BIOR
PĀRTIKAS DROŠĪBAS, DZĪVNIEKU VESELĪBAS
UN VIDES ZINĀTNISKAIS INSTITŪTS

«VIENAS VESELĪBAS» KONCEPCIJA ZINĀTNĒ

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LZA un LLMZA īstenais loceklis
LBTU Veterinārmedicīnas fakultātes profesors
Eiropas Pārtikas nekaitīguma iestādes *(European Food Safety Authority, EFSA)* valdes priekšsēdētājs

*“Between **animal** and **human medicine** there is no dividing line nor should there be.*
*The object is different but the experience obtained constitutes the basis of **all medicine**.”*

Rudolf Virchow (1958)

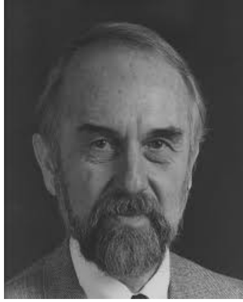
VĒSTURISKAIS KONTEKSTS

“Comparative medicine” (*end of 19th century)*

“One Medicine” (*Calvin Schwabe, 20th century)*

“One Medicine” ➔ **“One Health”**

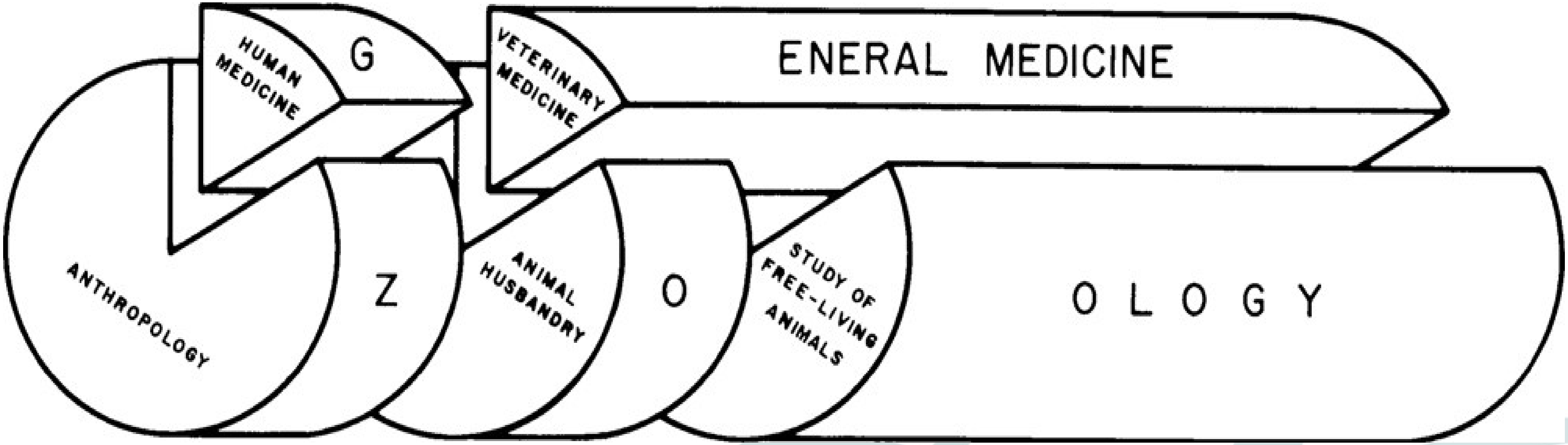
“Veterinary Public Health”



IN MEMORIAM

Calvin W. Schwabe
Professor Emeritus of Veterinary Epidemiology
Davis
1927 – 2006

Calvin W. Schwabe, widely known as the father of veterinary epidemiology, died in his home on June 24, 2006. Truly a Renaissance Man, in a 52-year career he made important scholarly contributions in a broad array of subjects including epidemiology, diseases of animals transmissible to people, interactions of veterinary and human medicine, parasitic zoonoses and their control, tropical health, public health practice, livestock health in pastoral societies, ancient origins of human and veterinary medicine and the philosophy of science. A member of the faculty of the UC Davis School of Veterinary Medicine, Cal also was one of eight founding faculty of the School of Medicine.



Calvin Schwabe’s “one medicine” as general medicine of humans, domestic and free-living animals (1984)

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],

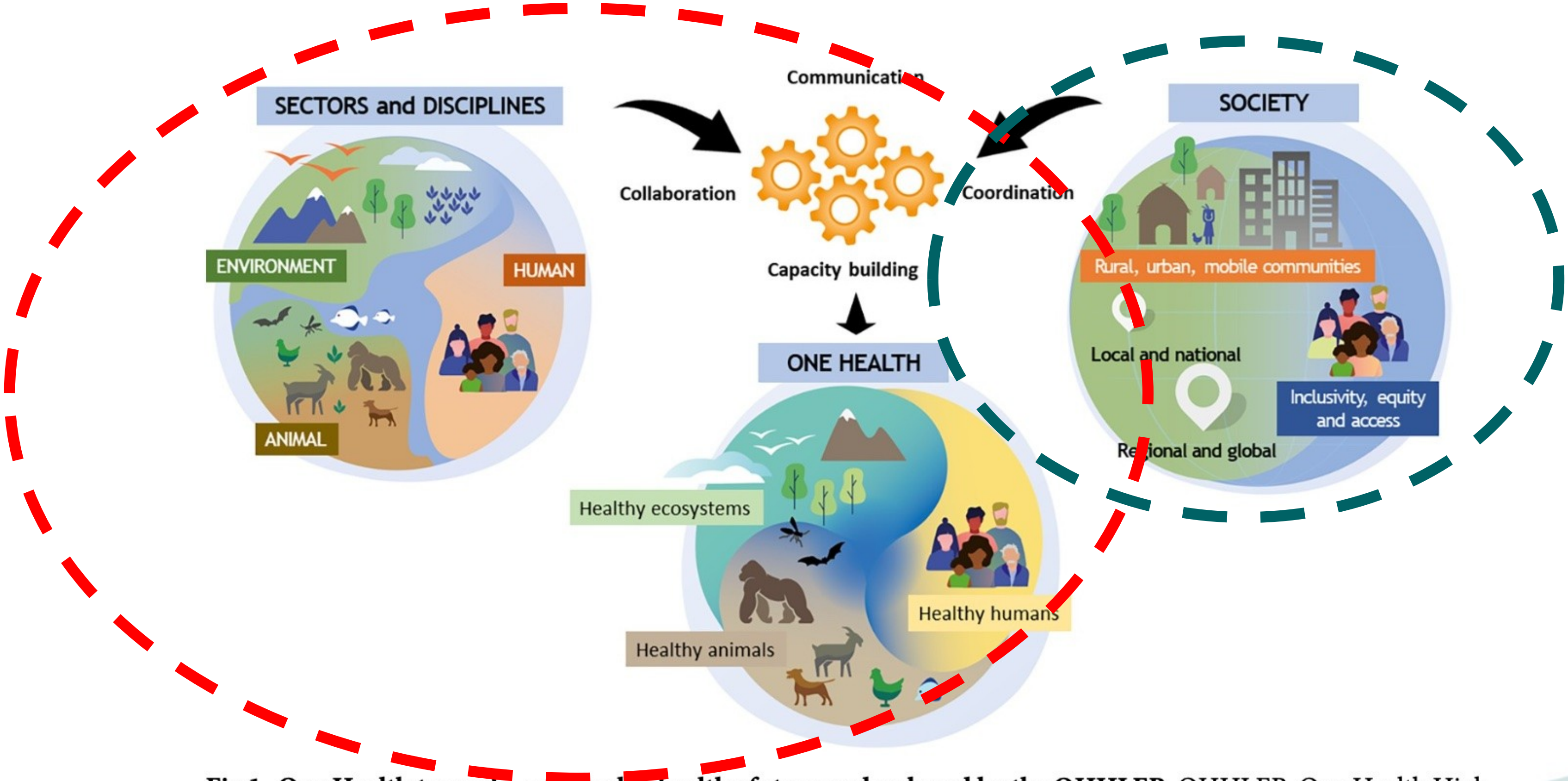
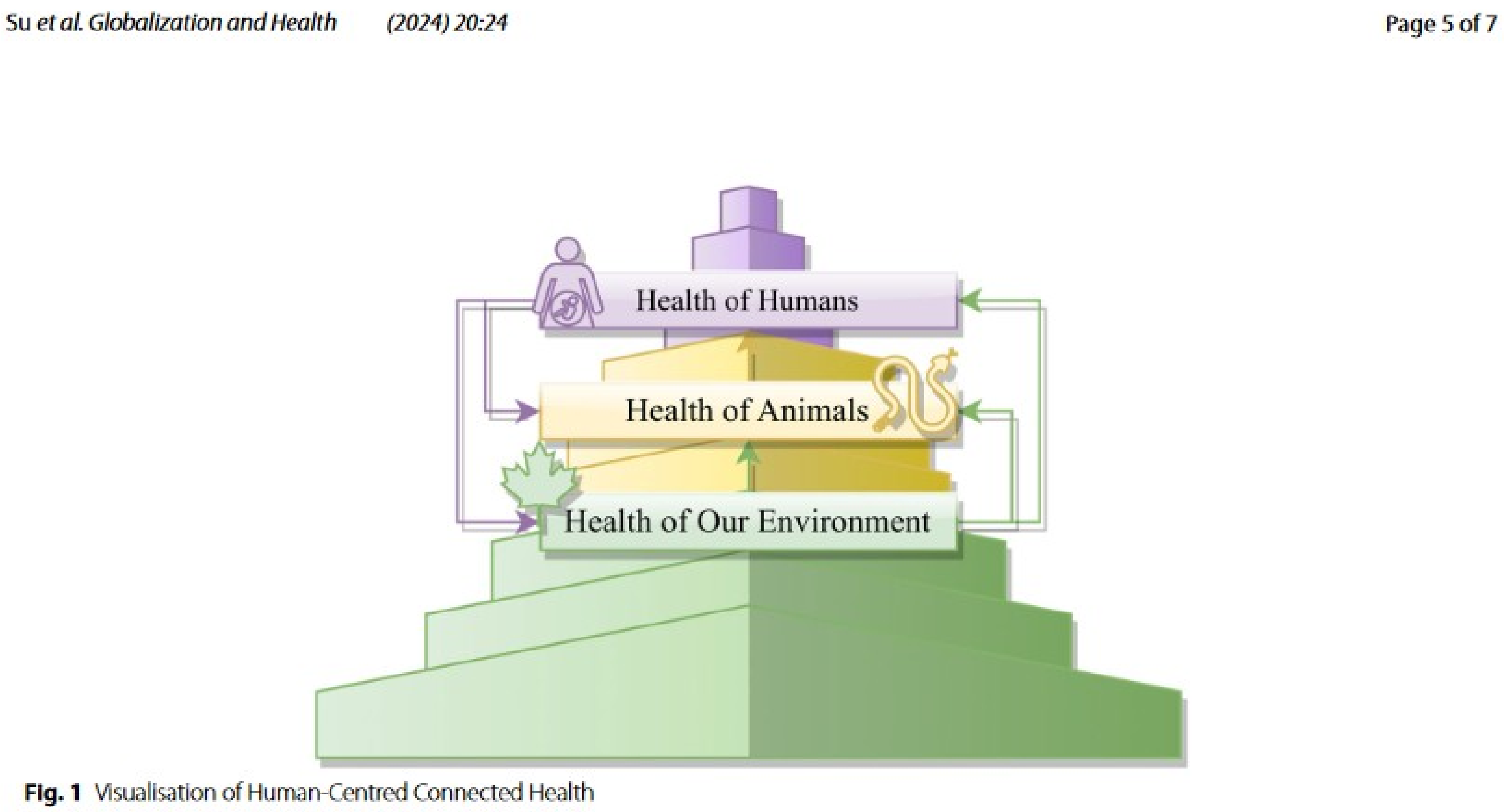


Fig 1. One Health toward a sustainable healthy future as developed by the OHHLEP. OHHLEP, One Health High-Level Expert Panel.

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

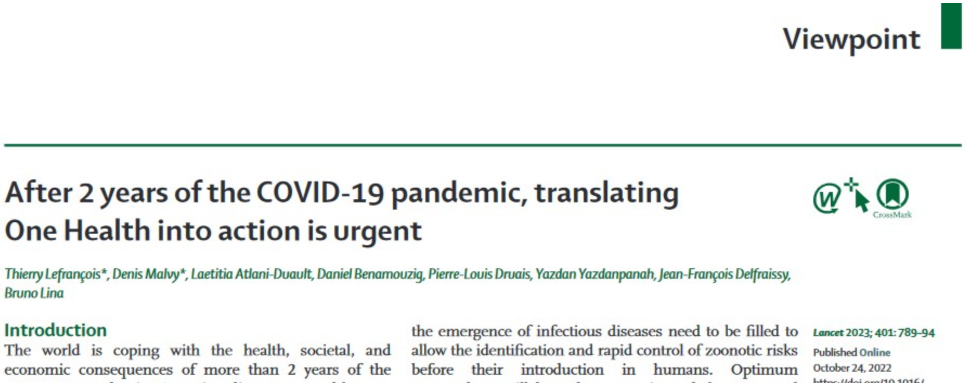
Adapted from WHO, OHHLEP et al. 2023



Su *et al. Globalization and Health* (2024) 20:24 Page 5 of 7

Fig. 1 Visualisation of Human-Centred Connected Health

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

Lancet 2023; 401: 789–94

Published Online

October 24, 2022

Points to be addressed:

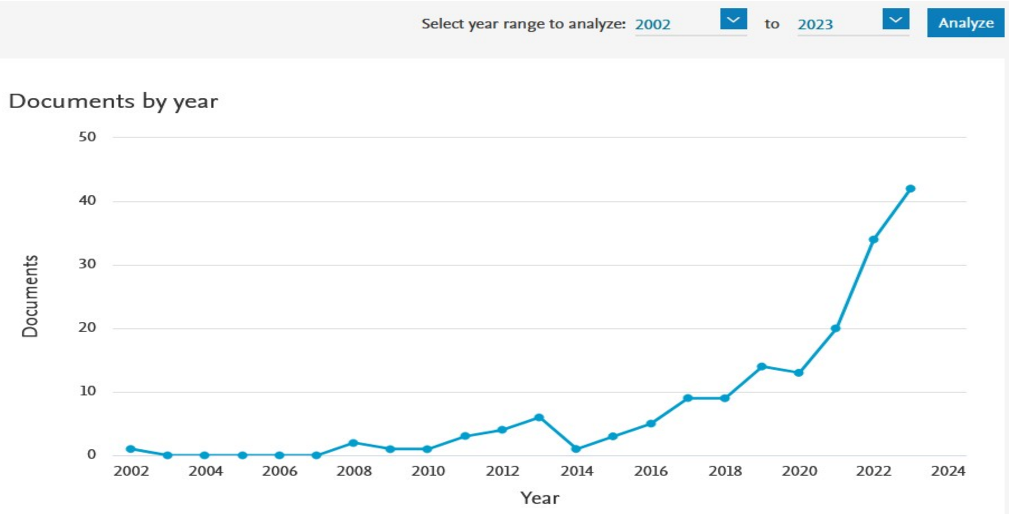
-developing **an ambitious roadmap** for each step of pandemic (outbreak) crisis;

- developing One Health **action plans;**

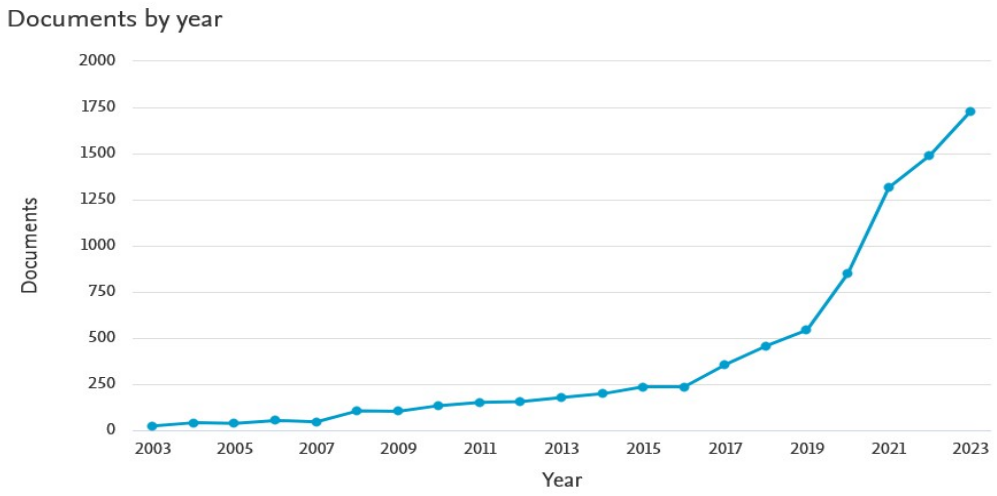
- improving surveillance and prevention by reinforcing both upstream and operational **research**;

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

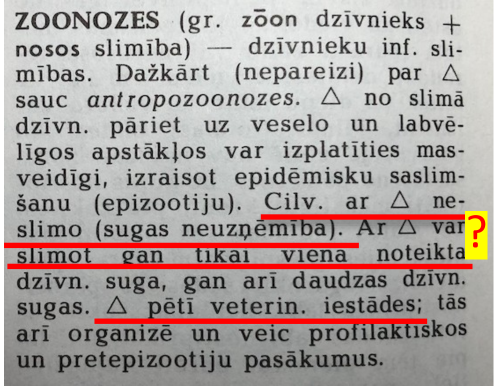
- ensuring adequate **education and training** of One Health;



Select year range to analyze: 2002 to 2023

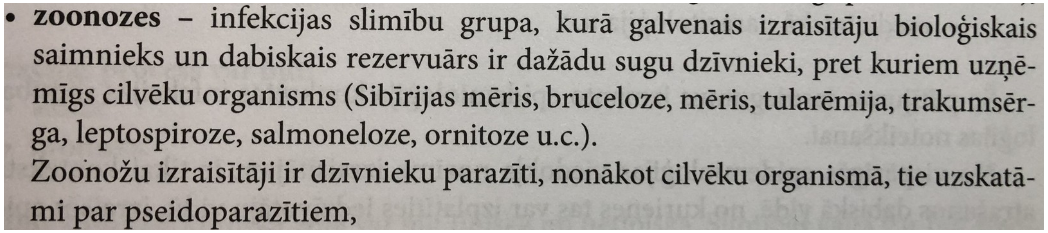


ZOONOZES … (REVERSĀS ZOONOZES)



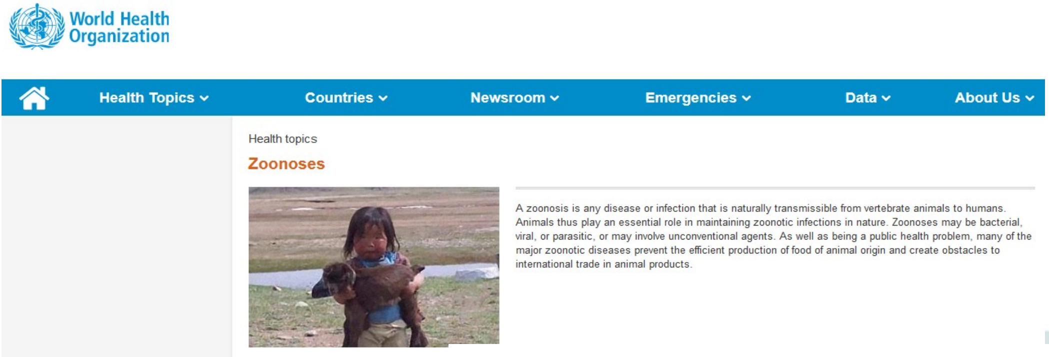
ZOONOZES (gr. zōon dzīvnieks + nosos slimība) — dzīvnieku inf. slimības. Dažkārt (nepareizi) par △ sauc *antropozoonozes.* △ no slimā dzīvn. pāriet uz veselo un labvēlīgos apstākļos var izplatīties masveidīgi, izraisot epidēmisku saslimšanu (epizootiju). Cilv. ar △ neslimo (sugas neuzņēmība). Ar △ var? slimot gan tikai viena noteikta dzīvn. suga, gan arī daudzas dzīvn. sugas. △ pēti veterin. iestādes; tās arī organizē un veic profilaktiskos un pretepizootiju pasākumus.

Populārā medicīnas enciklopēdija, 1984



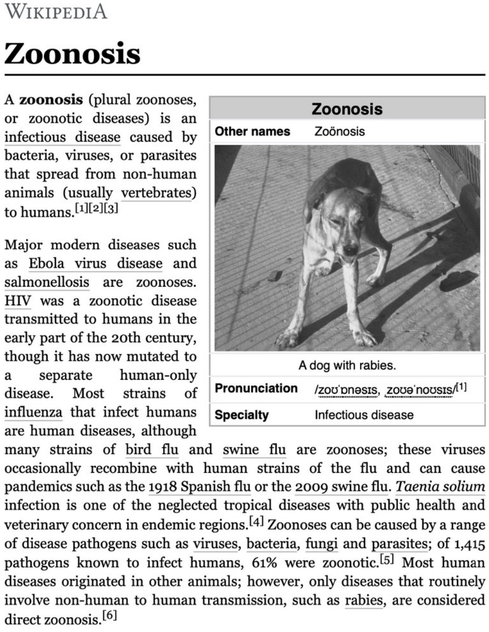
- **zoonozes** – infekcijas slimību grupa, kurā galvenais izraisītāju bioloģiskais saimnieks un dabiskais rezervuārs ir dažādu sugu dzīvnieki, pret kuriem uzņēmīgs cilvēku organisms (Sibīrijas mēris, bruceloze, mēris, tularēmija, trakumsērga, leptospiroze, salmoneloze, ornitoze u.c.). Zoonožu izraisītāji ir dzīvnieku parazīti, nonākot cilvēku organismā, tie uzskatāmi par pseidoparazītiem,

Brila A. Infekcijas slimību epidemioloģija. Nacionālais apgāds, 2009



Zoonoses

A zoonosis is any disease or infection that is naturally transmissible from vertebrate animals to humans. Animals thus play an essential role in maintaining zoonotic infections in nature. Zoonoses may be bacterial, viral, or parasitic, or may involve unconventional agents. As well as being a public health problem, many of the major zoonotic diseases prevent the efficient production of food of animal origin and create obstacles to international trade in animal products.



Zoonosis

A **zoonosis** (plural zoonoses, or zoonotic diseases) is an infectious disease caused by bacteria, viruses, or parasites that spread from non-human animals (usually vertebrates) to humans.[1][2][3]

Major modern diseases such as Ebola virus disease and salmonellosis are zoonoses. HIV was a zoonotic disease transmitted to humans in the early part of the 20th century, though it has now mutated to a separate human-only disease. Most strains of influenza that infect humans are human diseases, although many strains of bird flu and swine flu are zoonoses; these viruses occasionally recombine with human strains of the flu and can cause pandemics such as the 1918 Spanish flu or the 2009 swine flu. *Taenia solium* infection is one of the neglected tropical diseases with public health and veterinary concern in endemic regions.[4] Zoonoses can be caused by a range of disease pathogens such as viruses, bacteria, fungi and parasites; of 1,415 pathogens known to infect humans, 61% were zoonotic.[5] Most human diseases originated in other animals; however, only diseases that routinely involve non-human to human transmission, such as rabies, are considered direct zoonosis.[6]

Zoonosis	
Other names	Zoönosis
A dog with rabies.	
Pronunciation	/zoʊˈɒnəsɪs, zoʊəˈnoʊsɪs/[1]
Specialty	Infectious disease

LV "Epidemioloģiskās drošības likums":

zoonoze — infekcijas slimība, ar kuru slimo gan cilvēki, gan dzīvnieki;

Food and Agriculture Organization of the United Nations

WORLD ORGANISATION FOR ANIMAL HEALTH

World Health Organization

Zoonotic diseases (zoonoses): Infectious diseases that can be spread between animals and humans; can be spread by food, water, fomites, or vectors.

Latvijas ārsts

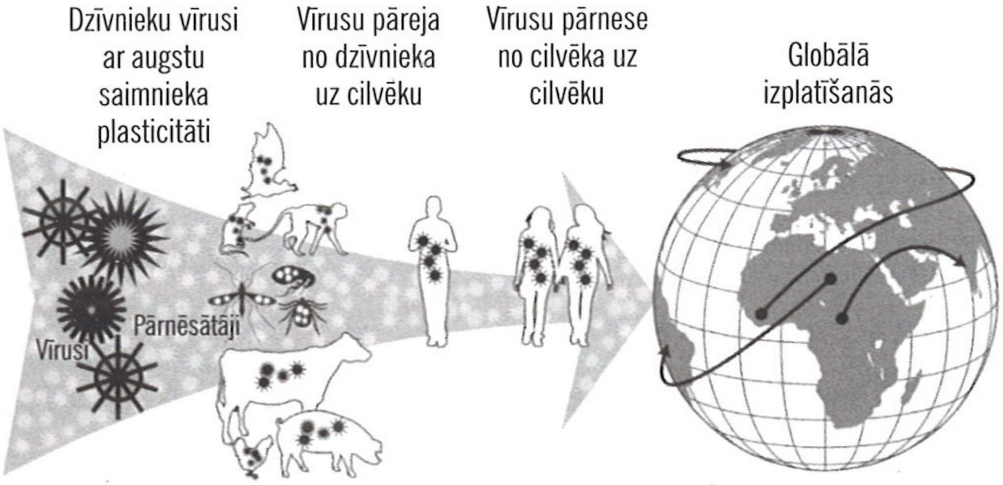
Zoonozes – izaicinājums sabiedrības veselībai

Aivars Bērziņš, *Dr.med.vet., Ph. D.*
Pārtikas drošības, dzīvnieku veselības un vides zinātniskā institūta „BIOR” direktors.
LLU Veterinārmedicīnas fakultātes profesors

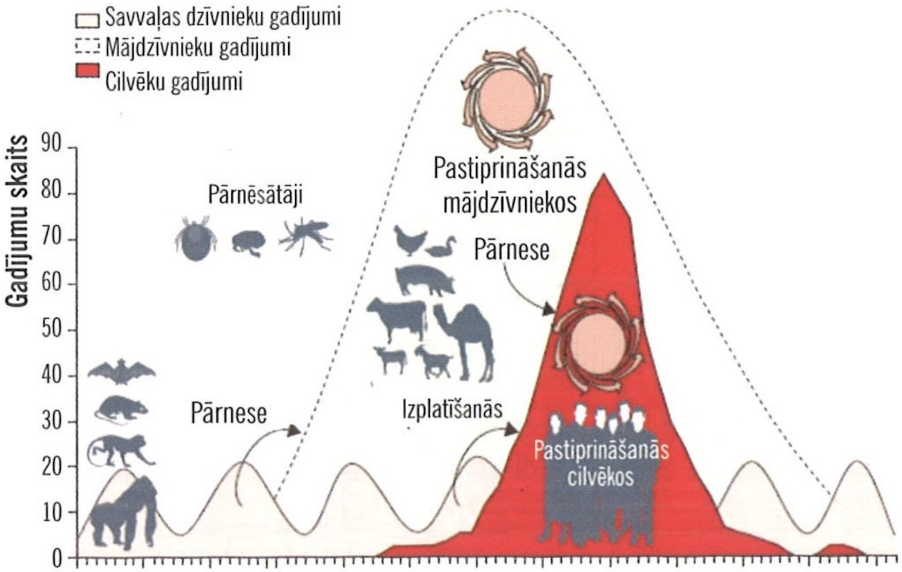
Zoonožu definīcija pēdējo 40 gadu laikā ir būtiski pilnveidota un pielāgota mūsdienu izaicinājumiem, ko pauž Pasaules Veselības organizācija (PVO), Pasaules Dzīvnieku veselības organizācija (O.I.E.) un Eiropas Komisija „zoonožu direktīvā” (2003/99/

mieļi u.c.) [6,7]. Šie ir pēd
gākie piemēri, kur infekciju
atstājuši liela mēroga negat

1. attēls **Zoonotisko vīrusu pandēmijas potenciāls.** Adaptēts no: *Johnson C.K. et al. 2015. Spillover and pandemic properties of zoonotic viruses with high host plasticity. Nature Scientific Reports. 5:14830*



2. attēls **Infekciju pārneses cikli no savvaļas dzīvniekiem uz mājdzīvniekiem un cilvēkiem.** Adaptēts no: *The Lancet, Vol 380 December 1, 2012*



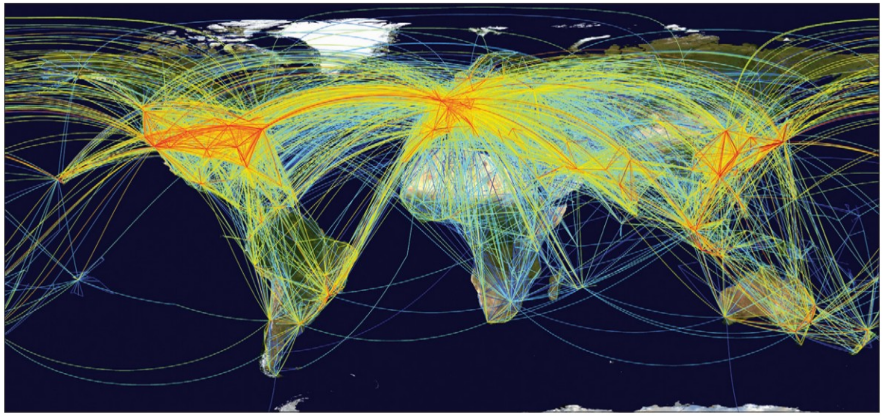
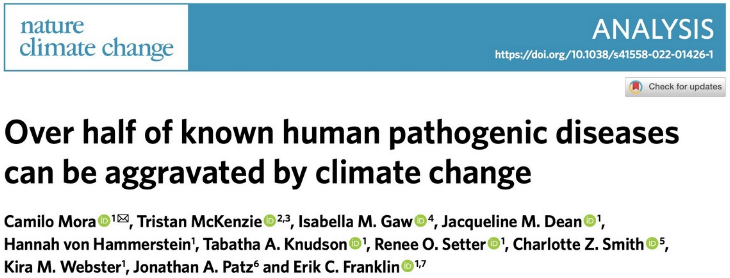


Figure 2: **The global aviation network**
Lines show direct links between airports, and the colour indicates passenger capacity in people per day (thousands [red]; hundreds [yellow]; tens [blue]). Routes linking regions at similar latitudes (in the northern or southern hemisphere) represent pathways that pathogens can move along to reach novel regions. Notably, air traffic to most places in Africa, regions of South America, and parts of central Asia is low. If travel increases in these regions, additional introductions of vector-borne pathogens are probable. Adapted from Hufnagal and colleagues.[30]

(Kilpatrick A.M., et al. 2012. *Lancet.* 380:1946-55)



nature climate change

ANALYSIS

https://doi.org/10.1038/s41558-022-01426-1

Check for updates

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]

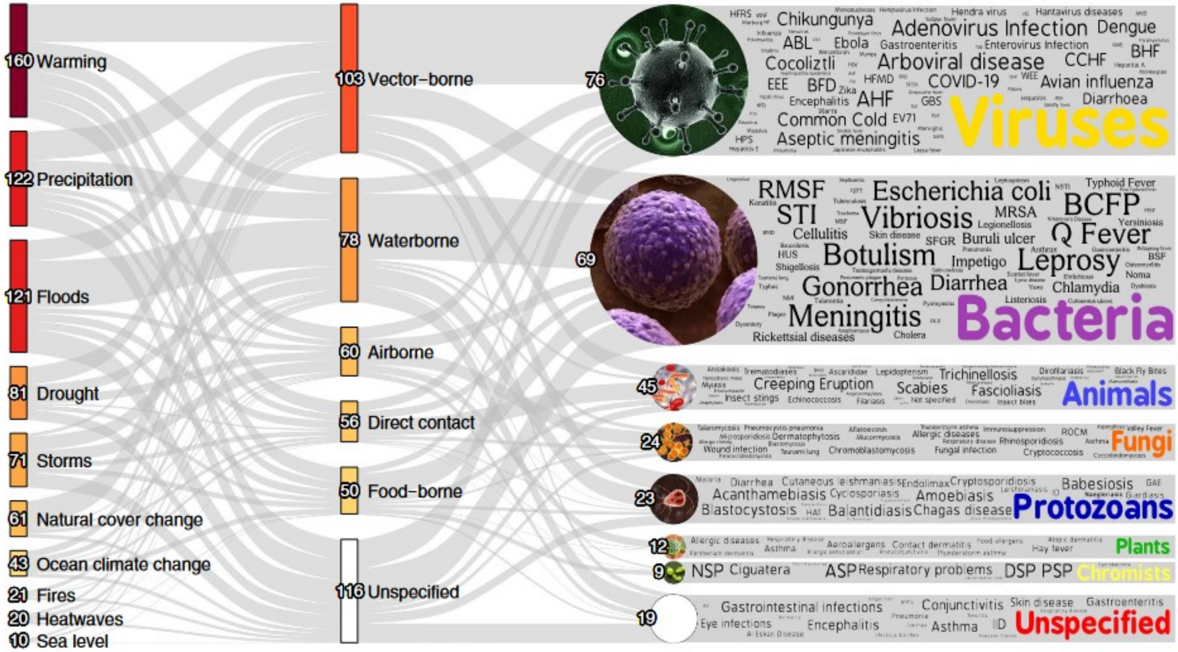
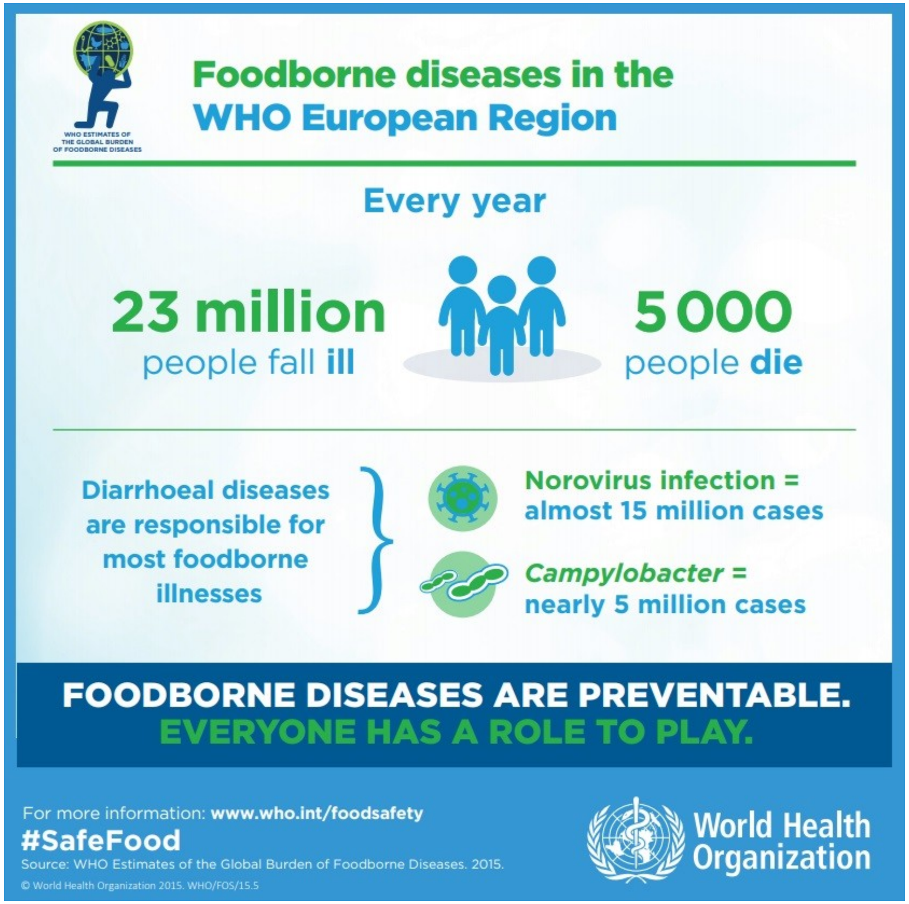


Fig. 3 | Pathogenic diseases aggravated by climatic hazards. Here we display the pathways in which climatic hazards, via specific transmission types, result in the aggravation of specific pathogenic diseases. The thickness of the lines is proportional to the number of unique pathogenic diseases. The 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.

AMR

PĀRTIKAS INFEKCIJAS UN AMR (PĀRTIKAS IZRAISĪTAS SASLIMŠANAS)



WHO ESTIMATES OF THE GLOBAL BURDEN OF FOODBORNE DISEASES

Foodborne diseases in the WHO European Region

Every year

23 million people fall **ill**

5 000 people **die**

Diarrhoeal diseases are responsible for most foodborne illnesses

- **Norovirus infection = almost 15 million cases**
- ***Campylobacter* = nearly 5 million cases**

FOODBORNE DISEASES ARE PREVENTABLE.
EVERYONE HAS A ROLE TO PLAY.

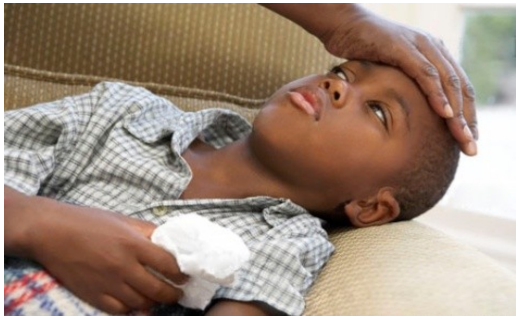
For more information: **www.who.int/foodsafety**

#SafeFood

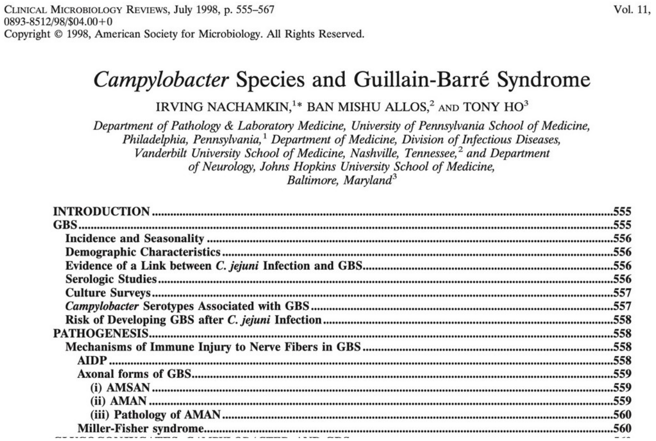
Source: WHO Estimates of the Global Burden of Foodborne Diseases. 2015.

© World Health Organization 2015. WHO/FOS/15.5

World Health Organization



https://www.unep.org/explore-topics/chemicals-waste/what-we-do/emerging-issues/antimicrobial-resistance-global-threat

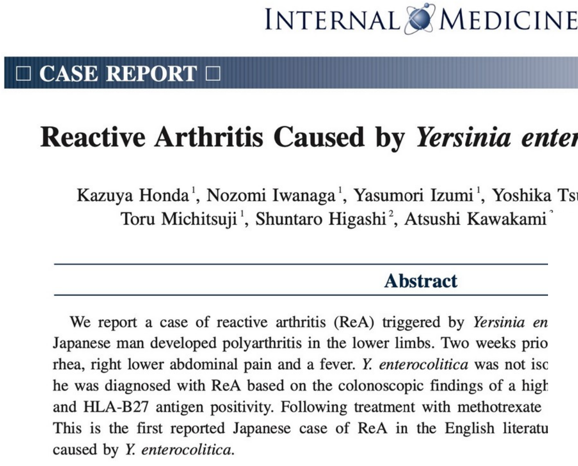


Clinical Microbiology Reviews, July 1998, p. 555–567 Vol. 11,
0893-8512/98/$04.00+0

Campylobacter Species and Guillain-Barré Syndrome

IRVING NACHAMKIN,[1]* BAN MISHU ALLOS,[2] AND TONY HO[3]

Department of Pathology & Laboratory Medicine, University of Pennsylvania School of Medicine,
Philadelphia, Pennsylvania,[1] *Department of Medicine, Division of Infectious Diseases,*
Vanderbilt University School of Medicine, Nashville, Tennessee,[2] *and Department*
of Neurology, Johns Hopkins University School of Medicine,
Baltimore, Maryland[3]



INTERNAL MEDICINE

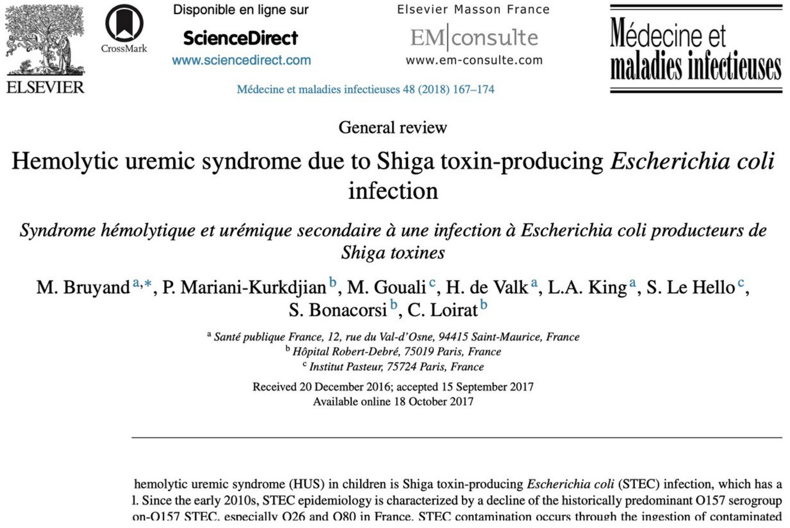
□ CASE REPORT □

Reactive Arthritis Caused by *Yersinia enterocolitica* Enteritis

Kazuya Honda[1], Nozomi Iwanaga[1], Yasumori Izumi[1], Yoshika Tsuji[1], Chieko Kawahara[1],
Toru Michitsuji[1], Shuntaro Higashi[2], Atsushi Kawakami

Abstract

We report a case of reactive arthritis (ReA) triggered by *Yersinia en*
Japanese man developed polyarthritis in the lower limbs. Two weeks prio
rhea, right lower abdominal pain and a fever. *Y. enterocolitica* was not isc
he was diagnosed with ReA based on the colonoscopic findings of a high
and HLA-B27 antigen positivity. Following treatment with methotrexate
This is the first reported Japanese case of ReA in the English literatu
caused by *Y. enterocolitica.*



ELSEVIER CrossMark Disponible en ligne sur ScienceDirect www.sciencedirect.com Elsevier Masson France EM|consulte www.em-consulte.com Médecine et maladies infectieuses
Médecine et maladies infectieuses 48 (2018) 167–174

General review

Hemolytic uremic syndrome due to Shiga toxin-producing *Escherichia coli* infection

Syndrome hémolytique et urémique secondaire à une infection à Escherichia coli producteurs de Shiga toxines

M. Bruyand[a,*], P. Mariani-Kurkdjian[b], M. Gouali[c], H. de Valk[a], L.A. King[a], S. Le Hello[c],
S. Bonacorsi[b], C. Loirat[b]

[a] *Santé publique France, 12, rue du Val-d'Osne, 94415 Saint-Maurice, France*
[b] *Hôpital Robert-Debré, 75019 Paris, France*
[c] *Institut Pasteur, 75724 Paris, France*

Received 20 December 2016; accepted 15 September 2017
Available online 18 October 2017

hemolytic uremic syndrome (HUS) in children is Shiga toxin-producing *Escherichia coli* (STEC) infection, which has a
l. Since the early 2010s, STEC epidemiology is characterized by a decline of the historically predominant O157 serogroup
on-O157 STEC, especially O26 and O80 in France. STEC contamination occurs through the ingestion of contaminated

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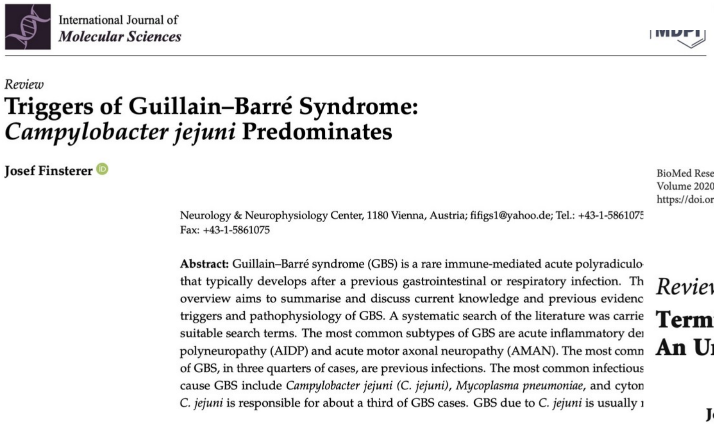

International Journal of
Molecular Sciences
MDPI

Review

Triggers of Guillain–Barré Syndrome: *Campylobacter jejuni* Predominates

Josef Finsterer

Neurology & Neurophysiology Center, 1180 Vienna, Austria; fifigs1@yahoo.de; Tel.: +43-1-5861075
Fax: +43-1-5861075

Abstract: Guillain–Barré syndrome (GBS) is a rare immune-mediated acute polyradiculo
that typically develops after a previous gastrointestinal or respiratory infection. Th
overview aims to summarise and discuss current knowledge and previous evidenc
triggers and pathophysiology of GBS. A systematic search of the literature was carrie
suitable search terms. The most common subtypes of GBS are acute inflammatory de
polyneuropathy (AIDP) and acute motor axonal neuropathy (AMAN). The most comm
of GBS, in three quarters of cases, are previous infections. The most common infectious
cause GBS include *Campylobacter jejuni (C. jejuni), Mycoplasma pneumoniae,* and cyton
C. jejuni is responsible for about a third of GBS cases. GBS due to *C. jejuni* is usually

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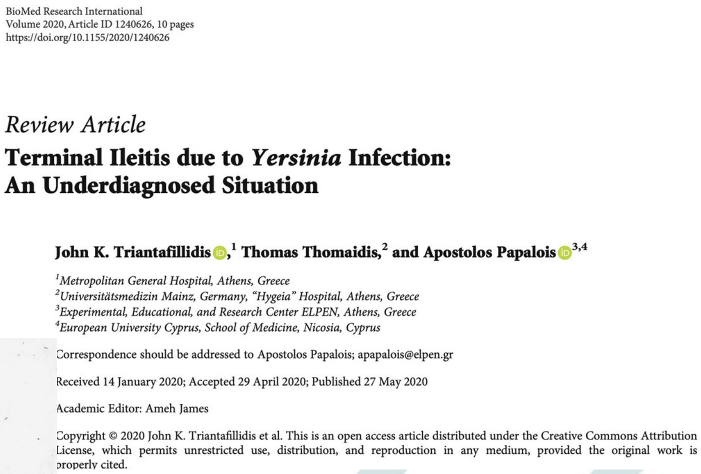


BioMed Research International
Volume 2020, Article ID 1240626, 10 pages
https://doi.org/10.1155/2020/1240626

Review Article

Terminal Ileitis due to *Yersinia* Infection: An Underdiagnosed Situation

John K. Triantafillidis,[1] **Thomas Thomaidis,**[2] **and Apostolos Papalois**[3,4]

[1]*Metropolitan General Hospital, Athens, Greece*
[2]*Universitätsmedizin Mainz, Germany, "Hygeia" Hospital, Athens, Greece*
[3]*Experimental, Educational, and Research Center ELPEN, Athens, Greece*
[4]*European University Cyprus, School of Medicine, Nicosia, Cyprus*

Correspondence should be addressed to Apostolos Papalois; apapalois@elpen.gr

Received 14 January 2020; Accepted 29 April 2020; Published 27 May 2020

Academic Editor: Ameh James

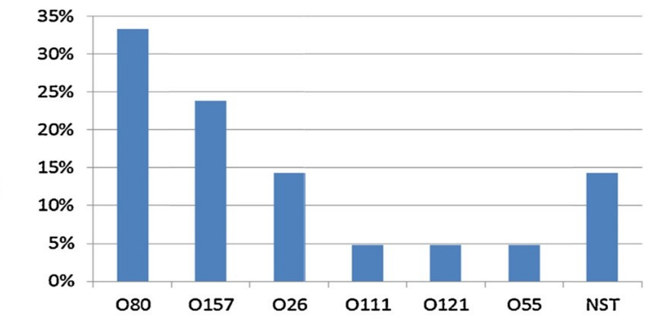
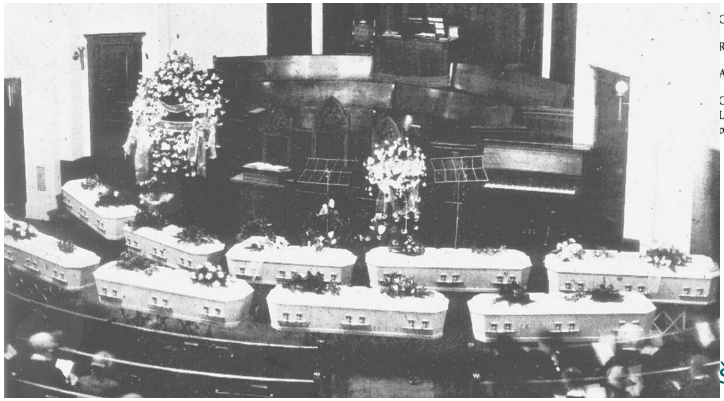
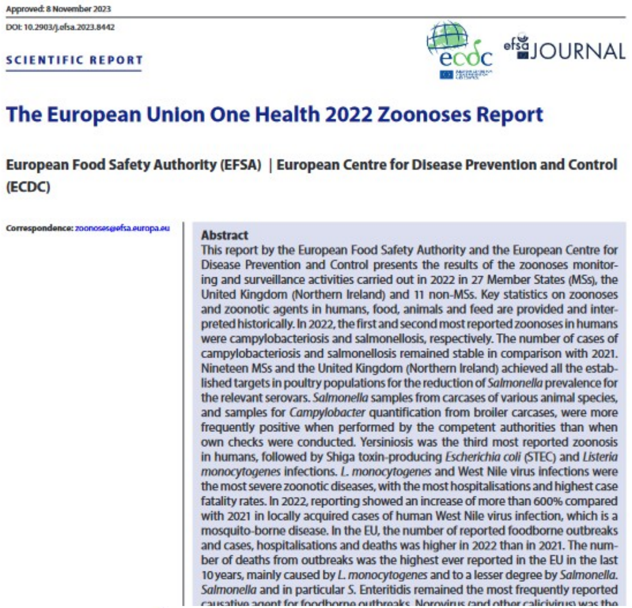


Fig. 1. Serogroups of STEC isolated in stool samples of children aged less than 15 years presenting with hemolytic uremic syndrome, France, 2015 [26]. NST: non-serotypable.





Approved: 8 November 2023
DOI: 10.2903/j.efsa.2023.8442

SCIENTIFIC REPORT

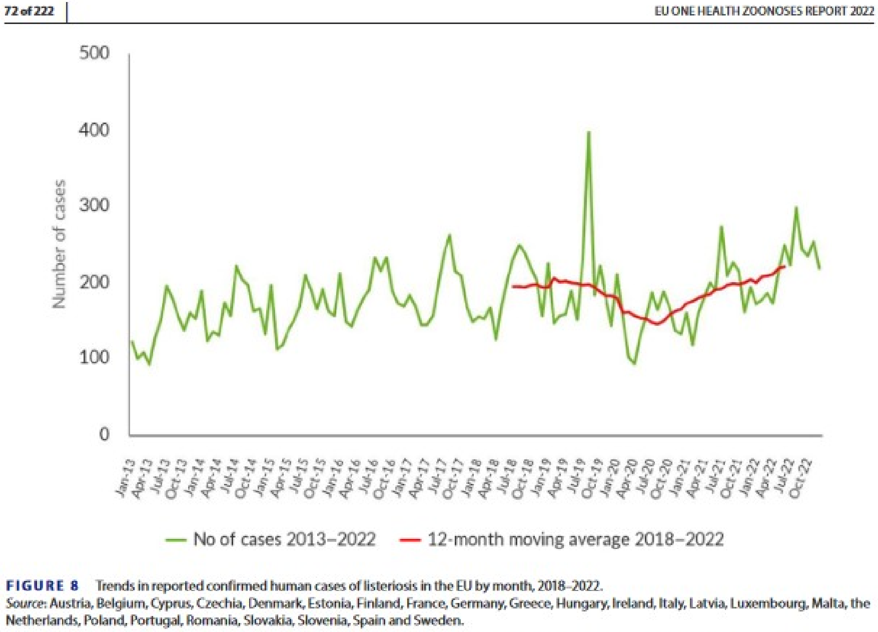
The European Union One Health 2022 Zoonoses Report

European Food Safety Authority (EFSA) | European Centre for Disease Prevention and Control (ECDC)

Correspondence: zoonoses@efsa.europa.eu

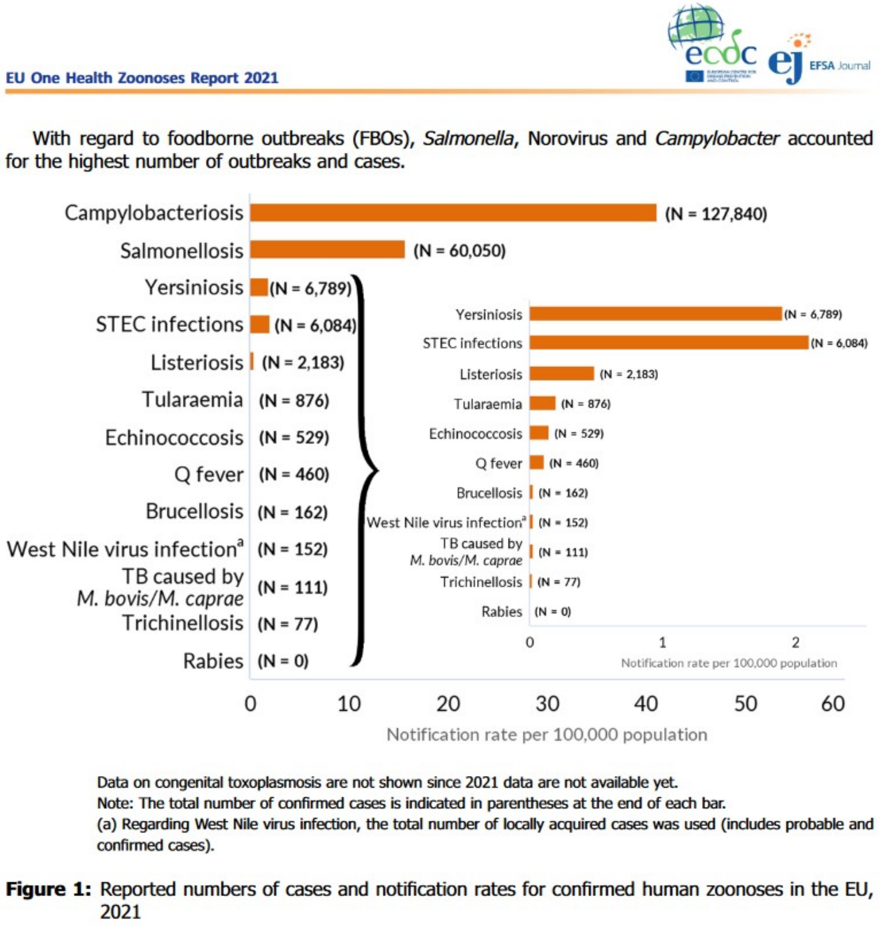
Abstract

This report by the European Food Safety Authority and the European Centre for Disease Prevention and Control presents the results of the zoonoses monitoring and surveillance activities carried out in 2022 in 27 Member States (MSs), the United Kingdom (Northern Ireland) and 11 non-MSs. Key statistics on zoonoses and zoonotic agents in humans, food, animals and feed are provided and interpreted historically. In 2022, the first and second most reported zoonoses in humans were campylobacteriosis and salmonellosis, respectively. The number of cases of campylobacteriosis and salmonellosis remained stable in comparison with 2021. Nineteen MSs and the United Kingdom (Northern Ireland) achieved all the established targets in poultry populations for the reduction of *Salmonella* prevalence for the relevant serovars. *Salmonella* samples from carcases of various animal species, and samples for *Campylobacter* quantification from broiler carcases, were more frequently positive when performed by the competent authorities than when own checks were conducted. Yersiniosis was the third most reported zoonosis in humans, followed by Shiga toxin-producing *Escherichia coli* (STEC) and *Listeria monocytogenes* infections. *L. monocytogenes* and West Nile virus infections were the most severe zoonotic diseases, with the most hospitalisations and highest case fatality rates. In 2022, reporting showed an increase of more than 600% compared with 2021 in locally acquired cases of human West Nile virus infection, which is a mosquito-borne disease. In the EU, the number of reported foodborne outbreaks and cases, hospitalisations and deaths was higher in 2022 than in 2021. The number of deaths from outbreaks was the highest ever reported in the EU in the last 10 years, mainly caused by *L. monocytogenes* and to a lesser degree by *Salmonella*. *Salmonella* and in particular *S.* Enteritidis remained the most frequently reported causative agent for foodborne outbreaks. Norovirus (and other calicivirus) was the



72 of 222 EU ONE HEALTH ZOONOSES REPORT 2022

FIGURE 8 Trends in reported confirmed human cases of listeriosis in the EU by month, 2018–2022.
Source: Austria, Belgium, Cyprus, Czechia, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Ireland, Italy, Latvia, Luxembourg, Malta, the Netherlands, Poland, Portugal, Romania, Slovakia, Slovenia, Spain and Sweden.

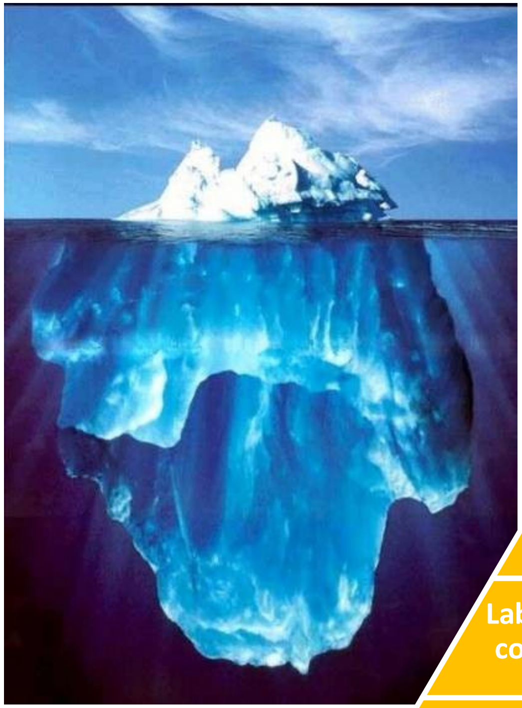


EU One Health Zoonoses Report 2021

With regard to foodborne outbreaks (FBOs), *Salmonella*, Norovirus and *Campylobacter* accounted for the highest number of outbreaks and cases.

Data on congenital toxoplasmosis are not shown since 2021 data are not available yet.
Note: The total number of confirmed cases is indicated in parentheses at the end of each bar.
(a) Regarding West Nile virus infection, the total number of locally acquired cases was used (includes probable and confirmed cases).

Figure 1: Reported numbers of cases and notification rates for confirmed human zoonoses in the EU, 2021



Re
po

Laboratory-confirmed cases

Tested in laboratory

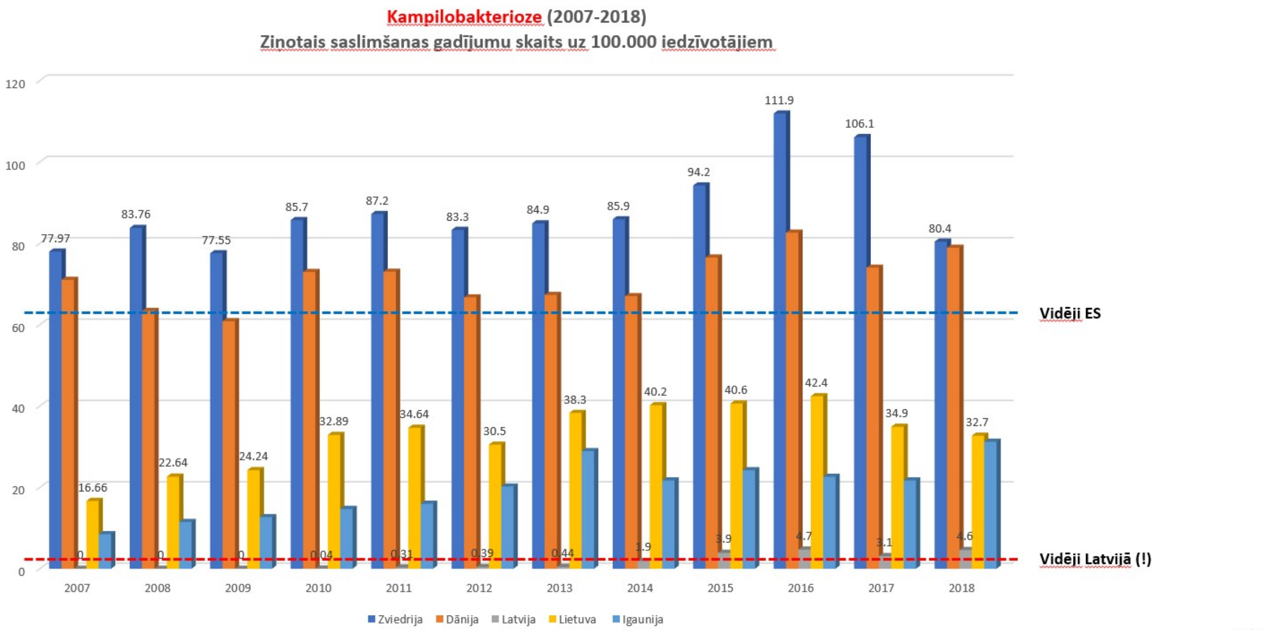
Cases when samples are requested from a patient

Persons who seek for help

Persons who get ill

Persons who had contact with agents

(Tauxe, 2010)



Archiv für Lebensmittelhygiene 60, Heft 5 (2009), Seiten 161–165

161

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State Public Health Agency, 1012 Riga, Latvia[3]

A 10-year retrospective study on listeriosis in Latvia, 1998–2007

Listeriose in Lettland – Retrospektive über die Jahre 1998–2007

Aivars Bērziņš[1, 2], Anita Brila[3], Sandra Magone[3], Jurijs Perevoščikovs[3], Hannu Korkeala[1]

Summary

This study was undertaken to describe the trends in human listeriosis in Latvia over the 10-year period from 1998 to 2007 as a means of characterizing the epidemiological and clinical features of this disease. A total of 90 listeriosis cases were identified for the period from 1998 to 2007. During the 10-year study period the overall incidence of listeriosis was 0.4 per 100 000 of the population. Overall, 77% of all described clinical cases were characterized by meningoencephalitis and/or sepsis. The overall mortality, including abortions and perinatal infant deaths, was 6.7% (6/90). A marked clustering of listeriosis cases was observed from September to December 2000 possibly indicating one large outbreak. The

LISTERIOZE

Listerioze *(non- invasive)*- slimība ar vāji izteiktiem simptomiem, dažreiz raksturīgs gastroenterīts, **caureja**, vemšana, drudzis, galvas sāpes (pašlimitējoša)

Listerioze *(invasive)*- slimība **ar augstu letalitāti (~20 līdz 30%)**, raksturīgs drudzis, muskuļu sāpes, caureja, slikta dūša, ar laiku izveidojas bakterēmija, septicēmija, **meningīts, meningoencefalīts;**

Grūtniecības periodā viegla pārslimošana ar gripai līdzīgiem simptomiem

grūtniecēm- pēdējā grūtniecības trešdaļā- spontāni aborti, vēlāk arī nedzīvi dzimuši augļi;

Resource: Hospital Materno Infantil La Paz, Madrid.

NEWS

IN BRIEF

Death penalty for two men over baby milk scandal: Two men who traded melamine used in infant formula milk have been sentenced to death in China. At least six children died and nearly 300 000 became sick after drinking the contaminated milk last year. Tian Wenhua, the chairwoman of the Sanlu Group, which was at the centre of the incident, was given a life sentence.

US rewards doctors for e-prescriptions: The Centers for Medicare and Medicaid are paying doctors a bonus to e-prescribe to reduce costs. The bonus amounts to 2% of charges billed to Medicare in 2009, and will decline to 0.5% by 2013; doctors who don't e-prescribe will get a penalty. The programme could prevent 1.9 million adverse drug events.

Allegations that AIDS doctors were tortured: The Iranian doctors Kamiar and Arash Alaei have been imprisoned for three and six years for conspiring with the United States to overthrow the government. Physicians for Human Rights claims that the trial was blatantly unfair. The doctors' televised confessions seemed to have been obtained under duress.

Screening in Europe needs to double: Public health authorities must increase their screening programmes for breast, cervical, and colorectal cancer, says the European Commission after a report showed that the number of screenings a

Deaths from listeriosis remain a cause for concern in Europe

Rory Watson BRUSSELS

The number of campylobacter infections in humans continues to rise across Europe, while the number of cases of salmonella is maintaining a downward trend, new data released in Brussels on 20 January show.

The report on zoonoses, jointly produced by the European Food Safety Authority in Parma, Italy, and the European Centre for Disease Prevention and Control in Stockholm, provides the latest picture on the extent to which infectious diseases are transmitted from animals to humans in 31 European countries.

Twenty two of the 27 European Union countries reported a rise in the number of confirmed cases of campylobacter in humans during 2007 (those that didn't were Estonia, Hungary, Lithuania, the Netherlands, and Spain). Mainly transmitted in fresh poultry meat, this organism can cause diarrhoea, fever, and headaches in patients. It affected 200 000 people across the continent in 2007. The biggest increases from the previous year were in Germany (number of cases up by 27%) and the United Kingdom (up by 11%).

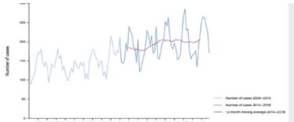
In contrast, the number of confirmed cases of human salmonellosis, which can induce fever, abdominal pain, nausea, and vomiting, fell for the fourth year in succession, from 2006: 1554 confirmed cases. However, the disease showed a high mortality rate of 20%, and mortality was especially high among vulnerable groups such as young babies and elderly people.

Andrea Ammon, the disease prevention centre's head of surveillance, said, "Although tackling salmonella and campylobacter infections remains a top priority, we are particularly concerned by the high proportion of deaths among older people as a result of infection with listeria. We have also noted a high proportion of newborn babies among the cases of listeriosis."

The report notes that listeria bacteria were seldom found above legal safety limits in ready to eat foods. However, they were detected above these levels in smoked fish and other ready to eat fishery products and also in certain meats and cheeses.

Throughout Europe the occurrence of bovine brucellosis remained largely unchanged from 2006, but there was a slight decrease in bovine tuberculosis and sheep and goat brucellosis. In humans, 542 confirmed cases of brucellosis were reported. Most were in Spain and Greece, and the overall trend is decreasing.

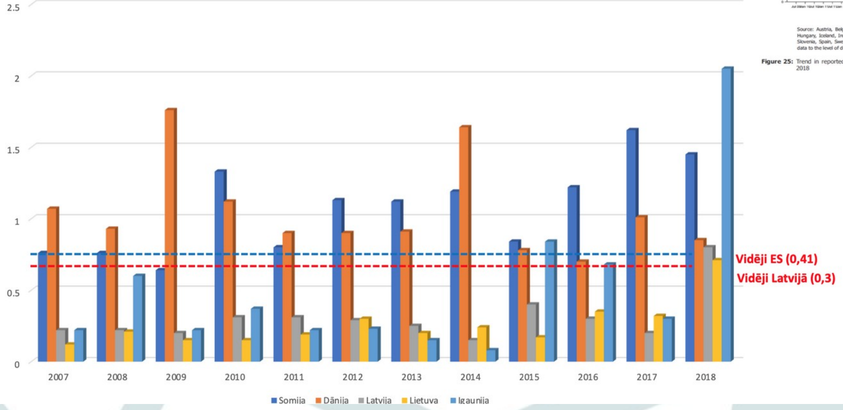
Although rabies is still found in domestic and wild animals in the Baltic and some

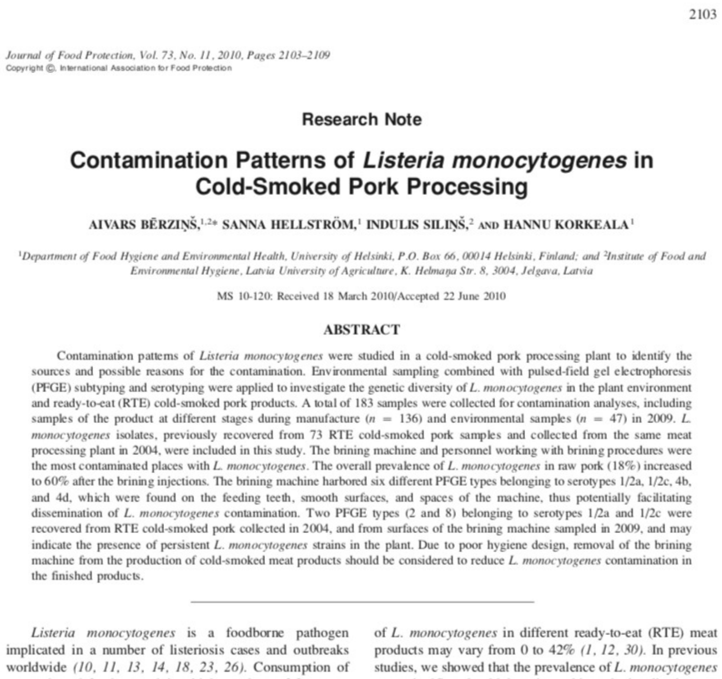


Source: Austria, Belgium, Cyprus, the Czech Republic, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Iceland, Ireland, Italy, Latvia, Lithuania, Malta, the Netherlands, Norway, Poland, Romania, Slovakia, Slovenia, Spain, Sweden and the United Kingdom. Bulgaria, Croatia, Luxembourg and Portugal did not report data to the level of detail required for the analysis.

Figure 25: Trend in reported confirmed human cases of listeriosis in the EU/EEA, by month, 2009–2018

Listerioze (2007-2018)
Ziņoto saslimšanas gadījumu skaits uz 100.000 iedzīvotāju





2103

Journal of Food Protection, Vol. 73, No. 11, 2010, Pages 2103–2109

Research Note

Contamination Patterns of *Listeria monocytogenes* in Cold-Smoked Pork Processing

AIVARS BĒRZIŅŠ,[1,2]* SANNA HELLSTRÖM,[1] INDULIS SILIŅŠ,[2] AND HANNU KORKEALA[1]

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MS 10-120: Received 18 March 2010/Accepted 22 June 2010

ABSTRACT

Contamination patterns of *Listeria monocytogenes* were studied in a cold-smoked pork processing plant to identify the sources and possible reasons for the contamination. Environmental sampling combined with pulsed-field gel electrophoresis (PFGE) subtyping and serotyping were applied to investigate the genetic diversity of *L. monocytogenes* in the plant environment and ready-to-eat (RTE) cold-smoked pork products. A total of 183 samples were collected for contamination analyses, including samples of the product at different stages during manufacture ($n = 136$) and environmental samples ($n = 47$) in 2009. *L. monocytogenes* isolates, previously recovered from 73 RTE cold-smoked pork samples and collected from the same meat processing plant in 2004, were included in this study. The brining machine and personnel working with brining procedures were the most contaminated places with *L. monocytogenes*. The overall prevalence of *L. monocytogenes* in raw pork (18%) increased to 60% after the brining injections. The brining machine harbored six different PFGE types belonging to serotypes 1/2a, 1/2c, 4b, and 4d, which were found on the feeding teeth, smooth surfaces, and spaces of the machine, thus potentially facilitating dissemination of *L. monocytogenes* contamination. Two PFGE types (2 and 8) belonging to serotypes 1/2a and 1/2c were recovered from RTE cold-smoked pork collected in 2004, and from surfaces of the brining machine sampled in 2009, and may indicate the presence of persistent *L. monocytogenes* strains in the plant. Due to poor hygiene design, removal of the brining machine from the production of cold-smoked meat products should be considered to reduce *L. monocytogenes* contamination in the finished products.

Listeria monocytogenes is a foodborne pathogen implicated in a number of listeriosis cases and outbreaks worldwide *(10, 11, 13, 14, 18, 23, 26)*. Consumption of contaminated foods containing high numbers of *L. mono-*

be transferred am g plants by persistently contaminated equipment. Recent udies have shown that the prevalence

of *L. monocytogenes* in different ready-to-eat (RTE) meat products may vary from 0 to 42% *(1, 12, 30)*. In previous studies, we showed that the prevalence of *L. monocytogenes* was significantly higher in cold-smoked, sliced meat

sliced meat products

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90 days) in vacuum
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MATERIALS AN METHO

Meat processing plant and the manufact cold-smoked pork products. Large-scale meat

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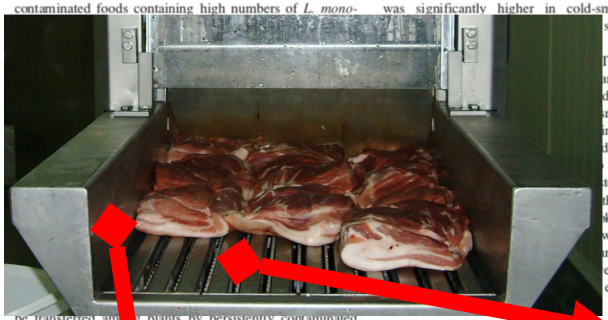
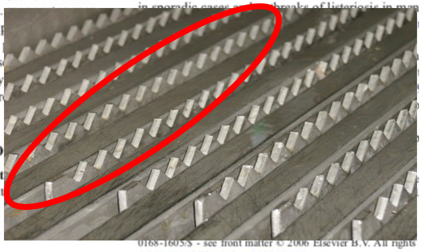
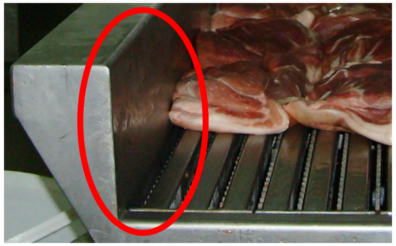
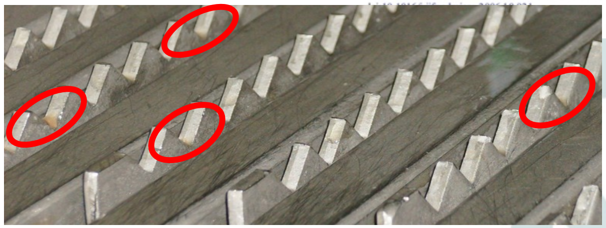
* Author for correspo Tel: +371 26520061; Fax: +358 9 19157101; E-mail: a rzins@helsinki.fi.









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INTERNATIONAL JOURNAL OF
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Factors associated with *Listeria monocytogenes* contamination of cold-smoked pork products produced in Latvia and Lithuania

Aivars Bērziņš [a,b,*], Ari Hörman [a], Janne Lundén [a], Hannu Korkeala [a]

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Received 19 April 2006; received in revised form 22 July 2006; accepted 25 October 2006

Abstract

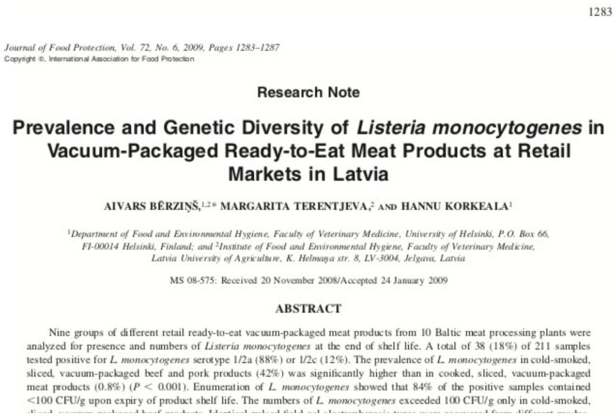
A total of 312 samples of sliced, vacuum packaged, cold-smoked pork from 15 meat processing plants in Latvia a 15-month period from 2003 until 2004, were analyzed for the presence of *Listeria monocytogenes* at the end of samples (38%) tested positive for *L. monocytogenes*. Despite the long storing period, the levels of *L. monocyt* products were low. Manufacturing processes were studied at seven meat processing plants. A new approach regression model was applied to identify the main factors associated with *L. monocytogenes* contamination durin smoked pork products. Brining by injection was a significant factor (odds ratio 10.66; $P<0.05$) for contam *monocytogenes*. Moreover, long cold-smoking times (≥12 h) had a significant predictive value (odds ratio 24.38; positive for *L. monocytogenes*. Pulsed-field gel electrophoresis results indicated that various sources of *L. monocyt* over periods of time in several meat processing plants. In two meat processing plants, persistent *L. monocytogenes* 1/2a and 1/2c were found.

Keywords: Listeria monocytogenes; Prevalence; Pork; Brine injection; Cold-smoking

1. Introduction

Since *Listeria monocytogenes* was found to be a food-borne pathogen (Schlech et al., 1983), epid studies have confirmed that meat products have bee

growth of *L. monocytogenes*, and are cooking (McLauchlin, 1996).



1283

Journal of Food Protection, Vol. 72, No. 6, 2009, Pages 1283–1287

Research Note

Prevalence and Genetic Diversity of *Listeria monocytogenes* in Vacuum-Packaged Ready-to-Eat Meat Products at Retail Markets in Latvia

AIVARS BĒRZIŅŠ,[1,2]* MARGARITA TERENTJEVA,[2] AND HANNU KORKEALA[1]

[1]*Department of Food and Environmental Hygiene, Faculty of Veterinary Medicine, University of Helsinki, P.O. Box 66, FI-00014 Helsinki, Finland; and* [2]*Institute of Food and Environmental Hygiene, Faculty of Veterinary Medicine, Latvia University of Agriculture, K. Helmaņa str. 8, LV-3004, Jelgava, Latvia*

MS 08-575: Received 20 November 2008/Accepted 24 January 2009

ABSTRACT

Nine groups of different retail ready-to-eat vacuum-packaged meat products from 10 Baltic meat processing plants were analyzed for presence and numbers of *Listeria monocytogenes* at the end of shelf life. A total of 38 (18%) of 211 samples tested positive for *L. monocytogenes* serotype 1/2a (88%) or 1/2c (12%). The prevalence of *L. monocytogenes* in cold-smoked, sliced, vacuum-packaged beef and pork products (42%) was significantly higher than in cooked, sliced, vacuum-packaged meat products (0.8%) ($P < 0.001$). Enumeration of *L. monocytogenes* showed that 84% of the positive samples contained <100 CFU/g upon expiry of product shelf life. The numbers of *L. monocytogenes* exceeded 100 CFU/g only in cold-smoked,

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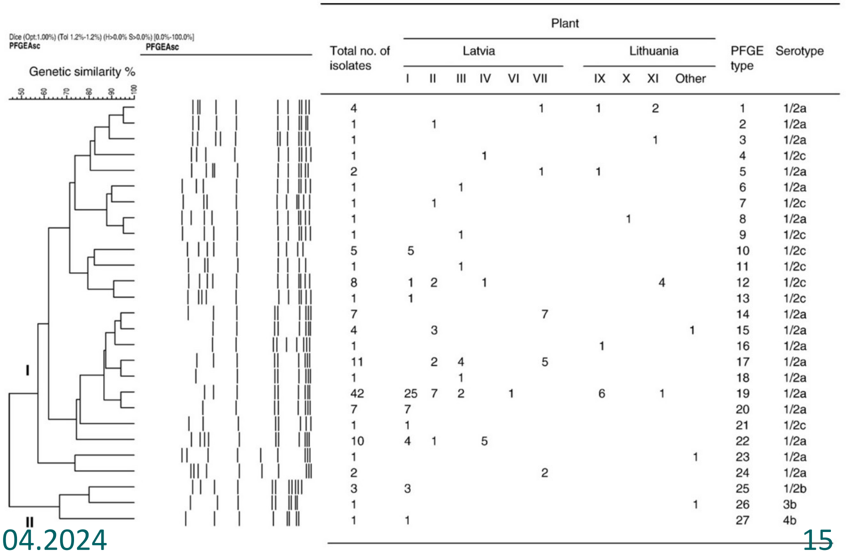

Total no. of isolates	Plant Latvia I	 II	 III	 IV	 VI	 VII	 Lithuania IX	 X	 XI	 Other	PFGE type	Serotype
4						1	1		2		1	1/2a
1		1									2	1/2a
1									1		3	1/2a
1				1							4	1/2c
2						1	1				5	1/2a
1			1								6	1/2a
1		1									7	1/2c
1								1			8	1/2a
1			1								9	1/2c
5	5										10	1/2c
1			1								11	1/2c
8	1	2		1					4		12	1/2c
1	1										13	1/2c
7						7					14	1/2a
4		3								1	15	1/2a
1							1				16	1/2a
11		2	4			5					17	1/2a
1			1								18	1/2a
42	25	7	2		1		6		1		19	1/2a
7	7										20	1/2a
1	1										21	1/2c
10	4	1		5							22	1/2a
1										1	23	1/2a
2						2					24	1/2a
3	3										25	1/2b
1										1	26	3b
1	1										27	4b

Fig. 2. Dendrogram demonstrating the genetic similarity among PFGE (*Asc*I) restriction profiles of *Listeria monocytogenes* isolated from sliced, vacuum packaged, cold-smoked pork products from Latvian and Lithuanian meat processing plants.

news

Pealtnägija: Deadly listeria traced to M.V.Wool fish factory

Fish at the M.V. Wool plant. Source: ERR

NEWS

ERR

25.09.2019 16:10

Listeria bacteria that has been traced back to the M.V.Wool fish plant in Estonia has been contracted by nine people in Estonia, two of whom died as a result.

LISTERIA UN TĀS EKOLOĢISKĀS NIŠAS

Veterinary and Animal Science 19 (2023) 100276

Contents lists available at ScienceDirect

Veterinary and Animal Science

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

Article

Genetic diversity and known virulence genes in *Listeria innocua* strains isolated from cattle abortions and farm environment

Silva Gradovska [a,*], Žanete Šteingolde [a,b], Juris Ķibilds [a], Irēna Meistere [a], Jeļena Avsejenko [a], Madara Streikiša [a], Laura Alksne [a], Margarita Terentjeva [a], Aivars Bērziņš [a,b]

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veterinary sciences

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Article

Characterization and Genetic Diversity of *Listeria monocytogenes* Isolated from Cattle Abortions in Latvia, 2013–2018

Žanete Šteingolde [1,2,*,†], Irēna Meistere [1,*,†], Jeļena Avsejenko [1], Juris Ķibilds [1], Ieva Bergšpica [1], Madara Streikiša [1], Silva Gradovska [1], Laura Alksne [1], Sophie Roussel [3], Margarita Terentjeva [2] and Aivars Bērziņš [1,2]

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[3] Maisons-Alfort Laboratory of Food Safety, University Paris-Est, French Agency for Food, Environmental and Occupational Health (ANSES), F-94701 Maisons-Alfort, France; sophie.roussel@anses.fr
* Correspondence: zanete.steingolde@bior.lv (Ž.Š.); irena.meistere@bior.lv (I.M.)
† These authors had equal contribution.

S. Gradovska et al. — Veterinary and Animal Science 19 (2023) 100276

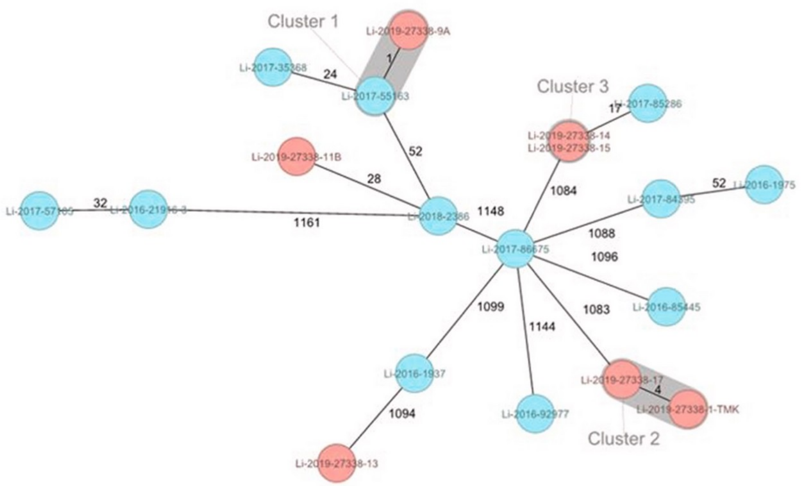


Fig. 3. MST includes L. *innocua* isolates of Farm A. Blue represents abortion sample; red – environmental samples such as soil, faeces, feed and water.

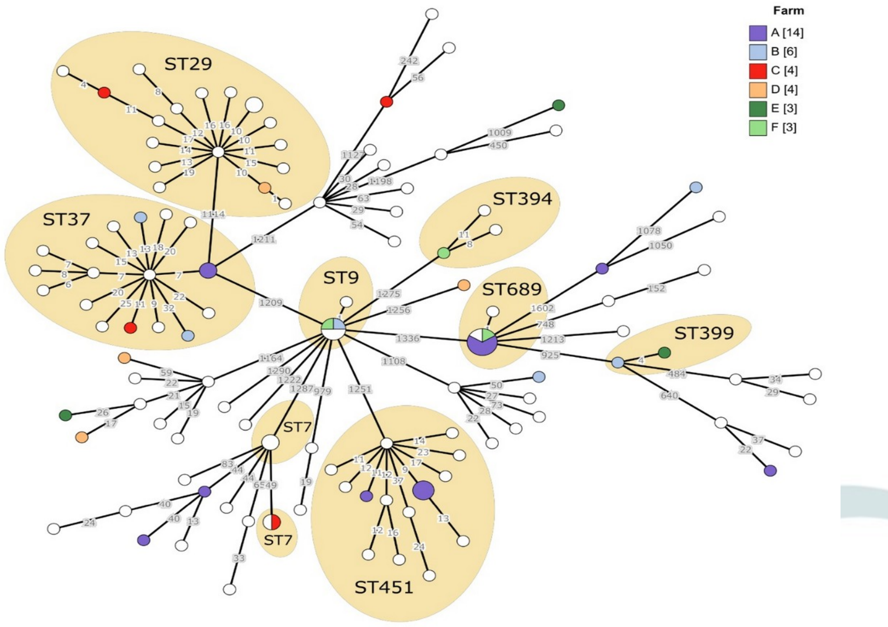
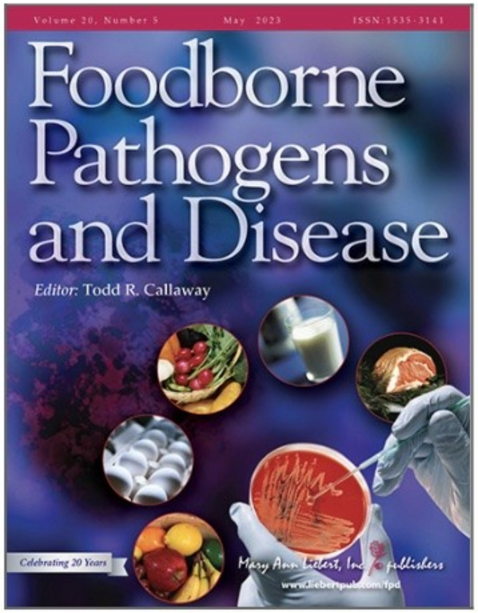
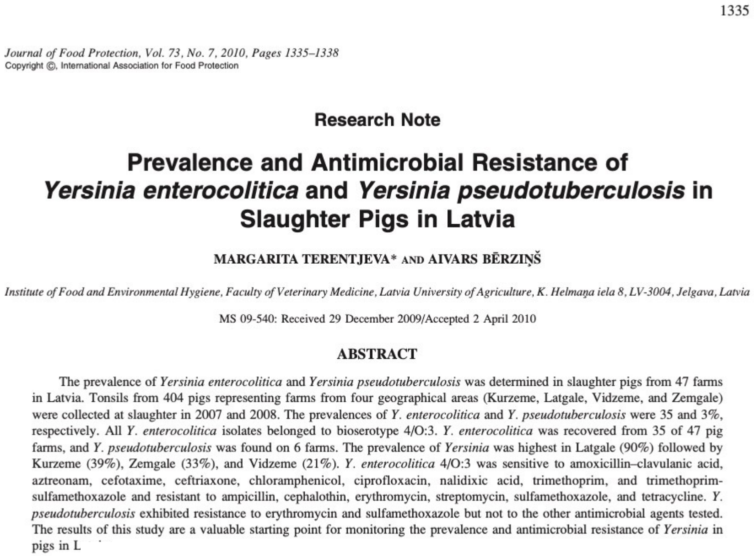


Figure 2. A minimum spanning tree showing the core genome allele diversity of *L. monocytogenes* isolates from cattle abortions. The tree is based on 1701 cgMLST loci. Farms with more than three isolates (designated as A–F) are represented with a color code, and the nod size is proportional to the isolate count per genotype. Depicted branch lengths are log-transformed but numbers on the branches represent the absolute distance between genotypes in the number of loci. The clusters within STs where the distance between a least two isolates is 10 alleles or less are highlighted as possible infection outbreak or transmission events.




1335

Journal of Food Protection, Vol. 73, No. 7, 2010, Pages 1335–1338
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Research Note

Prevalence and Antimicrobial Resistance of *Yersinia enterocolitica* and *Yersinia pseudotuberculosis* in Slaughter Pigs in Latvia

MARGARITA TERENTJEVA* AND AIVARS BĒRZIŅŠ

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MS 09-540: Received 29 December 2009/Accepted 2 April 2010

ABSTRACT

The prevalence of *Yersinia enterocolitica* and *Yersinia pseudotuberculosis* was determined in slaughter pigs from 47 farms in Latvia. Tonsils from 404 pigs representing farms from four geographical areas (Kurzeme, Latgale, Vidzeme, and Zemgale) were collected at slaughter in 2007 and 2008. The prevalences of *Y. enterocolitica* and *Y. pseudotuberculosis* were 35 and 3%, respectively. All *Y. enterocolitica* isolates belonged to bioserotype 4/O:3. *Y. enterocolitica* was recovered from 35 of 47 pig farms, and *Y. pseudotuberculosis* was found on 6 farms. The prevalence of *Yersinia* was highest in Latgale (90%) followed by Kurzeme (39%), Zemgale (33%), and Vidzeme (21%). *Y. enterocolitica* 4/O:3 was sensitive to amoxicillin–clavulanic acid, aztreonam, cefotaxime, ceftriaxone, chloramphenicol, ciprofloxacin, nalidixic acid, trimethoprim, and trimethoprim-sulfamethoxazole and resistant to ampicillin, cephalothin, erythromycin, streptomycin, sulfamethoxazole, and tetracycline. *Y. pseudotuberculosis* exhibited resistance to erythromycin and sulfamethoxazole but not to the other antimicrobial agents tested. The results of this study are a valuable starting point for monitoring the prevalence and antimicrobial resistance of *Yersinia* in pigs in L

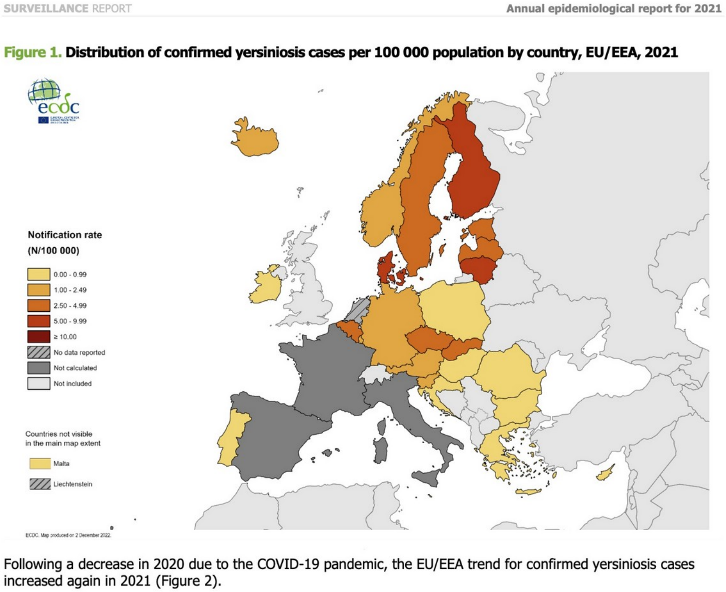
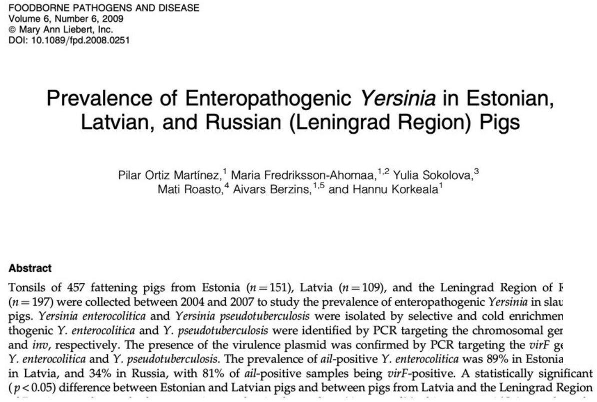

SURVEILLANCE REPORT Annual epidemiological report for 2021

Figure 1. Distribution of confirmed yersiniosis cases per 100 000 population by country, EU/EEA, 2021

ECDC. Map produced on 2 December 2022.

Following a decrease in 2020 due to the COVID-19 pandemic, the EU/EEA trend for confirmed yersiniosis cases increased again in 2021 (Figure 2).


FOODBORNE PATHOGENS AND DISEASE
Volume 6, Number 6, 2009
© Mary Ann Liebert, Inc.
DOI: 10.1089/fpd.2008.0251

Prevalence of Enteropathogenic *Yersinia* in Estonian, Latvian, and Russian (Leningrad Region) Pigs

Pilar Ortiz Martínez,[1] Maria Fredriksson-Ahomaa,[1,2] Yulia Sokolova,[3]
Mati Roasto,[4] Aivars Berzins,[1,5] and Hannu Korkeala[1]

Abstract

Tonsils of 457 fattening pigs from Estonia ($n = 151$), Latvia ($n = 109$), and the Leningrad Region of F
($n = 197$) were collected between 2004 and 2007 to study the prevalence of enteropathogenic *Yersinia* in slau
pigs. *Yersinia enterocolitica* and *Yersinia pseudotuberculosis* were isolated by selective and cold enrichmen
thogenic *Y. enterocolitica* and *Y. pseudotuberculosis* were identified by PCR targeting the chromosomal ger
and *inv*, respectively. The presence of the virulence plasmid was confirmed by PCR targeting the *virF* ge
Y. enterocolitica and *Y. pseudotuberculosis*. The prevalence of *ail*-positive *Y. enterocolitica* was 89% in Estonia
in Latvia, and 34% in Russia, with 81% of *ail*-positive samples being *virF*-positive. A statistically significant
($p < 0.05$) difference between Estonian and Latvian pigs and between pigs from Latvia and the Leningrad Region

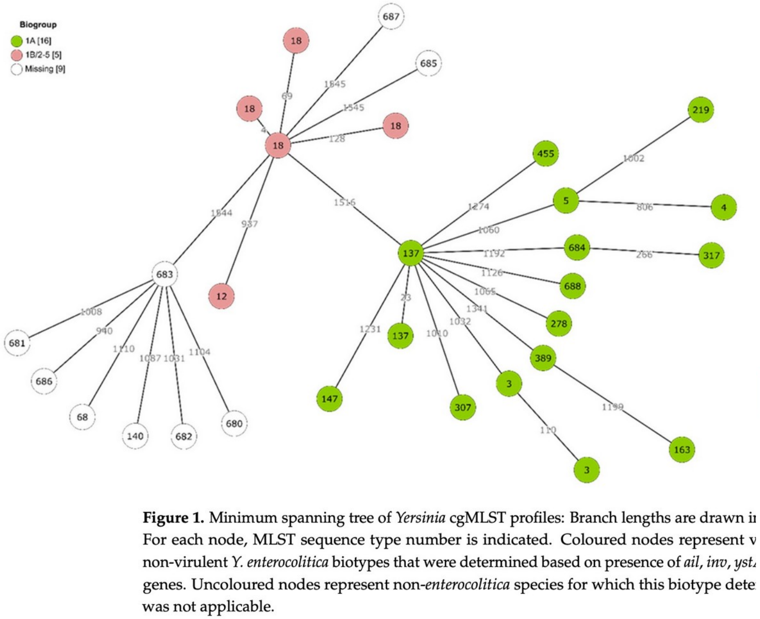


Figure 1. Minimum spanning tree of *Yersinia* cgMLST profiles: Branch lengths are drawn ii
For each node, MLST sequence type number is indicated. Coloured nodes represent v
non-virulent *Y. enterocolitica* biotypes that were determined based on presence of *ail*, *inv*, *yst*
genes. Uncoloured nodes represent non-*enterocolitica* species for which this biotype dete
was not applicable.


pathogens MDPI

Article

Virulence Determinants and Genetic Diversity of *Yersinia* Species Isolated from Retail Meat

Margarita Terentjeva [1,2,*], Juris Ķibilds [2], Irēna Meistere [2], Silva Gradovska [2], Laura Alksne [2], Madara Streikiša [2], Jevgēnija Ošmjana [2] and Olga Valciņa [2]

1 Institute of Food and Environmental Hygiene, Faculty of Veterinary Medicine, Latvia University of Life Sciences and Technologies, LV-3004 Jelgava, Latvia
2 Institute of Food Safety, Animal Health and Environment BIOR, LV-1076 Riga, Latvia; Juris.Kibilds@bior.lv (J.Ķ.); Irena.Meistere@bior.lv (I.M.); Silva.Gradovska@bior.lv (S.G.); Laura.Alksne@bior.lv (L.A.); Madara.Streikisa@bior.lv (M.S.); Jevgenija.Osmjana@bior.lv (J.O.); Olga.Valcina@bior.lv (O.V.)
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Abstract: *Yersinia enterocolitica* is an important foodborne pathogen, and the determination of its virulence factors and genetic diversity within the food chain could help understand the epidemiology of yersiniosis. The aim of the present study was to detect the prevalence, and characterize the

RESEARCH

Campylobacter species prevalence, characterisation of antimicrobial resistance and analysis of whole-genome sequence of isolates from livestock and humans, Latvia, 2008 to 2016

Irēna Meistere¹, Juris Ķibilds¹, Lāsma Eglīte¹, Laura Alksne¹, Jeļena Avsejenko¹, Alla Cibrovska¹, Svetlana Makarova¹, Madara Streikiša¹, Lelde Grantiņa-Ieviņa¹, Aivars Bērziņš¹
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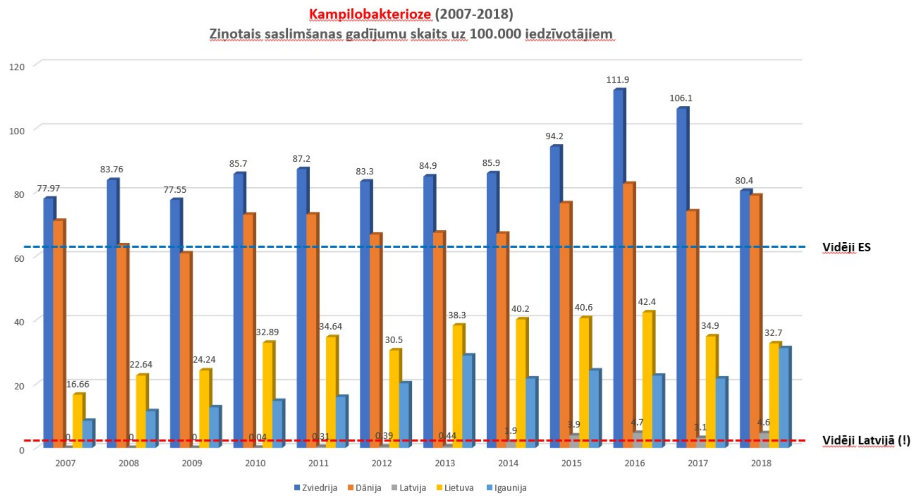
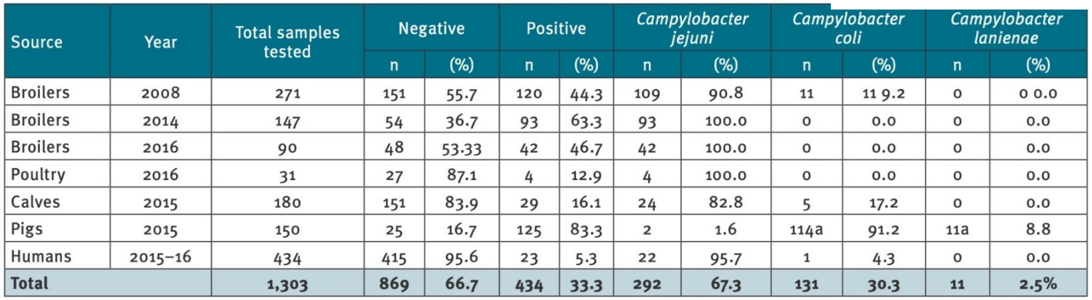

Kampilobakterioze (2007-2018)
Ziņotais saslimšanas gadījumu skaits uz 100.000 iedzīvotājiem

TABLE 1

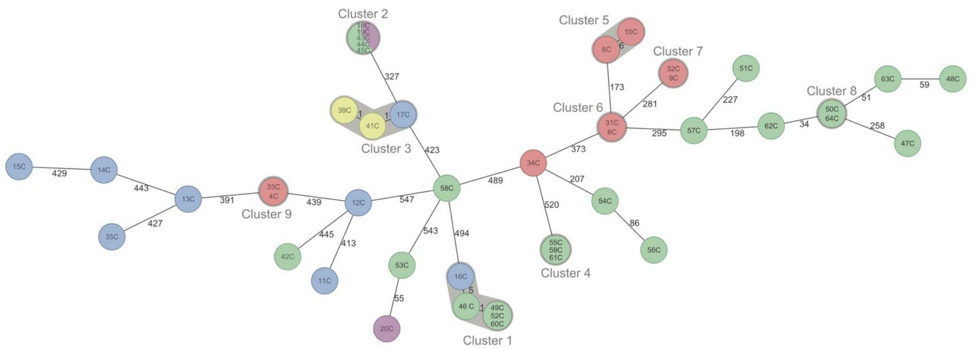
Campylobacter species prevalence in various sources, Latvia, 2008–2016 (n = 1,303)



Source	Year	Total samples tested	Negative		Positive		*Campylobacter jejuni*		*Campylobacter coli*		*Campylobacter lanienae*	
			n	(%)	n	(%)	n	(%)	n	(%)	n	(%)
Broilers	2008	271	151	55.7	120	44.3	109	90.8	11	11 9.2	0	0 0.0
Broilers	2014	147	54	36.7	93	63.3	93	100.0	0	0.0	0	0.0
Broilers	2016	90	48	53.33	42	46.7	42	100.0	0	0.0	0	0.0
Poultry	2016	31	27	87.1	4	12.9	4	100.0	0	0.0	0	0.0
Calves	2015	180	151	83.9	29	16.1	24	82.8	5	17.2	0	0.0
Pigs	2015	150	25	16.7	125	83.3	2	1.6	114a	91.2	11a	8.8
Humans	2015–16	434	415	95.6	23	5.3	22	95.7	1	4.3	0	0.0
Total		**1,303**	**869**	**66.7**	**434**	**33.3**	**292**	**67.3**	**131**	**30.3**	**11**	**2.5%**

FIGURE 2

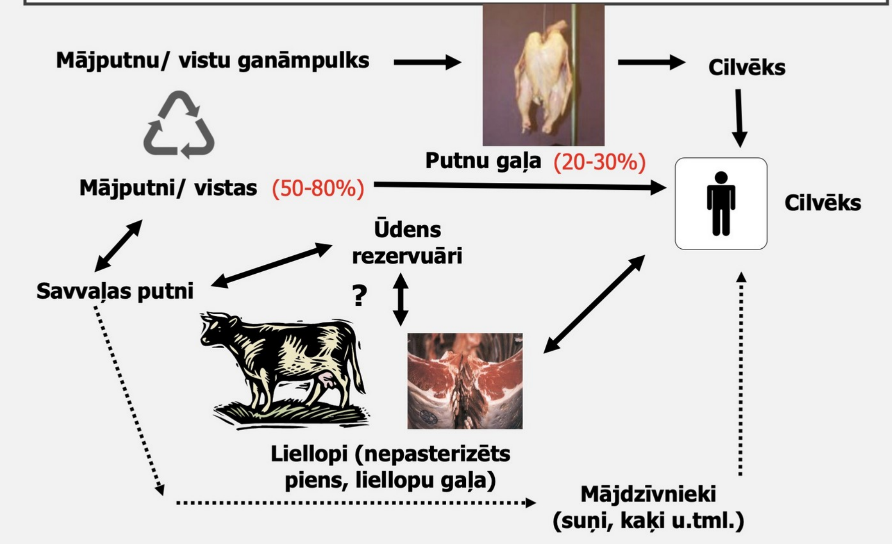
Minimum spanning tree of 45 *Campylobacter* isolates



C: *Campylobacter*; cgMLST: core genome multilocus sequence typing.

Distance based on 637 columns from *C. jejuni/coli* cgMLST, pairwise ignoring missing values. *C. jejuni/coli* cgMLST Complex Type/Cluster-Alert distance: 13. The lengths of the edges are not proportional to the numbers. Colours represent the following sample origin: green: human; red: calf; blue: pig; yellow: broiler; purple: poultry; grey background indicates genetically related isolates. Four different clusters (1;2;4;8) with human isolates involved were identified.

CAMPYLOBACTER SPP. PĀRTIKAS PRODUKTOS- PĀRNEŠANAS CEĻI:



Mājputnu/ vistu ganāmpulks

Cilvēks

Putnu gaļa (20-30%)

Mājputni/ vistas (50-80%)

Cilvēks

Ūdens rezervuāri

Savvaļas putni

?

Liellopi (nepasterizēts piens, liellopu gaļa)

Mājdzīvnieki (suņi, kaķi u.tml.)

ARTIFICIAL INTELLIGENCE AND **MACHINE LEARNING** FOR EPIDEMIOLOGICAL INVESTIGATIONS OF FOODBORNE DISEASE OUTBREAKS

frontiers
in Microbiology

MINI REVIEW
published: 06 August 2019
doi: 10.3389/fmicb.2019.01722

Machine Learning Approaches for Epidemiological Investigations of Food-Borne Disease Outbreaks

Baiba Vilne [1,2]*, Irēna Meistere [1], Lelde Grantiņa-Ieviņa [1] and Juris Ķibilds [1]

[1] Institute of Food Safety, Animal Health and Environment—"BIOR," Riga, Latvia, [2] SIA net-OMICS, Riga, Latvia

Foodborne diseases (FBDs) are infections of the gastrointestinal tract caused by foodborne pathogens (FBPs) such as bacteria [*Salmonella, Listeria monocytogenes* and Shiga toxin-producing *E. coli* (STEC)] and several viruses, but also parasites and some fungi. Artificial intelligence (AI) and its sub-discipline machine learning (ML) are re-emerging and gaining an ever increasing popularity in the scientific community and industry, and could lead to actionable knowledge in diverse ranges of sectors including epidemiological investigations of FBD outbreaks and antimicrobial resistance (AMR). As genotyping using whole-genome sequencing (WGS) is becoming more accessible and affordable, it is increasingly used as a routine tool for the detection of pathogens, and has the potential to differentiate between outbreak strains that are closely related, identify virulence/resistance genes and provide improved understanding of transmission events within hours to days. In most cases, the computational pipeline of WGS data analysis can be divided into four (though, not necessarily consecutive) major steps: *de novo* genome assembly, genome characterization, comparative genomics, and inference of phylogeny or phylogenomics. In each step, ML could be used to increase the speed and potentially the accuracy (provided increasing amounts of high-quality input data) of identification of the source of ongoing outbreaks, leading to more efficient treatment and prevention of additional cases. In this review, we explore whether ML or any other form of AI algorithms have already been proposed for the respective tasks and compare those with mechanistic model-based approaches.

Keywords: machine learning, food-borne disease, outbreaks, bacterial WGS, bioinformatics analysis pipeline

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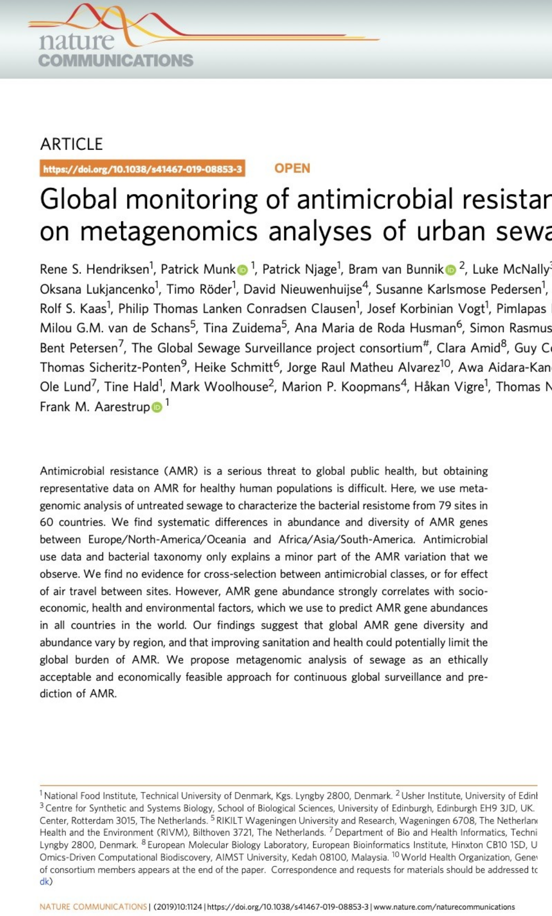
1. INTRODUCTION

Foodborne diseases (FBDs) are infections of the gastrointestinal tract caused by foodborne pathogens (FBPs) such as bacteria and several viruses, but also parasites and some fungi. *Salmonella, Listeria monocytogenes* and Shiga toxin-producing *Escherichia coli* (STEC) are some of the most important bacterial FBPs (Sekse et al., 2017), causing the most outbreaks and the largest number of sporadic cases with severe illness or even fatal outcome (EFSA, 2015; Sekse et al., 2017). *Salmonella* infections affect people at all ages and the main food sources of infection typically include ready-to-eat foods, eggs, swine and poultry. *L. monocytogenes* infections mostly affect elderly people, as well as immunocompromised patients and pregnant women, and display high mortality rates. Common food sources of *L. monocytogenes* include ready-to-eat foods such as smoked fish and soft cheeses. STEC has been associated with severe complications, e.g., acute kidney failure, often affecting elderly and immunocompromised people, and also small children.

Notekūdeņu monitoringa iespējas globālā līmenī (infekcijas, AMR u.c nākotnes izaicinājumi)



nature COMMUNICATIONS

ARTICLE

https://doi.org/10.1038/s41467-019-08853-3 OPEN

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[#], Clara Amid[8], Guy Cochrane[8], Thomas Sicheritz-Ponten[9], Heike Schmitt[6], Jorge Raul Matheu Alvarez[10], Awa Aidara-Kane[10], Sünje J. Pamp[1], Ole Lund[7], Tine Hald[1], Mark Woolhouse[2], Marion P. Koopmans[4], Håkan Vigre[1], Thomas Nordahl Petersen[1] & Frank M. Aarestrup[1]

Antimicrobial resistance (AMR) is a serious threat to global public health, but obtaining representative data on AMR for healthy human populations is difficult. Here, we use metagenomic analysis of untreated sewage to characterize the bacterial resistome from 79 sites in 60 countries. We find systematic differences in abundance and diversity of AMR genes between Europe/North-America/Oceania and Africa/Asia/South-America. Antimicrobial use data and bacterial taxonomy only explains a minor part of the AMR variation that we observe. We find no evidence for cross-selection between antimicrobial classes, or for effect of air travel between sites. However, AMR gene abundance strongly correlates with socio-economic, health and environmental factors, which we use to predict AMR gene abundances in all countries in the world. Our findings suggest that global AMR gene diversity and abundance vary by region, and that improving sanitation and health could potentially limit the global burden of AMR. We propose metagenomic analysis of sewage as an ethically acceptable and economically feasible approach for continuous global surveillance and prediction of AMR.

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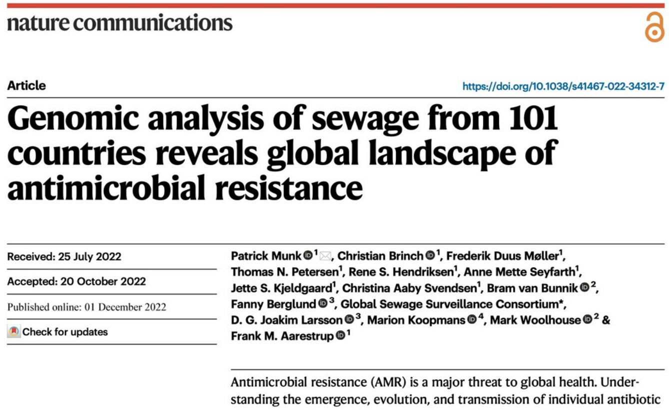
NATURE COMMUNICATIONS | (2019)10:1124 | https://doi.org/10.1038/s41467-019-08853-3 | www.nature.com/naturecommunications



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Article https://doi.org/10.1038/s41467-022-34312-7

Genomic analysis of sewage from 101 countries reveals global landscape of antimicrobial resistance

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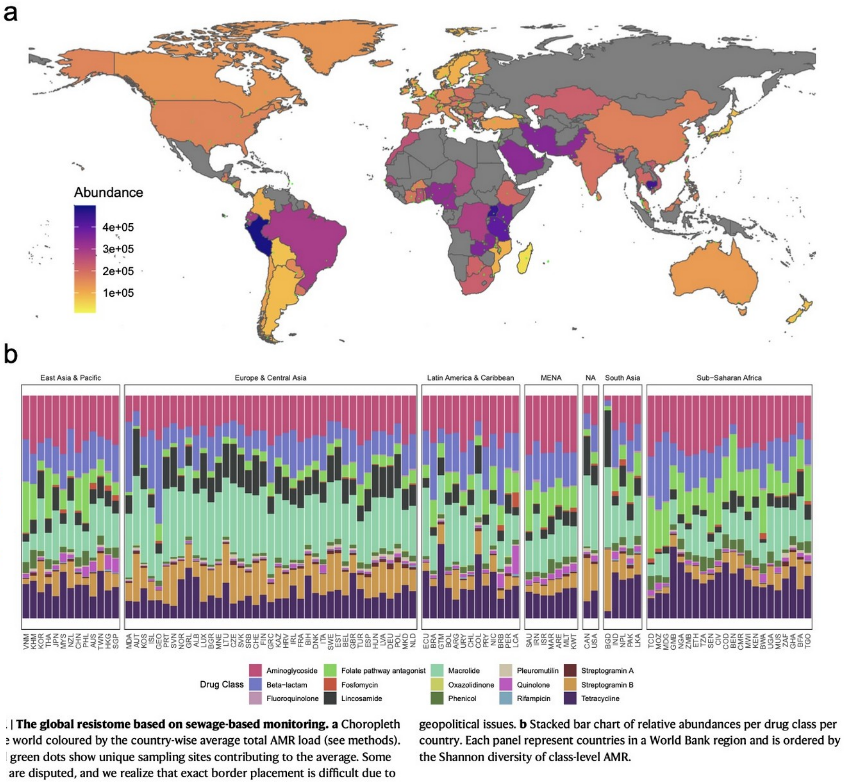
Check for updates

Patrick Munk[1], Christian Brinch[1], Frederik Duus Møller[1], Thomas N. Petersen[1], Rene S. Hendriksen[1], Anne Mette Seyfarth[1], Jette S. Kjeldgaard[1], Christina Aaby Svendsen[1], Bram van Bunnik[2], Fanny Berglund[3], Global Sewage Surveillance Consortium*, D. G. Joakim Larsson[3], Marion Koopmans[4], Mark Woolhouse[2] & Frank M. Aarestrup[1]

Antimicrobial resistance (AMR) is a major threat to global health. Understanding the emergence, evolution, and transmission of individual antibiotic



| **The global resistome based on sewage-based monitoring. a** Choropleth
world coloured by the country-wise average total AMR load (see methods).
green dots show unique sampling sites contributing to the average. Some
are disputed, and we realize that exact border placement is difficult due to geopolitical issues. **b** Stacked bar chart of relative abundances per drug class per country. Each panel represent countries in a World Bank region and is ordered by the Shannon diversity of class-level AMR.

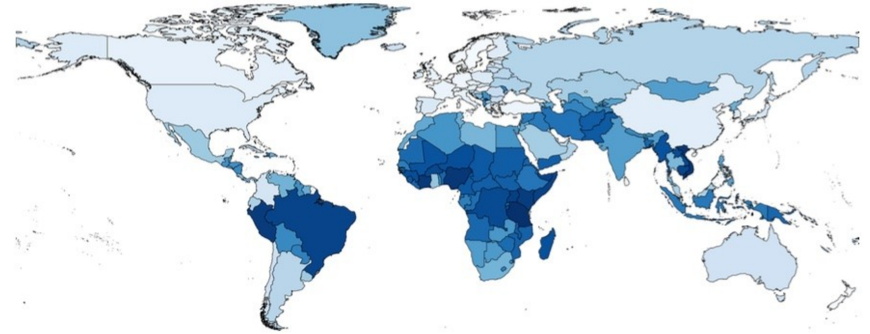


Fig. 4 Global predictions of antimicrobial resistance (AMR) abundance in all countries and territories in the world. Map colored according to predicted abundance of AMR from light blue (low AMR abundance) to dark blue (high AMR abundance). Global resistance predictions for the 259 countries and territories are shown in Supplementary Data 5

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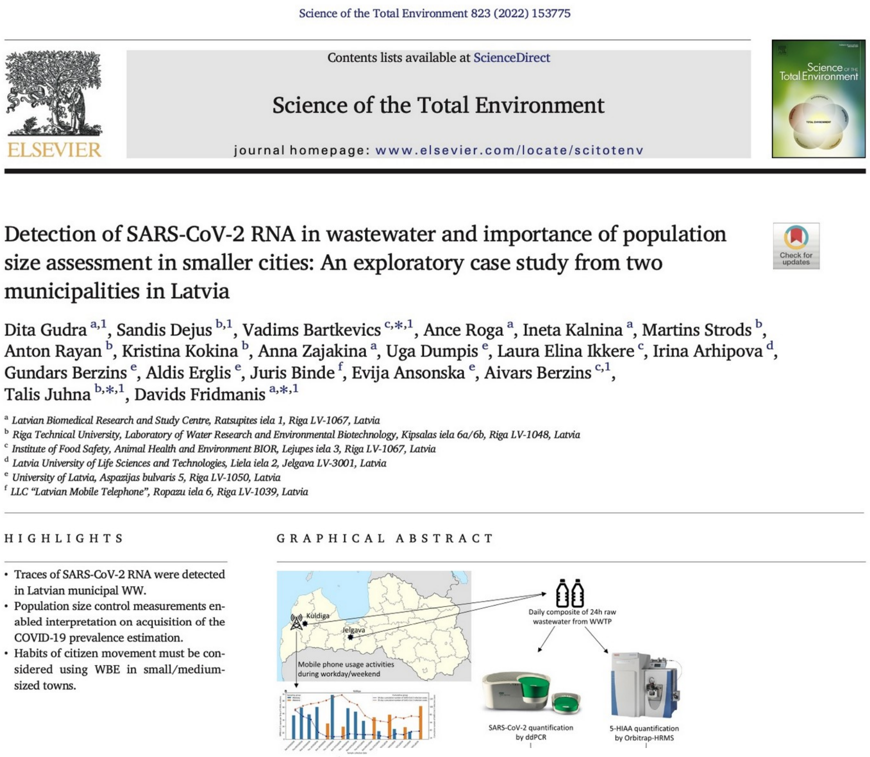
Setting a baseline for global urban virome surveillance in sewage

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 dynamics 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 show 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.



Science of the Total Environment 823 (2022) 153775

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Science of the Total Environment

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

Detection of SARS-CoV-2 RNA in wastewater and importance of population size assessment in smaller cities: An exploratory case study from two municipalities in Latvia

Dita Gudra [a,1], Sandis Dejus [b,1], Vadims Bartkevics [c,*,1], Ance Roga [a], Ineta Kalnina [a], Martins Strods [b], Anton Rayan [b], Kristina Kokina [b], Anna Zajakina [a], Uga Dumpis [e], Laura Elina Ikkere [c], Irina Arhipova [d], Gundars Berzins [e], Aldis Erglis [e], Juris Binde [f], Evija Ansonska [e], Aivars Berzins [c,1], Talis Juhna [b,*,1], Davids Fridmanis [a,*,1]

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HIGHLIGHTS

- Traces of SARS-CoV-2 RNA were detected in Latvian municipal WW.
- Population size control measurements enabled interpretation on acquisition of the COVID-19 prevalence estimation.
- Habits of citizen movement must be considered using WBE in small/medium-sized towns.

GRAPHICAL ABSTRACT

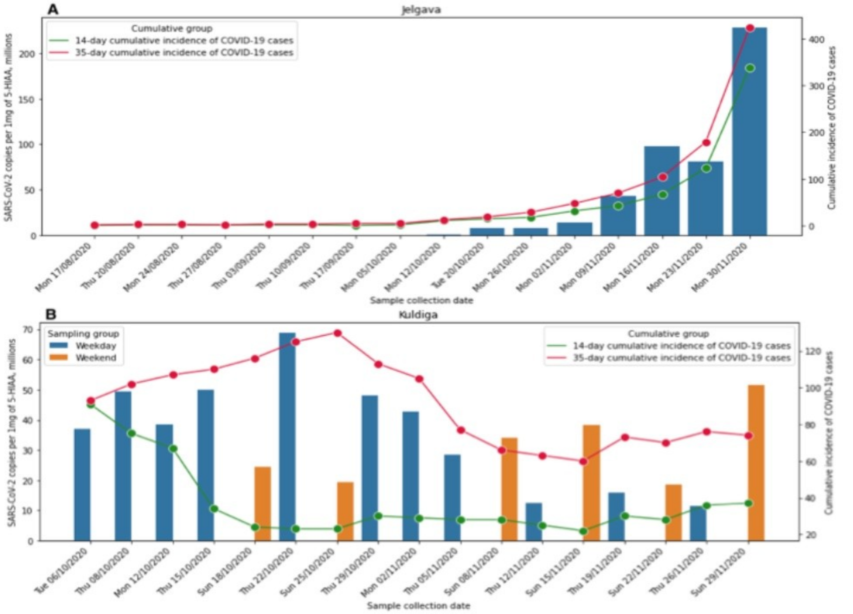
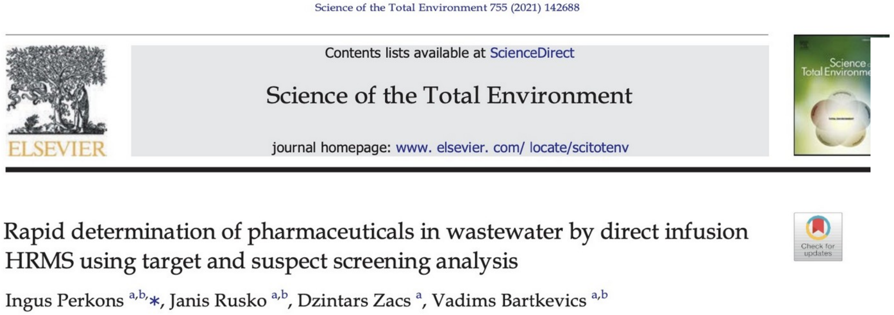


Figure 3. 5-HIAA normalized quantity of SARS-CoV-2 RNA within the wastewater of two Latvian locations A - Jelgava and B - Kuldiga.



Science of the Total Environment 755 (2021) 142688

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Rapid determination of pharmaceuticals in wastewater by direct infusion HRMS using target and suspect screening analysis

Ingus Perkons [a,b,*], Janis Rusko [a,b], Dzintars Zacs [a], Vadims Bartkevics [a,b]

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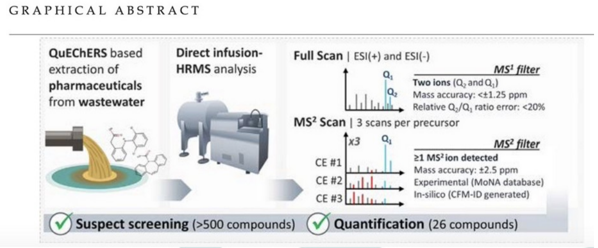
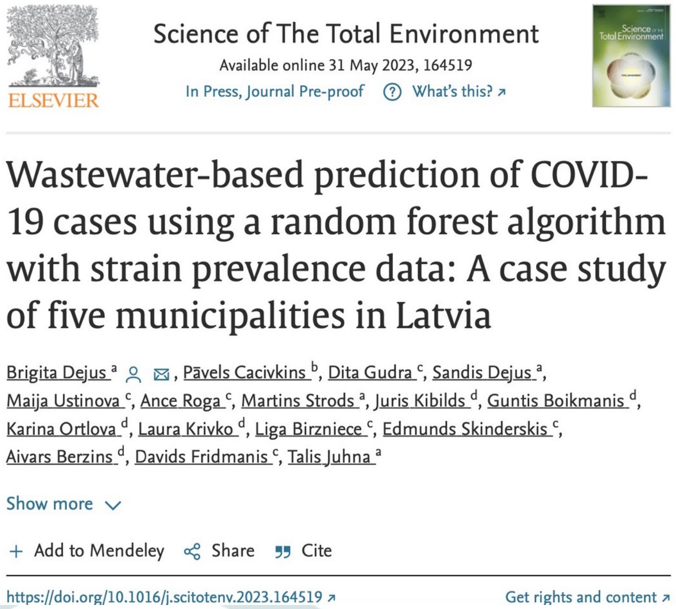
1, Riga LV-1004, Latvia

GRAPHICAL ABSTRACT





Science of The Total Environment

Available online 31 May 2023, 164519

In Press, Journal Pre-proof What's this?

Wastewater-based prediction of COVID-19 cases using a random forest algorithm with strain prevalence data: A case study of five municipalities in Latvia

Brigita Dejus [a], Pāvels Cacivkins [b], Dita Gudra [c], Sandis Dejus [a], Maija Ustinova [c], Ance Roga [c], Martins Strods [a], Juris Kibilds [d], Guntis Boikmanis [d], Karina Ortlova [d], Laura Krivko [d], Liga Birzniece [c], Edmunds Skinderskis [c], Aivars Berzins [d], Davids Fridmanis [c], Talis Juhna [a]

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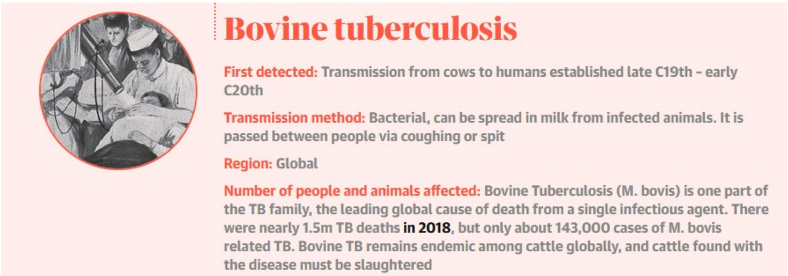


Bovine tuberculosis

First detected: Transmission from cows to humans established late C19th - early C20th

Transmission method: Bacterial, can be spread in milk from infected animals. It is passed between people via coughing or spit

Region: Global

Number of people and animals affected: Bovine Tuberculosis (M. bovis) is one part of the TB family, the leading global cause of death from a single infectious agent. There were nearly 1.5m TB deaths **in 2018**, but only about 143,000 cases of M. bovis related TB. Bovine TB remains endemic among cattle globally, and cattle found with the disease must be slaughtered

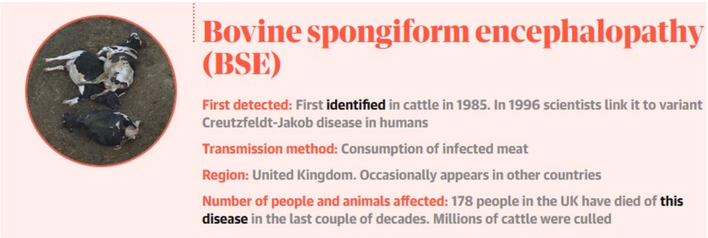
Q fever

First detected: First identified in humans in 1930s

Transmission method: Bacterial, airborne **transmission**

Region: The Netherlands experienced the largest ever outbreak. Q fever is found globally, commonly reported in France and Australia

Number of people and animals affected: By 2016, 74 people were **reported** to have died from the disease in the Netherlands after an outbreak began in 2007, with 50,000 people estimated to be infected. The Dutch government culled more than 50,000 dairy goats on 55 farms to control the spread of the disease



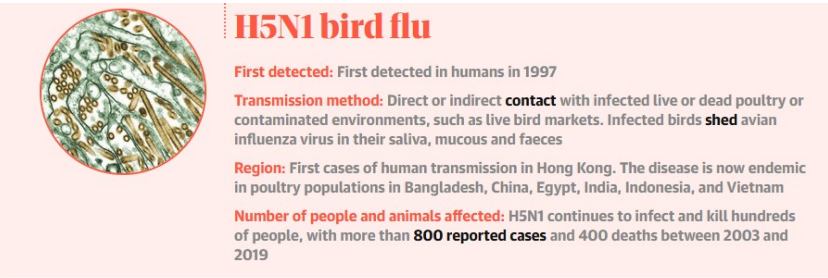
Bovine spongiform encephalopathy (BSE)

First detected: First **identified** in cattle in 1985. In 1996 scientists link it to variant Creutzfeldt-Jakob disease in humans

Transmission method: Consumption of infected meat

Region: United Kingdom. Occasionally appears in other countries

Number of people and animals affected: 178 people in the UK have died of **this disease** in the last couple of decades. Millions of cattle were culled



H5N1 bird flu

First detected: First detected in humans in 1997

Transmission method: Direct or indirect **contact** with infected live or dead poultry or contaminated environments, such as live bird markets. Infected birds **shed** avian influenza virus in their saliva, mucous and faeces

Region: First cases of human transmission in Hong Kong. The disease is now endemic in poultry populations in Bangladesh, China, Egypt, India, Indonesia, and Vietnam

Number of people and animals affected: H5N1 continues to infect and kill hundreds of people, with more than **800 reported cases** and 400 deaths between 2003 and 2019

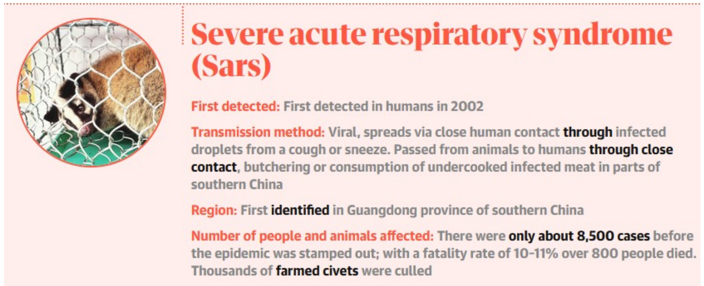
Nipah virus

First detected: First detected in humans in 1999

Transmission method: Viral, mainly from pigs, but can be transmitted between humans via intimate contact

Region: Came to light in Malaysia. **Subsequent outbreaks** in Bangladesh and eastern India

Number of people and animals affected: The initial outbreak saw 105 deaths, and led to the culling of almost **1 million animals**



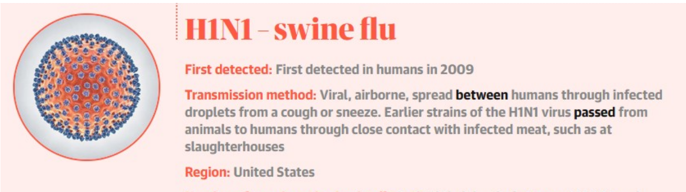
Severe acute respiratory syndrome (Sars)

First detected: First detected in humans in 2002

Transmission method: Viral, spreads via close human contact **through** infected droplets from a cough or sneeze. Passed from animals to humans **through close contact**, butchering or consumption of undercooked infected meat in parts of southern China

Region: First **identified** in Guangdong province of southern China

Number of people and animals affected: There were **only about 8,500 cases** before the epidemic was stamped out; with a fatality rate of 10-11% over 800 people died. Thousands of **farmed civets** were culled



H1N1 – swine flu

First detected: First detected in humans in 2009

Transmission method: Viral, airborne, spread **between** humans through infected droplets from a cough or sneeze. Earlier strains of the H1N1 virus **passed** from animals to humans through close contact with infected meat, such as at slaughterhouses

Region: United States

Number of people and animals affected: Global deaths **between** 151,700 and 575,000 people

Middle East respiratory syndrome (Mers)

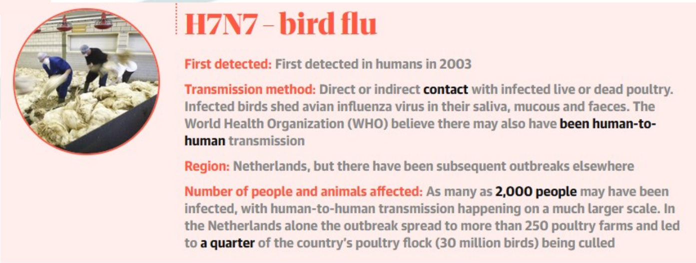
First detected: First detected in humans in 2012

Transmission method: Viral, spreads **through** direct or indirect contact with infected animals and between humans via **infected** droplets such as in a cough or sneeze

Region: First cases in Saudi Arabia, now spread to at least 27 countries, including the UK

Number of people and animals affected: More than 2,400 cases with least 912 human deaths

Middle East Respiratory Syndrome Coronavirus (MERS-CoV) particles (virions), computer illustration.
Credit: Alamy



H7N7 – bird flu

First detected: First detected in humans in 2003

Transmission method: Direct or indirect **contact** with infected live or dead poultry. Infected birds shed avian influenza virus in their saliva, mucous and faeces. The World Health Organization (WHO) believe there may also have **been human-to-human** transmission

Region: Netherlands, but there have been subsequent outbreaks elsewhere

Number of people and animals affected: As many as **2,000 people** may have been infected, with human-to-human transmission happening on a much larger scale. In the Netherlands alone the outbreak spread to more than 250 poultry farms and led to **a quarter** of the country's poultry flock (30 million birds) being culled

https://www.theguardian.com/environment/ng-interactive/2020/sep/15/covid-farm-animals-and-pandemics-diseases-that-changed-the-world

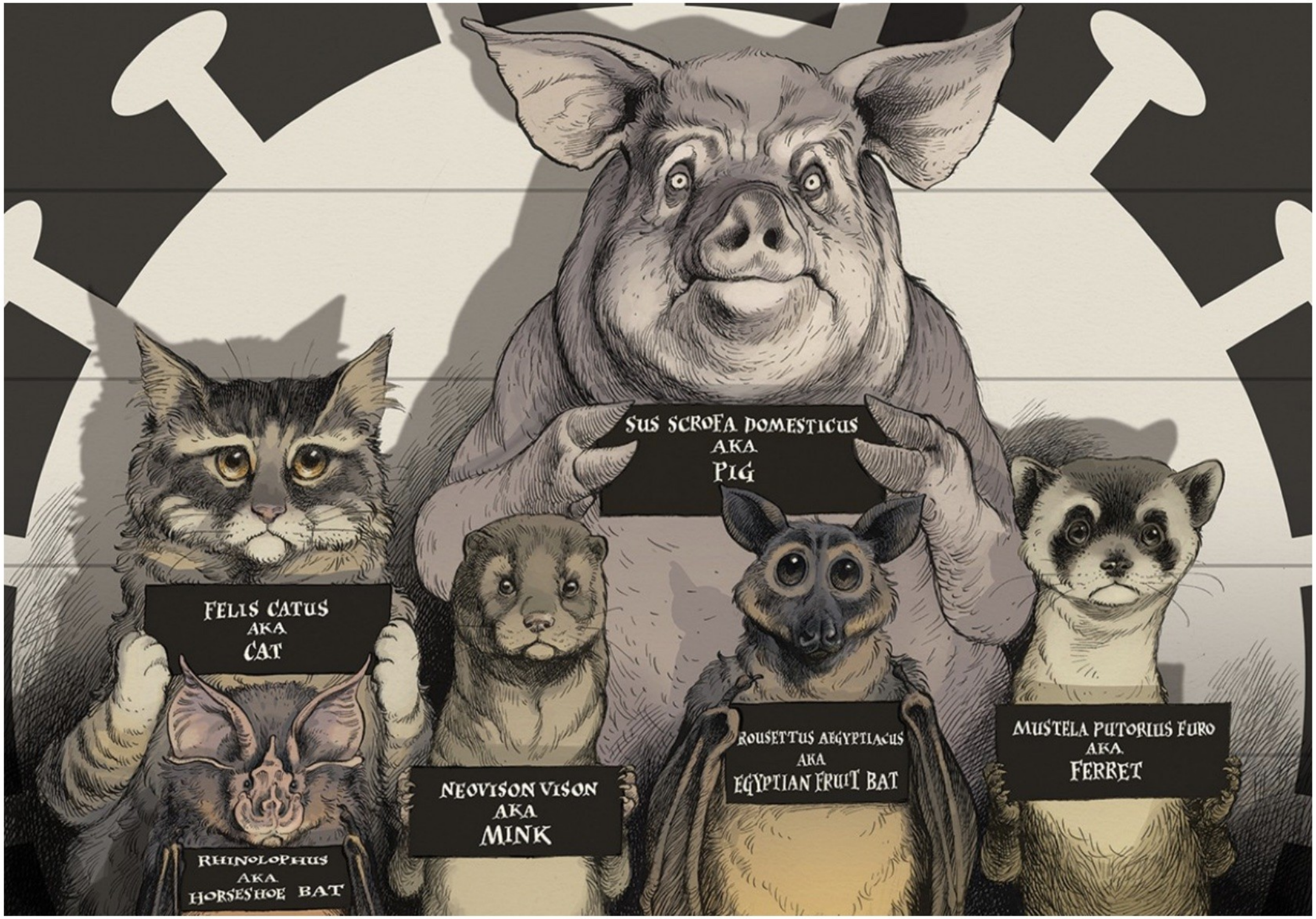


Illustration by David Parkins

*"**Surveillance efforts are becoming more unified.** The OIE, the WHO and the US Centers for Disease Control and Prevention have all published **guidance** on surveying animals (**none recommends widespread testing**, but the WHO advocates testing around infected fur farms)"*

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

NOSLĒGUMA KOMENTĀRI

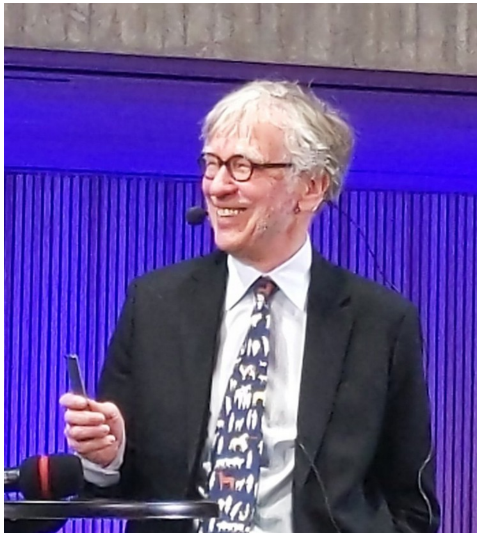
Kas ir nepieciešams, lai “Vienas veselības” koncepcija plašāk tiktu izmantota infekcijas slimību molekulārajā epidemioloģijā un kontrolē ?

- **starpsektoriāla sadarbība** valsts pārvaldes un slimību uzraudzības jomā;
- **koordinēts** (starpsektoriāls) **slimību monitorings** un uzraudzība;
- koordinēta starpdisciplināra pētniecība;
- **jaunu metožu izstrāde un ieviešana** infekcijas slimību monitoringā un uzraudzībā;
- laboratoriju **metodiskā vadība** un references funkcijas;
- vienota (riska) **komunikācija** ar sabiedrību.

Mūsu kopīgam mērķim ir jābūt vērstam uz infekcijas slimību (uzliesmojumu/ pandēmiju) novēršanu, izmantojot agrīnu noteikšanu/ detekciju, modelēšanu, kontroli u.c. mums pieejamas metodes visos sektoros!

ZINĀTNE UN PIERĀDĪJUMOS BALSTĪTA PIEEJA –
GATAVĪBA SLIMĪBU UZLIESMOJUMIEM/ PANDĒMIJĀM UN KRĪZĒM NĀKOTNĒ…

PATEICĪBAS … (PIRMS 20…25 GADIEM)



Prof. Hannu Korkeala, University of Helsinki

Prof. Edīte Birģele, LLU Veterinārmedicīnas fakultāte

Prof. Magne Yndestad, Norwegian School of Veterinary Science

Prof. Richard Linton, Purdue University/ President of Kansas State University)

Prof. David Gerrard, Purdue University/ Virginia Tech

PATEICĪBAS …

European Commission
HORIZON 2020

SEVENTH FRAMEWORK PROGRAMME

THEME [KBBE.2011.2.4-02]
[Pan-European Total Diet Study]

Grant agreement for: Collaborative project

Annex I - "Description of Work"

Project acronym: TDSEXPOSURE
Project full title: " Total Diet Study Exposure "
Grant agreement no: 289108
Version date: 2011-10-12

DURABLE
Research Network against Epidemics

SPICED
spices & herbs

VPP
Valsts pētījumu programma

cost
EUROPEAN COOPERATION IN SCIENCE & TECHNOLOGY

FLPP
FUNDAMENTĀLO UN LIETIŠĶO PĒTĪJUMU PROJEKTI

NACIONĀLAIS ATTĪSTĪBAS PLĀNS 2020

EIROPAS SAVIENĪBA
Eiropas Savienības struktūrfondi un Kohēzijas fonds

IEGULDĪJUMS TAVĀ NĀKOTNĒ

DOKTORI UN DOKTORANTI …


ETA/ Zane Bitere

Latvijas Biozinātņu un tehnoloģiju universitāte

BIOR
PĀRTIKAS DROŠĪBAS, DZĪVNIEKU VESELĪBAS UN VIDES ZINĀTNISKAIS INSTITŪTS

LATVIJAS UNIVERSITĀTE

RĪGAS STRADIŅA UNIVERSITĀTE


Izglītības un zinātnes ministrija

VPP

VALSTS PĒTĪJUMU PROGRAMMA COVID-19 SEKU MAZINĀŠANAI

Ministru kabineta sēde
2021.gada 8.aprīlis

LLU VETERINĀRMEDICĪNAS FAKULTĀTE 1919

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Latvijas Biomedicīnas pētījumu un studiju centrs
biomedicīnas pētījumi un izglītība no gēniem līdz cilvēkam

VPP
Valsts pētījumu programma

Valsts pētījumu programmas projekts biomedicīnā, medicīnas tehnoloģijās un farmācijā

VPP-EM-BIOMEDICĪNA-2022/1-0001