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ONE HEALTH SURVEILLANCE: THE NEED FOR INTERSECTORIAL COOPERATION

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One Health policy

efsa EUROPEAN FOOD SAFETY AUTHORITY

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ICES CIEM
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World Organisation for Animal Health
Founded as OIE

Latvian Academy of Sciences

One Health policy

Latvian Council of Sciences

Agricultural and food industry NVO's

Research institutes and academia

Municipalities

PLOS PATHOGENS

OPINION

One Health: A new definition for a sustainable and healthy future

One Health High-Level Expert Panel (OHHLEP), Wiku B. Adisasmito[1], Salama Almuhairi[2], Casey Barton Behravesh[3], Pépé Bilivogui[4], Salome A. Bukachi[5], Natalia Casas[6],

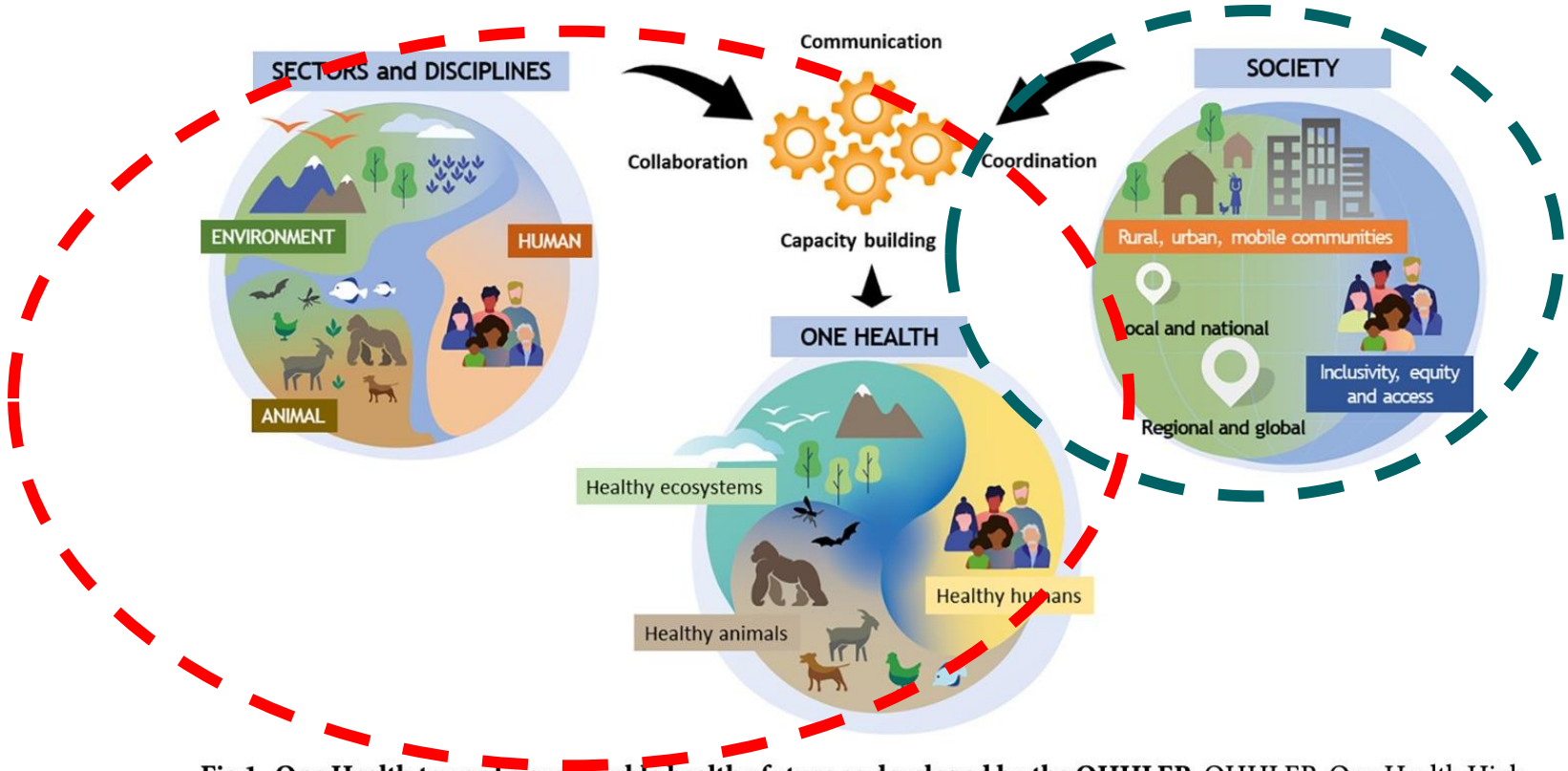

Fig 1. One Health toward a sustainable healthy future as developed by the OHHLEP. OHHLEP, One Health High-Level Expert Panel.

https://doi.org/10.1371/journal.ppat.1010537.g001

Adapted from WHO, OHHLEP et al. 2023

DEFINITION(S)….?!

One Health surveillance system is a system in which collaborative efforts exist between at least two sectors (among human health, animal health, plant health, food safety, wildlife and environmental health) at any stage of the surveillance process, to produce and disseminate information with the purpose of improving an aspect of human, animal or environmental health

(Bordier M. et al. 2020, Karimuribo et al., 2012, Berezowski et al., 2015, Stark et al. 2015, Hattendorf et al., 2107)

SCIENTIFIC ACTIVITY IMPACT ON *"ONE HEALTH SURVEILLANCE"*

Viewpoint

After 2 years of the COVID-19 pandemic, translating One Health into action is urgent

Thierry Lefrançois, Denis Malvy*, Laetitia Atlani-Duault, Daniel Benamouzig, Pierre-Louis Druais, Yazdan Yazdanpanah, Jean-François Delfraissy, Bruno Lina*

Introduction

The world is coping with the health, societal, and economic consequences of more than 2 years of the the emergence of infectious diseases need to be filled to allow the identification and rapid control of zoonotic risks before their introduction in humans. Optimum

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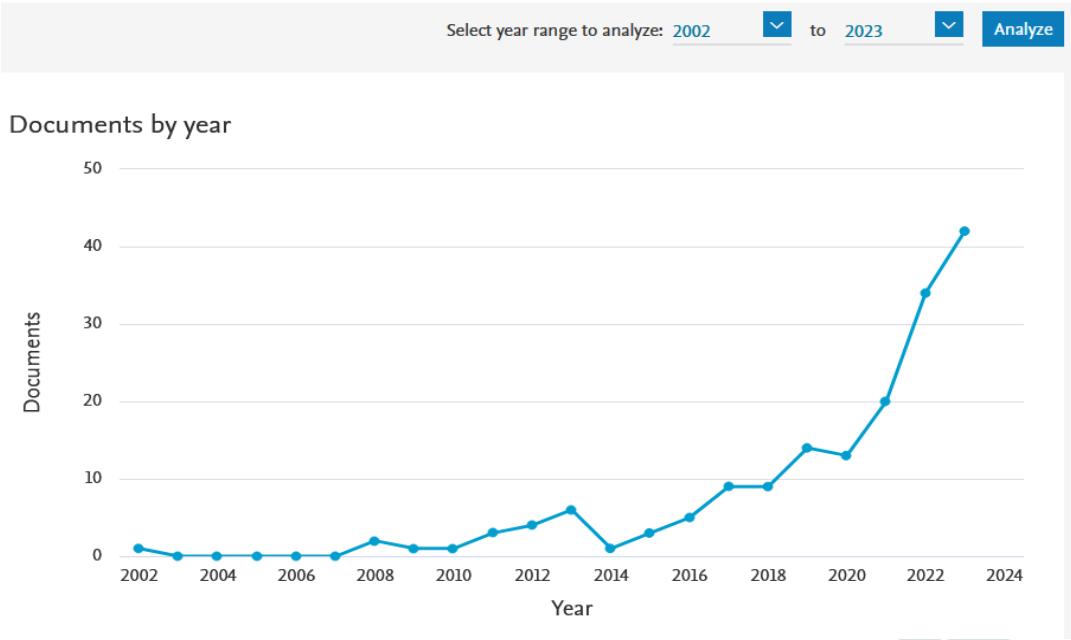

Points to be addressed:

-developing **an ambitious roadmap** for each step of pandemic (outbreak) crisis;

- developing One Health **action plans;**

- improving surveillance and prevention by reinforcing both upstream and operational **research**;

- developing a worldwide comprehensive and **united vision of health;**

- ensuring adequate **education and training** of One Health;

One Health cross-agency task force

Strengthening EU agencies' scientific advice on One Health

MED·VET·NET ASSOCIATION

One HEALTH EJP

EU agencies can help to bridge the gap between such knowledge and EU policy processes, make knowledge more accessible to relevant stakeholders, provide strategic direction to EU research funding, and directly engage with ongoing research projects (EFSA et al., 2018)

ADVANCING FOOD SAFETY: STRATEGIC RECOMMENDATIONS FROM THE "ONE – HEALTH, ENVIRONMENT & SOCIETY" CONFERENCE 2022

I. Keep up with science and technology, capitalising on **data** (Big Data, automation and AI)
II. Investment in future **preparedness** (develop and implement tools than can identify emerging food safety issues and risks, incl. strengthening foresight, horizon scanning, monitoring/ surveillance, hot spot mapping etc.)
III. Support the transition towards **sustainable food systems** (interaction with EU Green Deal, Farm to Fork Strategy and other EU policies)
IV. Increase relevance to **society** (build up, develop and strengthen relationships between science and society; covering communication and engagement, socieal sciences, Open Sciene)
V. Team up with **food safety actors** across the EU and beyond
VI. Apply the **One Health approach** (interinstitutional and transdisciplinary way of working, science and education, societal challenges…)

(Devos Y . et al., EFSA Journal 2022)

Preventive Veterinary Medicine 181 (2020) 104560

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journal homepage: www.elsevier.com/locate/prevetmed

Characteristics of One Health surveillance systems: A systematic literature review

Marion Bordier[a,b,c,*], Theethawat Uea-Anuwong[d,e], Aurélie Binot[b,f], Pascal Hendrikx[g], Flavie L. Goutard[b,d,e]

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[b] ASTRE, Univ Montpellier, CIRAD, INRA, Montpellier, France
[c] National Institute of Veterinary Research (NIVR), 86 Truong Ch
[d] CIRAD, UMR ASTRE, 10900 Bangkok, Thailand
[e] Kasetsart University, Faculty of Veterinary medicine, 50 Phahol
[f] CIRAD, ASTRE, Campus international de Baillarguet, 34398 Mo
[g] French Agency for Food, Environmental and Occupational Healt

Step of the surveillance process	Possible degrees of collaboration				
Planning	Undertaken separately in each sector	Undertaken by a single sector for all surveillance components	Cross-sectoral consultation but undertaken separately in each sector	Undertaken by a multi-sectoral working group	Undertaken by a multi-sectoral body
Data collection (sampling – laboratory testing)	Undertaken separately in each sector	Undertaken by a single sector for all components	Harmonisation across sectors	Joint activities across sectors	Undertaken by a multi-sectoral body
Data sharing	No data exchange	Notification of unusual events only	Ongoing data exchange		
Data analysis/ interpretation	Undertaken separately in each sector	Undertaken separately and then compared by a single sector	Jointly undertaken by a single sector for all components	Undertaken separately and then compared by a multi-sectoral working group	Jointly undertaken by a multi-sectoral working group or body
Results dissemination	Undertaken separately for each sector	Joint dissemination in separate sectoral activities	Joint dissemination by a single sector	Joint dissemination by a multi-sectoral working group	Joint dissemination by a multi-sectoral body

Fig. 2. Possible degrees of operational collaboration at the different steps of the surveillance process.

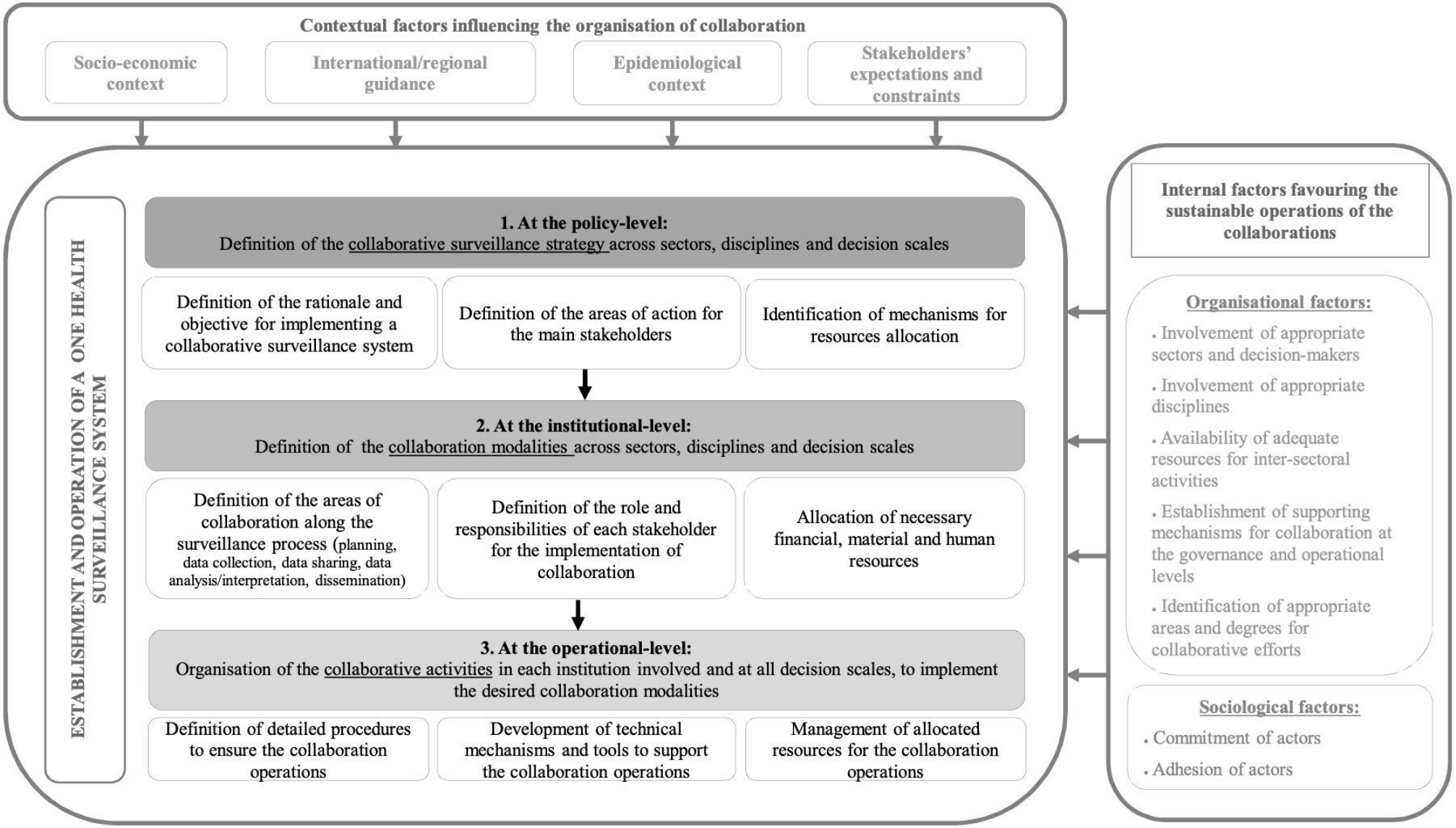

Fig. 3. Organisation of collaboration in a One Health surveillance system: a conceptual framework.

(Bordier M. et al. 2020. Preventive Veterinary Medicine)

nature climate change
ANALYSIS
https://doi.org/10.1038/s41558-022-01426-1
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Over half of known human pathogenic diseases can be aggravated by climate change

Camilo Mora[1✉], Tristan McKenzie[2,3], Isabella M. Gaw[4], Jacqueline M. Dean[1], Hannah von Hammerstein[1], Tabatha A. Knudson[1], Renee O. Setter[1], Charlotte Z. Smith[5], Kira M. Webster[1], Jonathan A. Patz[6] and Erik C. Franklin[1,7]

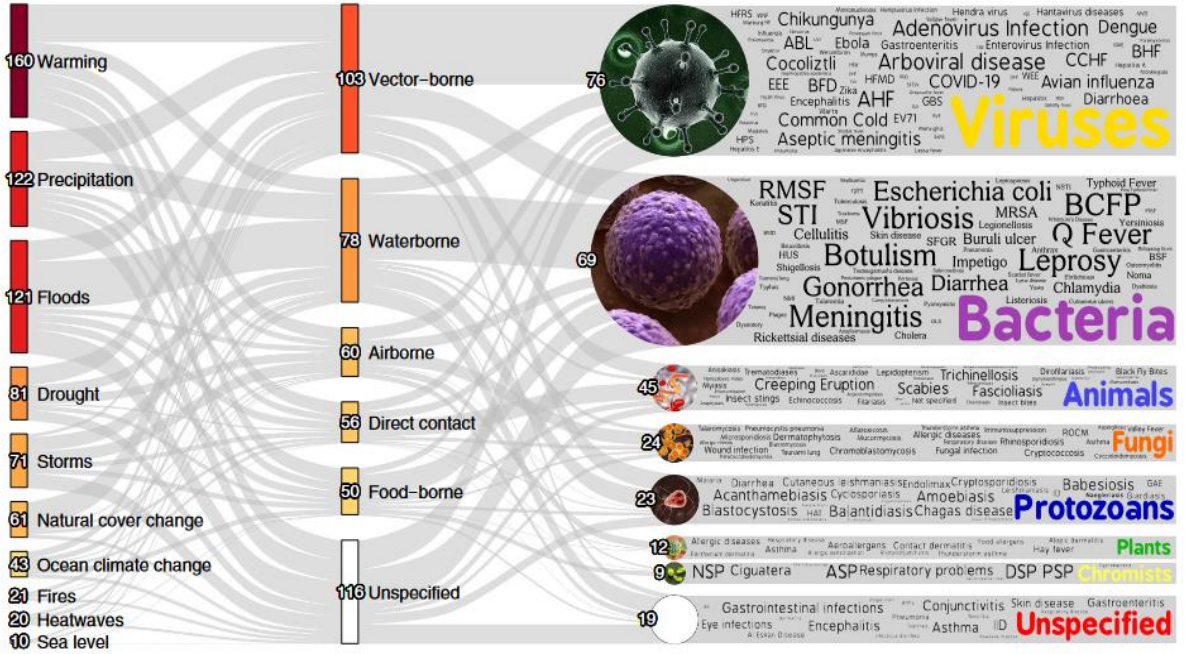

Fig. 3 | Pathogenic diseases aggravated by climatic hazards. Here we display the pathways in which climatic hazards, via specific transmission types, result in the aggravation of specific pathogenic diseases. The thickness of the lines is proportional to the number of unique pathogenic diseases. The colour gradient indicates the proportional quantity of diseases, with darker colours representing larger quantities and lighter colours representing fewer. Numbers at each node are indicative of the number of unique pathogenic diseases (caveats in Supplementary Information 1). An interactive display of the pathways and the underlying data are available at https://camilo-mora.github.io/Diseases/. Several disease names were abbreviated to optimize the use of space in the figure; their extended names are provided in Supplementary Table 1. Credits: word clouds, WordArt.com; bacteria, Wikimedia Commons (www.scientificanimations.com); other images, istockphoto.

INFECTIOUS DISEASES, AMR AND GLOBAL COOPERATION

nature COMMUNICATIONS

ARTICLE

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Global monitoring of antimicrobial resistance based on metagenomics analyses of urban sewage

Rene S. Hendriksen[1], Patrick Munk[1], Patrick Njage[1], Bram van Bunnik[2], Luke McNally[3], Oksana Lukjancenko[1], Timo Röder[1], David Nieuwenhuijse[4], Susanne Karlsmose Pedersen[1], Jette Kjeldgaard[1], Rolf S. Kaas[1], Philip Thomas Lanken Conradsen Clausen[1], Josef Korbinian Vogt[1], Pimlapas Leekitcharoenphon[1], Milou G.M. van de Schans[5], Tina Zuidema[5], Ana Maria de Roda Husman[6], Simon Rasmussen[7], Bent Petersen[7], The Global Sewage Surveillance project consortium, Thomas Sicheritz-Ponten[9], Heike Schmitt[6], Jorge Raul Matheu Alv, Ole Lund[7], Tine Hald[1], Mark Woolhouse[2], Marion P. Koopmans[4], I, Frank M. Aarestrup[1]

Antimicrobial resistance (AMR) is a serious threat to global public health, representative data on AMR for healthy human populations is difficult. Here, genomic analysis of untreated sewage to characterize the bacterial resistome f 60 countries. We find systematic differences in abundance and diversity between Europe/North-America/Oceania and Africa/Asia/South-America. use data and bacterial taxonomy only explains a minor part of the AMR va observe. We find no evidence for cross-selection between antimicrobial class of air travel between sites. However, AMR gene abundance strongly correla economic, health and environmental factors, which we use to predict AMR ge in all countries in the world. Our findings suggest that global AMR gene abundance vary by region, and that improving sanitation and health could pote global burden of AMR. We propose metagenomic analysis of sewage a acceptable and economically feasible approach for continuous global surveil diction of AMR.

[1] National Food Institute, Technical University of Denmark, Kgs. Lyngby 2800, Denmark. [2] Ush [3] Centre for Synthetic and Systems Biology, School of Biological Sciences, University of Edinbu Center, Rotterdam 3015, The Netherlands. [5] RIKILT Wageningen University and Research, Wa Health and the Environment (RIVM), Bilthoven 3721, The Netherlands. [7] Department of Bio a Lyngby 2800, Denmark. [8] European Molecular Biology Laboratory, European Bioinformatics I Omics-Driven Computational Biodiscovery, AIMST University, Kedah 08100, Malaysia. [10] Wo of consortium members appears at the end of the paper. Correspondence and requests for m dk)

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Setting a baseline for global urban virome surveillance in sewage

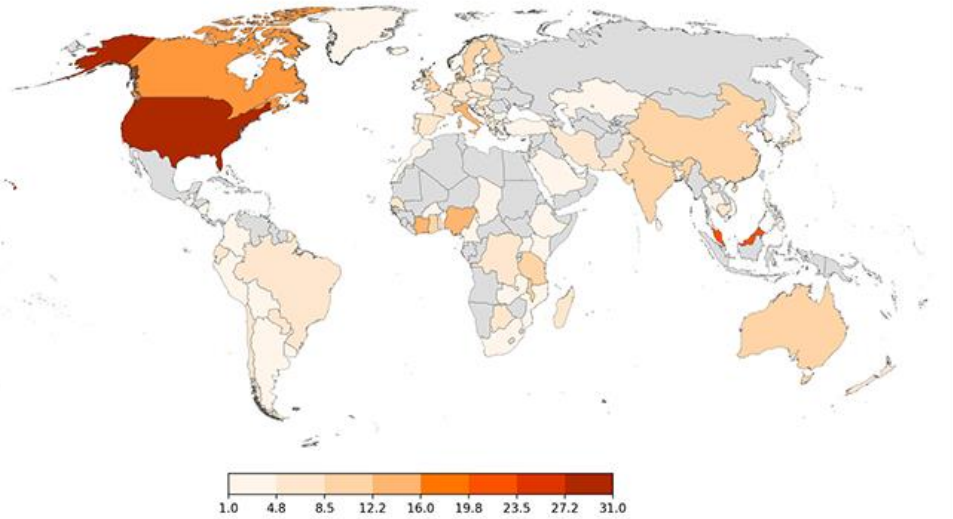
David F. Nieuwenhuijse[1,82], Bas B. Oude Munnink[1,82], My V. T. Phan[1,82], the Global Sewage Surveillance project consortium*, Patrick Munk[2], Shweta Venkatakrishnan[1], Frank M. Aarestrup[2], Matthew Cotten[1] & Marion P. G. Koopmans[1]✉

The rapid development of megacities, and their growing connectedness across the world is becoming a distinct driver for emerging disease outbreaks. Early detection of unusual disease emergence and spread should therefore include such cities as part of risk-based surveillance. A catch-all metagenomic sequencing approach of urban sewage could potentially provide an unbiased insight into the dynamic of viral pathogens circulating in a community irrespective of access to care, a potential which already has been proven for the surveillance of poliovirus. Here, we present a detailed characterization of sewage viromes from a snapshot of 81 high density urban areas across the globe, including in-depth assessment of potential biases, as a proof of concept for catch-all viral pathogen surveillance. We sho the ability to detect a wide range of viruses and geographical and seasonal differences for specific viral groups. Our findings offer a cross-sectional baseline for further research in viral surveillance from urban sewage samples and place previous studies in a global perspective.

The increasing connectivity of the modern world, changing demographics, and climate change increase th potential for novel and known viral pathogens to emerge and rapidly spread in new and unexpected areas, a could be seen during the emergence and global threat of Ebola virus in recent outbreaks[1]. Early detection c ruling out of high impact (emerging) infections as causes of disease is a hallmark of preparedness, but researc in response to recent outbreaks of Ebola, Zika and yellow fever has shown that these pathogens circulated fo extended periods of time before being recognized, leading to costly delays in public health response[2–5]. One c the key challenges is how to prioritize local investments in detection capacity, given the diversity of emergin diseases, the unpredictable nature of outbreaks, and the limited resources available for outbreak prepared ness. Understandably, surveillance of infectious diseases mainly targets common conditions and is scaled up i response to the emergence of pathogens and in particular disease outbreaks, rather than the costlier approac of broad range testing for any relevant infectious disease. The changing dynamics of infectious diseases relate to global change, however, require rethinking of this model for public health preparedness, as incidence-base surveillance provides a fragmented and limited scope of which pathogens are circulating in the general popula tion, particularly in low resource settings where access to healthcare and laboratory diagnostics is restricted[6]. Therefore, in its reorganization in response to the West African Ebola outbreak, the World Health Organizatio has launched the term "Disease X" to call for novel ideas for preparedness to unpredictable disease outbreaks Thus, there is a need for novel approaches to viral surveillance providing a broader and less biased insight int the circulation of viral pathogens to supplement the more targeted surveillance. Genomic epidemiology usin real-time pathogen sequencing has become part of the routine toolbox for outbreak tracking once the cause c the outbreak is known[8,10]. In addition, metagenomic sequencing has been put forward as a potential catch-a surveillance tool, but the step from research to routine implementation is extremely challenging[11,12], and thu careful validation is needed to avoid overpromise and wasting of resources.

Here, we set out to explore the potential use of metagenomic sequencing of urban sewage as an add-o strategy for global disease preparedness. One key driver of emergence is the amplification of rare zoonotic an vector-borne diseases in densely populated regions where infrastructure needs are outpaced by rapid urba developments. This leads to the formation of slums, favorable conditions for viral disease vectors, disparit in access to clean water, sanitation and healthcare, and an increase in close human-animal interaction due t deforestation[13,14]. The advantage of using sewage-based surveillance is that it represents the entire population c

[1] Viroscience Department, Erasmus Medical Center, Rotterdam, The Netherlands. [2] National Food Institute Technical University of Denmark, Lyngby, Denmark. [82] These authors contributed equally: David F. Nieuwenhuijse Bas B. Oude Munnink and My V. T. Phan. * A comprehensive list of consortium members appears at the end of the paper. ✉email: m.koopmans@erasmusmc.nl



SCIENTIFIC REPORT

efsa JOURNAL

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Coordinated surveillance system under the One Health approach for cross-border pathogens that threaten the Union – options for sustainable surveillance strategies for priority pathogens

European Food Safety Authority (EFSA),
John Berezowski, Katinka De Balogh, Fernanda C Dórea, Simon Ruegg, Alessandro Broglia, Gabriele Zancanaro and Andrea Gervelmeyer

A–Design of an EU coordinated surveillance system under the One Health approach for cross-border zoonotic pathogens that may threaten the Union

B–Collect Surveillance Data and Identify the Risks

C–Stakeholder Involvement….

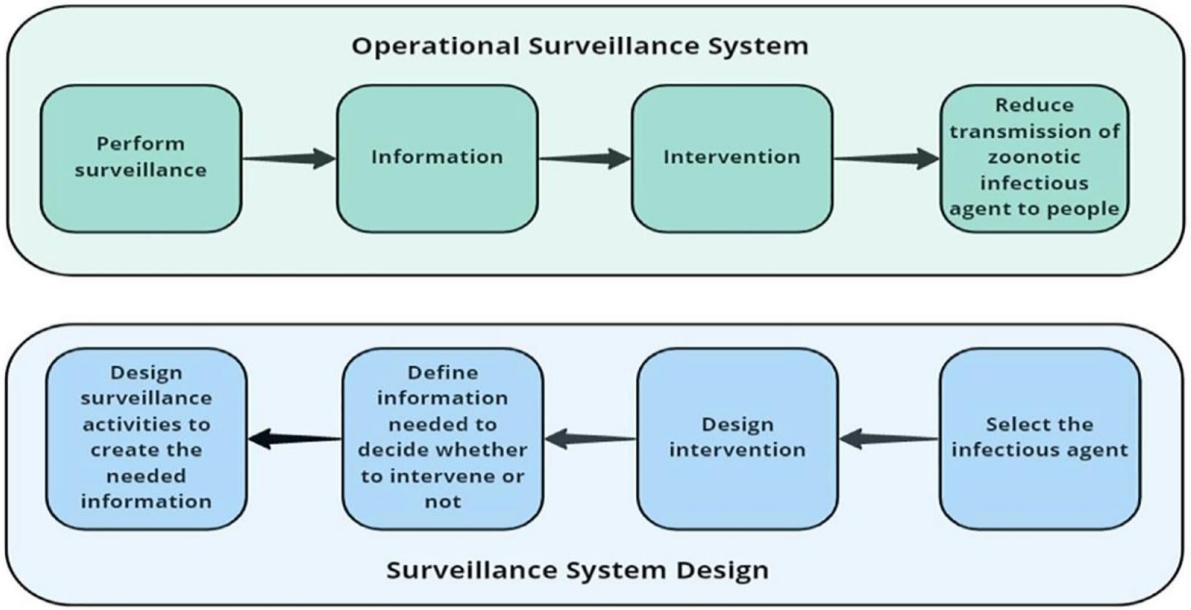

Figure 1: Sequence of steps in an operational surveillance system and the steps involved in the design of a surveillance system

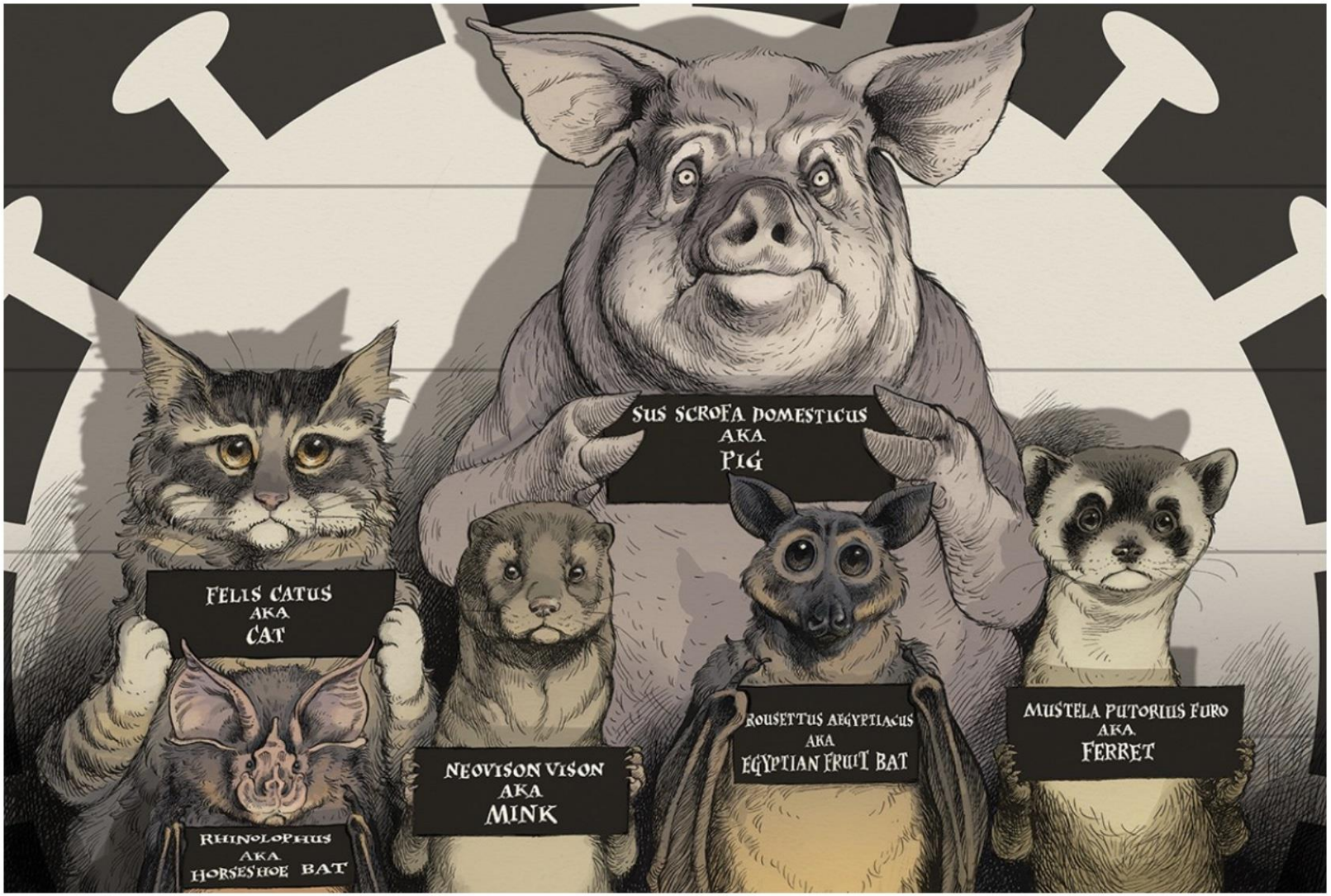

Illustration by David Parkins

"…During COVID-19 pandemic…"

*"**Surveillance efforts are becoming more unified.** The OIE (WOAH), the WHO and the US Centers for Disease Control and Prevention have all published common guidance on surveillance…."*

(Mallapaty S. et al. *Nature*. 591, 2021)