



# Session 2 : Strengthening the One Health vision and prospective



# The One Health EJP contribution to science, health policy and society

## Impact on science



Moderator:  
**Roberto La Ragione**  
University of Surrey

**Hein Imberechts**  
OHEJP Scientific Coordinator and Joint Research  
Projects Leader, Sciensano



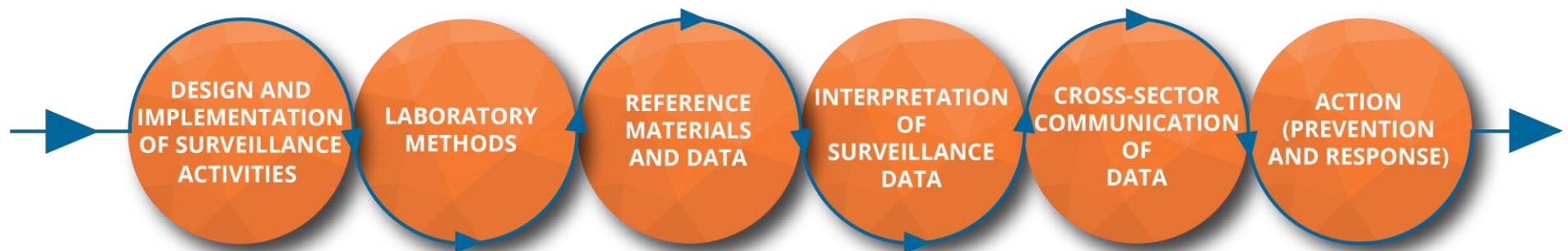


# One Health EJP and its impact on science

**Hein Imberechts**  
Scientific Coordinator One Health EJP  
One Health EJP Final Meeting  
*Paris, 12 September 2023*

# JRP, JIP and PhD

- JRP, JIP and PhD generated much **new knowledge and methodologies**; scientific collaboration to strengthen **networking**.
- The JRP calls were organized along **five themes**.
  - Detection; host-pathogen; epidemiology; risk assessment; prevention & response.
- All EJP activities were based on the **Strategic Research Agenda** with input from the national stakeholders and ECDC and EFSA; outcomes aligned with the **Integrative Strategy Matrix**.
  - Prevent-detect-response; preparedness.
  - See D7.1



# Analysis of outcomes of the One Health EJP likely to be utilised by stakeholders, also beyond the EJP

JOINT INTEGRATIVE PROJECTS (JIP)	INTEGRATIVE STRATEGIC ACTIVITIES	JOINT RESEARCH PROJECTS (JRP)		
		FOODBORNE ZOOSES	ANTIMICROBIAL RESISTANCE (AMR)	EMERGING THREATS
MATRIX: solutions to support and advance One Health surveillance COHESIVE: pathway analysis of detection of outbreaks	Design and implementation of surveillance activities	AIR-SAMPLE: air filters to detect <i>Campylobacter</i> in broiler houses NOVA: code to model disease spread and explore disease surveillance options		
OH-HARMONY-CAP: diagnostics, laboratories capabilities, capacities and interoperability collection tool	Laboratory methods	METASTAVA: Guidelines for sequence based metagenomics disease surveillance	IMPART: updated and improved detection protocols multicentre evaluation study results. New ECOFFs of veterinary antibiotics	TOX-Detect: database of protein profiles of foodborne toxigenic bacteria
		TOXOSOURCES: Harmonised Methods for detecting <i>Toxoplasma gondii</i> contamination in fresh produce	FARMED: Detection and Characterisation of unauthorised genetically modified microorganisms	MAD-Vir: Tool to detect known viruses and discover new viruses
			WORLDCOM: predict/detect AMR from microbial samples and genomic sequences	TELE-Vir: portable toolbox for identification and characterisation of emerging virus threats
			MedVetKlebs: The ZKIR Assay, a Real-Time PCR method for the detection of <i>Klebsiella pneumoniae</i> in environmental samples	IDEMBRU: toolbox for rapid detection/identification of emerging <i>Brucella</i> species
				MEmE: detection tools standardisation and data collection tools on <i>Echinococcus multilocularis/granulosus</i> in the food chain
				PARADISE: novel genotyping schemes and detection strategies for <i>Cryptosporidium</i> and <i>Giardia</i> detection

See document on One Health EJP website: [link](#)

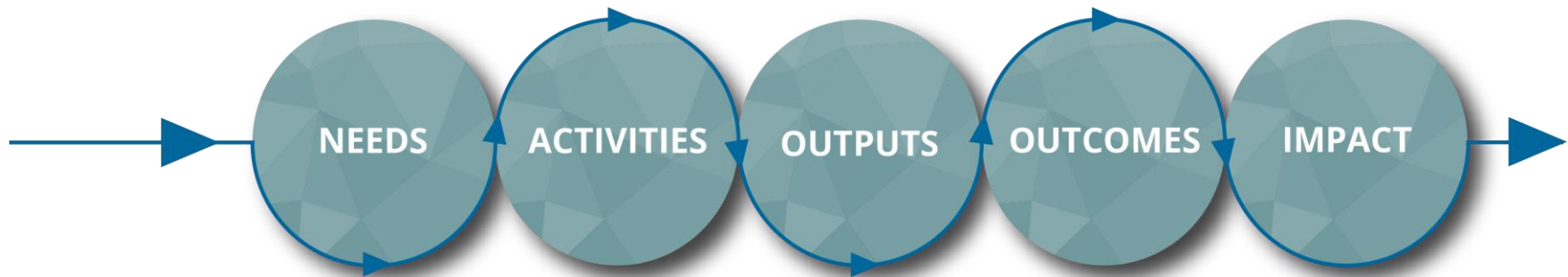


JOINT INTEGRATIVE PROJECTS (JIP)	INTEGRATIVE STRATEGIC ACTIVITIES	JOINT RESEARCH PROJECTS (JRP)		
		FOODBORNE ZOOSES	ANTIMICROBIAL RESISTANCE (AMR)	EMERGING THREATS
CARE: database of strains and genomes for quality control analysis in food safety	Reference material and data	LISTADAPT: Algorithm for selecting strains to explore the diversity of strains circulating	ARDIG: collection of large number of genomes that can be used as reference material for AMR confirmation	
ORION: framework for understanding and information exchange - One Health Surveillance Codex	Interpretation of surveillance data	ADONIS: decision making tool to determine causes and best interventions in human S. Enteritidis infections	ARDIG: Comparability between antimicrobial usage and AMR data to improve AMR surveillance	
COVRIN: models for risk assessment of SARS-CoV-2		BeONE: integrative solutions for foodborne pathogens surveillance	FULL-FORCE: data on plasmid structure and variability of drug resistant organisms	
COHESIVE: information system that stores genomics data and metadata of pathogens from different countries (demo)		DISCoVeR: models and methods for attributing human foodborne infections to animal, food and environment sources		
		TOXOSOURCES: methods to evaluate the relative contribution of different sources of <i>Toxoplasma gondii</i> infections		
		MedVetKlebs: Multicentric Study of <i>Klebsiella Pneumoniae</i> in European food products		
COHESIVE: Risk Analysis System for zoonoses; FoodChain-Lab web application to trace suspicious food items; quantitative shiny Risk application assessment toolbox; risk assessment Decision Support Tool	Cross-sector communication of data	BIOPIGEE: education and training activities	FULL-FORCE: tool box for Single Molecule Real Time sequencing for AMR surveillance	
		NOVA: mathematic models for data combination and analysis for One Health syndromic surveillance systems	FED-AMR: new data on the role of extracellular DNA as an AMR source and on AMR spread in agricultural environment	
ORION: solutions for interoperability to improve data FAIRness - OHEJP Glossary, One Health Linked Data Toolbox, Health Surveillance Ontology			RaDAR: modelling methodology for AMR specific source attribution, disease burden	
COHESIVE: review on economic analysis of foodborne zoonoses	Action (prevention and	MoMIR-PPC: Prevention & Control Measures against <i>Salmonella</i> at the poultry production level		



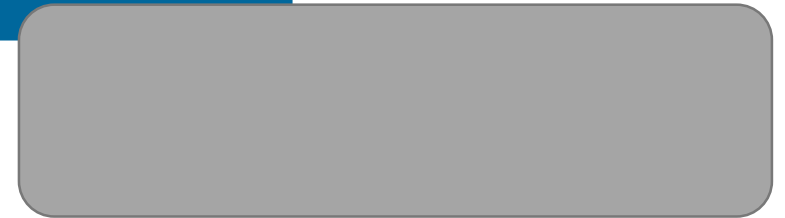
# Scientific results

- Large number of publications (over 265); new scientific projects have been launched based on this scientific work in the EJP.
- Cross-sector and cross border collaboration encourages (young) researchers and facilitates networking with peers; domains: FBZ, AMR, also parasitology; building trust, needed when responding to outbreaks.
- The importance of communication, dissemination and exploitation; within the consortium and beyond; promote uptake!





# One Health EJP Research Projects





## JRPs cover a broad area

- Three **domains**: Foodborne zoonoses, antimicrobial resistance, emerging threats.
- **Pathogens**: bacteria, virus, parasites; animal species (livestock).
  - *Acinetobacter, Brucella, Campylobacter, E. coli* incl. VTEC, *Klebsiella, Ochrobactrum, Salmonella*
  - Viruses incl. Hepatitis E
  - *Cryptosporidium, Echinococcus, Giardia, Toxoplasma*
- **Areas of work**
  - Free extracellular DNA, use of food purchase data as proxy for exposure, plasmid sequencing, bacterial toxins, specific resistances (carbapenem, colistin, etc.), specific technology (MALDI-ToF, Hi-C a.o. sequencing techniques, risk modelling, etc.), super-shedders, syndromic surveillance, etc.
- All fit into the **expected outcomes and impact** of the One Health EJP.

# All outcomes fit into 'prevent-detect-response'

- **Surveillance**
  - Sampling techniques, assessment of surveillance, syndromic surveillance, recommendations
- **Laboratory techniques**, incl. reference material
  - Metagenomics, bioinformatics, microarray, on-site / Point-of-Incidence (LAMP, ONT, etc.), ELISA and serological tests, mass-spectrophotometry
- **Data bases & data analysis**, interpretation of data
  - Samples and strains, sequences, MALDI-ToF, modelling
  - Exposure (and food purchase data)
- **Cross-sector communication**
  - Source attribution, tools to combine epidemiological and genomic data
- **Action (prevention & response)**
  - Pre- & probiotics, biosecurity

# Main areas of research

To identify JRPs:



Use the [search function!](#)

	JRP IDEMBRU	JRP PARADISE	JRP MEME	JRP TELE-VIR	JRP TOX-DETECT	JRP MAD-VIR	JRP NOVA	JRP LISTADAPT	JRP METASTAVA	JRP AIR-SAMPLE	JRP MOMIR-PPC	JRP MEDVETKLEBS	JRP DISCOVER	JRP BIOPIGEE	JRP TOXOSOURCES	JRP ADONIS	JRP BEONE	JRP IMPART	JRP ARDIG	JRP RADAR	JRP FARMED	JRP FULL-FORCE	JRP WORLDCOM	JRP FED-AMR
Bioinformatics				x									x								x	x		
Biomarkers					x						x				x								x	
Biosecurity							x			x	x			x										
Collection of strains	x				x			x				x	x		x								x	
Database of sequences		x		x				x	x			X	x		x							x		x
Detection & characterization	x	x	x	x	x	x		x	x	x		x	x		x			x	x		x	x	x	x
Environment	x	x	x	x	x	x		x	x	x		x	x	x	x				x		x		x	
Exposure							x	x							x	x				x				
Long-read / WGS	x	x						x	x				x		x						x	x		x
Machine-learning																				x		x	x	x
MALDI-ToF	x				x							x												
Metagenomics		x		x					x	x											x	x		x
Microarray						x																		
Modelling							x					x			x	x	x			x				
On-site tests (POI)				x						x											x		x	
Pre- & probiotics											x													
Reservoirs	x							x			x	x	x		x	x				x				x
Risk assessment	x	x	x				x					x	x	x	x	x	x		x	x				
Sampling	x		x			x	x			x		x			x									x
Serological tests					x										x									
Source attribution	x	x										x	x		x					x				
Surveillance systems							x										x					x		x
Wildlife	x		x										x		x									x

*This table aims to identify the main areas of research covered by the JRP.*

## Second call JRP

- JRP12-AMRSH5-FARMED
- JRP13-AMRSH5-WORLDCOM
- JRP14-AMR2.1-FULL-FORCE
- JRP15-AMR2.1-FED-AMR
- JRP16-ET2.2-TELE-Vir
- JRP17-ET2.2-IDEMBRU
- JRP18-ET1.1-MEmE
- JRP19-ET1.1-PARADISE
- JRP20-FBZSH3-DISCoVeR
- JRP21-FBZ3.1-BIOPIGEE
- JRP22-FBZ4.1-TOXOSOURCES
- JRP23-FBZSH5-ADONIS
- JRP24-FBZSH9-BeONE



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- JRP12-AMRSH5-FARMED
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- JRP22-FBZ4.1-TOXOSOURCES
- JRP23-FBZSH5-ADONIS
- JRP24-FBZSH9-BeONE

## D2.6 Updated list and descriptions of priority research and integrative topics

September 2018

	Foodborne zoonoses (FBZ) <i>Solveig Jore</i>	Antimicrobial resistance (AMR) <i>Jean-Yves Madec</i>	Emerging threats (ET) <i>Dan Horton</i>
Analytical methods <i>Stefano Morabito</i>	FBZSH9	AMR6.1	ET1.1
Host-microbe interactions <i>Bruno Gonzalez-Zorn</i>			
Epidemiology <i>Dariusz Wasyl</i>	FBZSH3; FBZ4.1; FBZSH5	AMRSH5; AMR2.1	ET2.2; ET5.2; ET2.1
Risk assessment <i>Maarten Nauta</i>	FBZSH8; FBZ7.1		
Intervention <i>Marete Hofshagen</i>	FBZ3.1; FBZSH6	AMRSH1; AMR4.1	

The ID code of the topic identifies the domain (FBZ, AMR or ET) and the original topic number therein, but if the letters "SH" are present in the topic code, it means that the topic was originally proposed by a stakeholder. The final versions of the topic descriptions have been validated by the members of the Programme Management Team.

## Second call JRP, the stakeholders' choice

- JRP12-AMRSH5-FARMED
- JRP13-AMRSH5-WORLDCOM
- JRP14-AMR2.1-FULL-FORCE
- JRP15-AMR2.1-FED-AMR
- JRP16-ET2.2-TELE-Vir
- JRP17-ET2.2-IDEMBRU
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- JRP19-ET1.1-PARADISE
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- JRP22-FBZ4.1-TOXOSOURCES
- JRP23-FBZSH5-ADONIS
- JRP24-FBZSH9-BeONE

Development of new tools for **early (real-time) detection of resistant pathogens** in humans and animals, as well as new diagnostic tools, in particular **on-site tests** for humans and animals.

**Source attribution of bacterial foodborne zoonoses and antimicrobial resistance** considering also the environment and non-livestock reservoirs (e.g. pets and wildlife) as sources.

Determinants of the **reversal of the decreasing trend in Salmonella incidence** in humans and poultry in the EU.

Better tools for **detection and investigation of foodborne outbreaks, including antimicrobial resistant pathogens**, as well as economic assessments of potentially increased cluster detection through whole genome sequencing

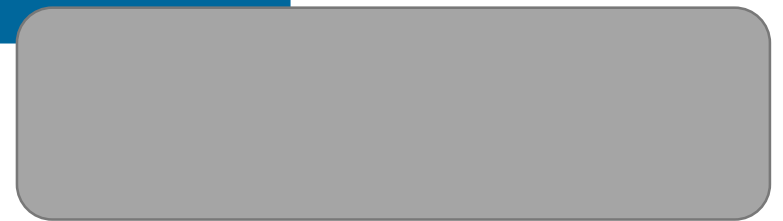


# Parasitology projects

- One Health EJP has offered a great opportunity.
- Parasitology cross-project approaches
  - Cooperation between MEmE, PARADISE and TOXOSOURCES
- Collaboration with the European Reference Laboratory for Parasites (EURLP).
- Collaboration with the WHO Collaborating Centre, with EFSA and ECDC.
- And with other national and international projects



# Conclusion





## In general

- Despite the COVID-19 crisis: creation and consolidation of **specific** (FBZ, AMR, ET, parasitology) **networks**, supporting **integrative activities** like capacity building, sharing of data, strengthening **prevent-detect-response** (see the Integrative Strategy Matrix).
- The **project specific webpages** on [www.onehealthejp.eu](http://www.onehealthejp.eu) are very complete (**search function!**) and will guide you and all stakeholders through the results and outcomes of the work done.



## Take-home message

- The cross-sector, **One Health approach** is very profitable; the existing Med-Vet/Food network is an excellent basis for a **unique European One Health consortium!**
- As legal entity, the [MedVetNet Association](#) will offer its partners a convenient European One Health forum and continue the uptake of practical One Health outcomes.



Thank you for your  
attention!



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OneHealthEJP.eu

# The One Health EJP contribution to science, health policy and society

## Impact on science



Moderator:  
**Roberto La Ragione**  
University of Surrey

**Verónica Pinho Mixão**  
One Health EJP BeONE project  
INSA





# BeONE

## Building Integrative Tools for One Health Surveillance

**Verónica Mixão**

One Health EJP Final Meeting

Paris, 11-12 September 2023



# BeONE: Building Integrative Tools for One Health Surveillance

- Enhancing evidence-informed public-health decision-making
- Connecting European genomic surveillance laboratories
- Promoting comparability and innovation in One Health surveillance



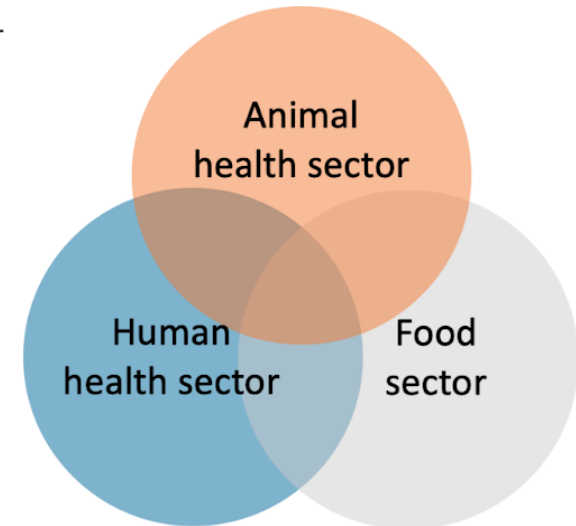
**Foodborne bacterial pathogens**

# WP1. Multi-country and intersectoral assessment of cluster congruence between genomic surveillance pipelines

- Comparison of typing methods used by different countries/sectors at all levels of resolution, including outbreak detection/investigation

	<i>L. monocytogenes</i>	<i>S. enterica</i>	<i>E. coli</i>	<i>C. jejuni</i>
Denmark	■ □	■ □	■ □	■ □
The Netherlands	■	■	■	■
Germany	■	■	■	■
Portugal	■	■	■	■
United Kingdom		□		
Germany	□	□	□	□
Italy	■ □	■ □	■ □	■ □
Poland	■	■	■	■
Germany	■ □	■ □	■ □	■ □

■ Allele-based    □ SNP-based    ■ Commercial software



Diverse datasets



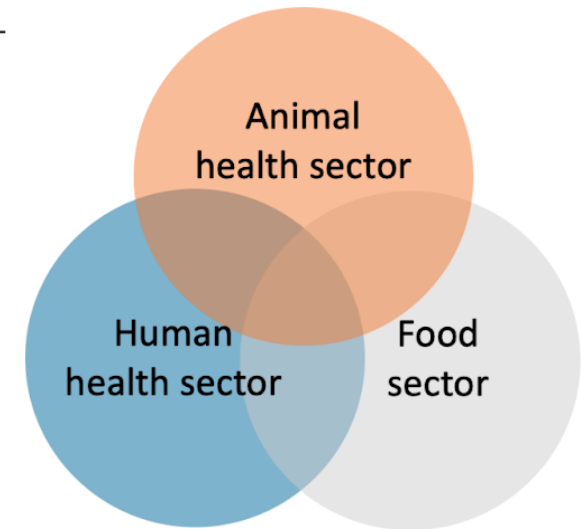
Useful asset for future surveillance and research works

# WP1. Multi-country and intersectoral assessment of cluster congruence between genomic surveillance pipelines

- Comparison of typing methods used by different countries/sectors at all levels of resolution, including outbreak detection/investigation

	<i>L. monocytogenes</i>	<i>S. enterica</i>	<i>E. coli</i>	<i>C. jejuni</i>
Denmark	■ □	■ □	■ □	■ □
The Netherlands	■	■	■	■
Germany	■	■	■	■
Portugal	■	■	■	■
United Kingdom		□		
Germany	□	□	□	□
Italy	■ □	■ □	■ □	■ □
Poland	■	■	■	■
Germany	■ □	■ □	■ □	■ □

■ Allele-based   □ SNP-based   ■ Commercial software



Diverse datasets

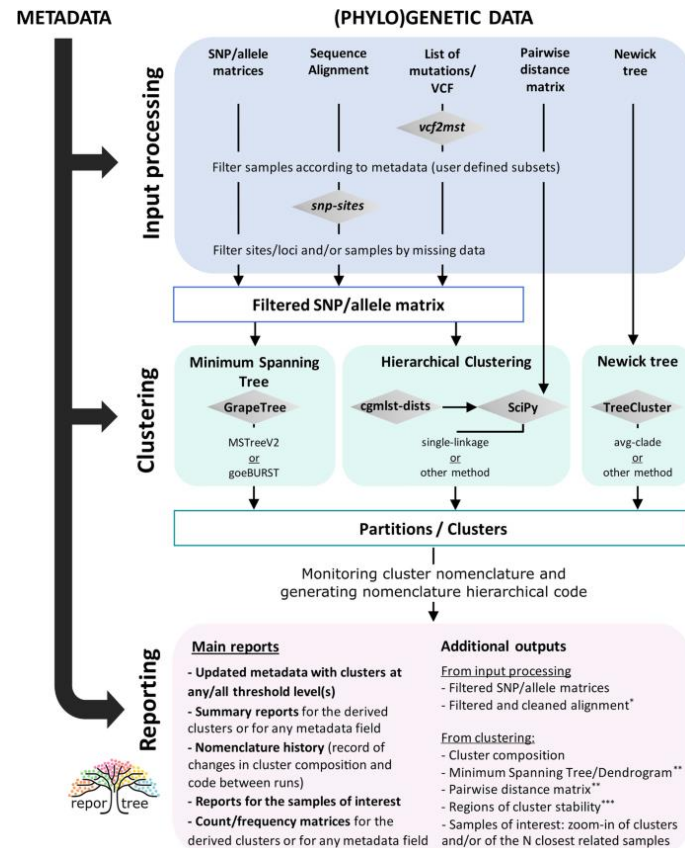


Useful asset for future surveillance and research works

How to harmonize the outputs and obtain clustering at multiple levels?



# ReporTree: a surveillance-oriented tool to strengthen the linkage between genetic clusters and epidemiological data

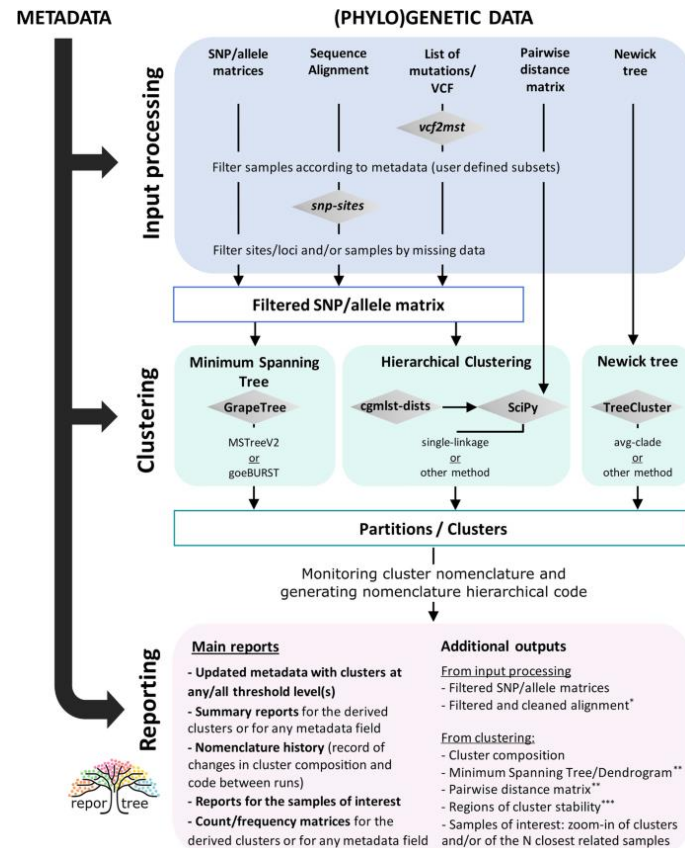


- Identification of genetic clusters at all resolution levels
- Surveillance-oriented reports



Mixão et al. (2023) *Genome Medicine* 15:43

# ReporTree: a surveillance-oriented tool to strengthen the linkage between genetic clusters and epidemiological data



Mixão et al. (2023) *Genome Medicine* 15:43

- Identification of genetic clusters at all resolution levels
- Surveillance-oriented reports

**Outcomes**

- ✓ Key-role in routine surveillance and outbreak investigation of bacterial and viral pathogens in Portugal
- ✓ Integration in the **COHESIVE** platform

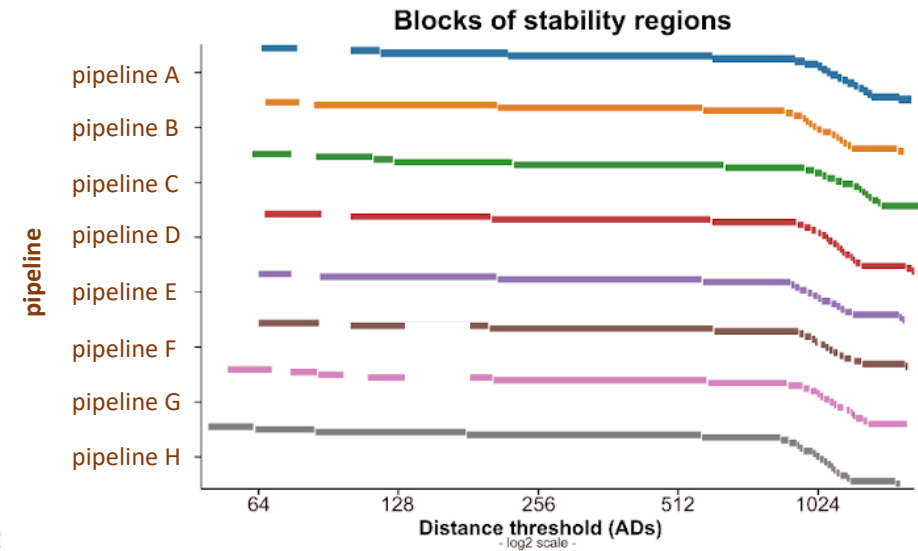


Collaboration with:



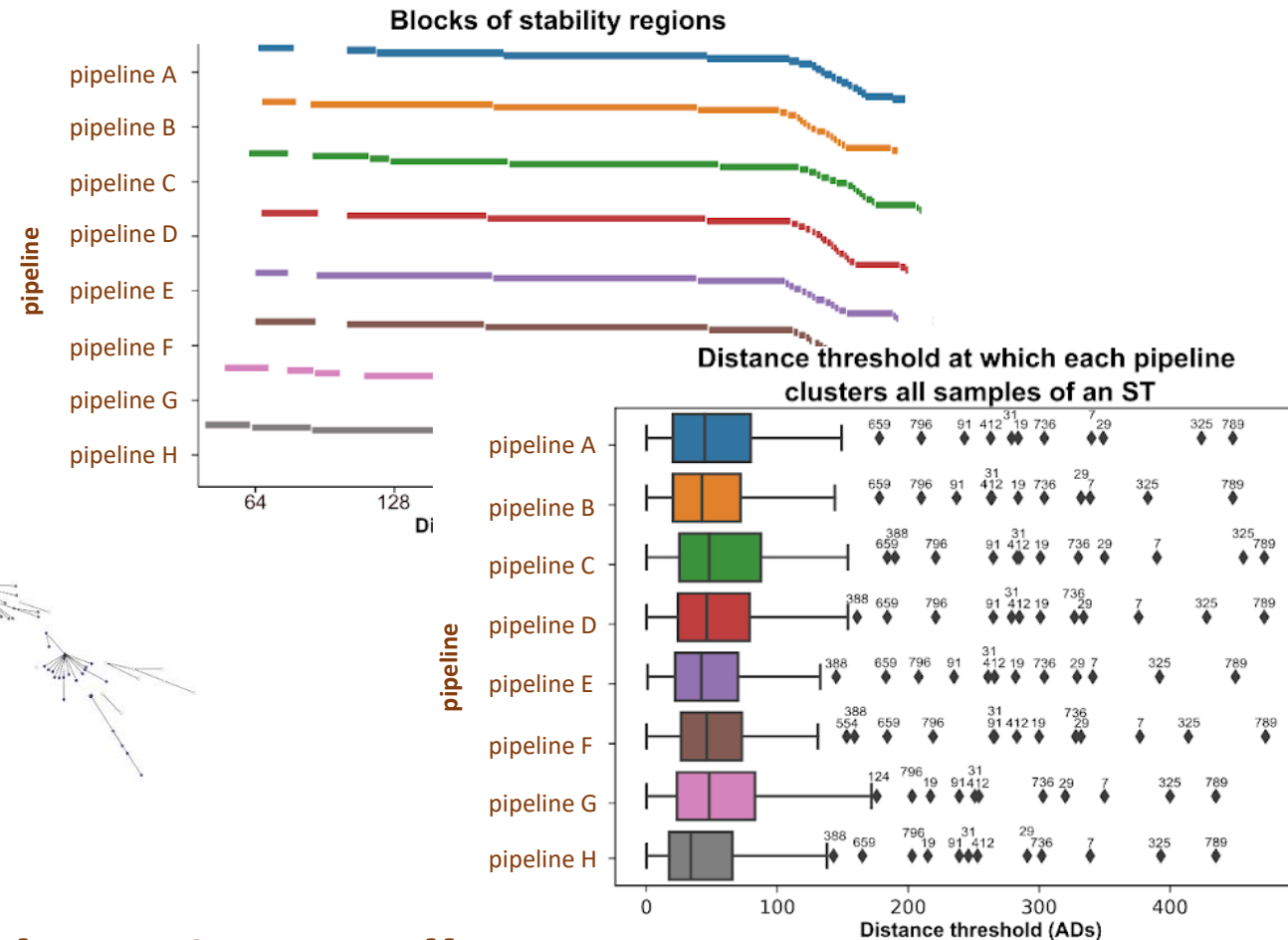
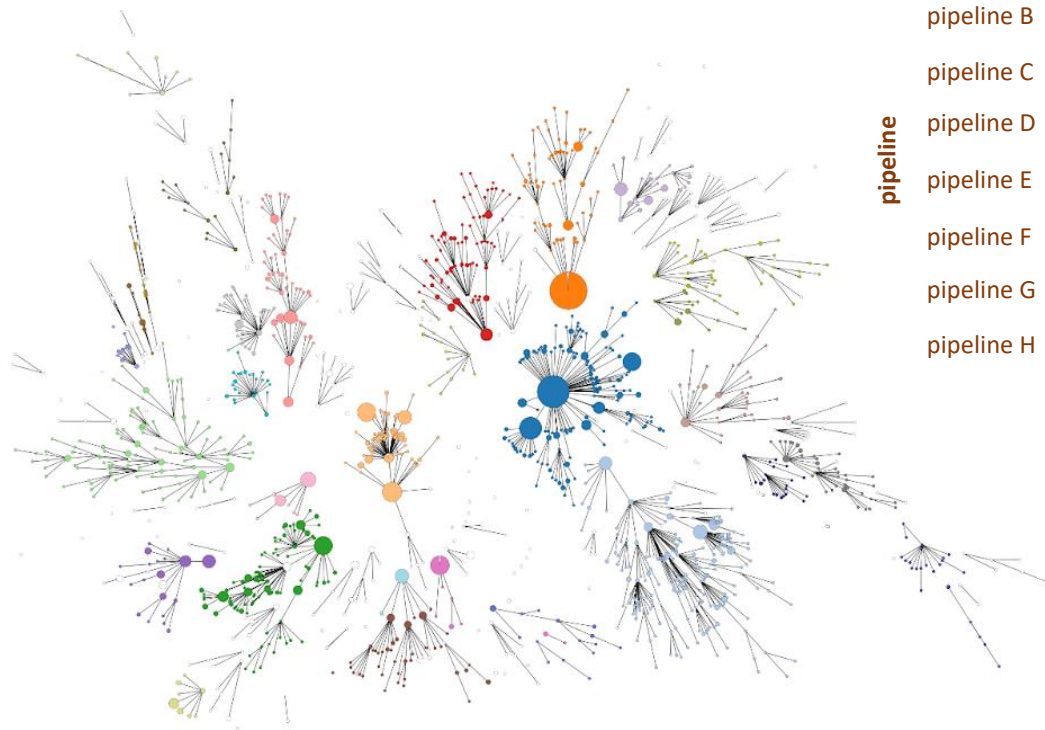
**Contributes to a sustainable and efficient public health genomics-informed pathogen surveillance**

# WP1. Multi-country and intersectoral assessment of cluster congruence between genomic surveillance pipelines



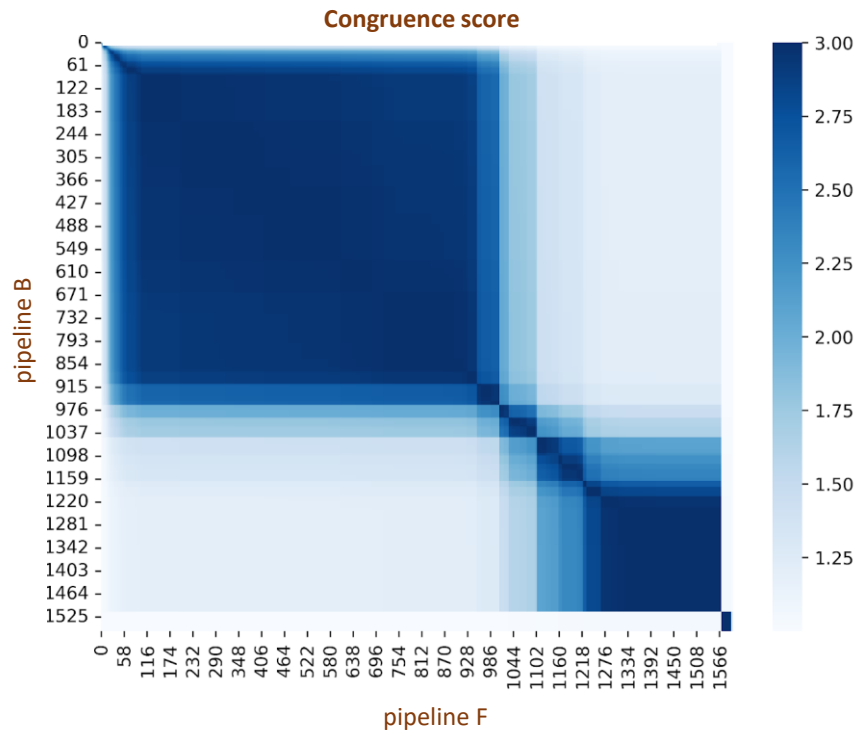
***Evaluation of allele-based clustering at all possible threshold levels and comparison of stability regions***

# WP1. Multi-country and intersectoral assessment of cluster congruence between genomic surveillance pipelines



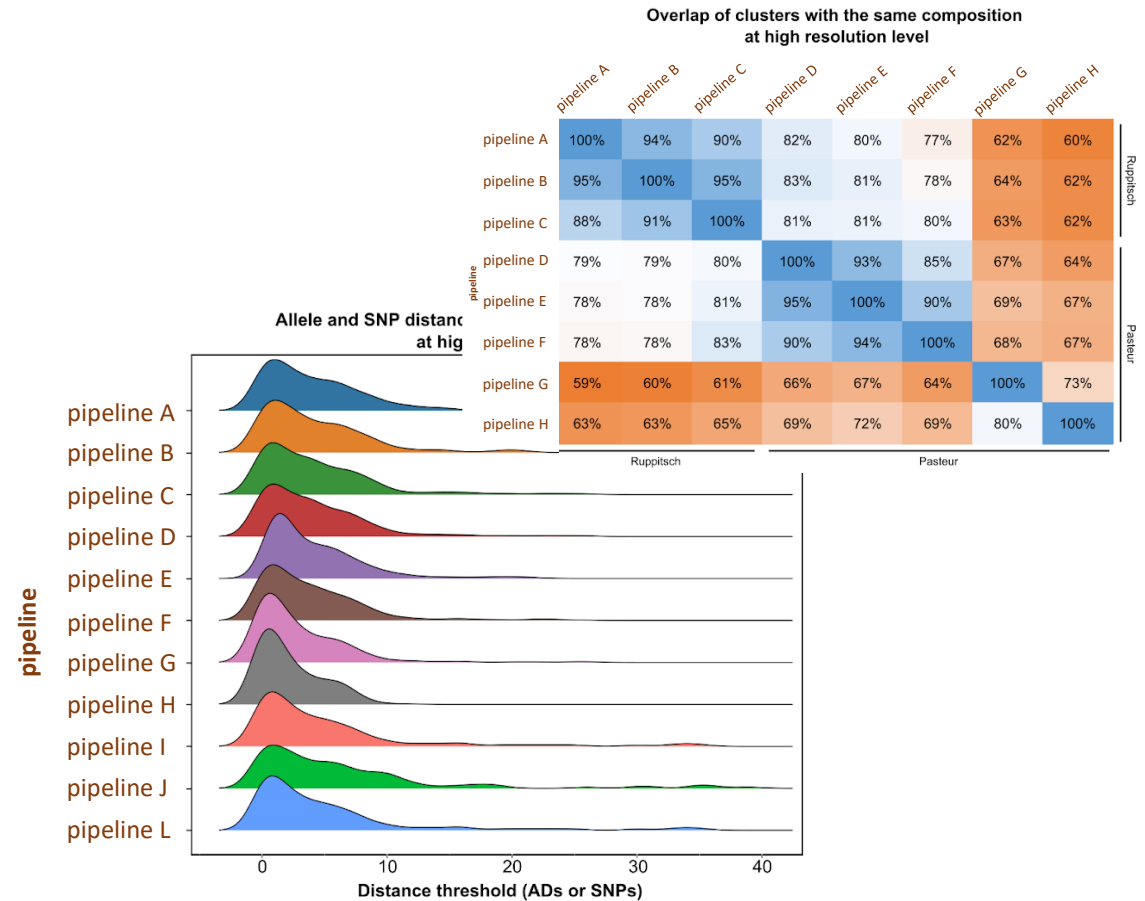
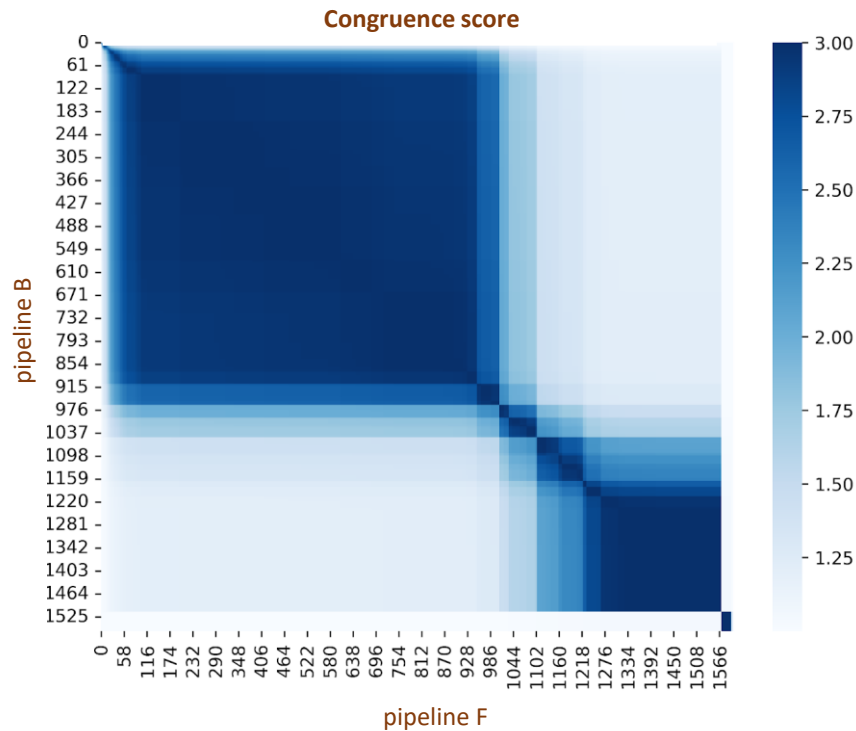
**Evaluation of allele-based clustering at all possible threshold levels and comparison of stability regions**

# WP1. Multi-country and intersectoral assessment of cluster congruence between genomic surveillance pipelines



***Global evaluation of cluster congruence  
between different pipelines at all threshold levels***

# WP1. Multi-country and intersectoral assessment of cluster congruence between genomic surveillance pipelines



**Global evaluation of cluster congruence  
between different pipelines at all threshold levels**



# WP1. BeONE: Building Integrative Tools for One Health Surveillance

Besides the comparative results, this work will provide a new set of tools that...

- Facilitate the technological transition by increasing the confidence of the laboratories when adopting new surveillance-oriented pipelines
- Support the continuous evaluation and long-term sustainability of any pipeline (e.g., by providing new insight on the impact of software updates)
- Promote the establishment of a fully integrative and efficient One Health genomic surveillance framework by facilitating the communication and integration of data obtained by different laboratories or promoting the transition by all laboratories to a unique “gold-standard” genomics-surveillance approach



# Acknowledgements



Instituto **Nacional de Saúde**  
*Doutor Ricardo Jorge*

FRIEDRICH-LOEFFLER-INSTITUT

**FLI**

Bundesforschungsinstitut für Tiergesundheit  
Federal Research Institute for Animal Health



German Federal Institute for Risk Assessment



IZSAM G. CAPORALE  
TERAMO



STATENS  
SERUM  
INSTITUT

ROBERT KOCH INSTITUT



Animal &  
Plant Health  
Agency



National Institute for Public Health  
and the Environment  
*Ministry of Health, Welfare and Sport*



**Veterinærinstituttet**  
*Norwegian Veterinary Institute*





Thank you for your  
attention!

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# The One Health EJP contribution to science, health policy and society

## Impact on science



Moderator:  
**Roberto La Ragione**  
University of Surrey

**Yacine Nia**  
One Health EJP TOX-DETECT project  
ANSES





# Outcomes of the OH EJP ToxDetect

**Yacine Nia, Jacques-Antoine Hennekinne**

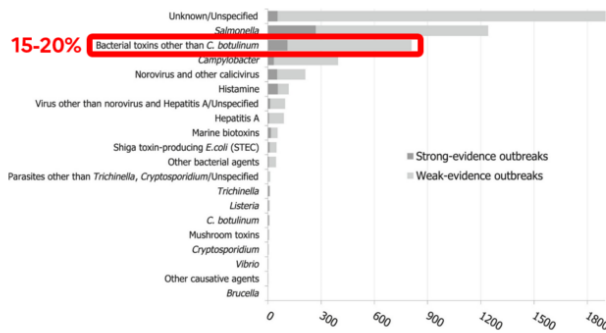
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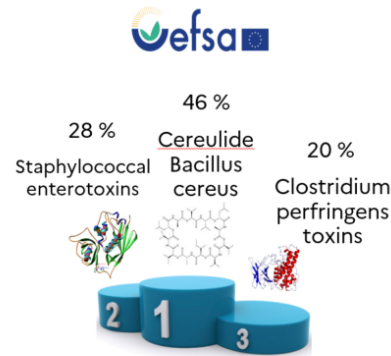
# Starting point and ... .. main objectives



- In 2020, 27 EU MSs reported 3086 outbreaks.
- Foodborne outbreaks due to bacterial toxins: **second causative agent**.



Efsa and ECDC report (2021). <https://doi.org/10.2903/j.efsa.2021.6406>



-Establishment of an EU-wide network focusing on the detection and identification of *S. aureus*, *B. cereus* and *C. perfringens*,

-Evaluation of different diagnostic approaches (e.g. mass spectrometry, immunological, functional approaches) to characterize *S. aureus*, *B. cereus* and *C. perfringens*,

-Generation and characterization of a reference collection of bacterial strains,

-Implementation and development of methods to identify bacteria and associated toxins and/or virulence factors,

-Transfer of the developed methods through proficiency trial organization.

## ➔ EJP OH ToxDetect (01/18 – 06/21)

(6 EU partners including 3 NRL CPS + EURL CPS as coordinator)

Development and harmonization of innovative methods for comprehensive analysis of food-borne toxigenic bacteria, ie. *Staphylococci*, *Bacillus cereus* and *Clostridium perfringens*



# Main results

- **Exchange** on quality assurance practices, SOP and materials to **promote work on bacteria producing toxins**
  - Fully characterized strains library (100) available
  - MaldiToF library available
  - 15 SOPs and 6 methods available and proof of concept of robustness and transferability by organization of 5 inter laboratory studies
- Presentation of ToxDetect outcomes during **cross-sector collaborative projects**
  - EuroBioTox project (H2020 security call)
  - TWG of the OPCW on bacterial toxins (security field)
  - EURL for CPS and NRL network = **key pillars** for dissemination (but for SEs only!)

**A question remains .... How to disseminate developments and results for bacteria and toxins not covered by the EC reg 2073/2005 ?**

# Scientific and societal impacts

- Development of a tool box strategy including various complementary principles with a **direct impact on FBO characterization**
- Improve consumer protection by filling gaps of lacking methodologies especially for non targeted toxins
- Improve FBO characterization (strong vs weak evidence)
- Improve implementation of Dir 2003/99

// with the EURL for CPS working program on harmonization of reporting of SFPO across EU MS

// with Standardization activities at the CEN TC 463 on bacterial toxins ?

// with Standardization activities at the ISO TC 34 SC9 level on

- Dvpt of a Std for validation/verification of bacterial toxins analysis (WG3)
- Dvpt of a Std for SEs quantification (WG30)
- Dvpt of EN ISO 6888-4 for *se* gene content by PCR tools (WG13)



 Veterinærinstituttet National Veterinary Institute	Taran Skjerdal
 INRAE In science, deep in life. From soil, to farm.	Nalini Rama Rao Michel Gohar Michel Hébraud
 BfR Risiken erkennen – Gesundheit schützen	Stephen S. Marino Hendrick Frentzel
 sciensano	Julien Masquelier
 Institut Pasteur	Dominique Clermont Julia Chamot-Rooke Christelle Mazuet
 anses	Valerie Fessard Benoit Gassiloud Manon Michaut Abdelrahim Abakabir

# Thank you for your attention!



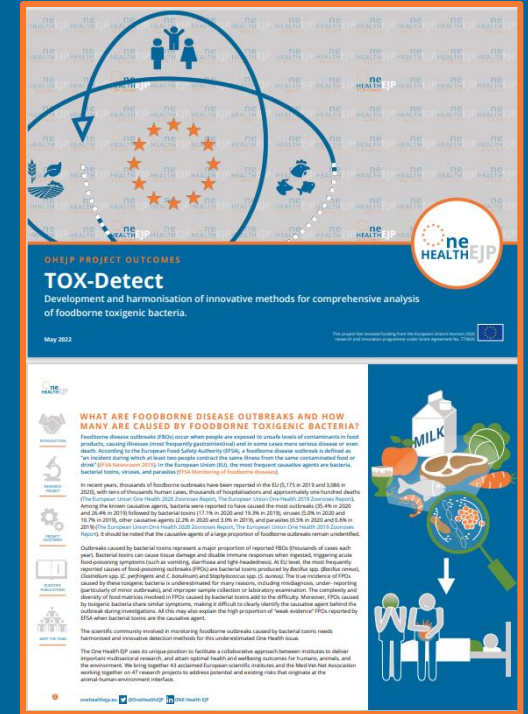
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**TOX-Detect**  
Development and harmonisation of innovative methods for comprehensive analysis of foodborne toxigenic bacteria.

May 2022

**WHAT ARE FOODBORNE DISEASE OUTBREAKS AND HOW MANY ARE CAUSED BY FOODBORNE TOXIGENIC BACTERIA?**

Foodborne disease outbreaks (FDOs) occur when people are exposed to levels of contaminants in food products, causing illnesses that frequently go unreported, and in some cases more serious disease or even death. According to the European Food Safety Authority (EFSA), foodborne disease outbreaks is defined as "an incident during which at least two people contract the same illness from the same contaminated food or drink" (EFSA Occurrence, 2019). The European Centre for Disease Prevention (ECDC) defines foodborne outbreaks as "bacterial, viral, and parasitic infections of foodborne origin".

In recent years, thousands of foodborne outbreaks have been reported in the EU (EFSA 2019 and EFSA 2022), with tens of thousands human cases, thousands of hospitalisations and approximately one hundred deaths (The European Centre for Disease Control 2020 Disease Report, The European Union One Health 2019 Disease Report). Among the known causative agents, bacteria were reported to have caused the most outbreaks (58.4% in 2020 and 56.4% in 2019), followed by parasites (17.7% in 2020 and 17.9% in 2019), viruses (12.2% in 2020 and 12.7% in 2019), other causative agents (6.2% in 2020 and 5.8% in 2019), and prion agents (4.5% in 2020 and 4.6% in 2019). In particular, in the 2020 and in 2019 the European Union One Health 2020 Disease Report, The European Union One Health 2019 Disease Report, it should be noted that the causative agent of a large proportion of foodborne outbreaks remain unidentified.

Outbreaks caused by bacterial toxins represent a major proportion of reported FDOs (thousands of cases each year). Bacterial toxins can cause tissue damage and elicit immune responses when ingested, triggering acute food poisoning symptoms such as vomiting, diarrhoea and light-headedness. ECDC stated that most frequently reported causes of food poisoning outbreaks (FPOs) are bacterial toxins produced by *Staphylococcus aureus*, *Clostridium perfringens*, and *C. botulinum* and *Shiga toxin* (see ECDC Annual Report on Foodborne Outbreaks, 2020). The true incidence of FPOs caused by these toxins is underestimated by many reasons, including misdiagnosis, under-reporting (particularly of minor outbreaks), and improper sample collection or laboratory contamination. The complexity and diversity of foodborne toxins (FDTs) caused by bacterial toxins and the difficulty to trace FDTs caused by temperate bacteria share similar symptoms, making it difficult to clearly identify the causative agent behind the outbreak during investigations. All this may also explain the high proportion of "weak evidence" FPOs reported by EFSA when bacterial toxins are the causative agent.

The scientific community involved in monitoring foodborne outbreaks caused by bacterial toxins needs harmonised and innovative detector methods for this understudied One Health issue.

The One Health EJP uses its unique position to facilitate a collaborative approach between institutes to deliver impactful multidisciplinary research and grant optimal health and wellbeing outcomes for humans, animals, and the environment. We bring together 43 excellent European scientific institutes and the best of best Association working together on 27 research projects to address potential and existing risks that originate at the animal-human-environment interfaces.

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# The One Health EJP contribution to science, health policy and society

## Impact on science



Moderator:  
**Roberto La Ragione**  
University of Surrey

**Cécile Boland**  
LIN-RES PhD  
Sciensano







# PhD02-LIN-RES:

Investigation of the molecular basis, origin, transferability and risk factors associated with linezolid-resistance emergence in Gram-positive bacteria of human and animal origin

**Dr. Cécile Boland**

One Health EJP Final Meeting

Paris, 11-12 September 2023

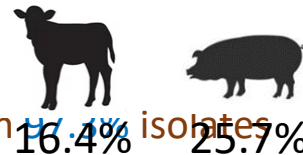
# Key outputs

✓ Research paper published in 2021

- Linezolid resistance (LR)

- Critical for

- Animal reservoir highlighted through selective monitoring



- **Transferable** LR genes in 16.4% isolates
  - Threat for AMR transmission to humans
  - **Cross-selection** with the use of **florfenicol** will maintain LR genes

✓ PhD thesis defended in 2022

J Antimicrob Chemother  
<https://doi.org/10.1093/jac/dkab376>

Journal of  
Antimicrobial  
Chemotherapy

## Large diversity of linezolid-resistant isolates discovered in food-producing animals through linezolid selective monitoring in Belgium in 2019

Michaël Timmermans<sup>1,2</sup>, Bert Bogaerts<sup>3</sup>, Kevin Vanneste<sup>3</sup>, Sigrid C. J. De Keersmaecker<sup>3</sup>, Nancy H. C. Roosens<sup>3</sup>, Carole Kowalewicz<sup>1</sup>, Guillaume Simon<sup>1</sup>, Maria A. Argudin<sup>†</sup>, Ariane Deplano<sup>4,5</sup>, Marie Hallin<sup>4,5,6</sup>, Pierre Wattiau<sup>1</sup>, David Fretin<sup>1</sup>, Olivier Denis<sup>6,7</sup> and Cécile Boland<sup>1\*</sup>



# Outcomes

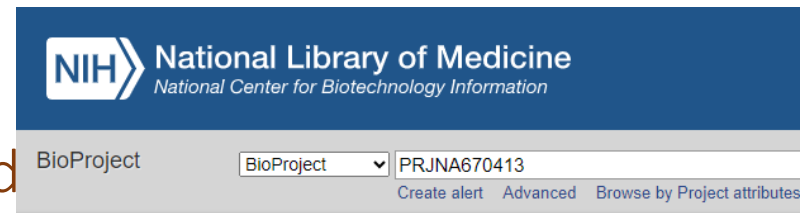
- Key results shared with:
  - Belgian institutions: FASFC, FAMHP, AMCRA
  - European institutions: EURL-AR/EFSA/EC
- Creation of a **technical working group** in Belgium on the question of the **use of florfenicol in animals** and cross-selection of linezolid resistance
- **EURL-AR working group** is being settled to agree on an harmonized launch soon a voluntary selective linezolid monitoring in several EU countries
  - Aim: carefully monitor this resistance in animals



# Impact

- Outputs of this project highlighted the needs:
  - for a good surveillance and understanding of the mechanisms and spread of resistance
  - to promote a prudent use of ALL antibiotics in a One Health perspective
- Results publically available to compare with future monitorings/researches

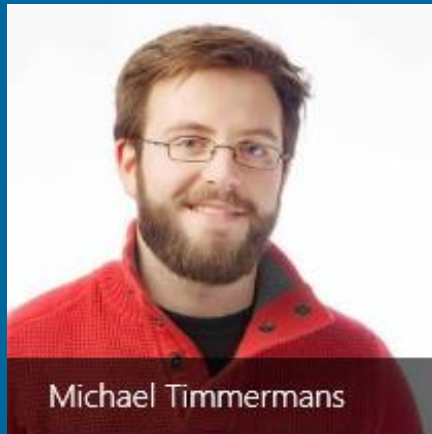
- Awareness of the human and



- Reflection and adaptation of the Belgian guidelines on the use of fluoroquinolones in animals is ongoing
  - Limit the risk of selection and spread of LR bacteria in animals



Special thanks to  
the PhD



# Thank you for your attention!

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& Thanks to:

- A. Radu and D. Petrone
- B. Bogaerts, K. Vanneste, S. De Keersmaecker, N. Roosens and the TAG technical team
- C. Kowalewicz
- G. Simon
- M. Argudin, A. Deplano, M. Hallin (NRC S. aureus)
- VET-EPI (M. Driesen and X. Simons)
- Hygiene hospitalière from St Luc Hospital
- P. Wattiau
- D. Fretin
- O. Denis



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