions and scope of pathogen genetic resources (PGR) need to be broad and flexible to enable effective pandemic prevention preparedness and response (PPR).**
2. **Open access to pathogen sequence data should be preserved with a harmonized set of digitally-appropriate access and benefit sharing (ABS) rules that enable science to continue to thrive and be inter-operable.**
3. **Established pathogen sharing infrastructures need to be preserved and promoted to enable efficient global pandemic PPR.**

1. Definitions and scope of PGR need to be broad and flexible to enable effective pandemic PPR

Beyond pandemic pathogens: When infectious diseases threats (re-)emerge, front-line responders must quickly react to contain their spread. At the beginning of an emergence, the pandemic or epidemic potential from causative agents is often unclear. Rapid and open access to pre-existing and epidemic-associated PGR, from different sources and locations is crucial to harness the skills of scientists globally to identify and investigate such threats independent of pandemic potential. The development of the first SARS-CoV-2 diagnostic tests was only possible due to the availability of the historical severe acute respiratory syndrome materials and associated sequences (Corman et al 2020). Continuous surveillance of circulating strains (and their relatives) is essential to spot new variants and to ensure that public health measures and medical countermeasures remain effective. Similarly, for example, the Moderna COVID vaccine depended on the use of 179 old and new virus sequences, not all of which had pandemic potential (Moderna case study).

Other than trying to identify the causative agent, responders also work to determine the origin of any new outbreak, assess host susceptibility, viral infectiousness, possible zoonotic transmission routes, and spill over from environmental reservoirs. The scope of the Pathogen Access and Benefit Sharing (PABS) System should not be limited to "pathogens with pandemic potential" as in many cases, this denomination can only be attributed retroactively. In case of new emerging diseases, one cannot know the identity of the causative agent of "Disease X" in advance. Instead, pandemic PPR needs continuous sharing and monitoring of existing and new pathogens and related species across the environmental-animal-human interface, under the One Health approach.

Beyond Genetic Sequence Data: The use of the terms "genetic" or "genomic sequence data" restricts the PABS System to nucleotide sequence data. This definition should be broadened to include the rapidly-evolving "omics" fields or data resulting from the application of biotechnology. New technologies can drastically change daily practice and emerge quickly. It is crucial to use language that would also include other forms of digital information such as metabolomics and artificial intelligence outcomes in order to better future-proof the text. Furthermore, **to create legal certainty for all stakeholders, a single, global and predictable set of rules for benefit-sharing from pathogen data is highly desirable**. A "universal solution" that harmonizes ABS for pathogens, across all R&D activities, and under all relevant international policy fora, would facilitate sequence data use across different disciplines, sources and locations enabling science, including pandemic PPR, to thrive. To this end, the PABS System needs to align with the multilateral mechanism on digital sequence information (DSI) being developed under the Convention on Biological Diversity.

Text proposals
We suggest broadening the scope of paragraph 2 of Article 10 of the WHO CA+ Zero Draft to encompass all pathogens (i.e., human, animal, and plant), activities within pandemic PPR, and all forms of R&D involving pathogen genomics, including One Health collaborations. These suggestions are in line with statements made on behalf of the African region regarding Article 10, and naturally, would need to be adopted throughout the whole text of Article 10, as indicated below:
"The PABS System shall cover all pathogens ~~with pandemic potential~~ ***across the environmental-animal-human interface****, including their genomic sequences* ***data and other forms of digital sequence information on genetic resources****, as well as access to benefits arising therefrom, and ensure that it operates synergistically with other relevant access and benefit-sharing instruments".*

2. Open access to pathogen sequence data should be preserved with a harmonized set of digitally-appropriate ABS rules that enable science to continue to thrive and be inter-operable

The benefit-sharing mechanism proposed in the PABS System is based on standard material transfer agreement (sMTA) contracts, as described in paragraph 3 of Article 10:
"(g) Facilitated access shall be provided pursuant to a Standard Material Transfer Agreement, the form of which shall be set out in the PABS System and that shall contain the benefit-sharing options available to entities accessing pathogens with pandemic potential;"

This is a well-grounded ABS strategy for *physical* influenza samples in the Pandemic Influenza Preparedness (PIP) Framework and for viral materials in e.g. the EVA project (Sett et al. *Lancet Microbe*) and other biobanks. **However, there is no explanation on how a contract-based (sMTA) approach to benefit-sharing would apply (or not) to pathogen sequence data, One Health data, and how it would align with Open Science policies, practices and structures.** New language is needed to indicate how access to digital data will **be compatible with Open Science and open-access databases**, avoiding limiting conditions for their access, use and redistribution, and interoperability.

Benefit-sharing from pathogen sequence data should be fair and equitable, but must be decoupled from access. A contract-based approach e.g., pre-access sMTA, or a trigger point for benefit-sharing from individual sequences or access to public databases (e.g. data access agreement) will impede science and response time. Author contributions must be recognized, but access controls are an inappropriate mechanism to achieve this end.

Any barrier and delays for access and use of pathogen sequence data will translate into delays in developing and implementing response measures and ultimately the loss of lives and livelihoods. **Having a controlled and siloed approach for sharing pathogen sequence data based on concepts developed for physical samples, will impede scientific access and comparison of the global data set.** The functionality and operability of sequence databases, where extremely large volumes of different

origins are directly being (re-)searched, differ fundamentally from biobanks where single samples of known origin are physically transferred before any research can be done.

Text proposals
We suggest to add to paragraph 3 of Article 10, the following:
"(h)bis Open access to genetic sequence data and other forms of digital sequence information on pathogen genetic resources are essential non-monetary benefits that shall be ensured by parties. Benefit-sharing from digital data shall include recognition of the contributing scientist but shall not hinder science and innovation. The PABS System benefit-sharing options shall guarantee open science standards including the FAIR principles;"

The PABS System needs to be compatible with scientific practice. Users of pathogen sequence data work with the global dataset, not just a few sequences from one source and country. Researchers compare and select among millions of sequences, merge and edit them. It is very difficult (if not impossible) to define which sequences were used to develop a product and which types/amount of benefits will be linked to which sequences (Ebola case study). Integrated, open, and biodiversity-rich databases are critical to enable scientists to research across sectors and disciplines, perform quality control checks, and efficiently work for pandemic PPR. Open access to sequence data offers irreplaceable benefits to global health security by enabling rapid reaction to evolving public health emergencies such as the fast identification and characterization of the causative agent, outbreak origin, zoonotic transmission, and the subsequent measures to control and counteract its spread (e.g. developing diagnostic methods, medical treatments, epidemiological monitoring and vaccines).

3. Established pathogen sharing infrastructures need to be preserved and promoted to enable efficient global pandemic PPR

Biobanks, related networks and databases are critical for pandemic PPR. They are the main actors for rapid, efficient, impartial, and safe access to PGR, and fair and equitable benefit-sharing. These infrastructures are global public goods, and should be brought to the forefront of PABS. Restricting which structures can share PGR, in the Zero Draft, is concerning. To be viable, the PABS System must synergize and work with established pathogen sharing infrastructures (i.e. biobanks, scientific networks, and databases including the International Nucleotide Sequence Database Collaboration and the Global Biodata Coalition) from developed and developing countries, integrating their extensive experience and expertise without trying to "re-invent the wheel."

All relevant infrastructures should be given fair and equal opportunity to participate in sharing PGR under the same terms and conditions. These institutions could self-nominate or become recognized laboratories under the WHO CA+ if they fulfil certain criteria (e.g. biosafety and benefit-sharing standards). Biobanks in developing countries should also be promoted and expanded, to improve response capacity in those regions. Any (bilateral or exclusive) ABS arrangements or "free access" outside the PABS System would provoke undesirable forum shopping, in which users can seek out access to pathogens not subject to ABS conditions. Furthermore, PABS terms and conditions should not be negotiable but must be standardized from the start. Otherwise, unaffordable delays, transactional costs, and an unfair playing field to parties with different negotiation power will result.

Text proposals
The PABS System needs to be harmonized and all-encompassing: covering all types of access and use, for all pathogens, across all different types of organisations and actors, from all countries and sectors through standardized conditions via paragraph 3 of Article 10:
"(a) Each Party, ~~through its relevant and authorized laboratories~~, shall ***ensure****, in a rapid, systematic and timely manner: (i)* ~~*provide*~~ *pathogens* ***are provided to globally accessible pathogen sharing structures, such as established biobanks, and*** ~~*with pandemic potential from early infections*~~

~~due to pathogens with pandemic potential or subsequent variants to a laboratory recognized or designated as part of an established WHO coordinated~~ laboratory network~~s~~; and (ii) upload the genomic sequence of such pathogens ~~with pandemic potential~~ to one or more publicly accessible databases of its choice.

Bis (b) Pathogen sharing infrastructures can be recognized at the international, national, or regional level based on compliance with published criteria such as biosecurity, biosafety, and benefit-sharing.

*(c) Access shall be accorded expeditiously ~~by the laboratory recognized or designated as part of an established WHO coordinated laboratory network, subject to conclusion of a Standard Material Transfer Agreement~~ **following the pre-established standardised conditions**, developed for the purposes of the PABS System…"*

To conclude

During the COVID-19 pandemic, the EVA consortium accrued extensive hands-on experience with rapid and efficient exchange of pathogen material and related data, particularly during the crucial first three months after the WHO declared it a pandemic. This enabled not only the characterization of the virus itself but also unmatched speed in the development of detection kits and vaccines. EVA has openly manifested its support for a multilateral benefit-sharing system for sequence data that is compatible with Open Science by signing the DSI Scientific Network's Open Letter, and by endorsing the position paper "Keep DSI a common good", the policy position letter submitted to the Convention on Biological Diversity via CBD/WG2020/3/4.

Based on scientific evidence as well as EVA's extensive empirical experience in pathogen sharing during and in-between pandemics, we believe the proposed suggestions and recommendations are critical for improving pandemic PPR in the short and long term and hope they will be carefully considered by the INB bureau, the WHO's Member States, and all relevant stakeholders. Transparency and stakeholder engagement are core values of the UN system. We hope EVA and other biobank leaders can be further involved in the WHO processes as a key stakeholder group.