the bmj

Preventing the Next Pandemic: The Power of a Global Viral Surveillance Network

SCHOLARONE™
Manuscripts

Preventing the Next Pandemic: The Power of a Global Viral Surveillance Network

Dennis Carroll (0000-0001-8529-4164) [1], Subhash Morzaria (0000-0003-3905-6979) [2], Sylvie

Briand [3] (0000-0001-6929-5335), Christine Kreuder Johnson [4] (0000-0001-6673-8743), David

Morens [5] (0000-0002-0968-3800), Keith Sumption [6] (0000-0002-3638-9869), Oyewale Tomori [7]

(0000-0002-6959-5749), Supaporn Wacharphaueasadee [8] (0000-0001-7636-1900)

Correspondence to: Dennis Carroll dcarroll008@gmail.com; 800 Wharf St, S.W. #70,

Washington DC, 20024 USA

Authors Details

[1] Dennis Carroll, Chair, Leadership Board, Global Virome Project, Washington DC, USA

[2] Subhash Morzaria, Independent Consultant, Loule, Portugal

[3] Sylvie Briand, Director, Global Infectious Hazard Preparedness, WHO, Geneva, Switzerland

[4] Cristine Kreuder Johnson, One Health Institute, School of Veterinary Medicine, University of

California, Davis, CA, USA

[5] David Morens, National Institute of Allergy and Infectious Diseases at the National Institutes of

Health, Bethesda, MD, USA.

[6] Keith Sumption, Chief Veterinary Officer, FAO, and Director, Joint Centre for Zoonotic Infections and AMR. Headquarters, Rome, Italy

[7] Oyewale Tomori, Professor, Redeemer's University, Ede, Osun, Osun State, Nigeria.

[8] Supaporn Wacharphaueasadee, Thai Red Cross Emerging Infectious Diseases Health Science Centre, World Health Organization Collaborating Centre for Research and Training on Viral Zoonoses, King Chulalongkorn University, Pathumwan, Thailand

Introduction

The ongoing COVID-19 pandemic has laid bare our collective weaknesses in being able to effectively respond to the emergence of a highly contagious and lethal microbial threat. Despite extraordinary advances over the past century in science and unprecedented improvement in global health standards, as evidenced by the COVID-19 pandemic, we still live in a world where the threat of an infectious agent can emerge anytime and any place without warning and spread rapidly to every community and every household without regard to national borders.

Importantly, COVID-19 is not the first pandemic of this century and is unlikely to be the last. Over the last 20 years a number of high impact epidemics and pandemics have emerged or reemerged. In this short period of time, we have had emergence of three new coronaviruses (CoV), namely Severe Acute Respiratory Syndrome (SARS) in 2003; Middle East Respiratory Syndrome (MERS) in 2012; and the ongoing COVID-19 pandemic caused by SARS-CoV-2, a number of highly pathogenic influenza A viruses (e.g. H5N1 in 2003; H7N9 in 2013; and the H1N1 pandemic of 2009), the Zika virus as a global health emergency in 2016, and the continuing rise and spread of Ebola in West and Central Africa since 2013. All these epidemic and pandemic viruses have jumped from wild animals, either directly into humans or indirectly through domestic animals. Once they have made the inter-species jump, they tend to persist and evolve in the human systems presenting a continuous danger to the global community.

Over the course of the remainder of this century, the likely frequency of epidemics and

pandemics will continue to increase, driven to a large extent by demographic trends, including

urbanization, and environmental degradation, climate change, persistent social and economic

inequalities, and globalized trade and travel (1,2,3). The burden of these diseases is not equally

distributed across the world; the economically disenfranchised, displaced populations and

people living with pre-existing conditions are disproportionately impacted (4).

Importantly, the drivers underlying the emergence of novel disease threats are complex human

behaviors and their impact on animal populations and the environment[5]. Changing

environmental and climatic conditions have been closely linked to the emergence of novel

infectious diseases and the redistribution of those already existing (6,7). Their aggregate impact

will continue to increase.

While the upgrading of the health security apparatus over the last decade has been welcomed,

COVID-19 underscores that these processes and institutional arrangements are not sufficient to

responding to events such as those caused by SARS-COV-2. Compliance with the International

Health Regulations (8), that provide a normative framework for surveillance, preparedness,

notification and international support and coordination has also been shown to be inadequate.

The experience of the COVID-19 pandemic, yet again underscores that new efforts need to be

made to craft global strategies, policies and regulatory frameworks that more directly address

the multi-sectoral aspects of disease emergence in order to improve our collective capacities to

prevent, as well as rapidly detect and respond to threats. Key is building a global surveillance

system spanning wildlife, livestock and human populations that is able through the collection of

detailed meta-data to identify geographic "hot spots" where the risk of spill-over into human

and livestock populations is greatest, and to use this detailed understanding of "risk" to target

surveillance to those places for the early detection of spillover events in humans and livestock

at a local level. Further, understanding where the threat of spillover is greatest allows for the

targeting of pre-emptive measures to disrupt spillovers. Current efforts to address pandemics

after they have emerged, through the traditional approaches such as quarantine, and drug and

vaccine development are woefully inadequate to contain a raging pandemic such as COVID-19.

Jones et al[7] created the first hot-spot maps based on comprehensive literature review of all

emerging and re-emerging infectious diseases in the last 60 years. This map was recently

updated (9). It shows that the tropical regions of Africa, Asia and South America are still

represented as high-risk ecological locations for majority of the zoonotic pathogens. These are

also the regions where the wildlife biodiversity is rich and the land use changes are

accelerating. These regions are likely to be most cost-effective for surveillance at the

intersection of wildlife, livestock and humans.

There are a huge number of pathogens globally, and given limited resources to address these,

World Health Organization (WHO) (10) under their Research and Development Blueprint

developed a first list of priority pathogens that have the greatest public health risks. This list

was updated in 2020 and includes members of the families of coronaviridae (SARS-CoV 1, SARS-

CoV-2 and MERS CoV), filoviridae (Ebola and Marburg), flaviviridae (Zika), paramyxoviridae

(Nipah, Henipa), arenaviridae (Lassa), bunyaviridae (Crimean-Congo haemorrhagic fever) and

phenuviridae (Rift Valley fever) and "Disease X". The Centres for Disease Control (CDC) (11), in

their list of priority diseases includes zoonotic influenzas as their top priority zoonotic viral

disease as they continue to persist and evolve generating new phenotypes in livestock

production sectors, particularly in Asia and Africa. The "Disease X" referred to in the WHO list

represents a disease caused by a pathogen as yet unknown to humans but may cause a serious

international health crisis. There are tens of thousands of such zoonotic viruses that are yet to

be discovered (12).

Creating a Global Viral Surveillance Atlas

In 2018 two papers were published (12,13) that proposed the Global Virome Project (GVP)

that had a bold and ambitious global-scale 'big science' plan to develop an atlas of the majority of

the planet's naturally-occurring zoonotic viral threats over a 10 year time frame, transforming

the world of emerging diseases into a data-rich field. The GVP was established as a legal non-

governmental entity in early 2020 with a planned launch of field operations in 2021. The vision

behind the GVP is that if we develop a comprehensive profile of viruses while they are

circulating in wildlife – their natural hosts – we can better prevent, detect, and respond to

viruses as they jump to us and before they begin to transmit among human population. The

expectation is that the GVP will transform our public health culture from one that responds to

the latest outbreak, to one that is better able prevent their emergence and spread among

human and livestock populations, detect spillover events early when they do occur, respond

quickly to preempt their spread and support the scientific community in generating far more

effectively biomedical countermeasures to respond to future outbreaks should they occur.

This power to "prevent, detect, and respond" will protect against not only human infections but

similarly protect domesticated animal populations which share our vulnerability to emerging

viral threats, and by extension protect against the devastating effects of viral threats such as

the recent emergence of the zoonotic H5N1 highly pathogenic avian influenza, and recent

incursion and spread of African Swine fever in Asia causing serious concerns of food security

and livelihoods of poor farming communities of the world (14,15,16,17).

At the heart of the GVP is an open and transparent data portal that will manage the array of

data generated – and enable the building of a comprehensive Global Viral Atlas, enhanced by a

large set of meta-data and a growing collection of new zoonotic viruses for further research.

The Need for a Global Viral Surveillance Network

While the GVP will contribute to a dramatic expansion of what is known about viruses circulating

in wildlife and enable the identification of future viral threats *before* they emerge – these "big

data" will by virtue of GVP's 10 year temporal boundaries, represent a "snap shot in time" – that

provide a specific point in time data-set spanning viral genetics and ecology. What will be true

of these "high risk" viruses is that they will, over time, continue to evolve – acquiring new

genetic features, diversifying their distribution across animal species – and in effect evolving

their risk profile (18). The initial data generated by the GVP will contribute critical insight into

establishing a "viral watch list" composed of those viruses circulating in wild life that possess the most significant threat to human and animal populations.

The GVP will make substantive contributions to enhancing the multi-sectoral capacities across countries for the collection and analysis of viral samples from the across wildlife (and under certain circumstance livestock and humans) and provide a baseline against which to monitor their evolution over time.   What the GVP will not do is sustain the kind of long-term surveillance that will be needed to monitor the critical biological and ecological changes among the "watch list" that could signal elevated risk to human and animal health.

Though time-limited, the GVP is laying the groundwork for a longitudinal, multi-sectoral global surveillance system to detect early spillover events, track and monitor the evolution of the viral "watch list". While information and knowledge about hundreds of thousand of yet undiscovered viruses is essential, it is only a piece of a complex multifactorial reality.   What is needed is a comprehensive surveillance system that will build on the country-level capacities developed by GVP and use the "watch list" to track genetic and ecologic evolution over time. This system should also look at the human side of the equation. Among the millions of viruses present in nature, only very few have the capcity to infect humans and even fewer have the capacity to spread. However, even if the likelihood of an effective spill over is very low, the impact can be disastrous and therefore specific investment in systems that can prevent such events is justified. Many of the epidemics with pandemic potential were discovered early through an unusual cluster of severe cases or deaths in humans. This is a weak signal, and is often missed by the

classical surveillance systems. In the future to improve our capacity to detect early viruses with

pandemic potential, it also critical to strengthen further the global capacity to pick-up unusual

clusters of severe morbidities and mortalities for further investigation and response. This can be

achieved by dual strategy of strengthening the existing health care systems and improving the

surveillance and diagnostic capacities to detect above-mentioned viral watch list in hot spot

regions. Such a multi-sectoral system will contribute to an enhanced capacity to forecast future

threats and enable early intervention before they pose a threat.

Examples of Viral Surveillance Exist but Need to Be Broadened

There is precedent for establishing a global scope for the longitudinal monitoring of a select

pathogen. WHO's Global Influenza Surveillance and Response System (GISRS) for more than

half a century has been tasked with monitoring the evolution of influenza viruses for

development of the annual influenza vaccine, as well as serving as a global alert mechanism for

the emergence of influenza viruses with pandemic potential (19). The GISRS has grown into a

global partnership of 143 National Influenza Centers (NICs), 6 highly specialized Collaborating

Centres for Reference and Research on Influenza and 4 national licensing agencies or Essential

Regulatory Laboratories and 13 H5 Reference Laboratories. The NICs collect, identify and ana-

lyze influenza strains isolated from clinical specimens and forward representative or unusual

virus isolates to a WHO Collaborating Centres for detailed characterization. Although

individual-level epidemiological or clinical data are not collected, NICs provide weekly reports

to WHO of geographically-based influenza like activity using FluNet, a web-based electronic

interactive data reporting, query and mapping system (20).   The network over 65 years has

provided information on circulating seasonal influenza viruses, as well as supporting response

to the influenza pandemics in 1957, 1968, and 2009, and to threats caused by animal influenza

viruses and by zoonotic transmission of coronaviruses.

Before the H1N1 2009 pandemic, WHO developed FluID, which is a global platform for data

sharing that links regional influenza epidemiological data into a single global database

(https://www.who.int/influenza/surveillance_monitoring/fluid/en/) to monitor the influenza

disease. It complements FLuNet by providing critical information of the impact of the viruses on

human health.

The 2009 H1N1 pandemic showed that only monitoring for viruses does not provide adequate

information for decision makers to respond to and mitigate the health impacts of an epidemic.

Information on the severity of the disease and the real time impact on populations health is

essential. After the 2009 H1N1 pandemic most of the influenza surveillance systems in the

world started to include surveillance for respiratory symptoms with standardized case

definitions for Influenza Like Illnesses (ILI) and Severe Acute Respiratory Influenza (SARI), and

real time modelling into the existing viral surveillance. Similarly, OFFLU, the World Organization

for Animal Health (OIE)/Food and Agriculture Organization (FAO) Animal Influenza Surveillance

platform, established in 2005 to interface with the existing WHO influenza network (21)

routinely shares as well as promotes the collection, exchange and characterization of animal

influenza viruses, including selection of viruses for seasonal influenza and deposition of

sequence data in genome banks.

GISRS and OFFLU are excellent examples of a robust global longitudinal surveillance system, however, they are focused on influenzas. While it is important to maintain these surveillance systems, forging the alliances essential for sustaining a multi-dimensional data base that encompasses virtually all zoonotic viral families and spans the wildlife-livestock-human ecosystems will require an order of magnitude higher level of political and institutional commitments of the key international stakeholders, in particular WHO, FAO and OIE, and a buy-in from their membership and the global development partners.

Fortunately, WHO, FAO and OIE, recognizing the need for enhanced multisectoral collaboration for effective strategies for improving national, regional and community level pandemic preparedness and response, have been strengthening their partnerships over the past decade through a formal tripartite agreement (22). Recently, this agreement was further strengthened through a Memorandum of Understanding (23) to set up joint action to combat health threats emerging from interactions between humans, animals and the environment.

One example of a formalized monitoring and reporting platform for disease events involving the WHO, FAO and OIE is the Global Early Warning and Response System (GLEWS). Established in 2006, it aims to combine the strengths of three organizations to enhance a public and animal health early warning system intended to reduce incidence and impacts of emerging infectious diseases in animals and humans (24). Partners in GLEWS, which incorporates both animal and public health sectors, share information from all over the world on disease outbreaks in real time, conduct rapid cross-sectoral risk assessments, evaluate control and prevention options, and coordinate their responses.

GLEWS combines and coordinates the alert and response mechanisms of the OIE, FAO, and

WHO to assist in prediction, prevention, and control of emerging infectious diseases. This

international platform is among the most effective means by which these agencies currently

collaborate. The scope of GLEWS, however, is focused on early detection of ongoing outbreaks

and does not address monitoring for and detection of emerging pathogens in animals and

humans before outbreaks occur, or support the "pre-event" surveillance of viruses in wildlife

population enabled by the GVP.

The Time for Building a Sustained, Multi-sectoral Global Viral Surveillance Network is Now

While GISRS offers an important model for a longitudinal monitoring platform with its global

network of National Influenza Centers and Collaborating Centers, the "watch list" of a large

number of new viruses being generated by the GVP will necessitate an expanded scope – from a

focus on one viral family to the inclusion of all zoonotic viral families characterized as "high risk".

In addition, a multi-sectoral partnership, much more like GLEWS, will be needed to ensure the

systems and capacities are able to track the evolution of these viruses as they spill over from

wildlife into livestock and humans. The GVP over its 10 year life will make critical investments in

building such multi-sectoral surveillance capacities at national, regional and global level as it

captures the initial "baseline" data (11). Sustaining such an effort, however, will require an

expanded partnership across WHO, FAO and OIE and their national constituencies and regional

economic communities to the long-term monitoring of genetic, epidemiologic and ecologic

changes that signal the potential emergence of a new viral threat.   Equally important will be

sustaining and broadening the open and transparent data platform established by the GVP; and, that like GISRS and GLEWS this data will be the basis for further risk analysis, targeted surveillance in humans and livestock, forecasting disease emergence, and effective response and prevention.

Nearly all the surveillance systems that currently exist are very much event based, or syndromic in nature. Most pathogens that are identified are from outbreaks.   Apart from GISRS, all other multi-sectoral collaborations are focused on disease information sharing through their respective networks and country offices. There is no formal system that is in place in any country that routinely conducts active viral surveillance combined with rapid clinical assessment for a list of priority emerging and re-emerging viral diseases. Identifying viral spillover events from wildlife to livestock and humans, well before they manifest in localised outbreaks, is a pre-requisite for pre-empting high consequence epidemics and pandemics. While such an approach under a global coordination mechanism has never been attempted before, given the frequency with which new epidemics and pandemics are now emerging, this approach necessitates further discussion and investment. Given the magnitude of the dual, health and socio-economic impact of current COVID-19 crisis, the benefits of such an approach can be easily justified.

Introduction of a formalized and sustained, longitudinal surveillance for detection of spill-over events at the interface of wild and domestic animals and humans of priority viruses in pre-defined hot-spot regions of the world is not without significant challenges. This approach is fundamentally different in scope and scale from syndromic, passive surveillance and require

sustainable investment at the interface of multiple sectors. Dealing with high impact emerging

and re-emerging infectious diseases is of international public good (25) and hence will require a

strong buy-in and financing from national public, animal and environmental sectors, with

support from UN technical agencies (e.g. WHO, FAO and OIE), as well as numerous bilateral

donors, multi-lateral development partners and Foundations (e.g. United States Agency for

International Development, Department for International Development of UK, the European

Union, World Bank and Bill and Melinda Gates Foundation). The technical challenges in

designing sampling frames, availability of trained human resource, infrastructural support for

joint public health and animal health collection of biological samples, transportation and

laboratory testing in target countries are complex. In addition, mechanism of sharing

information for rare spillover events that may occur in distant and remote places at evolving

interfaces, and in dynamic livestock and wild animal production systems and their value chains,

driven by a complex set of factors such as climate change, land use and demographic changes

cannot be under-estimated. Challenges of handling large volumes of data, standardization,

establishment of databases, multi-dimensional data analysis, and regulatory and legislative

framework for sharing information pose significant challenges.

Coordination among the United Nations and other international agencies, together with relevant

national and regional partners and financing institutions is needed urgently to discuss and plan

such a global venture and to develop a shared vision leading to a formal agreement on the

principle of the establishment of an active, targeted global, innovative one health surveillance

programme as an essential basis for preventing future pandemics. Technical, policy and

regulatory framework can then be coordinated under the aegis of the FAO-OIE-WHO 'tripartite'.

The products of GVP will offer a unique opportunity to the global community for the first time in

providing information on the precise geographical location of the new high-risk viruses that are

being detected. New virus discovery will enable generation of multiplex diagnostic platforms

with appropriate pathogen specific molecular primers and probes for rapid and affordable

detection of these viruses through active virological surveillance. In addition, rapidly evolving

next generation or 'deep' DNA sequencing technologies and real time digital pathogen

surveillance allow a generic approach (non-specific method) to virus identification that does not

require *a priori* knowledge on the targeted pathogens but can deliver a species/strain specific

result (26,27). Combining these technologies with associated bioinformatics tools can greatly

enhance the power of active viral surveillance programme for early spill over events of novel

viruses from wild life to domestic animals and humans.

The time for establishing such a long-term surveillance platform is not, however, at the end of

the GVP's ten-year lifespan. The projected discovery curves under the GVP for new viral threats

will be rapid (11). By year three of the GVP tens of thousands of new viruses are projected to

have been identified and the first "viral watch-lists" will have been generated. Given the time

sensitivity of the "baseline data" there will be an urgent need to begin the immediate

monitoring of this "list".   Current plans for the GVP have the first phase of its launch beginning

in 2021– a two year "incubation period" in a limited number of "start up" countries to test the

ability of the GVP to go to operational scale (both sampling and data management). The full

scale 10 year "steady-state" phase of the GVP will begin in 2023– with an expected rapid generation of viral data. The ongoing COVID-19 pandemic, the worst since the influenza pandemic 100 years ago, has heightened the sensitivity of the global community to devastating socio-political and economic damage to the planet. This is a significant opportunity to initiate a high-level dialogue to embark on how to formalize and support a sustainable global surveillance system for emerging pathogens to avert future epidemics and pandemics that continue to emerge and re-emerge at increasing frequency from wild animals.

The global community has an opportunity over the next three years to partner with and build on the knowledge and information that will be generated by the GVP to early detect and prevent pandemics through longitudinal tracking of high risk viral threats –and realize the promise of the GVP to make the world safer and better able to prevent the next pandemic.

Ultimately, multi-pronged approaches are needed to address the challenges of mitigating the impacts of epidemics and pandemics of new viruses originating from wild animals. These should include harnessing the large volume of new meta-data generated through the GVP and the proposed longitudinal viral surveillance programmes to address the root causes of spill-overs and spread of new pathogens, addressing risky practices, improving livestock food systems, and in parallel continue significant investments in the development of innovative diagnostic, vaccines (28) and chemotherapeutics.

Abbreviations

CDC: Centres for Disease Control, CoV: Coronavirus; COVID-19: Coronavirus Disease; FAO: Food

and Agriculture Organization; GISR: Global Influenza Surveillance; GLEWS: Global Early Warning

System; GVP: Global Virome Project; HPAI: Highly Pathogenic Influenza; ILI: Influenza like

Illnesses; MERS: Middle East Respiratory Syndrome; OFFLU: OIE/FAO; OIE: The World

Organization for Animal Health; SARI: Severe Acute Respiratory Infections; SARS: Severe Acute

Respiratory Syndrome; WHO: World Health Organization

Ethics approval and consent to participate: Not applicable in view of the nature of the paper.

Consent for publication: Not applicable.

References

1. Woolhouse MEJ, Gowtage-Sequeria S. Host range and emerging and reemerging

    pathogens. Emerg Infect Dis. 2005;11(12):1842–7.

2. Patz JA, Epstein PR, Burke TA, Balbus JM. Global climate change and emerging infectious

    diseases. JAMA. 1996;275(3):217–23.

3. Semenza JC, Suk JE. Vector-borne diseases and climate change: a European perspective.

    FEMS Microbiol Lett [Internet]. 2018;365(2). Available from:

    http://dx.doi.org/10.1093/femsle/fnx244

4. Morens DM, Fauci AS. Emerging infectious diseases: threats to human health and global

    stability. PLoS Pathog. 2013;9(7): e1003467.

5. Semenza JC, Lindgren E, Balkanyi L, Espinosa L, Almqvist MS, Penttinen P, et al.

    Determinants and drivers of infectious disease threat events in Europe. Emerg Infect Dis.

    2016;22(4):581–9.

6. Morens DM, Folkers GK, Fauci AS. Emerging infections: a perpetual challenge. Lancet Infect

    Dis. 2008;8(11):710–9.

7. Jones KE, Patel NG, Levy MA, Storeygard A, Balk D, Gittleman JL, et al. Global trends in

    emerging infectious diseases. Nature. 2008;451(7181):990–3.

8. World Health Organization. Strengthening health security by implementing the

    International Health Regulations. 2005 http://www.who.int/ihr/about/en/

9. Allen T, Murray KA, Zambrana-Torrelio C, Morse SS, Rondinini C, Di Marco M, et al. Global

    hotspots and correlates of emerging zoonotic diseases. Nat Commun. 2017;8(1):1124.

10. WHO (2015). Blueprint for R&D preparedness and response to public health emergencies due to highly infectious pathogens. 1-7

11. Centres for Disease Control. Prioritizing zoonotic diseases for multisectoral, one health collaboration in the United States. https://www.cdc.gov/one health/pdfs/us-ohzp-report-508.pdf . 2017:1-63.

12. Carroll D, Daszak P, Wolfe ND, Gao GF, Morel CM, Morzaria S, et al. The global virome project. Science. 2018;359(6378):872–4.

13. Carroll D, Watson B, Togami E, Daszak P, Mazet JA, Chrisman CJ, et al. Building a global atlas of zoonotic viruses. Bull World Health Organ. 2018b;96(4):292–4.

14. Burgos, S., Otte, J., Roland-Holst, D., 2012. Poultry, HPAI and Livelihoods in Lao People's Democratic Republic–A Review.,

15. Otte J. Impacts of avian influenza virus on animal production in developing countries. CAB Rev Perspect Agric Vet Sci Nutr Nat Resour [Internet]. 2008;3(080). Available from: http://dx.doi.org/10.1079/pavsnnr20083080

16. FAO, 2019. One year on, close to 5 million pigs lost to Asia's swine fever outbreak. http://www.fao.org/news/story/en/item/1204563/icode/.

17. Mistreanu S. China's swine fever crisis will impact global trade well into 2020. Forbes Magazine [Internet]. 2019 Dec 28 [cited 2020 Sep 24]; Available from: https://www.forbes.com/sites/siminamistreanu/2019/12/28/chinas-swine-fever-crisis-will-impact-global-trade-well-into-2020/

18. Kreuder Johnson C, Hitchens PL, Smiley Evans T, Goldstein T, Thomas K, Clements A, et al.

   Spillover and pandemic properties of zoonotic viruses with high host plasticity. Sci Rep.

   2015;5(1):14830.

19. Ziegler T, Mamahit A, Cox NJ. 65 years of influenza surveillance by a World Health

   Organization-coordinated global network. Influenza Other Respi Viruses. 2018;12(5):558–

   65.

20. FluNet. Available from: http://www.who.int/influenza/gisrs_laboratory/flunet/en/.

   Accessed November 27, 2017.

21. Edwards, S. OFFLU Network on Avian Influenza. Emerging infectious diseases. 2008;

   12(8):1287-88.

22. FAO-OIE-WHO (2010). Collaboration: Sharing responsibilities and coordinating global

   activities to address health risks at the animal-human-ecosystems interfaces. A Tripartite

   Concept Note.

   https://www.who.int/foodsafety/zoonoses/final_concept_note_Hanoi.pdf?ua=1.

23. WHO, FAO, OIE, (2018). Collaboration between the United Nations FAO, WHO and OIE

   Regarding cooperation to combat health risks at the animal-human-ecosystems interface

   in the context of the 'one health' approach and including antimicrobial resistance.

   https://www.who.int/zoonoses/MoU-Tripartite-May-2018.pdf?ua=1, 2018)

24. FAO-OIE-WHO. (2006). Global Early Warning and Response System for major animal

   diseases, including zoonoses.

25. Smith, RD. Global public goods and health. Bulletin of the World Health

Organization. 2003;81(7):475. World Health

Organization. https://apps.who.int/iris/handle/10665/268992

26. Tang P, Chiu C. Metagenomics for the discovery of novel human viruses. Future Microbiol.

2010;5(2):177–89.

27. Gardy JL, Loman NJ. Towards a genomics-informed, real-time, global pathogen surveillance

system. Nat Rev Genet. 2018;19(1):9–20.

28. Gouglas D, Christodoulou M, Plotkin SA, Hatchett R. CEPI: Driving progress toward
epidemic preparedness and response. Epidemiologic Reviews. 2019 Jan 31;41(1):28-33.