



| <b>Minutes</b><br><b>One Health EJP</b><br><b>Grant Agreement number 773830</b> |  |
|---|--|
| <b>Date</b>   | <b>22 November 2022 (8:30 – 13:00) CET</b>                     |
| <b>Venue</b>  | FoHM's Headquarters<br>Nobels väg 18, Solna, Sweden            |
| <b>Meeting</b>  | Joint Programme Managers/Owners/Stakeholders Committee Meeting |

## 1. Opening and welcome address

Pikka Jokelainen (WP3 and WP5 deputy leader - SSI) welcomed the participants and presented the agenda of the meeting.

## 2. One Health EJP key facts

Pikka introduced the speakers presenting the highlights of the One Health EJP, beginning with a brief history of the Consortium and then reviewing the achievements based on perspectives from an earlier SWOT analysis.

**To describe the “One Health EJP journey”**, Arnaud Callegari (Coordinator - Anses) presented the successive steps conducted, from 2000 (with CoVetLab that initiated the FP6 MedVetNet Network of Excellence between 2004 and 2009, which then gave birth to the Med-Vet-Net Association in 2009 until now) to 2023 (end of the One Health EJP and new perspectives for the future), to create and enhance a Med-Vet network in One Health approach. The community formed by the One Health EJP, gathers more than 500 researchers from Public Health (PH), Animal Health (AH) and in Food Safety (FS) fields, from 44 partners from 22 EU countries. As conclusion, Arnaud addressed the question of the future. He pointed out that while there is no concrete continuation foreseen at this stage of progress of the One Health EJP, the EJP remains nevertheless in a position to expect a continuation in the future, notably thanks to its input in raising awareness of importance of One Health approach and to the MedVetNet Association, which can play the role of refugee solution until next EU funding opportunity. Arnaud also underlined that welcoming the environmental sector would be a step forward.

Pikka then gave the floor to the Project Management Team members to present the key points from analysis of Threats, Weaknesses, Strengths and Opportunities.

Firstly, Annemarie Kaesbohrer (WP5 Science to policy leader – BfR) listed the main **Threats** including:

- Duplication of work instead of synergies and complementarity;
- Duration of One Health EJP too short to achieve measurable impact;
- Cross-sectoral collaboration and cooperation hampered by different priorities and capabilities;
- Institutional landscape not ready for One Health approach.

Secondly, Arjen van de Giessen (WP2 SRA leader – RIVM) addressed the **Weaknesses** by raising that:

- One Health EJP is limited in scope;
- One Health EJP is limited in geographic distribution;
- One Health EJP financial structure details proved not to fit all equally well;
- One Health EJP consortium balance is suboptimal.

Then Roberto La Ragione (WP6 Training & Education leader – UoS) underlined important **Strengths** of the One Health EJP:

- Highly visible One Health consortium focusing on Med-Vet-Food;
- New One Health database and tools;
- Harmonisation of One Health protocols;



- Improved preparedness of public Med-Vet-Food institutes;
- New One Health education programmes training future One Health experts;
- Established collaborations for the future with strong legacy and sustainability plans.

The presentation was concluded with the **Opportunities** presented by Hein Imberechts (Scientific Coordinator – Sciensano), who pointed out:

- High public interest, increased by the COVID-19 crisis;
- Innovative tools and practices are available to support the One Health approach;
- One Health EJP is an excellent basis for creating a true One Health consortium in Europe;
- International bodies and funding programmes advocate the One Health approach, creating an excellent opportunity;
- However, a joint One Health initiative is not (yet!) planned.

Pikka thanked the presenters, encouraged to discuss the points during later sessions, and introduced the poster session.

### 3. Poster Session

The poster session intended to present selected key outcomes of Joint Research Projects for consideration of uptake by stakeholders. Two separate meeting rooms enabled the presentation of selected projects in each of the three domains of the One Health EJP: Foodborne Zoonoses, Antimicrobial Resistance and Emerging Threats.

→ **All the posters presented are available on the meeting website, by clicking [here](#).**

The following projects were presented and discussed with the audience.

#### 3.1. Foodborne Zoonoses

Session moderated by Karin Artursson, Pikka Jokelainen and Annemarie Käsbohrer.

- ❖ **Design and implementation of surveillance activities were presented with the projects:**
  - **NOVA:** Novel approaches for design and evaluation of cost-effective surveillance across the food chain – presented by Jenny Frössling (Project leader, SVA),
  - **Air Sample:** Air-sampling, A Low-Cost Screening Tool in Biosecured Broiler Production – presented by Gro Johannessen (project contact person, NVI).
- ❖ **Outcomes obtained in Interpretation of surveillance data & cross-sector communication of data were presented with the projects:**
  - **DISCoVer:** Discovering the sources of *Salmonella*, *Campylobacter*, VTEC and antimicrobial resistance – presented by Lapo Mughini Gras (Project representative, RIVM),
  - **TOXOSOURCES:** *Toxoplasma gondii* sources quantified – presented by Pikka Jokelainen (Project leader, SSI),
  - **ADONIS:** Assessing Determinants of the Non-Decreasing Incidence of Salmonella – presented by Lapo Mughini Gras (Project representative, RIVM),
  - **BeONE:** Building Integrative Tools for One Health Surveillance – presented by Verónica Mixão (INSA).
- ❖ **Action (prevention & response) was illustrated by the project:**
  - **BIOPIGEE:** Biosecurity practices for pig farming across Europe – presented by Annemarie Käsbohrer (Project representative, BfR).

#### 3.2. Antimicrobial Resistance

Session moderated by Arjen van de Giessen and Roberto La Ragione.



❖ **Laboratory methods were discussed with the project:**

- **IMPART**: Improving phenotypic Antimicrobial Resistance Testing by development of sensitive screening assays for emerging resistances, and setting missing ECOFFs – presented by Kees Veldman (Project leader, WBVR).

❖ **Outcomes in Interpretation of surveillance data & Cross-sector communication of data were discussed with the projects:**

- **FULL-FORCE**: Full-length sequencing for an enhanced EFFORT to map and understand drivers and reservoirs of antimicrobial resistance – presented by Pieter-Jan Ceysens (Project leader, Sciensano),
- **FED-AMR**: The role of free extracellular DNA in dissemination of antimicrobial resistance over ecosystem boundaries along the food/feed chain – presented by Manuela Caniça (Project representative, INSA).

### 3.3. Emerging Threats

Session moderated by Dolores Gavier-Widén and Dan Horton.

❖ **Laboratory methods were discussed with the projects:**

- **TOX-DETECT**: Development and harmonisation of innovative methods for comprehensive analysis of foodborne toxigenic bacteria, i.e. *Staphylococci*, *Bacillus cereus* and *Clostridium perfringens* – presented by Yacine Nia (Project co-leader, Anses),
- **TELE-Vir**: Point-of-incidence toolbox for emerging virus threats, presented by Katja Spiess (Project leader, SSI).
- **PARADISE**: Parasite Detection, Isolation and Evaluation – presented by Simone Mario Cacciò (Project leader, ISS).
- **MEEmE**: Multi-centre study on *Echinococcus multilocularis* and *Echinococcus granulosus* s.l. in Europe: development and harmonisation of diagnostic methods in the food chain – briefly presented by Dolores Gavier-Widén in the absence of MEEmE's project leader.

## 4. Plenary Session: Main outcomes of the Joint Integration Projects

Karin Artursson (WP4 – Integrative activities leader, SVA) introduced the session intended to present the methods, tools and protocols of the Joint Integrative Projects that have been produced and are now available for uptake and further use by stakeholders.

→ **All the presentations given during the session are annexed to this meeting report.**

The presentation started with the JIP ORION presented by Mia Torpdahl (SSI) on behalf of Matthias Filter, Project leader (BfR) and Fernanda Dórea, co-leader (SVA). **JIP ORION** “One health surveillance Initiative on harmonization of data collection and interpretation” is a high-level framework that supports collaboration, mutual understanding, knowledge exchange and data interoperability between OH sectors. Among the tools developed by ORION, Mia presented:

- One Health surveillance Codex.
- OHEJP Glossary and OHS Inspirational catalogue to support OHS collaboration & cross sectorial communication.
- OH knowledgebase-Epi and OH knowledgebase-NGS to improve the OHS knowledge base.
- Health Surveillance Ontology (HSO) and Tools to annotate data and meta data to support OHS data interoperability, integration & interpretation.
- Consensus Report, Annotation Checklist, National OHS Report Templates to support external communication of OHS outcomes.

The second integrative project presented was the **JIP COHESIVE**: One Health Structure in Europe, presented by Elina Lahti (SVA) on behalf of the project team with Kitty Maassen, (RIVM), Frits



Vlaanderen (RIVM), Marion Gottschald (BfR), Adriano Di Pasquale (IZS) and Thomas Selhorst (BfR) and Rob Dewar (APHA).

The main aim of COHESIVE was to develop sustainable One Health approaches with respect to signalling, assessing, responding and controlling zoonoses at the national and regional level within EU countries. This objective has been achieved by setting up an integrated human-veterinary-food risk analysis structure for efficient signalling, risk-assessment, response and control of (emerging) zoonoses and the development of a suite of software tools to support surveillance and management of outbreaks.

Some selected outcomes & tools:

- Guidelines to support countries to strengthen the One Health collaboration in the area of risk ([www.ohras.eu](http://www.ohras.eu) / [www.onehealthguidelines.eu](http://www.onehealthguidelines.eu))
- Online Risk Assessment Decision Support tool (<https://cohesive.onehealthjep.eu>)
- COHESIVE prototype Information System (CIS) (<https://cohesive.izs.it>)
- FoodChain-Lab: Free open-source software (<https://foodrisklabs.bfr.bund.de/foodchain-lab/>)
- Shiny Risk (<https://github.com/RobertOpitz/shinyRisk>)

Elina concluded by explaining that to further improve preparedness, the efforts are pursued to improve interoperability with main data exchange systems at EU level (EFSA, ECDC, RASFF and MS systems).

Current cooperation highlighted:

- Framework of the CIS: Contacts with relevant whole-genome sequencing (WGS) projects (BeONE, MATRIX, CARE, COVRIN and TELEVIR) and further harmonization with EFSA WGS tool and BeONE.
- Framework of FoodChain-Lab: EFSA co-operation on establishment of data standards for supply chain tracing for authorities and creation of a European tracing tool ecosystem.

The presentations followed with [JIP CARE](#): *Cross-sectoral framework for quality Assurance Resources for countries in the European Union*, presented by the co-leader of the project, Mia Torpdahl (SSI). JIP CARE is focused on the development of a new One Health concepts for proficiency testing of laboratories, reference materials and quality/availability of demographic data for risk analysis.

Some selected project outcomes:

- Creation of a collection of reference materials for seven foodborne bacterial pathogens: *Salmonella* / *Listeria* / *Campylobacter* / *E. coli* / *Staphylococcus* / *Bacillus* / *Yersinia*. The purpose of this collection is to strengthen the links between food safety, veterinaries, public health.
- Guide for accessing relevant data and models for quantitative microbial risk assessment, aiming to help to identify data/knowledge that risk assessors and data scientists need and to support the whole risk assessment community including national and international risk assessment agencies, and academic institutions.

[JIP OH-HARMONY-CAP](#): *Harmonised protocols and common best practice* was presented by Mia Torpdahl (SSI) on behalf of Nadia Boisen (Project leader, SSI).

Mia presented the objectives and some selected outcomes of the project:

- Development of a Benchmarking Instrument OHLabCap to measure and provide a description of the microbiology system in the OH-field;
- One Health laboratory interoperability guidance for model organisms;
- Design of harmonised protocols for model organisms: protocols proposed by CARE, should contribute to an improvement in the standardisation of protocols for STEC/ETEC and *Cryptosporidium* spp. It also allows to develop new primers for the detection of STEC and ETEC related genes and represent an update reflecting the current epidemiology and current knowledge of microbiology organisms
- Dissemination and Increase the EU laboratory capacity.

[JIP MATRIX](#): *Connecting dimensions in One Health surveillance* was presented by Guido Benedetti, Project leader (SSI). MATRIX created solutions for European countries to improve implementation of





the One Health Surveillance. MATRIX invites European institutes working in the animal health, public health and food safety sectors, to adopt the MATRIX solutions and to further build upon them.

Guido presented examples of tools developed by MATRIX:

- One Health – EpiCap Tool - to evaluate the capacities and capabilities for One Health Surveillance of a specific sector and/or pathogen of choice.  
Three dimensions are evaluated: Organization of One Health, One Health in operational activities and Impact of One Health.
- Manual for One Health Surveillance Dashboards <https://sva-se.github.io/MATRIX-dashboards/> to facilitate the design and implementation of One Health Surveillance dashboards using open source tools.

**JIP COVRIN:** *One Health research integration on SARS-CoV-2 emergence, risk assessment and preparedness* was presented by Dan Horton, co-leader of the project (UoS). Firstly, Dan presented two main integrative research objectives: to identify drivers for the emergence and spread of SARS-CoV2 and to generate data and build models for risk assessment of SARS-CoV2.

Selected outputs describes by Dan:

- SARS-CoV2 detection: Animal samples: Protocol database and comparison exercise are provided. Detection in environmental samples: Environmental RNA quantifications provided; input risk assessment.
- SARS-CoV2 Characterization: Next generation sequencing protocol repository was set up; Cell line sensitivity->report; Animal model protocols collated -> catalogue; Pathology toolbox per species -> report
- Risk assessment and surveillance: procedure for integration of surveillance data; Evaluation of the current surveillance activities; Analyse of risk of transmission in pets with epidemiological surveys. A case study in SARS-CoV2 sampling in animals has been conducted by the partners Institutes.

As conclusion, Dan highlighted the expected impact of the JIP COVRIN: the societal and policy impact consists in improvement of risk assessment and health risks control. The preparedness research and risk assessment and control research should be considered as an important research output.

The last integration activity presented during the session was the **SimEx:** *Table-top exercise that covered a realistic foodborne outbreak at a national level*, implemented from September 2021 to December 2022 and gathering 257 participants from 11 countries. The actual exercise was conducted at the national level during 2-3 days in the period of May to September 2022.

Federico Alves (SVA) provided feedback from the exercise aimed at testing the One Health capability, capacity and interoperability of authorities in PH, AH and FS to work together. The main objectives were: increasing knowledge, increasing understanding of One Health, increasing capability to communicate. Federico explained that the exercise was conducted as a table-top exercise with an adaptable scenario, designed to encourage cross-sectoral communication and information sharing between PH, AH and FS authorities.

The exercise resulted in increased knowledge focusing on collaboration, roles and responsibilities during a zoonotic outbreak and also how to use guidelines and available tools (declared by 88% of participants) and in enhanced understanding of One Health and data sharing (90% of participants claimed to have increased their understanding on the importance of data harmonization practices and 18% feel their own organisation does not prioritize the improvement of such practices). National reports highlighted common gaps in the One Health approach and defined a roadmap for future challenges.

94% reported feeling encouraged to pursue a One Health approach and try to work closer with the other health sectors in a future outbreak situation. For the future, it will help to support decision makers in the implementation of structural changes at institutional level by raising awareness to the benefits of a One Health strategy and by highlighting the current gaps and define strategies to address them.



The presentations were followed by an active discussion.

Hein Imberechts asked if the instrument JIP was a good way to reply to emergency (concerning the JIP COVRIN). Dan Horton responded affirmative: it allowed to get partners involved in testing engaged. The impact is already visible.

Pikka Jokelainen asked the presenters about the cross-sector collaboration between the JIPs; experiences and how it was facilitated. Mia Torpdahl reported a positive experience of collaboration across projects, and that a lot of researchers from different institutes are participating in different JIPs. Guido Benedetti added that it is easy to build on the experience from different countries and corpus of knowledge, it should allow the researchers to talk together, communicate more and collaborate more. Strengthening collaboration and sharing experiences are crucial to the advancement of science and research. Elina Lahti said that from COHESIVE project, it is easy now to continue the development, but it was really challenging to establish collaboration, notably in the COVID-19 context when people worked together digitally.

Stef Bronzwaer (EFSA) asked the project leaders what they consider as success factor. Guido Benedetti said that there are no easy solutions, it is necessary to go through the total production obtained and summarize it.

Mia Torpdahl and Ann Lindberg commented the work undertaken by the OHEJP during the COVID-19 pandemic, when the Partner Institutes dedicated the resources to support Public Health. The researchers should be telling their part in the story. The future of the Consortium should be taken into account as well as the sustainability of the integrative activities.

Arnaud Callegari defended the idea of continuation of the EJP One Health: "Now we have the results, we will continue to disseminate them in 2023 and we hope that ECDC, EFSA, REA, DG Agri will support the continuation of the work after 2023."

Carlos das Neves (EFSA) stated that to push the work done a success story is needed, for example out of the AMR domain.

Ole Heuer (ECDC) stated that the presented outcomes are much appreciated: alignment of data/ JIPs etc. However, the needs of the EU members to reinforce the OH concept need to be further explored.

## 5. Plenary session on Institutionalization of One Health

Ludovico Sepe (WP5, BfR) introduced the speakers and the session's objectives: firstly to show how the One Health EJP contributed to institutionalisation of the One Health approach across Europe and secondly to inspire the participants to implement the OH approach in their respective countries. Ludovico underlined the importance of the national level to implement the One Health solutions and to overcome barriers to cross sectoral cooperation, including sharing data, different sectors using different languages, overlooking some sectors, organization, ownership, and funding issues. Some of the tools to overcome barriers are provided by OHEJP: tools to One Health surveillance, harmonisation and integration of approaches, knowledge on One Health issues along whole prevent-detect-respond axis.

The examples of Sweden and Italy show national efforts in putting in place a One Health approach at the national level. The Swedish context was presented by Ann Lindberg, Director General of the National Veterinary Institute of Sweden (SVA). Umberto Agrimi, Director of the department of Food safety, nutrition and veterinary public health of the Istituto Superiore di Sanità (ISS), presented the Italian example.

### 5.1. Institutionalisation of the One Health approach in Sweden

Ann Lindberg firstly underlined the high-level political commitment to advocate and support the implementation of OH e.g. One Health Joint Plan of Action 2022-2026 of the Quadripartite (the Food and Agriculture Organization of the United Nations (FAO), the United Nations Environment Programme (UNEP), the World Health Organization (WHO), and the World Organisation for Animal Health (WOAH)).



She also recalled that the health challenges threatening humans, animals, plants and the environment require holistic, integrated solutions with a systemic approach that incorporates wider structural factors, as well as systemic prevention measures integrating the health of humans, animals, plants and the environment. This shift requires the embrace of One Health to move beyond the “siloed” approaches still adopted by many sectors.

A survey, conducted in Sweden in the framework in the [PhD Sustain](#), has shown how the One Health EJP impacts the actors at individual, institutional and country levels. The survey's results showed notably: wider and stronger networks and development of competence at individual and institutional levels; improved crisis prevention and preparedness and expanded knowledge on OH among managers at different levels were underlined, as well as a further development of national collaborative processes (mandate of Zoonosis council, joint reporting, joint work in ad hoc commissions). According to the survey respondents, at EU level, the EJP One Health boosted multi-sectoral collaboration and deepened collaboration within the EU.

Ann concluded that in the Swedish context the institutionalisation of the OH is effective. If institutionalisation is defined as the “action of establishing something as a convention or norm in an organization or culture”, it can be confirmed that the OH concept is now known and understood not only by experts but also at management level and the OH approach is the platform for discussion on how to develop collaborative mechanisms, both nationally and with partners outside Sweden. Ann also underlined that there is still a lot to do; among the main aspects to take into account, she mentioned:

- Maintain networks (incl. secure financing),
- Share and use the outputs produced more broadly, not only in scientific contexts,
- Learn from the experience (also from all the challenges along the way, changes of plans etc).
- Get the environmental perspective truly and practically on board;
- Set national ambitions for collaborative efforts.

## 5.2. Institutionalisation of the One Health approach in Italy

Umberto Agrimi described the structure of the Italian National Health System and pointed out that since its implementation in 1978, the Italian public veterinary services have been integrated in the health administration. Under the current reform of the system, additional directorate Health and the Environment will be created to, among other functions, carry out “definition of a public health model based on the principles of “One health” and focused on monitoring exposure to environmental pollutants with harmful consequences for health”. Umberto also added that during the COVID-19 pandemic, the Medical-Veterinary integration has been enhanced through diagnosis and sequencing activities and the National genomic surveillance platform.

Umberto concluded that thanks to the contribution of the OHEJP community, a widespread awareness has been created in Italy among health professionals and decision-makers on the need to adopt the One Health approach to address issues of prevention and fight against zoonoses, AMR, climate change and many other environmental issues. The scientific foundations and approaches developed by OHEJP are robust and allow to build the future of One Health at national and European level. We all have to seize the moment!

## 6. Mentimeter Session

The final session of the meeting was chaired by Lapo Mughini Gras and was conducted as an interactive Mentimeter session. It allowed the audience to express what they have gotten from the One Health EJP and how the project, over its lifespan, has contributed to using a One Health approach.

The results of the session (in Annex) showed that extended and consolidated International One Health network comes as main legacy of OHEJP, followed by a positive learning curve for cross-sectoral collaboration. The scientific output and evidence base (research activities) and the capacity building and joint infrastructures were considered principal outcomes produced over the last 5 years. A large majority of participants (92%) supported the continuation of the OHEJP beyond 2023. Finally, the components



of an OHEJP 2.0 were designed with notably: animal welfare, environment, training, social sciences, wildlife, data sharing, citizen engagements, and health economy aspects to be taken into consideration.

Amanda-Jane Ozin-Hofhaess (Policy Officer at REA) commented on the suitable format of an OHEJP 2.0: it should include citizen engagement. To continue, a networking concept is needed, a reflection on how to keep the project going not necessarily with a single funding, but with multiple financial instruments.

## 7. Conclusions and closing remarks

Arnaud Callegari and Hein Imbrechts closed the meeting by thanking Public Health Agency of Sweden (FoHM) and Swedish National Veterinary Institute (SVA) for hosting the meeting. They acknowledged the presenters, participants and all that contributed putting the meeting together. They also asked for a common engagement to support implementation of the EJP's outcomes at national and European level and to advocacy for a sustainability of the project.

## 8. Annex:

- Meeting Agenda
- Attendance List
- JRPs Posters
- Presentations from JIPs session
- Results of Mentimeter session



## Joint Programme Managers/Owners/ Stakeholders Committee Meeting

FoHM's Headquarters

Nobels väg 18, Solna, Sweden

Expected participants: Programme Managers Committee (PMC) members, Programme Owners Committee (POC) members, Scientific projects Leaders, Stakeholders Committee (SC) members (ECDC / EFSA / EMA / EEA / EC DGs AGRI/SANTE/ENV / WHO / FAO / WOA)H)



21st-22nd NOVEMBER 2022

CET 21st NOVEMBER

19.00 Social Dinner

Elite Hotel Carolina Tower, Eugeniovägen 6, 171 64 Solna, Sweden

[MAP](#)

22nd NOVEMBER

Joint PMC-POC meeting

08.30 Welcome

08.35 Plenary Session

One Health EJP key facts

History of the One Health EJP: from origination, our journey, and where the future may be.

From the SWOT analysis, issued at the beginning of the project, we will discuss one main question for each segment respectively **T**hreats, **W**eaknesses, **S**trengths and **O**pportunities. Responses will be provided by consortium members, and the OHEJP will be illustrated with key facts and figures.

09.00 Poster Session

Main outcomes of the Joint Research Projects for consideration of uptake by stakeholders

Three separate meeting rooms will allow presenting selected projects in each of the three domains of intervention of the One Health EJP: Foodborne Zoonoses, Antimicrobial Resistance and Emerging Threats.

Project Leaders will present their poster highlighting project outcomes obtained and expected impact. *A table at the end of this document summarises which partner institute is involved in each JRP/JIPs.*

The selected projects are:

**Foodborne Zoonoses**

**Design and implementation of surveillance activities**

- [NOVA](#): Novel approaches for design and evaluation of cost-effective surveillance across the food chain
- [Air Sample](#): Air-sampling, A Low-Cost Screening Tool in Biosecured Broiler Production

**Interpretation of surveillance data & cross-sector communication of data**

- [DISCoVeR](#): Discovering the sources of *Salmonella*, *Campylobacter*, VTEC and antimicrobial resistance
- [TOXOSOURCES](#): *Toxoplasma gondii* sources quantified
- [ADONIS](#): Assessing Determinants of the Non-Decreasing Incidence of *Salmonella*
- [BeONE](#): Building Integrative Tools for One Health Surveillance



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**Joint Programme Managers/Owners/  
Stakeholders Committee Meeting**  
**FoHM's Headquarters**  
**Nobels väg 18, Solna, Sweden**

**21st-22nd NOVEMBER 2022**



**Action (prevention & response)**

- [BIOPIGEE](#): Biosecurity practices for pig farming across Europe

**Antimicrobial Resistance**

**Laboratory methods**

- [IMPART](#): Improving phenotypic Antimicrobial Resistance Testing by development of sensitive screening assays for emerging resistances, and setting missing ECOFFs

**Interpretation of surveillance data & Cross-sector communication of data**

- [RaDAR](#): Risk and Disease burden of Antimicrobial Resistance
- [FULL-FORCE](#): Full-length sequencing for an enhanced EFFORT to map and understand drivers and reservoirs of antimicrobial resistance
- [FED-AMR](#): The role of free extracellular DNA in dissemination of antimicrobial resistance over ecosystem boundaries along the food/feed chain

**Emerging Threats**

**Laboratory methods**

- [TOX-DETECT](#): Development and harmonisation of innovative methods for comprehensive analysis of foodborne toxigenic bacteria, ie. *Staphylococci*, *Bacillus cereus* and *Clostridium perfringens*
- [TELE-Vir](#): Point-of-incidence toolbox for emerging virus threats
- [MEmE](#): Multi-centre study on *Echinococcus multilocularis* and *Echinococcus granulosus* s.l. in Europe: development and harmonisation of diagnostic methods in the food chain
- [PARADISE](#): Parasite Detection, Isolation and Evaluation

**10.30 Plenary Session**

**Main outcomes of the Joint Integration Projects for consideration of uptake by stakeholders**

The methods, tools and protocols of the Joint Integrative Projects will be presented by each of the Project Leaders, for uptake and further use by stakeholders.

The project are:

**Design and implementation of surveillance activities**

- [ORION](#): One Health surveillance initiative on harmonisation of data collection and interpretation
- [COHESIVE](#): One Health structure in Europe
- [CARE](#): Cross-sectoral framework for quality Assurance Resources for countries in the European Union
- [OH-HARMONY-CAP](#): One Health Harmonisation of Protocols for the Detection of Foodborne Pathogens and AMR Determinants
- [MATRIX](#): Connecting dimensions in One Health surveillance
- [COVRIN](#): One Health research integration on SARS-CoV-2 emergence, risk assessment and preparedness
- [SIMEX](#): Table-top exercise that covered a realistic foodborne outbreak at a national level



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## Joint Programme Managers/Owners/ Stakeholders Committee Meeting

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21st-22nd NOVEMBER 2022

### 11.45 Round Table

How the One Health EJP contributed to institutionalisation of the One Health approach across Europe – two examples: Sweden and Italy

The One Health EJP has contributed positively to raising the awareness towards governments of participating countries, to consider and put in place a One Health approach in their outbreak surveillance system. The two examples will illustrate the progress of adoption of the One Health approach across Europe. The aim being to raise awareness the other countries present at the meeting to do the same.

### 12.15 Mentimeter Session

What did you get from the One Health EJP?

In conclusion, we will have a live audience participation Mentimeter session (please pre-download app on [Google Store](#), or on [Apple Store](#)). Questions will be themed to see the audience response to how the One Health EJP, over its 6 years lifespan, has contributed to improve surveillance in food security using a One Health approach.

### 12.35 Conclusions and closing remarks

12.40 Close



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# Joint Programme Managers/Owners/ stakeholders committee meeting

FoHM's Headquarters  
Nobels väg 18, Solna, Sweden

21st-22nd NOVEMBER 2022



| ORION  | COHESIVE   | CARE   | OH-HARMO-<br>NY-CAP   | MATRIX   | COVRIN  | IMPART  | ARDIG   | RADAR   | MADVir  | TOXdetect  | NOVA   | LISTADAPT  | METASTAVA   | AIR-Sample                          | MoMIR-PPC   |
|--|--|--|---|--|---|---|---|---|---|--|--|--|---|-------------------------------------|---|
| Sciensano<br>BfR<br>FLI<br>DTU<br>SSI<br>APHA<br>PHE<br>RIVM<br>WbvR<br>NIPH<br>NVI<br>FoHM<br>SVA | ANSES<br>AGES<br>Sciensano<br>BfR<br>FLI<br>DTU<br>APHA<br>PHE<br>ISS<br>IZSAM<br>IZSLER<br>RIVM<br>WbvR<br>NIPH<br>NVI<br>INIAV<br>SLV<br>FoHM<br>SVA | ANSES<br>DTU<br>SSI<br>UCM<br>ISCIII<br>INRA<br>IP<br>APHA<br>ISS<br>IZSAM<br>IZSLER<br>RIVM<br>WbvR<br>PIWET<br>SLV<br>FoHM<br>SVA<br>BIOR<br>RUOKA | ANSES<br>BfR<br>SSI<br>ISCIII<br>APHA<br>TEAGASC<br>ISS<br>RIVM<br>NIPH<br>NVI<br>PIWET<br>INIAV<br>INSA<br>SLV<br>FoHM<br>SVA<br>BIOR<br>RUOKA | ANSES<br>BfR<br>FLI<br>DTU<br>SSI<br>INIA<br>UCM<br>APHA<br>UoS<br>ISS<br>IZSAM<br>RIVM<br>WbvR<br>NIPH<br>NVI<br>PIWET<br>INIAV<br>INSA<br>FoHM<br>SVA<br>BIOR<br>RUOKA | ANSES<br>AGES<br>Sciensano<br>VRI<br>BfR<br>FLI<br>INIA<br>UCM<br>APHA<br>UoS<br>ISS<br>IZSAM<br>IZSLER<br>RIVM<br>WbvR<br>NIPH<br>NVI<br>PIWET<br>INIAV<br>INSA<br>FoHM<br>SVA<br>BIOR | ANSES<br>BfR<br>DTU<br>SSI<br>APHA<br>IP<br>APHA<br>PHE<br>UoS<br>WbvR<br>NVI | ANSES<br>BfR<br>RKI<br>UCM<br>IP<br>APHA<br>PHE<br>UoS<br>WbvR<br>NVI                   | ANSES<br>BfR<br>DTU<br>APHA<br>ISS<br>RIVM<br>WbvR<br>NVI   | ANSES<br>VRI<br>SSI<br>INIA<br>APHA<br>UoS<br>OKI<br>IZSAM<br>IZSLER<br>PIWET   | ANSES<br>Sciensano<br>BfR<br>INRA<br>IP<br>NVI   | ANSES<br>Sciensano<br>BfR<br>FLI<br>RKI<br>DTU<br>SSI<br>INIA<br>UCM<br>APHA<br>PHE<br>ISS<br>IZSAM<br>RIVM<br>NIPH<br>NVI<br>FoHM<br>SVA          | ANSES<br>AGES<br>VRI<br>DTU<br>INRA<br>IZSAM<br>NVI<br>SLV   | ANSES<br>Sciensano<br>WbvR<br>SVA   | VRI<br>DTU<br>IZSAM<br>NVI<br>PIWET | ANSES<br>NDRVMI<br>VRI<br>UCM<br>INRA<br>UoS<br>ISS<br>IZSLER<br>WbvR<br>NIPH |
| MedVet-<br>Klebs   | FARMED   | WORLD-<br>COM  | FULL-FORCE  | FED-AMR  | TELE-Vir  | IDEMBRU   | MEme  | PARADISE  | DISCoVer  | BIOPIGEE   | TOXO-<br>SOURCES   | ADONIS   | BeONE   | ECO-HEN                             | LIN-RES   |
| ANSES<br>AGES<br>DTU<br>SSI<br>INRA<br>IP<br>NUIG<br>IZSAM<br>RIVM                                 | Sciensano<br>BfR<br>DTU<br>SSI<br>UCM<br>APHA<br>ISS<br>IZSAM<br>WbvR  | FLI<br>UT<br>UCM<br>UoS<br>NUIG<br>INSA  | ANSES<br>Sciensano<br>BfR<br>DTU<br>SSI<br>INIA<br>INRA<br>APHA<br>ISS<br>RIVM<br>WbvR<br>NVI<br>PIWET<br>INSA<br>FoHM<br>SVA                   | AGES<br>SZU<br>BfR<br>FLI<br>SSI<br>UT<br>IP<br>UoS<br>NUIG<br>NVI<br>PIWET<br>INSA  | ANSES<br>Sciensano<br>VRI<br>SSI<br>INIA<br>UoS<br>IZSAM<br>IZSLER<br>NVI<br>PIWET<br>INSA<br>SVA   | ANSES<br>NDRVMI<br>BfR<br>FLI<br>APHA<br>IZSAM<br>WbvR<br>INIAV<br>INSA       | ANSES<br>FLI<br>SSI<br>UT<br>VFL<br>ISS<br>RIVM<br>NVI<br>PIWET<br>INIAV<br>INSA<br>SVA | ANSES<br>VRI<br>BfR<br>RKI<br>SSI<br>UoS<br>OKI<br>ISS<br>RIVM<br>NVI<br>PIWET<br>INIAV<br>SLV<br>FoHM<br>SVA | ANSES<br>VRI<br>BfR<br>DTU<br>SSI<br>UCM<br>APHA<br>PHE<br>TEAGASC<br>ISS<br>RIVM<br>WbvR<br>NIPH<br>NVI<br>PIWET<br>INIAV<br>INSA<br>SVA | ANSES<br>AGES<br>NDRVMI<br>VRI<br>BfR<br>FLI<br>RKI<br>DTU<br>SSI<br>UCM<br>APHA<br>PHE<br>ISS<br>IZSAM<br>IZSLER<br>RIVM<br>WbvR<br>NVI<br>PIWET<br>SVA | ANSES<br>SZU<br>VRI<br>BfR<br>FLI<br>RKI<br>DTU<br>SSI<br>UCM<br>UoS<br>ISS<br>RIVM<br>WbvR<br>NIPH<br>NVI<br>PIWET<br>INIAV<br>INSA<br>SLV<br>SVA | ANSES<br>AGES<br>Sciensano<br>SSI<br>UCM<br>IP<br>APHA<br>PHE<br>ISS<br>RIVM<br>WbvR<br>PIWET<br>INIAV<br>INSA | BfR<br>FLI<br>RKI<br>DTU<br>SSI<br>APHA<br>PHE<br>IZSAM<br>RIVM<br>NIPH<br>NVI<br>PIWET<br>INSA | DTU<br>UCM                          | Sciensano   |
| HME-AMR  | KEN-<br>TUCKY  | METAPRO  | PEMbo   | MACE   | DESIRE  | UDOFRIC   | WILBR   | EnvDis  | AptaTrich   | VIMOGUT  | ToxSau-<br>QMRA  | TRACE  | Codes4<br>strains   | SUSTAIN                             |   |
| NUIG<br>TEAGASC  | Sciensano<br>INRA  | UCM<br>UoS   | ANSES   | UoS<br>ISS   | RIVM<br>WbvR  | ANSES<br>APHA   | APHA<br>SVA   | UoS   | ANSES<br>BfR  | APHA<br>WbvR   | ANSES<br>RIVM  | RIVM<br>WbvR   | IP  | ISS<br>SVA                          |   |

PARTNER COORDINATOR



Folkhälsomyndigheten



NATIONAL  
VETERINARY  
INSTITUTE



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ONE Health EJP

#OneHealthEJP #StrongerTogether



## Participant list

### One Health EJP

Grant Agreement number 773830

| <b>Date &amp; Time</b> | 22 November 2022<br>8:30 – 13:00 CET                |   |                                      |
|------------------------|---|---|--------------------------------------|
| <b>Venue</b>           | FoHM's Headquarters<br>Nobels väg 18, Solna, Sweden |   |                                      |
| <b>Meeting</b>         | Joint PMC-POC meeting                               |   |                                      |
| Name                   |   | Institute / Organisation  | Role in the Project                  |
| Niloy                  | Acharyya  | UK-Veterinary Medicines Directorate, Defra                        | POC member                           |
| Umberto                | Agrimi  | P27-ISS   | PMC member                           |
| Frederico              | Alves   | P41-SVA   | JIP SImEX REP                        |
| Karin                  | Artursson   | P41-SVA   | PMT member / WP4 leader              |
| Dorte Lau              | Baggesen  | P12-DTU   | PMC member                           |
| Magdalena              | Bartosińska   | PL-Ministry of Agriculture and Rural Development                  | POC member                           |
| Guido                  | Benedetti   | P13-SSI   | JIP MATRIX Leader                    |
| Aivars                 | Berzins   | P44-BIOR  | PMC Member                           |
| Richard                | Boguifo   | P01-Anses   | ST member                            |
| Stefan                 | Borjesson   | P40-FoHM  | SSB member                           |
| Antra                  | Brinke  | LV-Ministry of Agriculture  | POC Member                           |
| Stef                   | Bronzwaer   | EFSA  | Stakeholder                          |
| Simone Mario           | Cacciò  | P27-ISS   | JRP PARADISE Leader / online         |
| Arnaud                 | Callegari   | P01-Anses   | PMT member / Coordinator             |
| Manuela                | Canica  | P36-INSa  | PMT member / WP4 deputy leader       |
| Jennifer               | Cantlay   | P23-UoS   | Communication Team                   |
| Jean-Charles           | Cavitte   | European Commission, DG Agriculture and Rural Development         | EC DG AGRI                           |
| Pieter-Jan             | Ceyssens  | P03-Sciensano   | JRP Full Force Leader                |
| Ildiko                 | Csolle Putzova                                      | P08-VRI   | PMC member                           |
| Carlos                 | das Neves   | EFSA  | Stakeholder                          |
| Lucia                  | De Juan   | P17-UCM   | PMC & PMT member / WP2 deputy leader |
| Yvonne                 | de Nas  | NL-Ministry of Health, Welfare and Sport/Public Health Department | POC Member                           |
| Racha                  | El Mounaged   | P03-Sciensano   | PMT collaborator / WP3               |



| Name        |               | Institute / Organisation                                 | Role in the Project                         |
|-------------|---------------|--|---|
| Anders      | Folkesson     | P39 SLV  | PMC Representative                          |
| Jenny       | Frössling     | P13-SSI  | JRP NOVA Leader / online                    |
| Susanne     | Frykman       | JPIAMR, Swedish Research Council                         | Stakeholder                                 |
| Dolores     | Gavier-Widen  | P41-SVA  | PMT member / WP7 deputy leader              |
| Lucyna      | Haaso-Bastin  | P01-Anses  | ST member                                   |
| Estelle     | Hamelin       | World Organisation for Animal Health                     | Stakeholder                                 |
| Ole         | Heuer         | ECDC   | Stakeholder                                 |
| Merete      | Hofshagen     | P33-NVI  | PMC & POC member                            |
| Dan         | Horton        | P23-UoS  | JIP COVRIN Co-leader / WP6 team             |
| Hein        | Imbrechts     | P03-Sciensano  | PMT member / Scientific Coordinator         |
| Patrícia    | Inácio        | P35-INIAV  | PMC Member                                  |
| Gro S.      | Johannessen   | P33-NVI  | JRP AIRSAMPLE Rep / online                  |
| Pikka       | Jokelainen    | P13-SSI  | PMT member / WP3 & WP5 deputy leader        |
| Annemarie   | Käsbohrer     | B09- BFR   | PMT member / WP5 leader                     |
| Veljo       | Kisand        | P14-UT   | PMC & POC member                            |
| Elina       | Lahti         | P41-SVA  | JIP COHESIVE REP                            |
| Roberto     | La Ragione    | P23-UoS  | PMC Representative<br>PMT member/WP6 leader |
| Alois       | Leidwein      | P02-AGES   | PMC Member                                  |
| Ann         | Lindberg      | P41-SVA  | PMC & POC member                            |
| Francesca   | Martelli      | P21-APHA   | PMC Representative / SSB member             |
| Auguste     | Matuleviciene | LT-Office of the Parliament of the Republic of Lithuania | POC Representative                          |
| Liisa       | Maunuksela    | P45- Ruokavirasto  | PMC member                                  |
| Axel        | Mauroy        | BE-Federal Agency for the Safety of the Food Chain       | POC member                                  |
| Verónica    | Mixão         | P36-INSA   | JRP BeONE REP                               |
| Lapo        | Mughini Gras  | P30-RIVM   | JRP DISCOVER REP / WP2 team                 |
| Yacine      | Nia           | P01-Anses  | JRP Tox-DETECT Co-leader                    |
| Amanda Jane | Ozin-Hofhaess | REA  | Project officer REA                         |
| Eveliina    | Palonen       | FI-Ministry of Agriculture and Forestry                  | POC Representative                          |
| Annette     | Perge         | DK-Ministry of Food, Agriculture and Fisheries           | POC member                                  |
| Dario       | Piselli       | European Environment Agency                              | Stakeholder                                 |
| Mirosław    | Polak         | P34-PIWET  | PMC member                                  |
| Egidijus    | Pumputis      | P42-NMVR   | PMC member                                  |
| Gilles      | Salvat        | P01-Anses  | PMC Representative / SSB member             |
| Cristina    | Santos        | P36-INSA   | PMC member                                  |





This meeting is part of the European Joint Programme One Health EJP. This project has received funding from the European Union's Horizon 2020 research and innovation programme under Grant Agreement No 773830.



| Name     |                | Institute / Organisation                                | Role in the Project                        |
|----------|----------------|---|--|
| Karin    | Schlesier      | P09-BfR   | PMC Representative / SSB member            |
| Karoline | Schollmeyer    | DE-Federal Ministry of Food and Agriculture             | POC Member                                 |
| Scott    | Sellers        | UK - Department for Environment, Food and Rural Affairs | POC member                                 |
| Ludovico | Sepe           | B09- BFR  | PMT collaborator / WP5                     |
| Joukje   | Siebenga       | P31-WbvR  | PMC Representative                         |
| Myriam   | Sneyers        | P06-Sciensano   | PMC Representative / SSB member            |
| Katja    | Spiess         | P13-SSI   | JRP TELEVIR Leader / online                |
| Karin    | Tegmark-Wisell | P40-FoHM  | PMC member / POC member                    |
| Mia      | Torpdahl       | P13-SSI   | JIP CARE REP                               |
| Lena     | Tuominen       | P41-SVA   | PMT Collaborator / WP4                     |
| Henrik   | Ullum          | P13-SSI   | PMC member                                 |
| Arjen    | van de Giessen | P30-RIVM & P18-MVNA                                     | PMC Representative / PMT member WP2 leader |
| Giorgio  | Varisco        | P29-IZSLER  | PMC member                                 |
| Kees     | Veldman        | P31-WbvR  | JRP IMPART Leader / online                 |



# Joint PMC POC Meeting Poster Session





# Novel approaches for design and evaluation of cost-effective surveillance across the food chain

J. Frössling<sup>1</sup> • S. Ethelberg<sup>2</sup> • M-E. Filippitzi<sup>3,4</sup> • A. Huneau<sup>5</sup> • A. de la Torre<sup>6</sup> • H. Vigre<sup>7</sup>

1. SVA, Sweden • 2. SSI, Denmark • 3. Sciensano, Belgium • 4. AUTH, Greece • 5. Anses, France • 6. INIA, Spain • 7. DTU-FOOD, Denmark

In this research project (JRP06), more than 65 project participants from 18 public health and veterinary institutes in 10 countries collaborated over a project period of 3½ years. NOVA has addressed improvement of disease surveillance through a large number of separate projects, organised into five main themes, as reflected in its overall work package structure:



Basic aspects and issues in connection with performing One Health surveillance



Use of electronic traces of purchase of food for surveillance and outbreak investigations



One Health developments of syndromic surveillance methods



Use and development of spatial risk mapping



Modelling the cost efficiency of surveillance programs

## OUTCOME HIGHLIGHT 1: METHODS FOR MODERN OUTPUT-BASED SURVEILLANCE

- Modelling of **disease spread and surveillance in the same model**
- Several spread scenarios investigated
- Alternative sampling strategies compared
- Traditional measures of surveillance sensitivity complemented by measures of **time to detection**, and outbreak size at time of detection
- National adaptation to new Animal Health Law: Output from this modelling has been important as a **basis for discussion and decision** with the Board of Agriculture, animal health organisations and other stakeholders.
- Continuing work on this modelling framework in other research projects, including second round of OHEJP projects (FullForce and Biopigee).

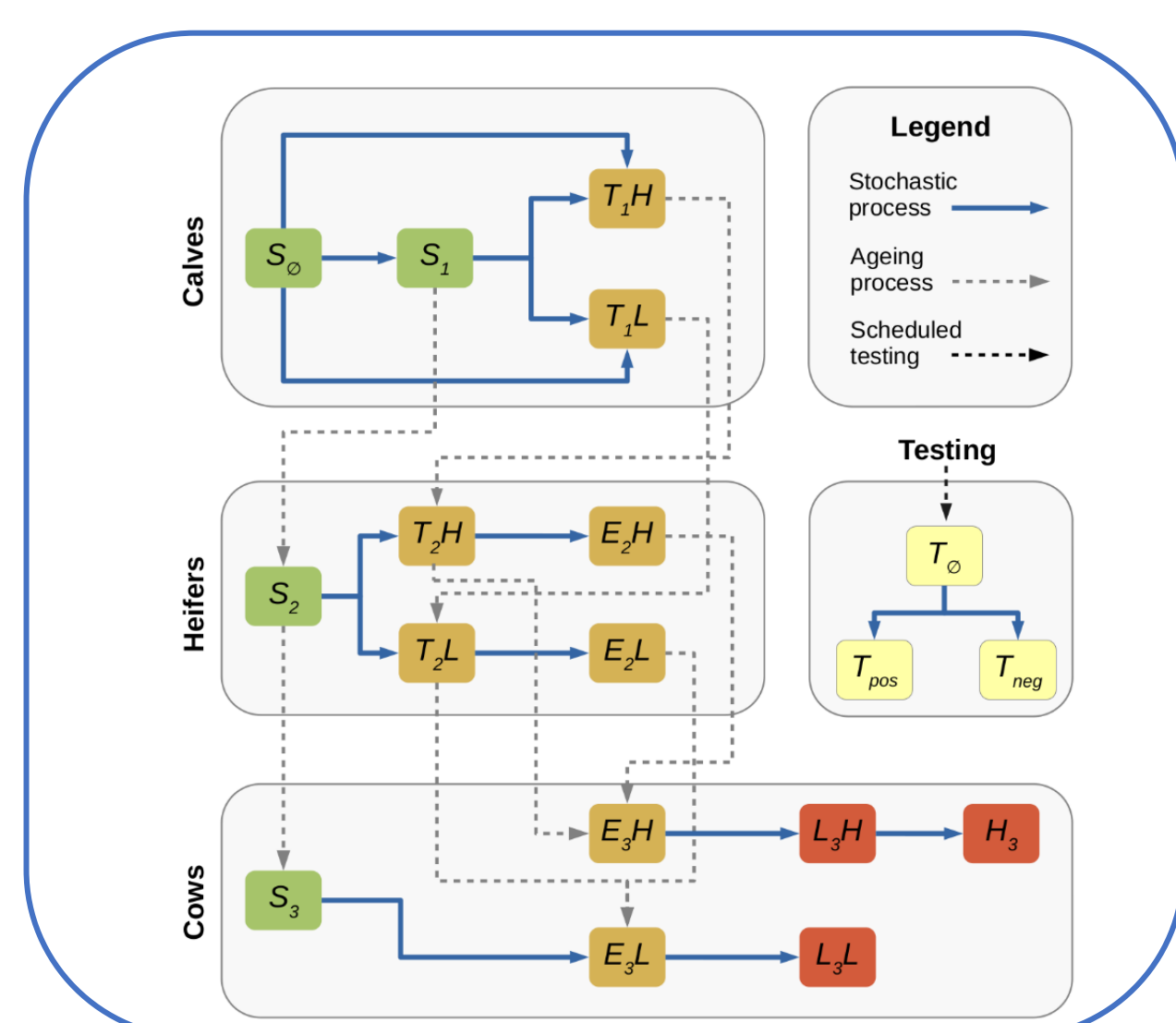


Fig 1 Compartments representing diagnostic testing (yellow) included in spread model

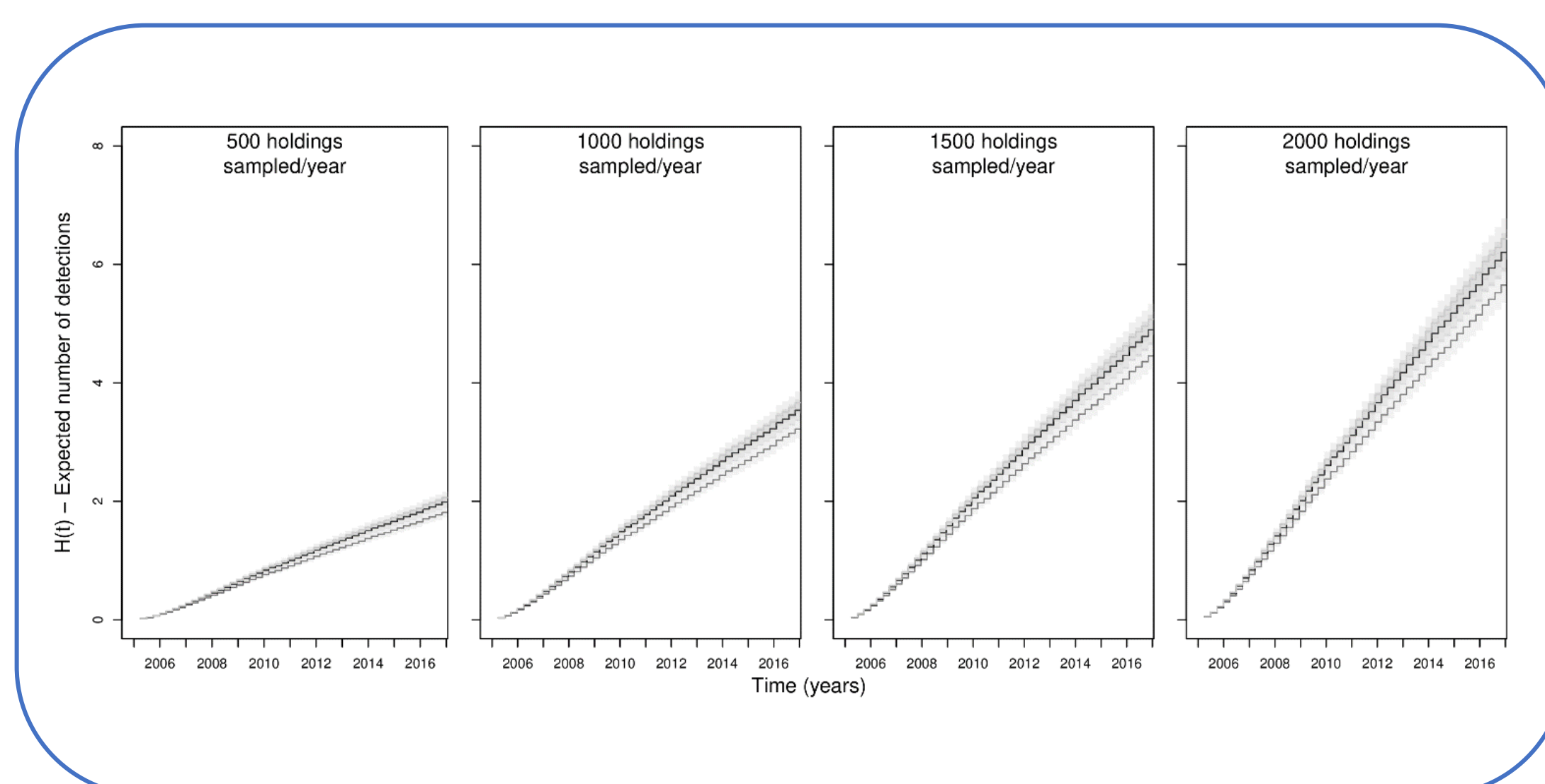
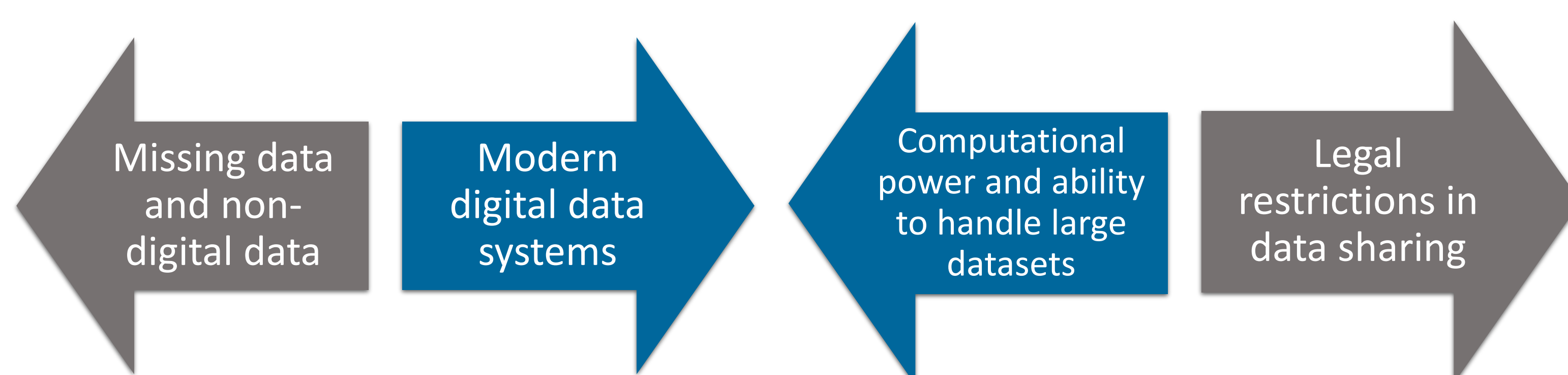


Fig 2 Time to detection of outbreak based on four surveillance strategies with different number of tested holdings



Photo: B. Ekberg/SVA

## OUTCOME HIGHLIGHT 2: DATA AVAILABILITY



- Data availability and access investigated in several WPs, from different perspectives.
- General difficulty to share data**, also between authorities in the same MS
- Imbalance in data formats and data access

## IMPACT SUMMARY

- Understanding and improving access to data → more information, lower cost, more cost-effective surveillance
- General models and open code → use in MS with similar data
- Support for outcome-based surveillance
- Outcomes used in ongoing surveillance and several research projects
- New network, increased contact across disciplines → improved collaboration



Photo: F. Dórea/SVA





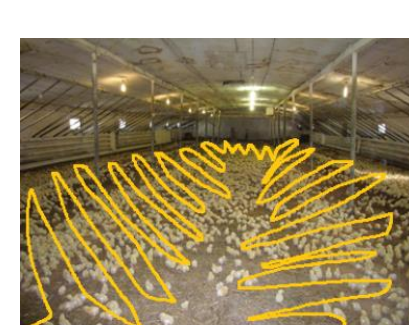
# AIR-SAMPLE

## A low-cost screening tool in bio-secured broiler production

Gro S. Johannessen  
Norwegian Veterinary Institute

### BACKGROUND AND AIM

- Monitoring of *Campylobacter* in poultry production is mandatory
- Current methods: boot swabs, fecal droppings



➔ Modernization of sampling is desirable

Sampling of ambient air in broiler houses has previously been successfully tested for screening of *Campylobacter*.



➔ In AIR-SAMPLE: further testing, harmonization and evaluation of protocols in five countries across Europe has been carried out.

### RESULTS IN BRIEF

Testing of air sampling was carried out over two seasons in five European countries.

- A pilot study (year 1) indicated suitability to detect *Campylobacter* in biosecured broiler production.
- A multi-centre evaluation (year 2) of harmonized protocols indicated that air sampling in combination with real-time PCR can produce fast and reliable results.
- The use of metagenomic (shot-gun) analyses of air samples to detect *Campylobacter* was tested.
- A SOP, guidelines and a video demonstration were produced.

#### Publications:

Johannessen et al. 2020. *Campylobacter* in chicken – critical parameters for international, multicentre evaluation of air sampling and detection methods. [doi:10.1016/j.jfm.2020.103455](https://doi.org/10.1016/j.jfm.2020.103455)

Hoorfar et al. 2020. A Multicenter proposal for a fast tool to screen biosecure chicken flock for the foodborne pathogen *Campylobacter*. doi: 10.1128/AEM.01051-20

Video demonstration: <https://youtu.be/LMD03UAAPUw>

### OUTCOMES AND IMPACT

#### Harmonized and multi-center evaluated protocols for collecting air samples in broiler houses, DNA extraction from filters and real-time PCR for *Campylobacter* detection.

Fast and sensitive method that increased the likelihood of detecting *Campylobacter* in infected flocks. Guidelines, SOPs, instructions videos, scientific publications and presentations have been developed.

- ➔ Air sampling can be implemented as an alternative to other methods for sampling for screening of *Campylobacter* in broiler houses.
- The use of air samples could be expanded to include more pathogen targets, thus being a simple tool for sampling of relevant organisms. Such further use needs testing.

#### Use of metagenomic (shot gun) analyses of air samples to detect *Campylobacter*

Identified and tested a DNA extraction protocol that can be used for both real-time PCR and metagenomic studies. Carried out a pilot study using inoculated samples to see if we were able to identify *Campylobacter* using shot-gun metagenomics

- ➔ A step towards using metagenomics for detection of pathogenic bacteria or other microorganisms in food production environment that can be used for multiple purposes. Area for further research that requires cooperation across many fields.

#### Impact

- ➔ Early detection of *Campylobacter* and potentially other microorganisms that may be harmful to humans and animals enables measures to be put in place to ensure the safety of the product, animal and public health.
- A step towards using metagenomics for the detection of foodborne pathogens, with its potential of use for multiple purposes.

**Acknowledgement:** Prof. Jeffrey Hoorfar (retired), DTU, initiator and coordinator of the project until December 2020. Project partners from DTU, IZSAM, PiWet, VUVeL and NVI.





# DiSCoVeR – Discovering the sources of *Salmonella*, *Campylobacter*, VTEC and antimicrobial Resistance

## OBJECTIVES

- To provide a hub for sharing genomic, other microbiological and epidemiological data to perform source attribution analyses for *Salmonella*, *Campylobacter*, Shiga toxin-producing *E. coli* (STEC), and antimicrobial resistance (AMR) across Europe.
- To critically assess existing source attribution models and to develop novel or improve current source attribution models suited to the data of the project or to be collected in the foreseeable future in human, animal, food and environmental samples to trace the origins of *Salmonella*, *Campylobacter*, STEC and AMR at different levels of the reservoir-to-exposure continuum.
- To produce quantitative estimates for the sources of *Salmonella*, *Campylobacter*, STEC and AMR that also account for the environment, non-livestock reservoirs, multi-directionality of transmission, and geographical differences.
- To evaluate existing data for source attribution, the applicability of existing and novel methods, and the interpretability of results to fill gaps in knowledge, data and methodologies.
- To liaise with decision makers and other stakeholders in order to evaluate how source attribution analyses and approaches can reinforce current and future control policies for *Salmonella*, *Campylobacter*, STEC and AMR, as well as integrated surveillance programmes.

## CONSORTIUM

DiSCoVeR brings together experts from different disciplines (microbiology, bioinformatics and epidemiology) and sectors (veterinary science, food safety, public and environmental health) from 19 institutes in 13 European countries (Fig. 1) to address source attribution in an interdisciplinary manner. The DiSCoVeR consortium is led by the DTU and RIVM.

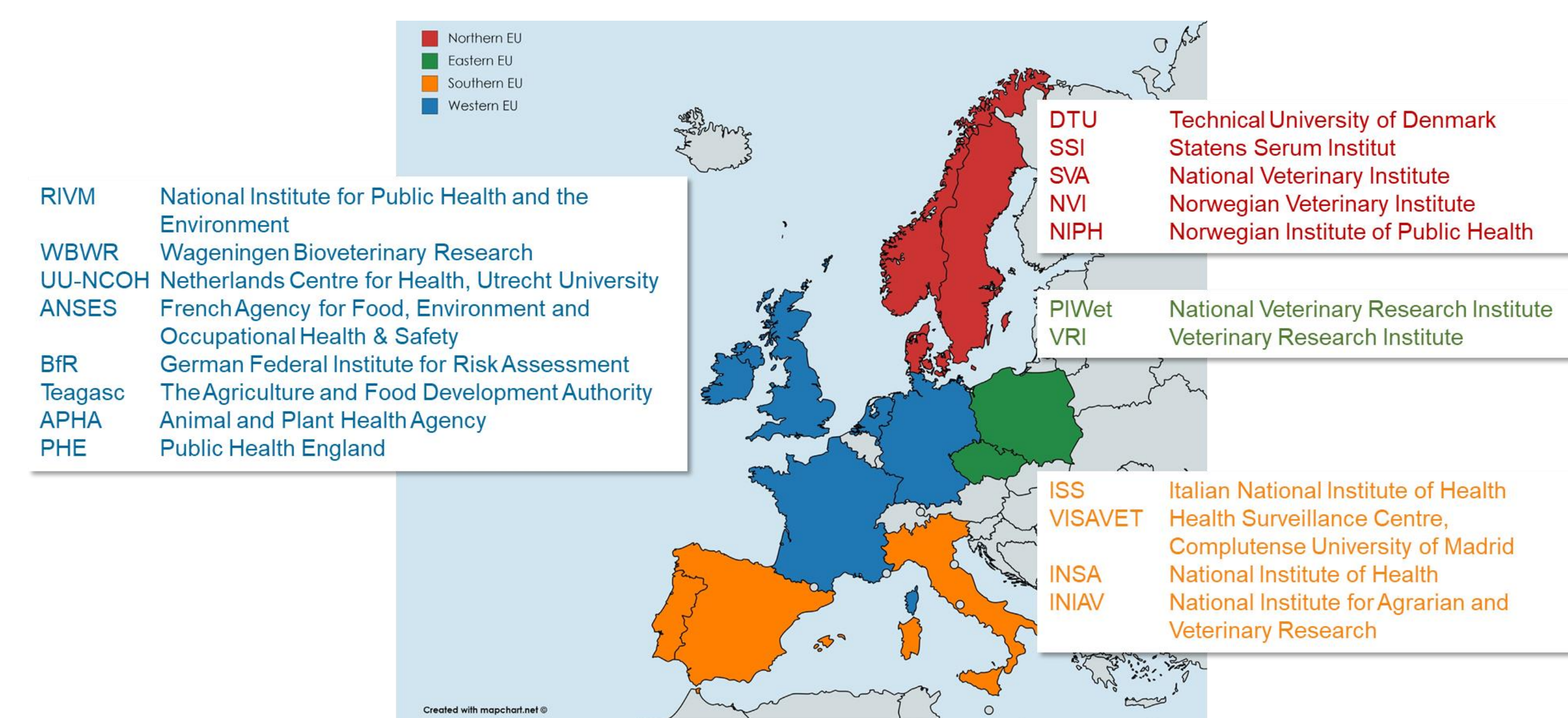


Fig. 1. Composition of the DiSCoVeR consortium.

## STRUCTURE

As shown in Fig.2, DiSCoVeR is structured in 5 interconnected work packages (WPs) encompassing project coordination (WP1), data collection (WP2), methodological assessment (WP3), estimate generation (WP4) and science-to-policy translation (WP5).

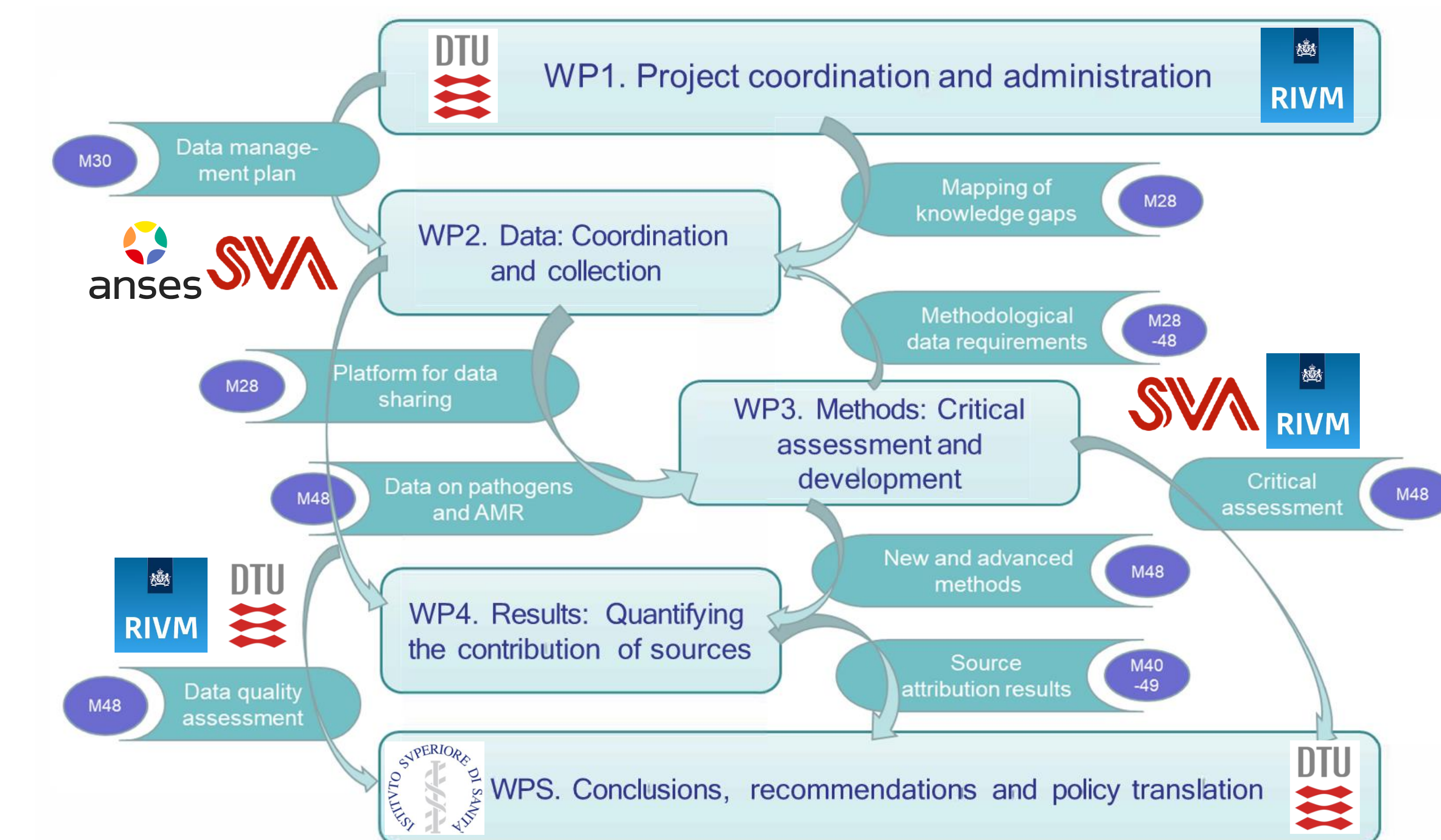


Fig. 2. Interrelationships and leadership of the different WPs of DiSCoVeR.

## OUTCOMES

Five different analytical approaches are applied to the three target pathogens and AMR (Table 1).

Table 1. Analytical approaches used in DiSCoVeR.

|                      | Subtyping (phenotype)                         | Subtyping (genotype)                                      | Outbreak data | Case-control study       | Comparative exposure assessment |
|----------------------|---|---|---------------|--------------------------|---------------------------------|
| <i>Salmonella</i>    | Serotyping (frequency-matching)               | cgMLST (population genetics, machine-learning)            | EFSA data     | Meta-analysis literature | Dogs and cats                   |
| <i>Campylobacter</i> | -   | cgMLST, Kmer, SNP   | -             | Meta-analysis literature | Dogs and cats                   |
| VTEC                 | Serotyping + stx, eae... (frequency-matching) | cgMLST, pangenome (population genetics, machine-learning) | -             | -                        | Dogs and cats                   |
| AMR                  | -   | ESBL genotypes (frequency-matching, dynamic modelling)    | -             | -                        | Dogs and cats                   |

- Results are presented per pathogen, method, data type and country, to identify country differences for pathogen-data-approach combinations that may reflect differences in epidemiology. Multi-country analyses are also performed.
- Particular attention is given to environmental and non-livestock (pets and wildlife) sources besides the 'traditional' livestock/food sources, although data for these sources generally are scarce.
- Existing and novel methods are improved and applied in parallel, notably the use of machine-learning methods like random forest using the increasingly available genomic data from WGS surveillance. See, as an example, the outcomes for *Salmonella* Typhimurium in Fig. 3 and comparable results obtained with other methods (Fig. 4).

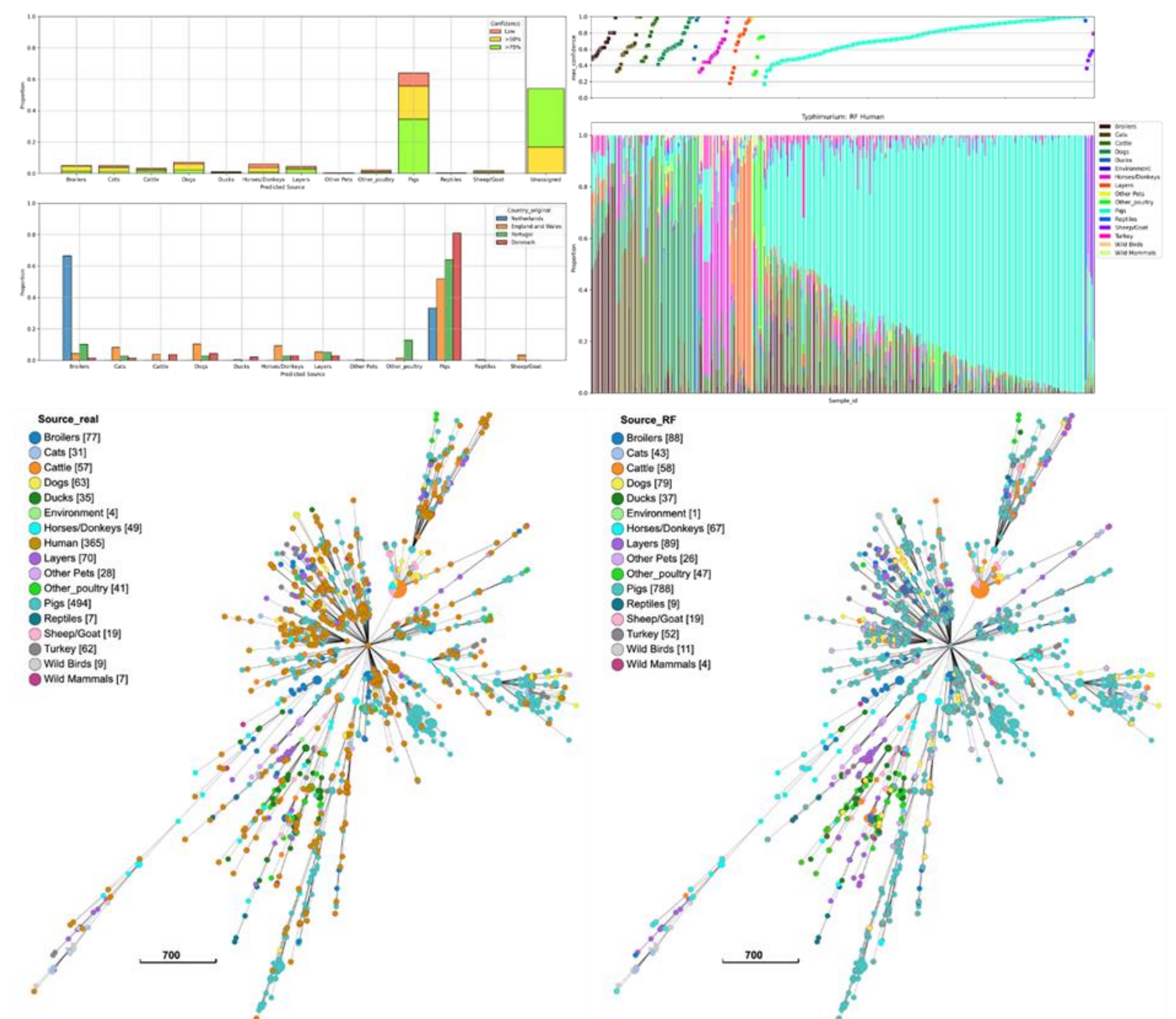


Fig. 3. Isolates of *Salmonella* Typhimurium and its monophasic variant attributed to each source based on cgMLST data using random forest.



Fig. 4. Attribution estimates of human *S. Typhimurium*/monophasic variant isolates using population genetics models (A), for *Salmonella* spp. analysis of outbreak data (B), and meta-analysis of case-control studies (C).

## IMPACT

- DiSCoVeR has identified and filled important knowledge, methodological and data gaps about source attribution of top-priority zoonotic pathogens in the EU and AMR through systematic collection and analysis of existing and new data and by applying existing, modified and novel approaches.
- Results allow for recommendations on how source attribution estimates can be translated into policy to support the surveillance, control and prevention of foodborne infections in Europe.





# TOXOSOURCES

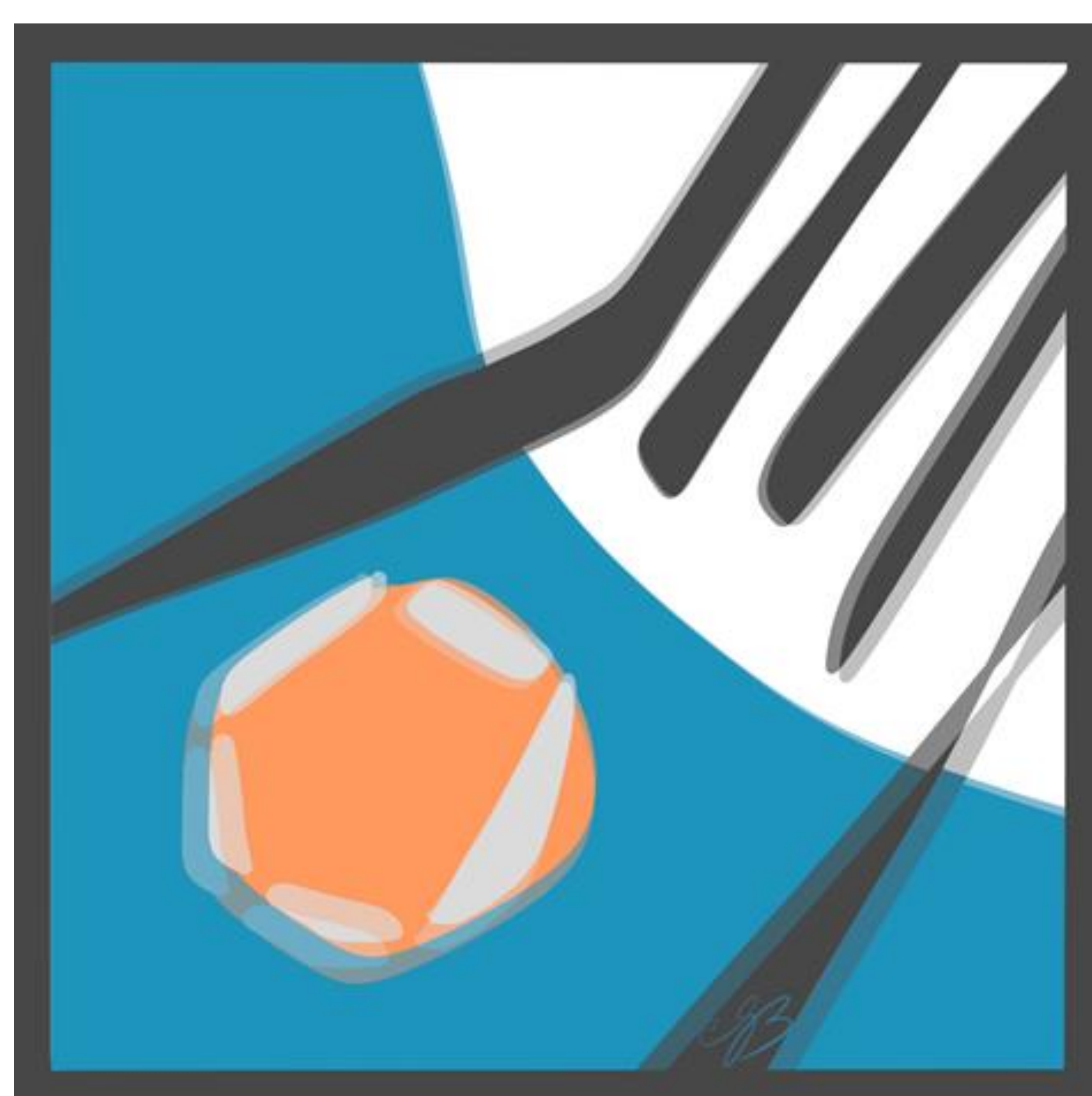
## *Toxoplasma gondii* sources quantified

Pikka Jokelainen (SSI, Denmark), Joke van der Giessen (RIVM, the Netherlands),  
Marieke Opsteegh (RIVM, the Netherlands), Sara Monteiro Pires (DTU-FOOD, Denmark),  
Marco Lalle (ISS, Italy), Anne Mayer-Scholl (BfR, Germany),  
Furio Spano (ISS, Italy), Frank Seeber (RKI, Germany),  
Gereon Schares (FLI, Germany), Simone Cacciò (ISS, Italy),  
and other TOXOSOURCES Consortium members

*Toxoplasma gondii* is a zoonotic parasite that causes a high disease burden.

### MAIN GAP ADDRESSED

Relative importance of the main transmission pathways, via the environment (oocyst-borne) or via meat (tissue-cyst-borne), has been a major issue and only answered with expert elicitations. (EFSA 2018)



Contact: [PIJO@ssi.dk](mailto:PIJO@ssi.dk)  
Twitter @PikkaJokelainen  
<https://onehealth.ejp.eu/jrp-toxosources/>

### Methods

- Harmonized approaches enabling comparable data
- Better preparedness to detect and investigate outbreaks and emerging strains
- New and improved methods
  - Improved quantitative microbial risk assessment (QMRA)
  - Standard operating procedure and interlaboratory validation of detection of oocyst contamination in leafy green vegetables
  - Serology to detect infections caused by oocysts explored
  - Harmonizing current state-of-the-art genotyping: ring trials
  - Novel typing method to detect within-genotype variation
- Methods already applied in several laboratories across Europe

### Science

- Major contributions to our understanding regarding sources and transmission pathways, epidemiology and molecular epidemiology, and performance of methods
  - Several literature reviews, high number of scientific publications
  - New data from multicenter exposure survey and QMRA
  - New data on role of ready-to-eat fresh produce from large multicenter study
  - Unique data on performance of a selection of antigens for stage-specific serology
  - Whole genome sequences of a high number of *Toxoplasma gondii* strains
  - Quantitative estimates of main sources of *Toxoplasma gondii* infections

### Consortium

- Multidisciplinary and cross-sectoral One Health collaborations
- 21 One Health EJP partners plus external collaborators
- Participation of early-career colleagues, career advancement
- Networking, including across projects within and beyond One Health EJP
- Active dissemination, including collaborations with social sciences and policy platforms, and using social media #TOXOSOURCES





# Understanding the changing epidemiology of *Salmonella* (the ADONIS project)

Project leader: Eelco Franz (RIVM)  
Work package leaders: Marianne Chemaly (ANSES), Roan Pijnacker (RIVM), Eva Litrup (SSI), Lapo Mughini Gras (RIVM)

## Background

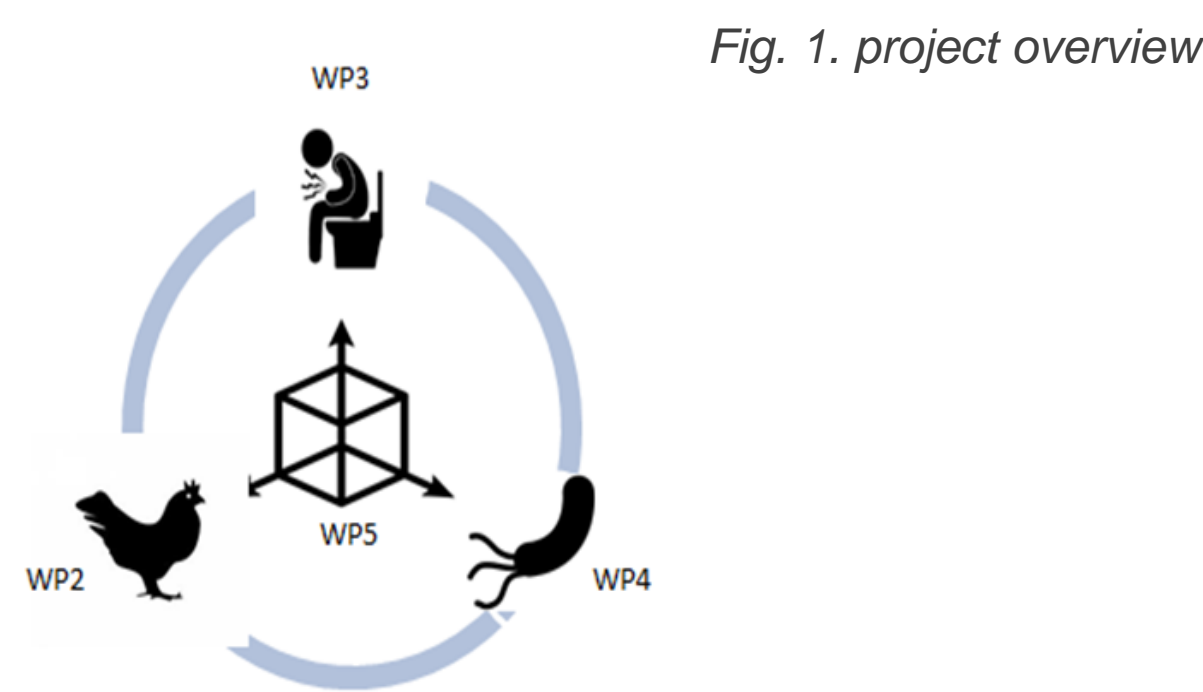
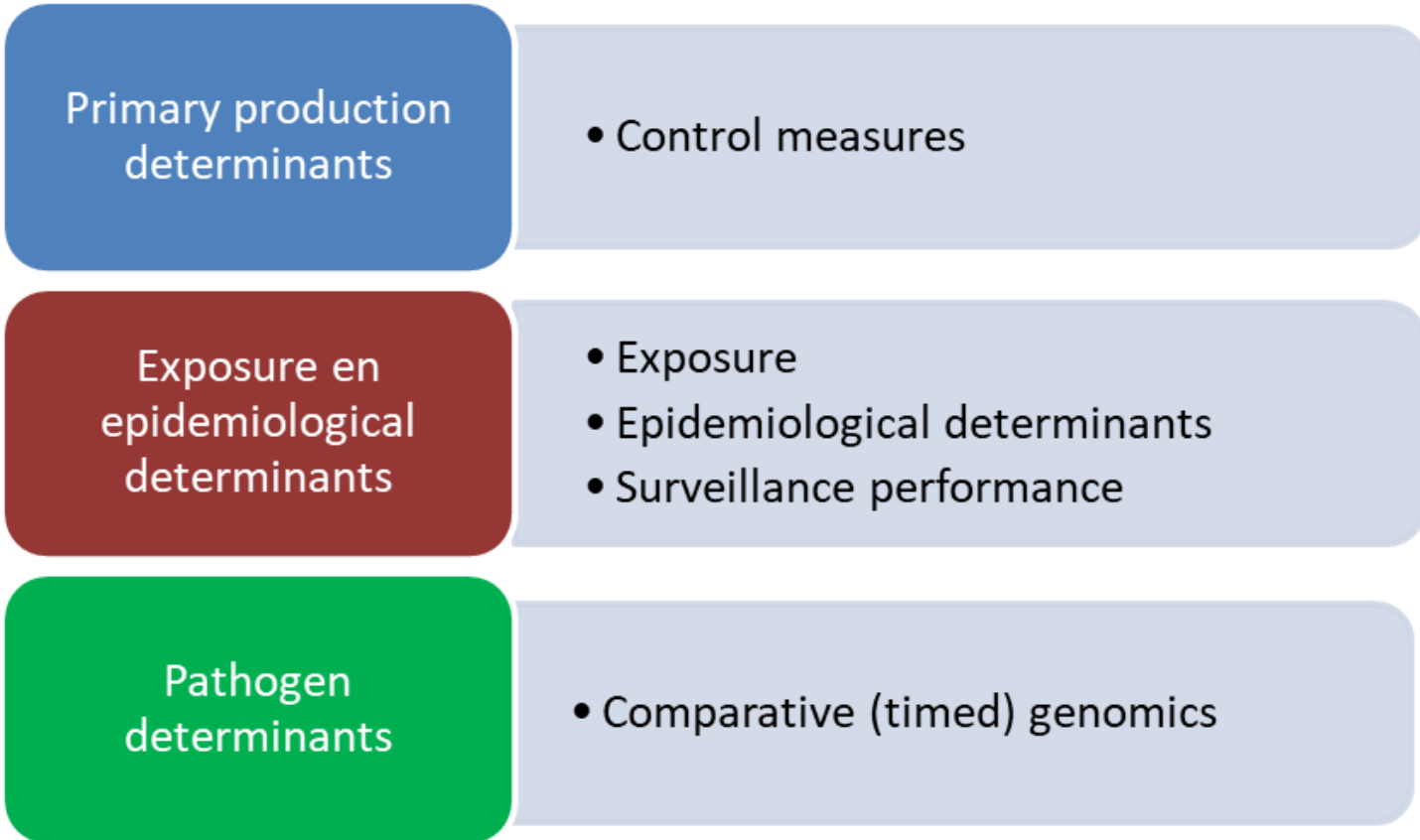
ECDC has revealed the decrease in *Salmonella* incidence in the EU has levelled off.

**ADONIS will identify determinants underlying the stagnation/reversal of the decreasing trend in *Salmonella* Enteritidis incidence in humans and poultry in the EU**

Deliver stakeholders and policy makers with anchor points to at least prevent a continued stagnation or even an re-establish a decreasing trend in *Salmonella* incidence in humans and poultry.

## Approach

The project approach is to investigate possible determinants at the level of primary production (WP2), epidemiology (WP3) and the pathogen (WP4); a multi-criteria- decision analysis (MCDA) is performed in WP5 (Fig. 1).



## Primary production

- Comparison of National Control Plans (NCPs) in poultry in ADONIS partners revealed a common framework that was nevertheless differed in certain aspects in terms of the predominant production systems and implementation details
- Factors associated with increased odds of *Salmonella* detection in poultry are very heterogenous depending on the study, but sampler (Competent authority vs. Food Business Operator) is strongly associated with an increased probability of detection.
- Analysis of NCP data from one MS found that the risk of detection has remained in similar levels in the last years

## Epidemiology

- Outbreaks (EU):** source attribution based on EU outbreak data showed poultry/eggs are still the main sources; Reported *Salmonella* outbreaks have increased significantly in occurrence from 2015 to 2019, particularly outbreaks caused by SE in Eastern European countries.

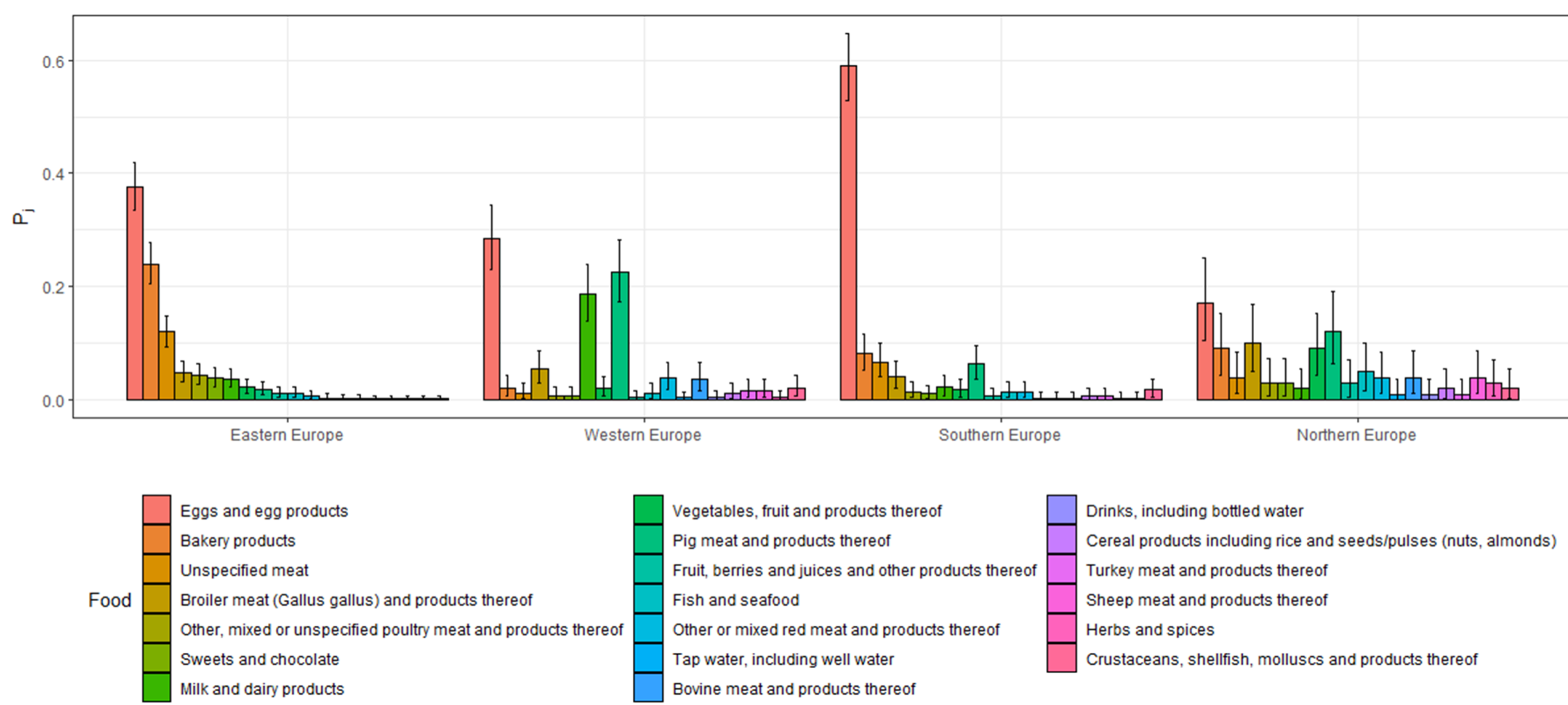


Fig. 2. Proportions of human salmonellosis outbreaks attributed to simple and unknown food-sources by European region with their respective 95% uncertainty intervals, 2015-2019

- Incidence (NL/BE):** *S. Enteritidis* incidence decreased significantly in both countries until 2015, followed by an increasing trend, which was particularly pronounced in the Netherlands. Potential SE outbreaks in both countries and invasive infections in the Netherlands also increased after 2015.

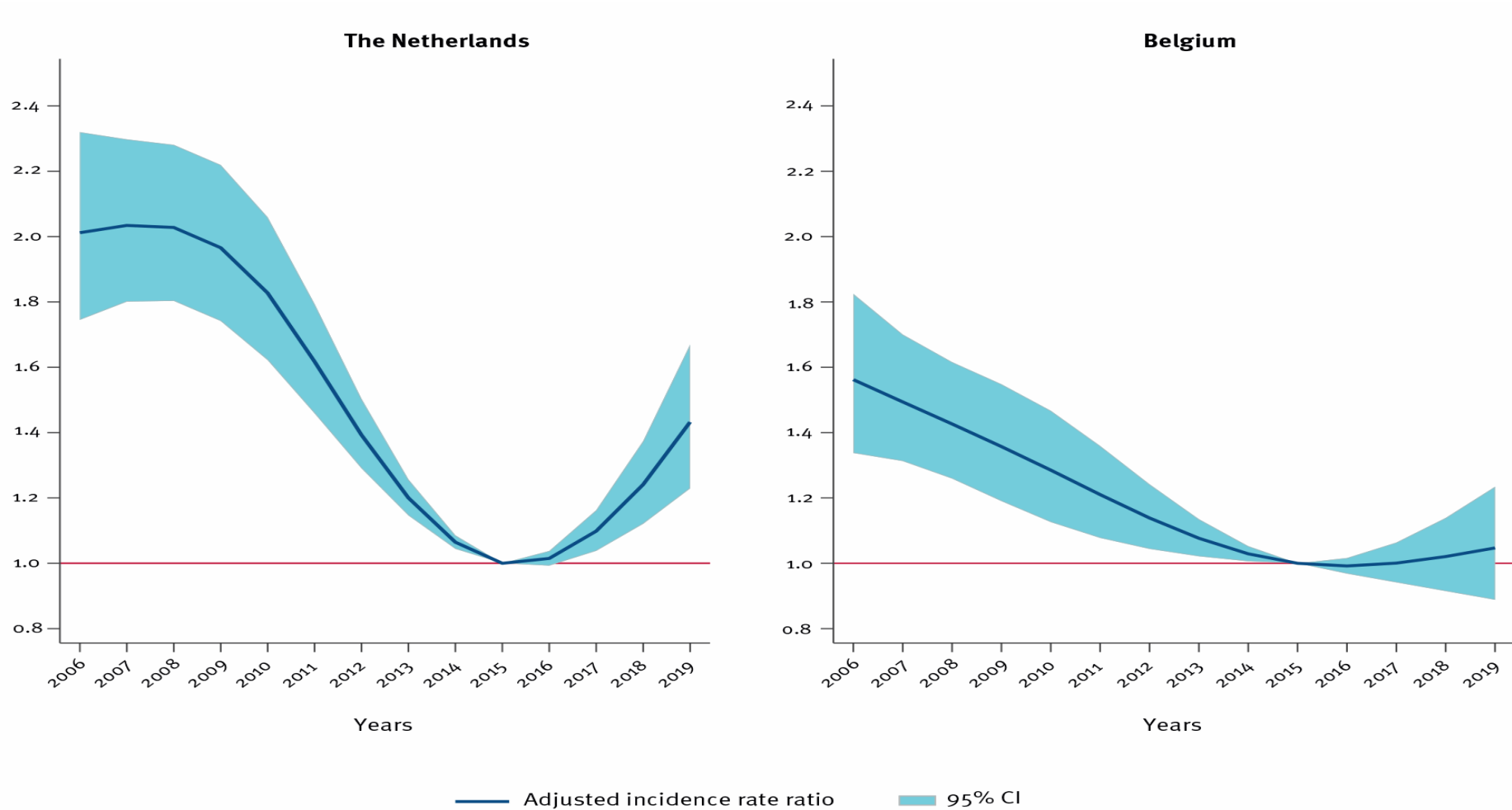


Fig. 3. Changes over time in the incidence of *Salmonella* Enteritidis (SE) human infection, with 2006 as reference year, in the Netherlands and Belgium, 2006-2019

## Pathogen

- AMR:** with decreasing antimicrobial use the resistance among *Salmonella* shows a decreasing trend; except third-generation cephalosporins and gentamycin (mainly driven by *S. Infantis*, and *S. Kentucky*).
- MGE:** Prophage specific for strains in old clade is undergoing mutant creation (removal of prophage) and phenotypic experiments.
- Geo-pyhologeny:** the population of *S. Enteritidis* is dominated by ST11 and characterized by relatively low geographical/niche structuring.
- Phyldynamics:** the presence of two large, relatively distant clades within the dominant ST instructs us towards an approach centered on distinct phyldynamics analyses.

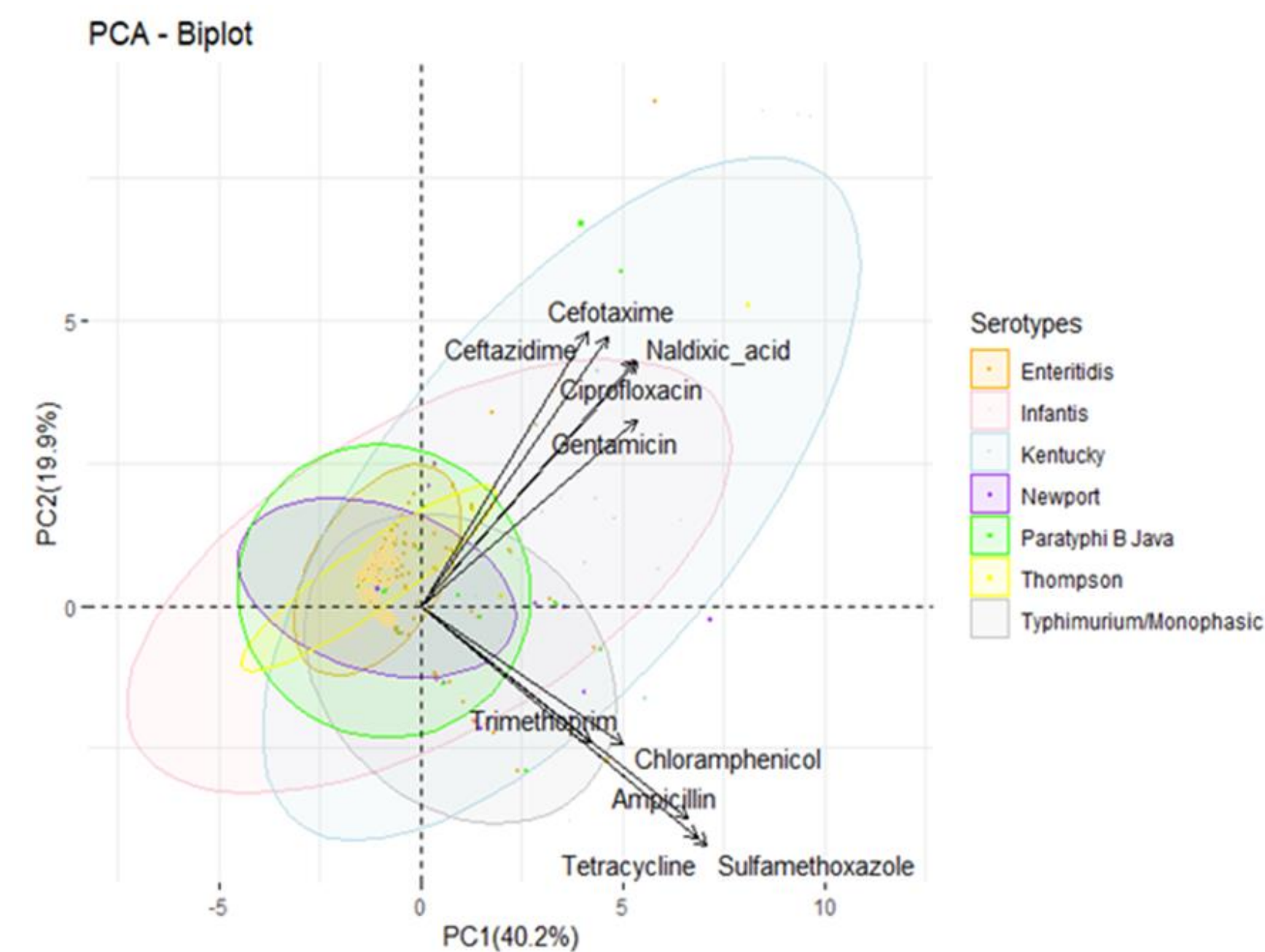


Fig. 4. Principal component plot of antimicrobial resistance by *Salmonella* serotype.

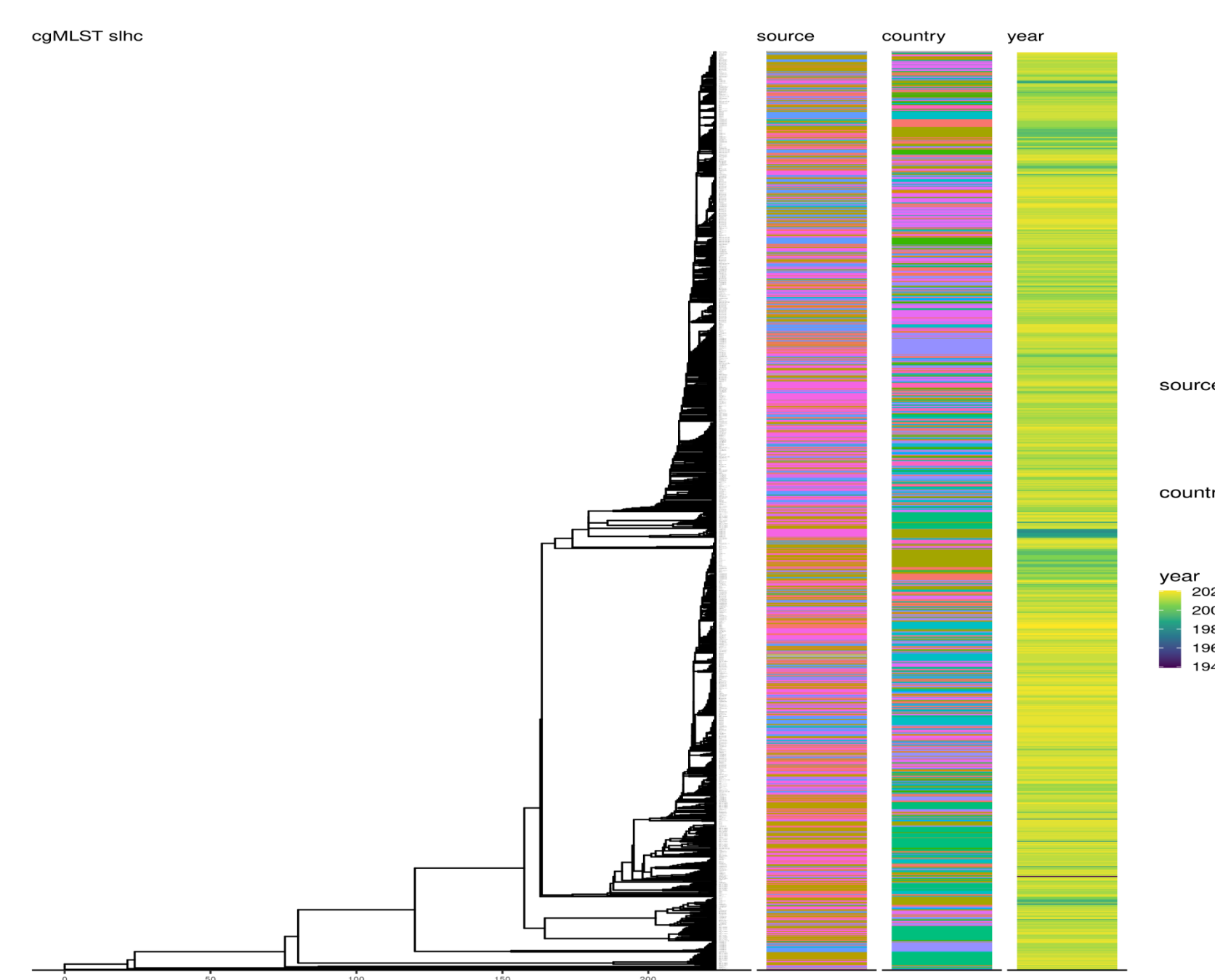


Fig. 5. Single linkage phylogenetic tree nnotated to country, source and year.

## Multi-criteria decision analysis

- The alternatives for the determinants and options for intervention that ranked the highest were consistently those related to the level of poultry health and production.

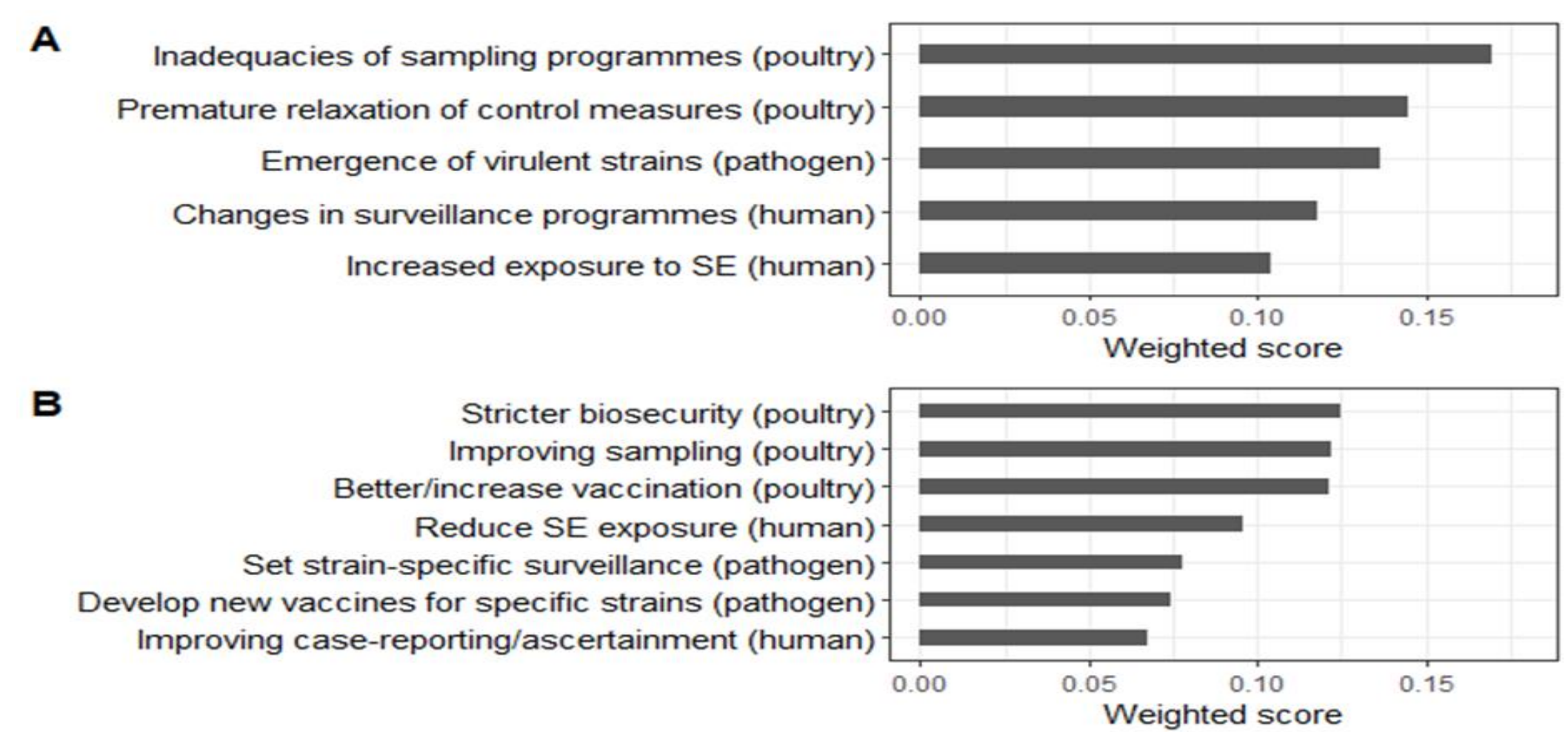


Fig. 7. Ranking of the determinants (A) and options for intervention (B) of the stagnating trend.

## Policy impact

- We observed a no longer decreasing trend in Salmonellosis, increased number of outbreaks and more severe infections
- Relaxation of sampling and control measures at poultry primary production was perceived as most important determinant
- Public health and veterinary institutes at national and supra-national level should prioritize salmonellosis control in terms of improved monitoring and surveillance as well as adequate source finding with outbreaks



# BeONE: Building Integrative Tools for One Health Surveillance

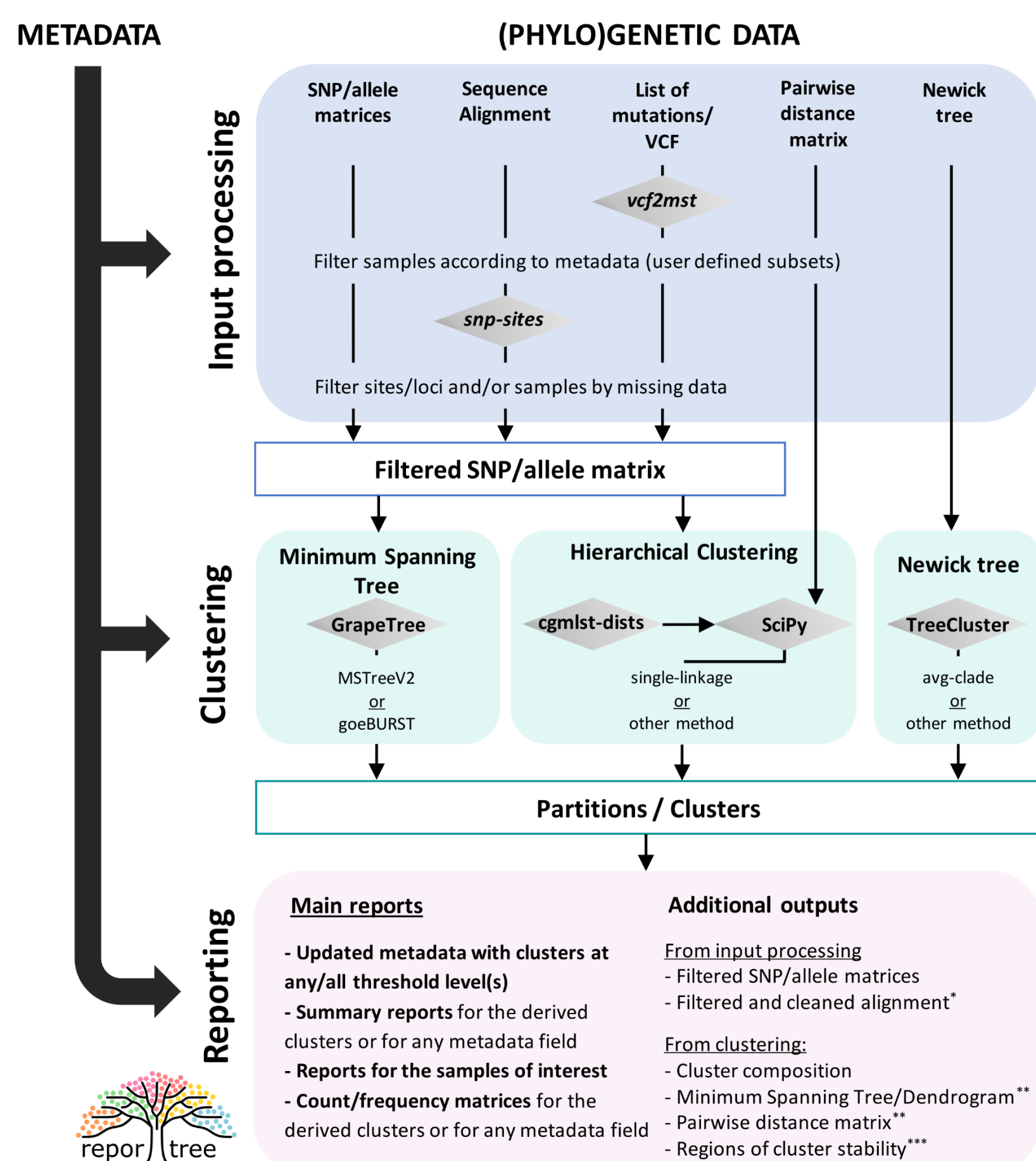
Verónica Mixão<sup>1</sup>, Vítor Borges<sup>1</sup>, Claudia Swart-Coipan<sup>2</sup>, Holger Brendebach<sup>3</sup>, Simon Tausch<sup>3</sup>,  
Finn Gruwier Larsen<sup>4</sup>, Katrine Joensen<sup>4</sup>, Kristoffer Kiil<sup>4</sup>, Sofie Holtsmark Nielsen<sup>4</sup> and BeONE Consortium

<sup>1</sup>National Institute of Health Doutor Ricardo Jorge (INSA, Portugal), <sup>2</sup>National Institute for Public Health and the Environment (RIVM, Netherlands),  
<sup>3</sup>German Federal Institute for Risk Assessment (BfR, Germany), <sup>4</sup>Statens Serum Institut (SSI, Denmark)

## Enhancing evidence-informed public-health decision-making

**Output:** A surveillance-oriented tool to strengthen the linkage between genetic clusters and epidemiological data

- Rapid identification of genetic clusters at any (or all) distance thresholds (e.g., high resolution thresholds used for **outbreak detection** or stable threshold ranges for **nomenclature design**)
- Generate **surveillance-oriented reports** based on the available metadata, such as timespan, geography or vaccination/clinical status



- Can be **smoothly implemented** in **routine surveillance**, with negligible computational and time costs
- Contributes to a **sustainable and efficient public health genomics-informed pathogen surveillance**

Collaboration with:



### Outcomes

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

**ReporTree** is an **automated and flexible pipeline**, applicable to **multiple pathogens**, with a concept aligned with **“One Health” perspectives**

## Promoting comparability and innovation in One Health surveillance

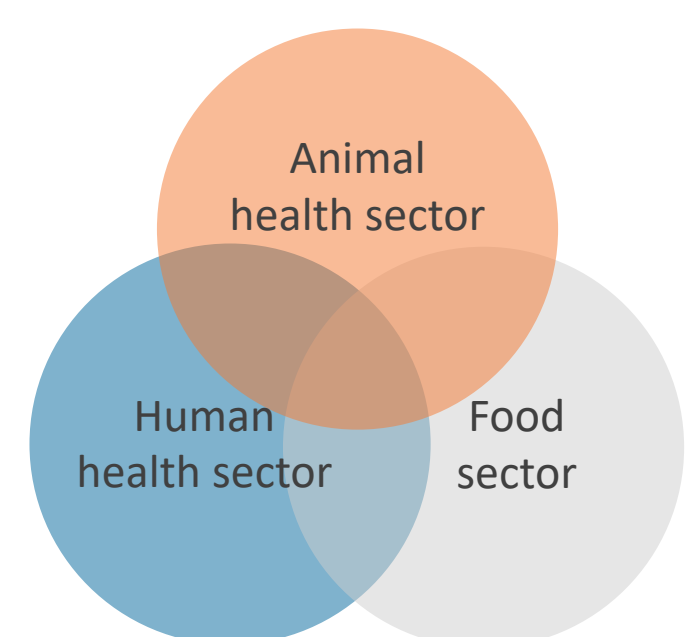
**Output:** Multi-country and inter-sectoral assessment of cluster congruence between different genomic surveillance pipelines

- Comparison of different typing methods used in the different countries/sectors, covering the levels of resolution needed for long-term routine surveillance and outbreak detection/investigation

✓ **Thresholds at several levels (for different “epidemiological” goals) that can be the basis for efficient nomenclature systems**

|                 | <i>Campylobacter jejuni</i> | <i>Escherichia coli</i> | <i>Listeria monocytogenes</i> | <i>Salmonella enterica</i> |
|-----------------|-----------------------------|-------------------------|-------------------------------|----------------------------|
| Denmark         | ■                           | ■                       | ■                             | ■                          |
| The Netherlands | ■                           | ■                       | ■                             | ■                          |
| Germany         | ■                           | ■                       | ■                             | ■                          |
| Portugal        | ■                           | ■                       | ■                             | ■                          |
| United Kingdom  | ■                           | ■                       | ■                             | ■                          |
| Germany         | ■                           | ■                       | ■                             | ■                          |
| Italy           | ■                           | ■                       | ■                             | ■                          |
| Poland          | ■                           | ■                       | ■                             | ■                          |
| Germany         | ■                           | ■                       | ■                             | ■                          |

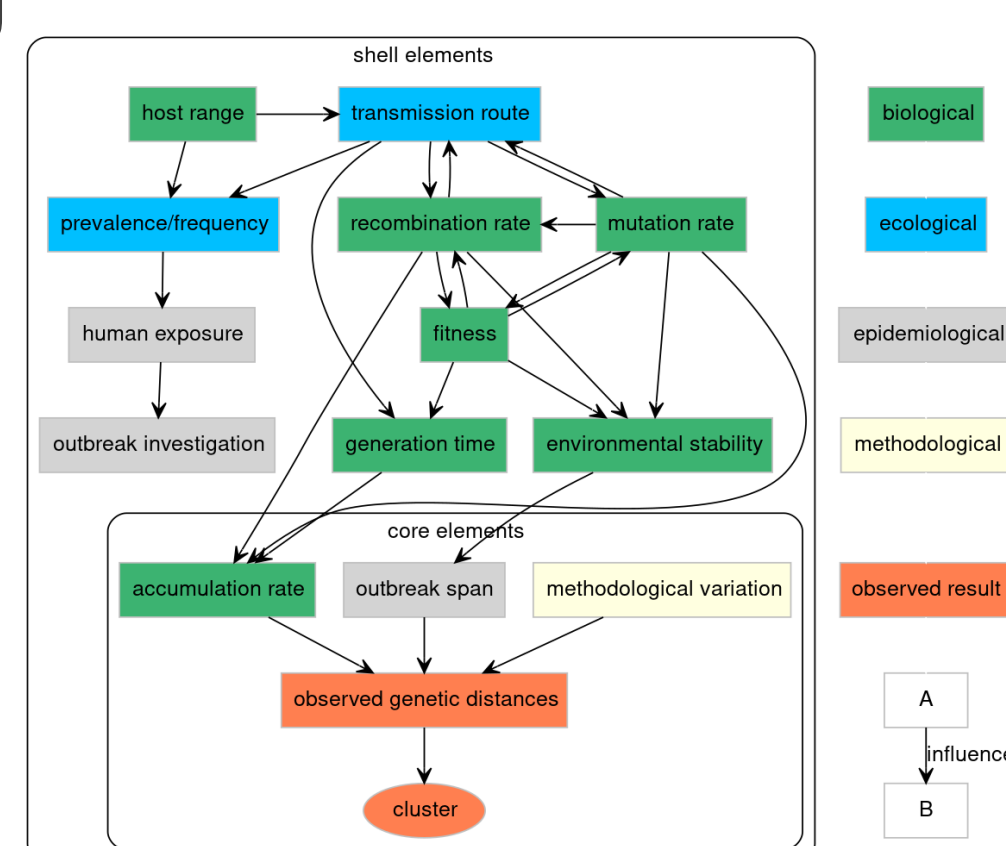
**Comparability between different pipelines, promoting a multi-country and intersectoral One Health approach**



**Output:** Conceptual model of genetic clustering

- Address the outbreak detection problem and outline a conceptual model that underlines the complex relations between the **biological and ecological factors at play in the evolution** of common foodborne pathogens

✓ **This model will be refined upon emergence of new data on this innovative topic**



**First step in developing and evaluating new algorithms for cluster definition/detection towards a transdisciplinary One Health approach**

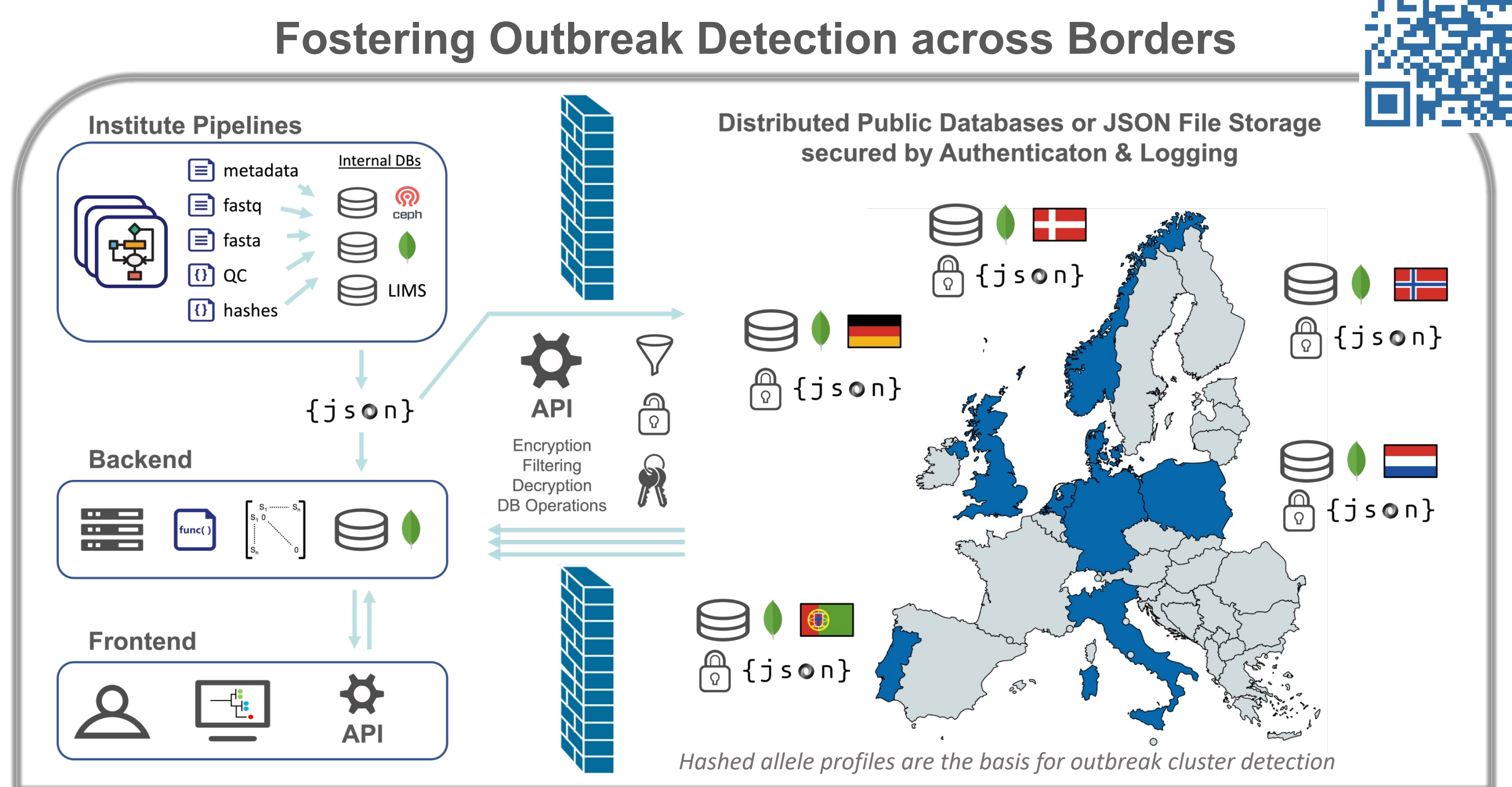
## Connecting European genomic surveillance laboratories

**Output:** Digital structure for the exchange of genomic and epidemiological data

- Structure of the epidemiological data shared between laboratories/countries utilizes controlled vocabulary based on the **EFSA Standard Sample Description**
- Data is imported into a publicly accessible MongoDB and may be **filtered and/or encrypted** concurrently in an information hierarchy-aware manner

### Outcomes

- ✓ Pilot tested in Germany
- ✓ Simulation of **multilateral data exchange within BeONE**



With this **harmonized data model** and **data aggregation in a non-relational database**, **bi- or multilateral automated data exchange under legal and GDPR considerations** becomes feasible

## Integrating different surveillance-oriented solutions

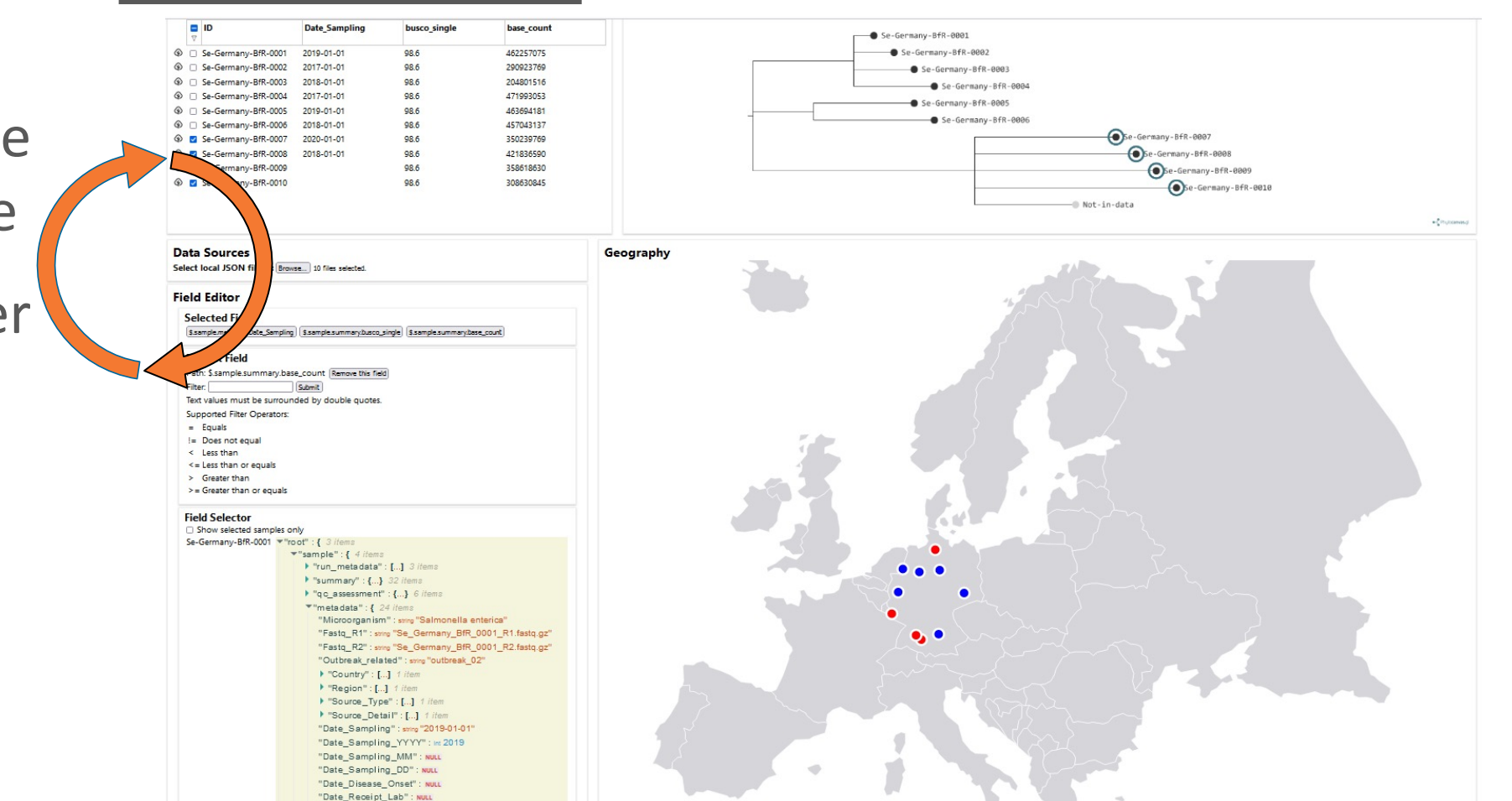
**Output:** BeONE datahub and dashboard

### BeONE datahub

- Web application connected to the BeONE MongoDB sample database
- Integration of ReporTree for cluster identification and reporting



### BeONE dashboard



**Integrative web application for the visualization of genetic clusters integrated with epidemiological and geographical data**

## ADDITIONAL OUTPUTS

### Diverse datasets of four important foodborne pathogens

Public datasets comprising genome assemblies and allelic profiles of *Listeria monocytogenes* (3,300 isolates), *Salmonella enterica* (2,766 isolates), *Escherichia coli* (2,307 isolates) and *Campylobacter jejuni* (3,686 isolates). Part of these isolates were anonymously shared within the BeONE Consortium. The remaining ones were carefully selected from public databases to ensure a wide genetic diversity in the dataset. **Useful asset for future surveillance and research works.**



### One Health Sequencing for Surveillance Handbook

Online handbook covering the main technical and practical aspects associated with the application of WGS for foodborne diseases surveillance. By following a simple and straightforward writing and structure, it can be easily understandable by laboratory staff starting in the field, thus **helping national and local labs to build capacity and competence** on the use of NGS methods for surveillance purposes.



## IMPACT

BeONE tools and outputs are expected to i) contribute to the **capacitation of EU laboratories** to carry out routine surveillance integrating both genomic and epidemiological data, ii) launch **new research lines** to improve food and waterborne diseases (FWD) genomic epidemiology, and iii) facilitate **data sharing and comparability** among EU countries, international organizations, and/or other stakeholders involved in FWD prevention and control. Fully aligned with the One Health concept, BeONE may ultimately promote an **enhanced interoperability** at multi-country and intersectoral levels towards an **evidence-informed public health policy- and decision-making** to decrease the FWD burden.

### Main publications

- Mixão V et al. (2022) ReporTree: a surveillance-oriented tool to strengthen the linkage between pathogen genetic clusters and epidemiological data. *Research Square*. doi: 10.21203/rs.3.rs-1404655/v2
- Deneke C et al. (2021) Species-Specific Quality Control, Assembly and Contamination Detection in Microbial Isolate Sequences with AQUAMIS. *Genes*. 12(5):644. doi: 10.3390/genes12050644
- Deneke C et al. (2021) Decentralized Investigation of Bacterial Outbreaks Based on Hashed cgMLST. *Front Microbiol*. 12:649517. doi: 10.3389/fmicb.2021.649517



This poster is part of the European Joint Programme One Health EJP. This project has received funding from the European Union's Horizon 2020 research and innovation programme under Grant Agreement No 773830





# BIOPIGEE

## Biosecurity practices in pig farming across Europe

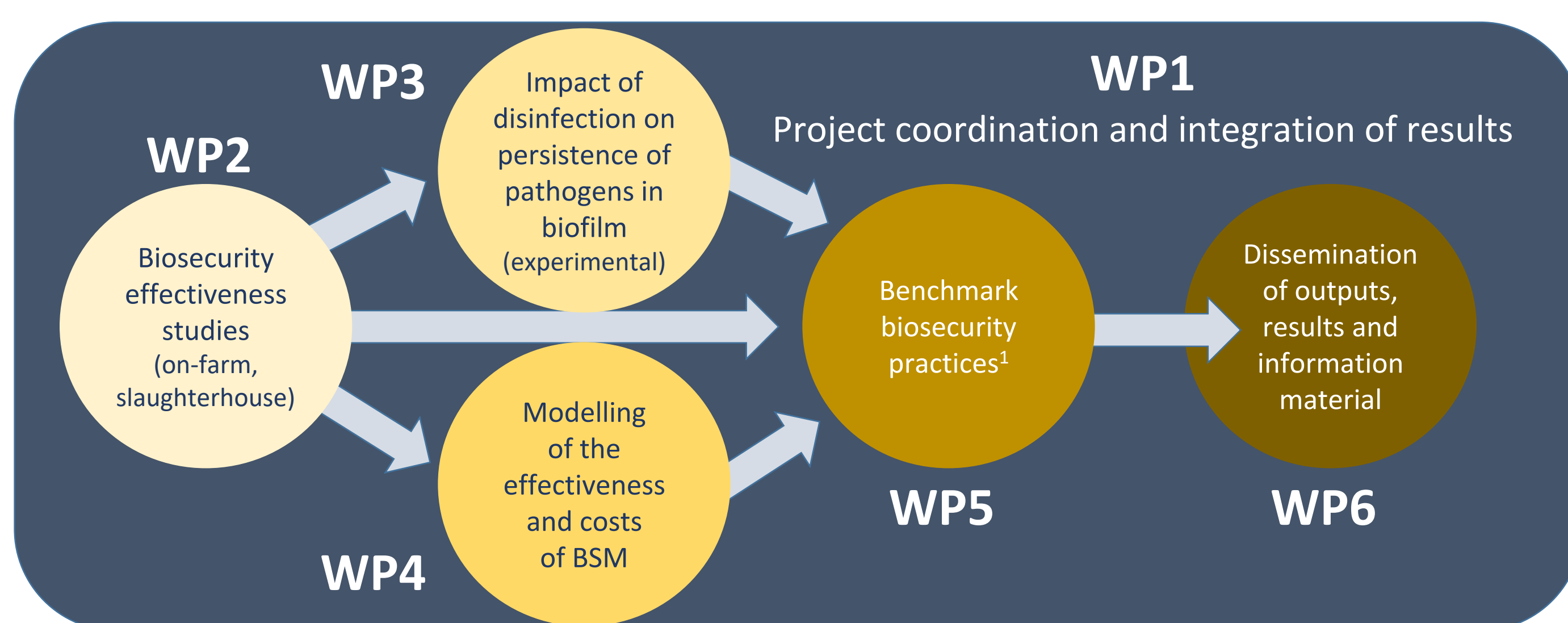
E. Burow (WP1, BfR), R. Smith (WP2, APHA), W. v.d. Poel (WP3, WBVR), R. Simons (WP4, APHA), V. Zoche-Golob (WP5, BfR), M. Sjölund (WP6, SVA), BIOPIGEE Consortium

### Project background

*Salmonella* (SAL) and hepatitis E virus (HEV) are considered zoonotic pathogens which rarely lead to clinical signs in pigs but can cause severe diseases in humans. Since pigs can serve as reservoirs, the relevance of biosecurity measures (BSM; defined by Huber et al. 2022) for controlling transmission of SAL and HEV into and within pig farming was studied.

**Objective:** Identification of effective and cost-efficient biosecurity measures along the pig production chain to prevent SAL and HEV from entering the food supply chain.

Briefly, work packages including literature, expert panel, field and experimental studies as well as modelling were arranged and finally informed a package disseminating the findings.



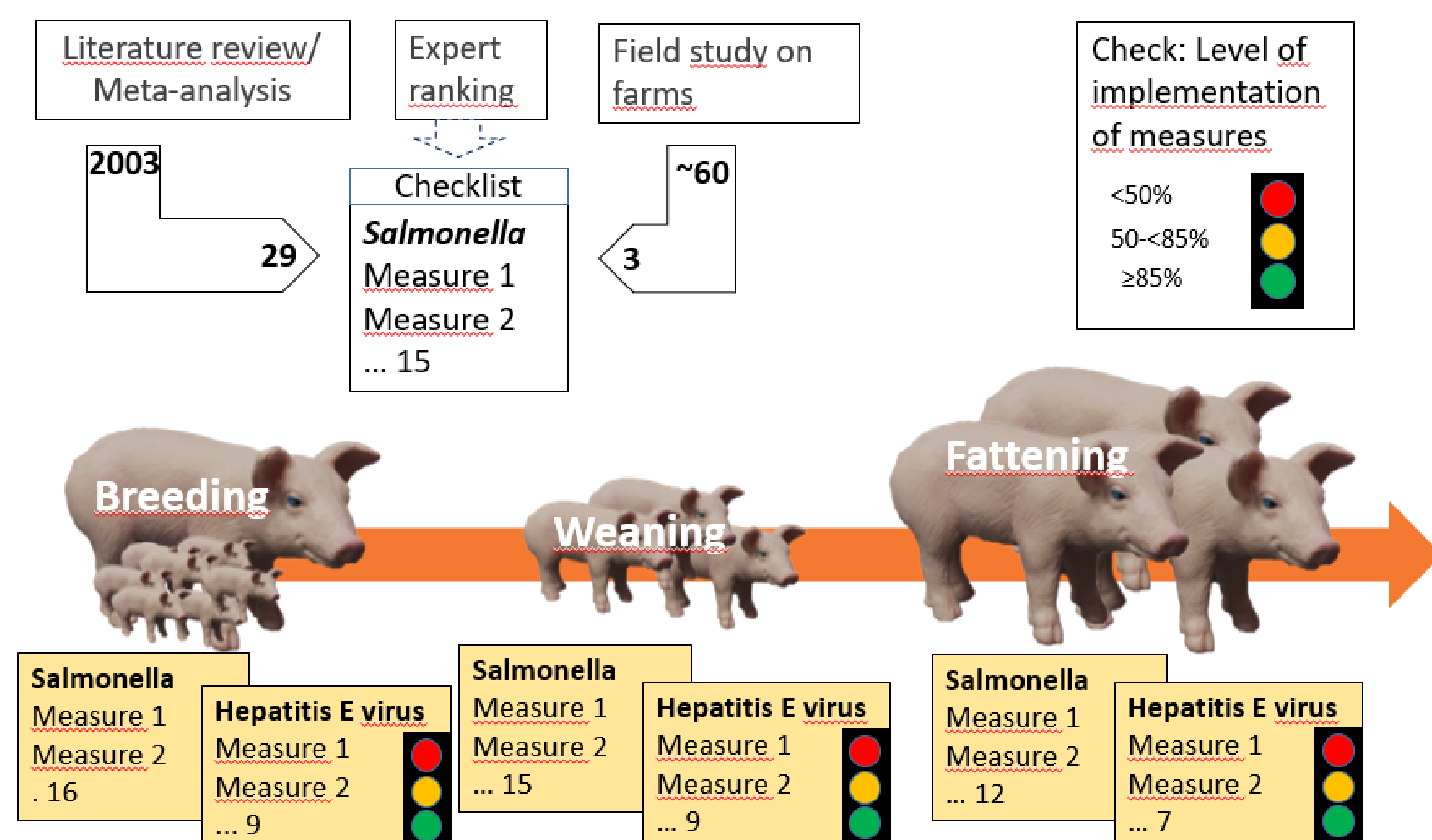
<sup>1</sup>WP5: Definition biosecurity measure, literature review, expert survey, checklist

### Key output: On-farm checklists

Checklists were developed (WP5.5) which include BSM

- proven to be effective for pig farms based on extractions from peer-reviewed papers (WP5.2) and BIOPIGEE field studies (WP2.2)
- meet the definition by Huber et al. 2022 (WP5.0).
- ordered based on expert opinion (highest ranked measures at the top of lists, WP5.4).

A traffic light system indicates implementation rate (WP5.5).

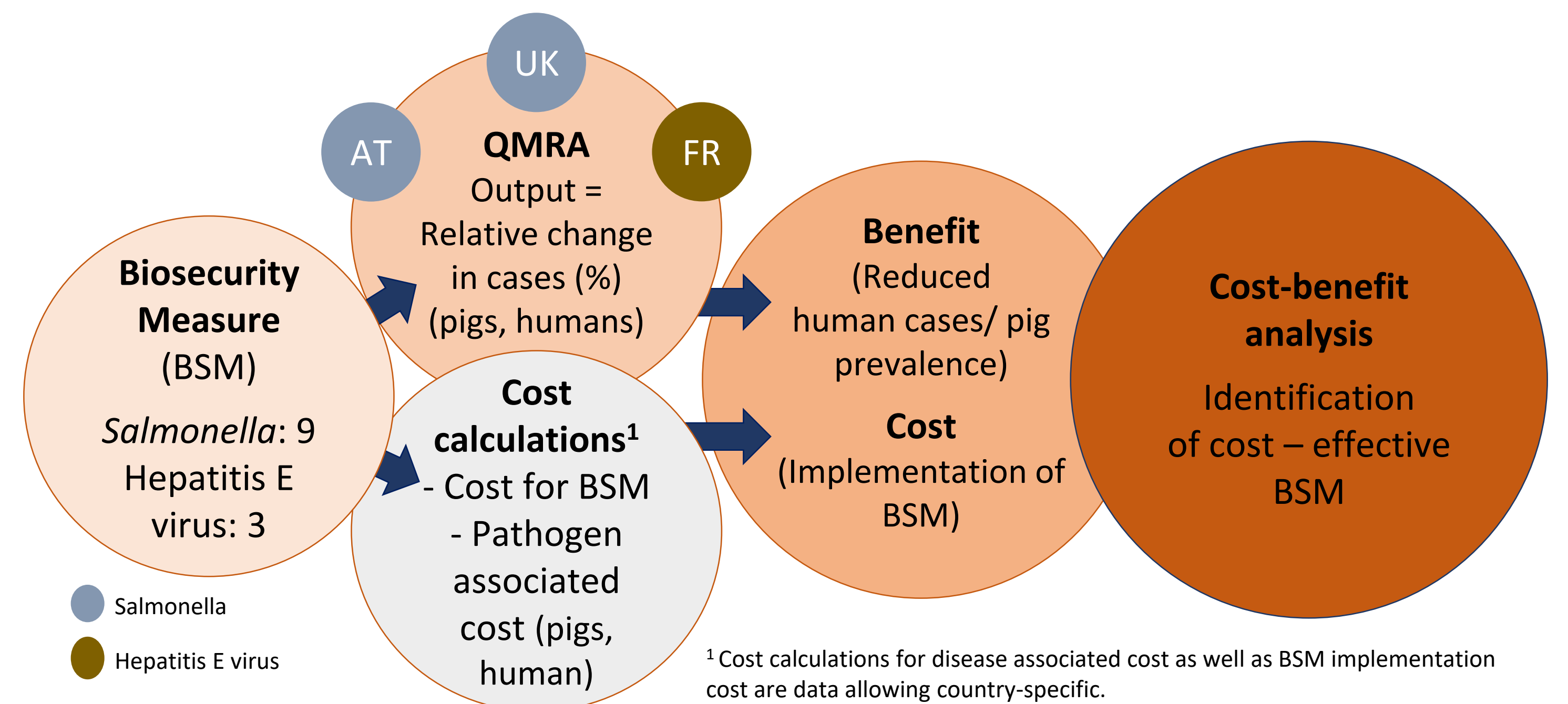


### Key output: Guidance document for abattoirs

A guidance document was produced (WP2.3), listing 23 quantitatively effective BSMs to control SAL and *E. coli* occurrence in slaughterhouses, identified from 51 relevant research papers & reports.

| Steps in slaughter process      | Number of effective BSMs/publications |
|---------------------------------|---------------------------------------|
| Lairage hygiene and management  | 4/10                                  |
| Scalding methods & conditions   | 2/8                                   |
| Singeing methods & conditions   | 1/3                                   |
| Polishing                       | 3/5                                   |
| Evisceration hygiene & technics | 3/7                                   |
| Carcass splitting               | 2/3                                   |
| Decontamination of carcasses    | 4/8                                   |
| Chilling of carcasses           | 4/4                                   |

### Key output: Cost-benefit of biosecurity measures



<sup>1</sup> Cost calculations for disease associated cost as well as BSM implementation cost are data allowing country-specific.

The impact on the number of human cases by as effective identified BSM (WP5.2) was evaluated using established quantitative microbial risk assessment models (QMRA) (WP4.2). In a cost-benefit analysis (WP4.4) the cost (€) of the applied BSM in 100% of farms/slaughter pigs within a country was compared against the resulting benefit (€) (i.e. reduced number of human cases, reduced prevalence in pig population) for the year 2019. The results of only 3 BSM for SAL showed a BCR >1 for the selected countries. Due to data gaps, only benefits resulting from a reduced number of human cases could be calculated for HEV. All evaluated BSM for HEV had a BCR <1.

| Economic assessment   |         |                |
|---|---------|----------------|
| BCR = Total benefit/Total cost  |         |                |
| Results for a 100% application rate of the BSM on farms/in slaughter pigs to reduce Salmonella. |         |                |
| Biosecurity measure   | Austria | United Kingdom |
| SALMONELLA  |         |                |
| Benefit Cost Ratio  |         |                |
| Acid in feed  | 1.49    | 1.50           |
| Acid in water   | 1.12    | 1.91           |
| Anal plugging   | 1.42    | 1.42           |
| Disinfection  | <1      | 1.02           |

### Project outcomes and impact

#### Outcomes

- Guidance for farmers, veterinarians, consultants, slaughterhouses in European countries
- Exchange with expert panel, stakeholders and head organizations at various workshops and other dissemination events was organized across partner countries
- Illustrative flyers and web content to inform stakeholders, incl. collaborating farm education centers and other projects is produced and offered in partner countries

#### Impact

##### Societal and policy

- **Reliable** guidance on **cost-efficient** measures
- **Reduction** of SAL & HEV **spread**, and of animal and human **diseases**
- Basis for **monitoring & regulation** in a One Health context

##### Scientific

Applied support tools can be developed further

- **Integration** of new evidence on cost-effective measures
- **Adaptation** to cover also **other pathogens, livestock species, production systems**
- **Definition** of **biosecurity measures** as fundamental basis for targeted implementation

#### Acknowledgements

Contribution: A. Viltrop (slaughterhouse study, Estonian University of Life Sciences), C. Bester (cost-benefit study, Vetmeduni Vienna)

#### Reference

N. Huber et al. 2022 <https://doi.org/10.1016/j.onehlt.2022.100433>

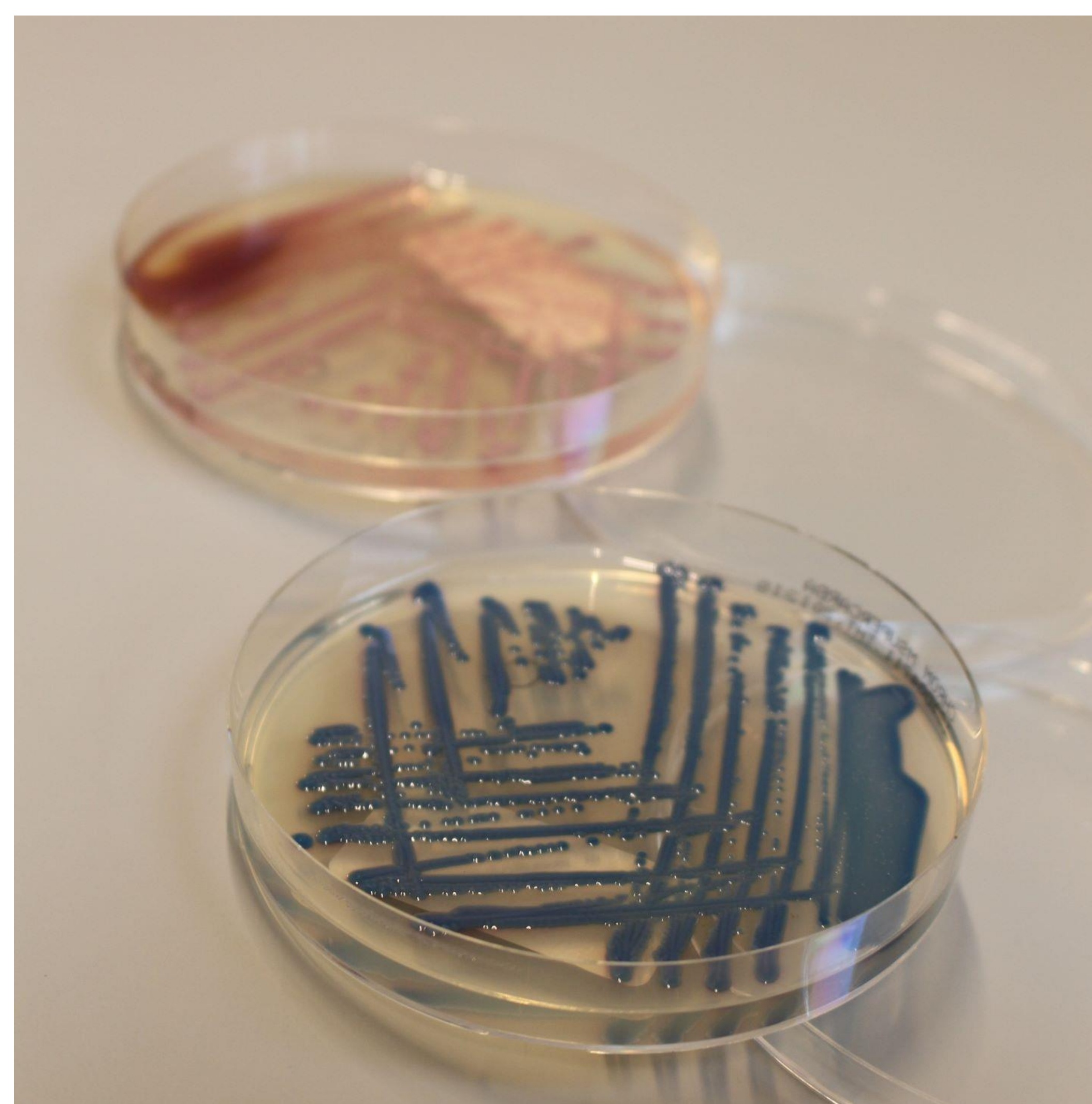


# IMPART: Improving Phenotypic Antimicrobial Resistance Testing

Project leader: **Kees Veldman**, Wageningen Bioveterinary Research (WBVR) part of Wageningen University & Research (WUR)  
Work package leaders: **Agnès Perrin-Guyomard** and **Sophie Granier**, The French Agency for Food, Environmental and Occupational Health and Safety (ANSES); **Jannice Schau Sletteameås**, Norwegian Veterinary Institute (NVI); **Kees Veldman**, Wageningen Bioveterinary Research (WBVR) ; **Sven Maurischat**, German Federal Institute for Risk Assessment (BfR).

## MAIN OBJECTIVES

- (1) Harmonising detection methods for specific types of AMR associated with bacteria relevant to public health, such as colistin-resistant and carbapenemase-producing Enterobacterales (CPE).
- (2) Establishing new laboratory test criteria (ECOFF) to improve international harmonisation of the monitoring of antimicrobial resistance in bacterial pathogens from animals and humans.

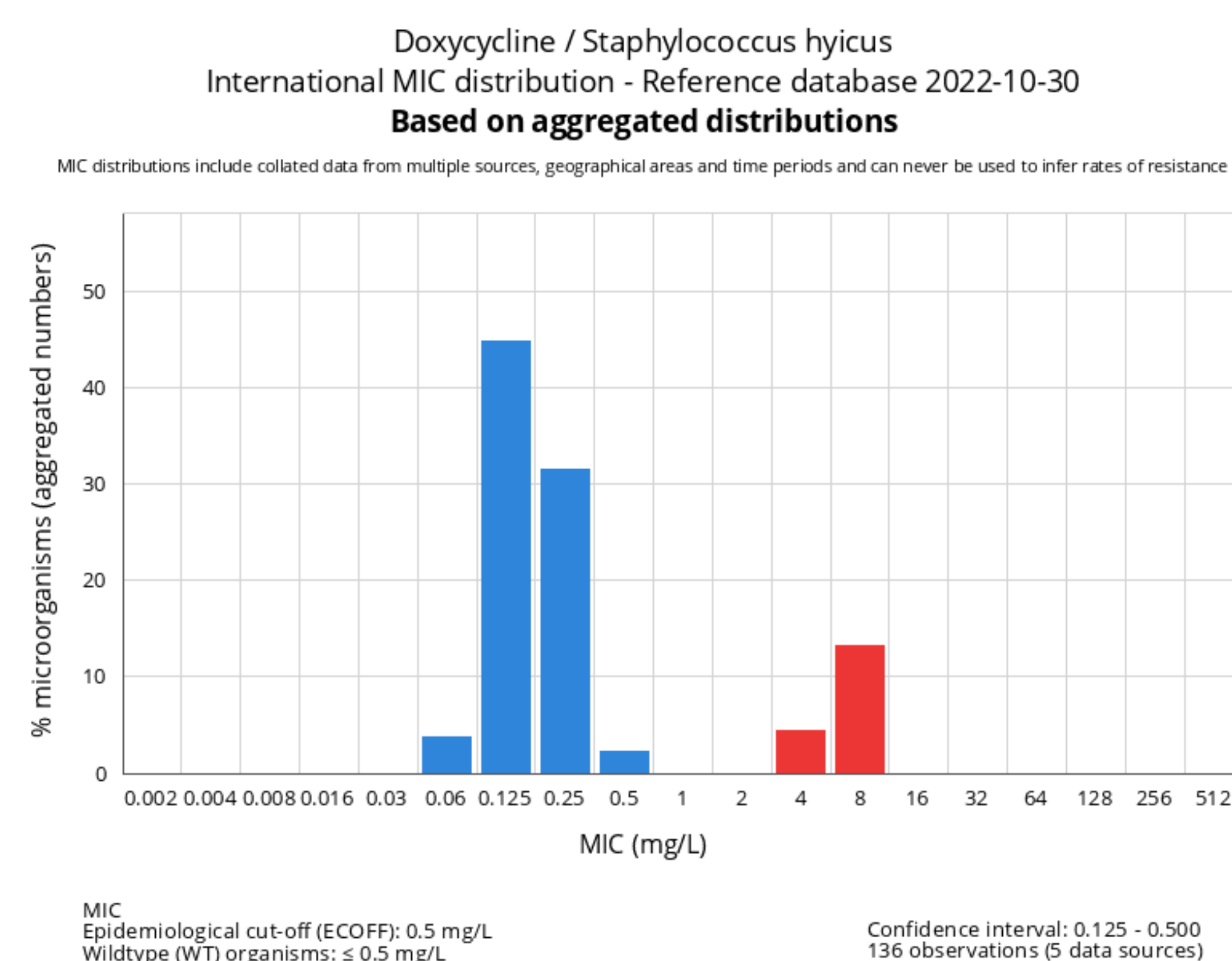


## KEY OUTPUTS

**WP1:** A two-step screening method involving a PCR amplification and culturing on chromogenic agars media was effective to detect most of the *E. coli* or *Salmonella* spp. strains harboring *mcr*-genes.

**WP2:** Most commercially available agars for the detection of CPE performed adequately. However, the evaluation showed that the investigated agars were not suitable for detection of non-chromogenic CPE strains nor for the detection of CPE with low meropenem MICs.

**WP3:** Facilitated by the production of >50.000 MIC values new epidemiological cut-off values (ECOFFs) were established for *Staphylococcus hyicus*, *S. pseudintermedius*, *Pasteurella multocida* and *Mannheimia haemolytica*.



## SCIENTIFIC IMPACT

**WP1:** The outcomes of IMPART stimulated different partner institutes to optimize their protocol for detection of colistin resistant bacteria which will result in additional publications on this subject.

**WP2:** Limitations to detect low-level meropenem resistance using the EURL-AR protocols for detection of ESBL/AmpC and CPE in caecal or meat samples encouraged partner institutes to perform additional CPE screening by using PCR and/or selective enrichment steps.

**WP3:** ECOFFs of animal pathogenic bacteria are essential for determining clinical breakpoints of veterinary antibiotics. The first clinical breakpoint for florfenicol in cattle was established by VetCAST after setting ECOFFs for *Mannheimia haemolytica* and *Pasteurella multocida*.

## POLICY IMPACT

**WP1:** Implementation of a selective screening protocol will generate valuable data for EFSA regarding the prevalence of *mcr*-carrying bacteria in food-producing animals and meat products to monitor the effect of the recent reduction of polymyxins usage in livestock.

**WP2:** Based on the outcomes of a questionnaire regarding the non-selective pre-enrichment step within the protocol for detection of ESBL/AmpC and CPE, the EURL-AR decided to stick to the current method because of the multi-purpose application of the broth for other objectives of the AMR monitoring.

**WP3:** Activities to harmonise susceptibility testing of veterinary pathogenic bacteria are continued within VetCAST and COST action ENOVAT (COST Action CA18217) and will support the EU One Health Action Plan against AMR.









## FED-AMR:

# The role of free extracellular DNA in dissemination of antimicrobial resistance over ecosystem boundaries along the food/feed chain

## INTRODUCTION

Free extracellular DNA (exDNA) is assumed to be a major contributor to the environmental resistome. Transformation is an important driver for genetic plasticity of bacterial genes and genomes. Natural transformation does not require physical contact between donor and recipient bacteria and is exclusively regulated by the recipient cell. This may facilitate antibiotic resistance genes (ARG) crossing ecosystem barriers and invading new habitats compared to HGT by conjugation.

**Keywords:** Bacterial transformation, free extracellular DNA, antimicrobial resistance, horizontal gene transfer, ecosystem boundaries.

## QUESTIONS

The design of the experiments are allowing to answer the following research questions:

- Question 1:** What are the most prevalent ARGs in the tested environmental compartments?
- Question 2:** Which environmental compartments show an especially high contamination with ARGs of anthropogenic origin?
- Question 3:** Does ARG-encoding free exDNA overcome ecosystem boundaries and bottlenecks more easily compared to the transfer of non-autochthonous bacteria in newly invaded ecosystems?
- Question 4:** What are the main drivers of AMR dissemination via free exDNA in the tested environmental compartments?
- Question 5:** Which strategies can be applied to reduce the spread of AMR caused by the transfer of free exDNA between ecosystems highly contaminated with ARGs of anthropogenic origin?

## SPECIFIC AIMS

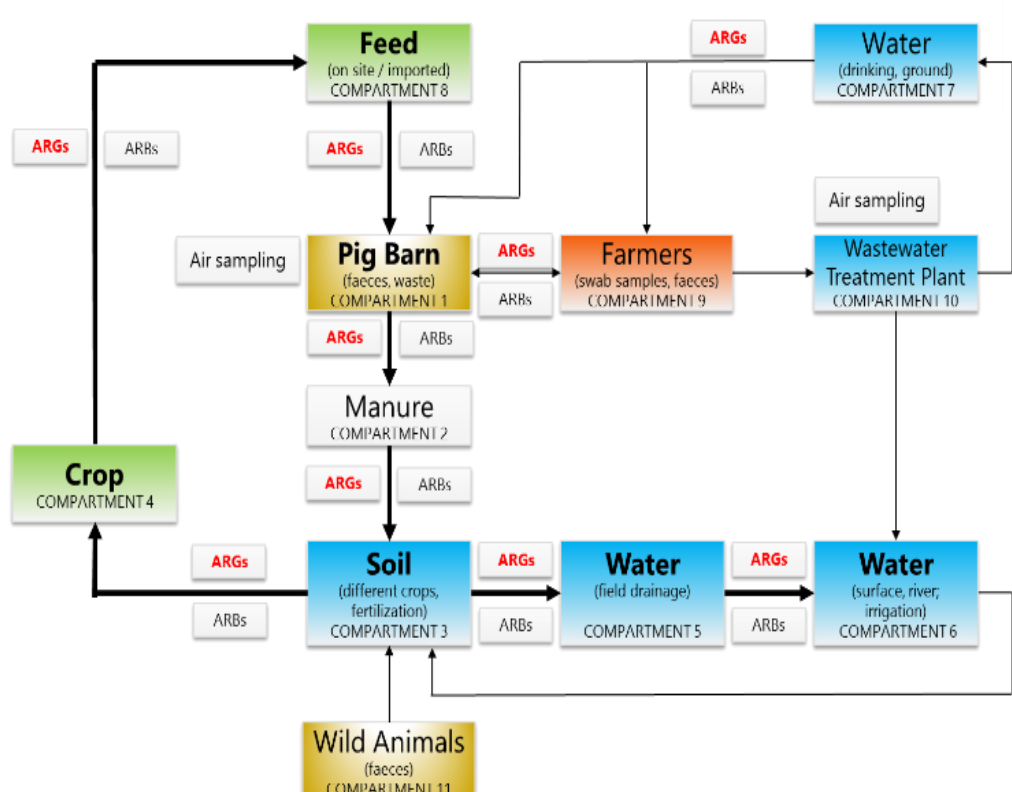
**Objective 1 (WP2):** Determination of the resistome and microbial biodiversity in the tested environmental compartments – longitudinal study over a crop-growing season (1 year; field studies). Identification of the role of exDNA for HGT in the tested compartments (**Fig. 1**).

**Objective 2 (WP3):** Elucidating the role of *C. difficile* as an ARG transfer platform over ecosystems boundaries and its linkage between human and non-human (zoonotic) reservoirs (**Fig. 1**).

**Objective 3 (WP4):** Determination of the selection pressures in the tested compartments of human, animal and environmental ecosystems (**Fig. 1**).

**Objective 4 (WP5):** Identification of environmental conditions modulating transformation frequencies in soil microcosms and porcine chemostat gut models (laboratory studies)

**Objective 5 (WP6):** Developing probabilistic and mechanistic models explaining the links between antimicrobial usage in animals, AMR in the environment, and the risks for public health.



**Fig. 1. Potential pathways for ARG dissemination over environmental ecosystem barriers.** Bold letters/arrows = compartments and pathways for ARG movement that are monitored on the HOAL testing range; ARGs: antimicrobial resistance genes; ARBs: antimicrobial resistant bacteria; Animal compartments (pigs, stable; wild animals in HOAL catchment area); gold: Human compartments (farmer, workers exposed to animal husbandry in HOAL); red: Compartments associated to plants (crops, animal feed); green: Genuine environmental compartments (soil, water); blue.

**Sampling:** 6 countries from 4 EU regions (East, North, South, West) collected in 2 HOALs (Hydrological Open Air Laboratory) (AU, PT), 2 conventional agricultural lands (EE, CZ), 1 mixed livestock farm (GB), 1 municipal WWTP & Forest (IE) samples from up to 11 compartments.

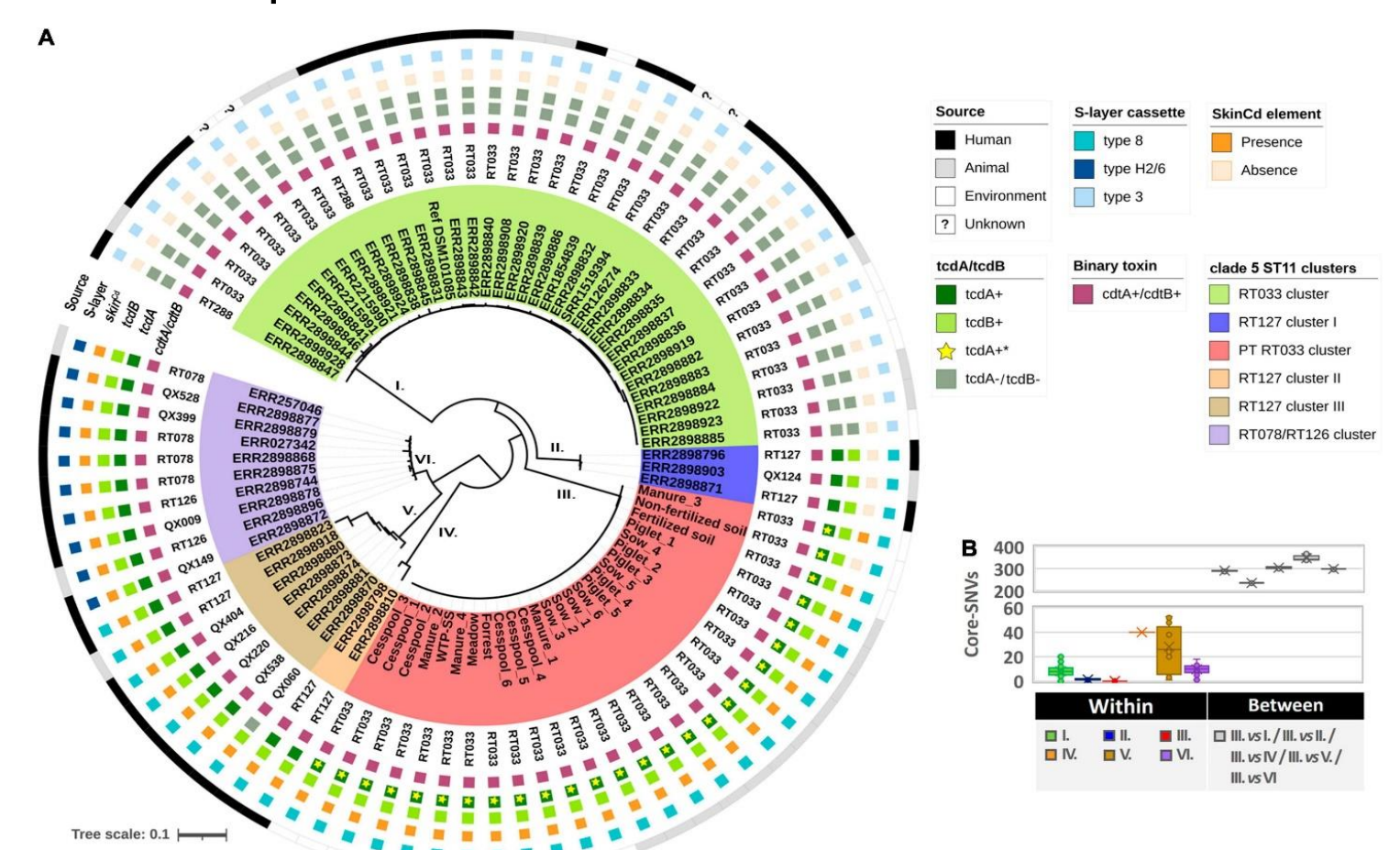
### Objective 2:

In each HOAL, a different ribotype was dominant.

All compartments connected to the swine production unit (pigs, swine cesspool/manure, agricultural soil and WTP) presented the highest *C. difficile* positivity rate, and RT033 was the predominant type found in those compartments.

**Conclusion:** The high genetic relatedness found among isolates (0.1 core-SNVs) (**Fig. 6B**) supports a clonal transmission between animal and environmental compartments.

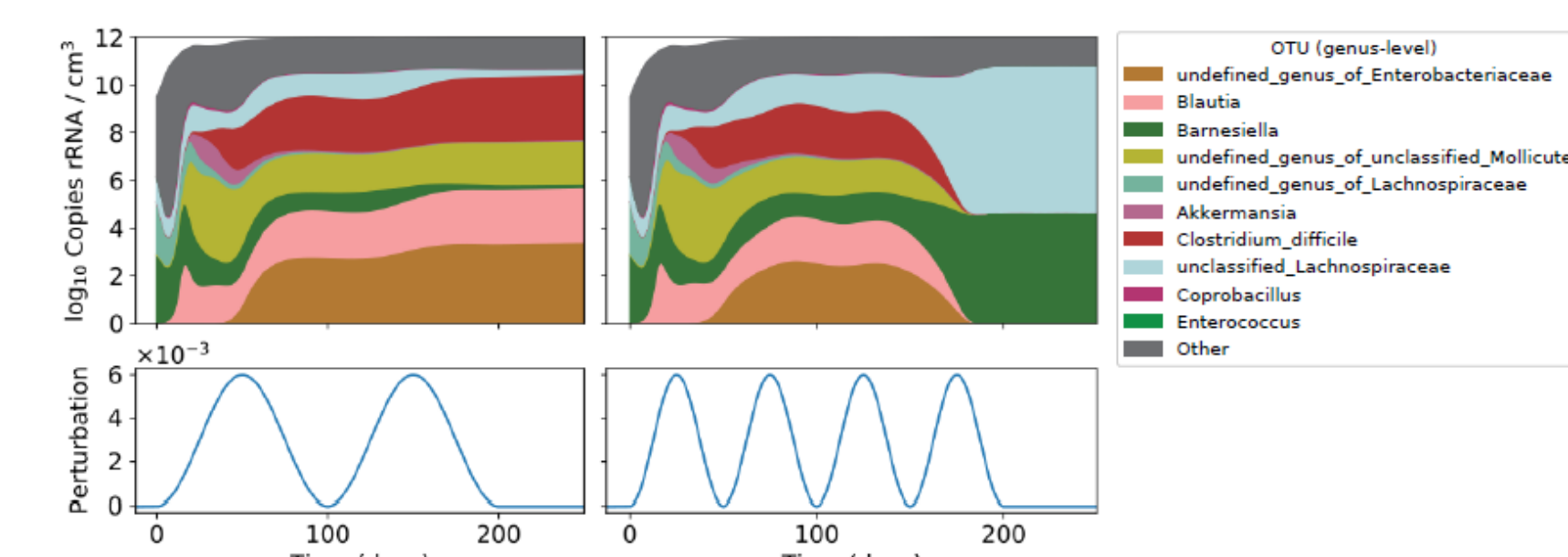
**Fig. 6 Phylogenetic positioning of PT RT033 clone within the *Clostridioides difficile* clade 5 ST11 lineage. (A) Core-genome SNP-based phylogenetic tree. (B) Box Plots depicting the number of SNVs observed within and between all clade ST11 clusters.**



### Objective 5:

We inferred bacterial growth, interaction and antibiotic susceptibility parameters for the Lotka-Volterra model, restricted to the top 10 most abundant genera to avoid overfitting. After simulations we identified a tipping point of the community in response to external perturbation: resulting in a persistent change in its composition and subsequent recovery from colonisation by *C. difficile* (**Fig. 7**). The areas under the curves for both perturbation signals are equivalent.

**Conclusion:** Ecological modelling of microbial communities affords additional insight into their stability, which cannot easily be determined from experimental studies alone. Our next step is to explore the impact of different perturbation regimes, with the long-term goal to model data obtained from chemostat experiments (WP5).



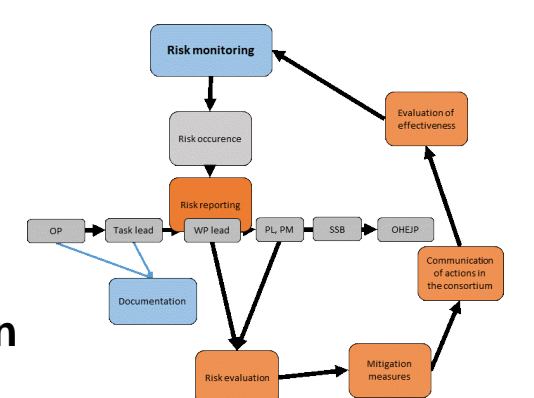
**Fig. 7. The microbial community composition (top) is influenced by a transient, periodic perturbation signal (e.g. the addition of antibiotics; see bottom). These signals differ in their frequency. (Left) Community displays resilience to this signal. (Right) Community is tipped into a different state, and recovers from colonisation by *C. difficile* (red shaded region).**

### Publications:

- ✓ Draft Genome Sequence of a Multidrug-Resistant *Escherichia coli* Sequence Type 1193 Pandemic Clone Isolated from Wastewater in Austria. Microbiol. Resour. Anounc., 2021, 10:e00762-21. doi: 10.1128/ MRA.00762-21
- ✓ Assessment of the Transmission Dynamics of *Clostridioides difficile* in a Farm Environment Reveals the Presence of a New Toxigenic Strain Connected to Swine Production. Front. Microbiol., 2022, 13:858310. doi: 10.3389/fmicb.2022.858310
- ✓ Characterizing Antimicrobial Resistance in Clinically Relevant Bacteria Isolated at the Human, Animal, Environment Interface Using Whole-Genome Sequencing in Austria Journal. Int. J. Mol. Sci. 2022, 23:11276. doi.org/10.3390/ijms231911276
- ✓ Airborne spores' dissemination of a swine associated *Clostridioides difficile* clone. Anaerobe, 2022, 78, 102651. doi.org/10.1016/j.anaerobe.2022.102651
- ✓ Factors associated with the prevalence of antibiotic resistance in the environment from a One Health perspective: Protocol for a systematic evidence map. Environ. Int. (in revision, 2022).
- ✓ Master thesis: Characterization of Antibiotic Resistance in Strains Isolated from Different Environmental Reservoirs [Caracterização da Resistência aos Antibióticos em estirpes isoladas de diferentes reservatórios ambientais] http://hdl.handle.net/10451/53801

### Other Outcomes:

- ✓ Oral Communications and Posters in national and international congresses and other meetings: **12**
- ✓ Webinars (e.g. "Biotechnology and Safety: Tracking and Analyzing Free-floating Extracellular DNA across Urban Waterways"): **5**
- ✓ Monthly meetings (with all Partners): **27**
- ✓ Supervisory Board meeting (13 Members): **1**
- ✓ Advisory Board meeting (7 Members): **1**
- ✓ Annual meetings (science and management) (with all Partners): 1 face-to-face (2020); 1 online (2021); 1 face-to-face & online (2022)
- ✓ New documents produced, e.g. Protocols (harmonization) (>30), Deliverables (**25**), Minutes of meetings (**27**), others: >**82**
- ✓ Data Management Plan: **1**
- ✓ Risk Management Plan: **1 (Fig. 8)**
- ✓ Networking and communication between partners and reference labs from different sectors and countries, leading to new knowledge.
- ✓ Training through research, e.g. a Master, collaborations among different experiences and countries.



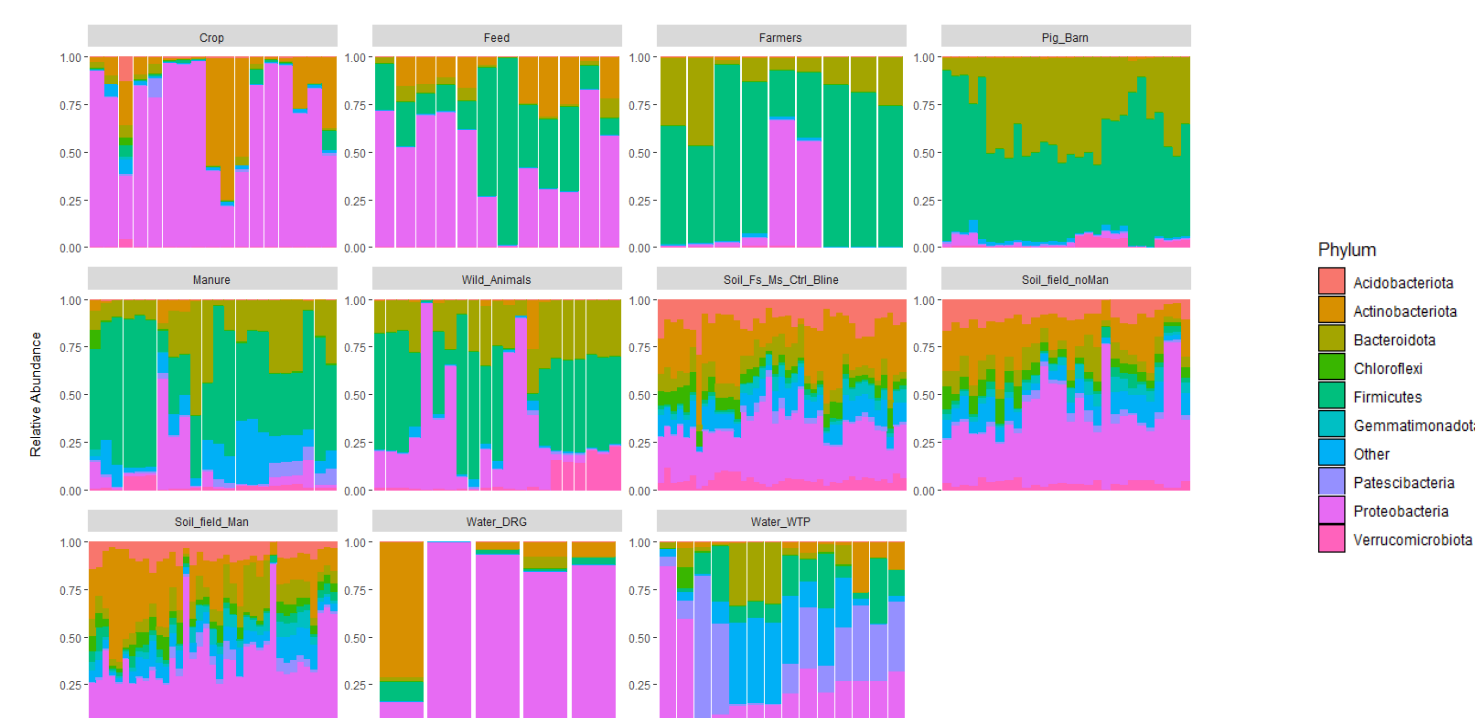
**Fig. 8. Risk Management Plan**

## KEY OUTPUTS

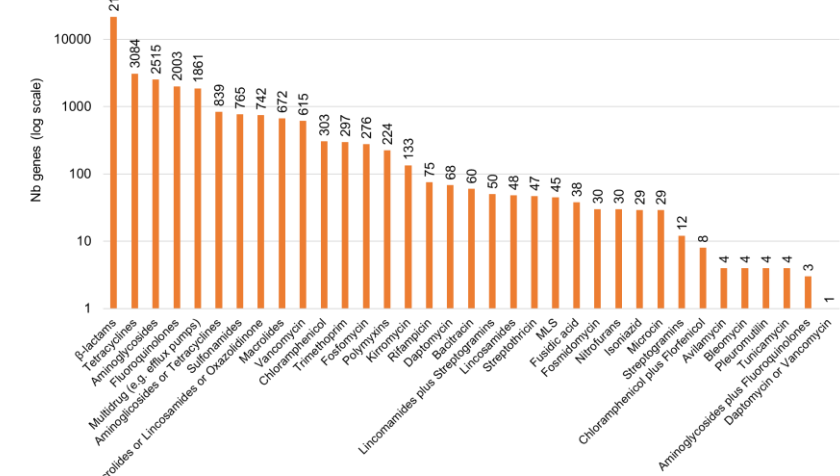
### Objective 1:

The microbial biodiversity and resistome in the tested environmental compartments were evaluated by characterising all 16S V1-V9 regions through 16S rRNA metagenomics and target gene enrichment.

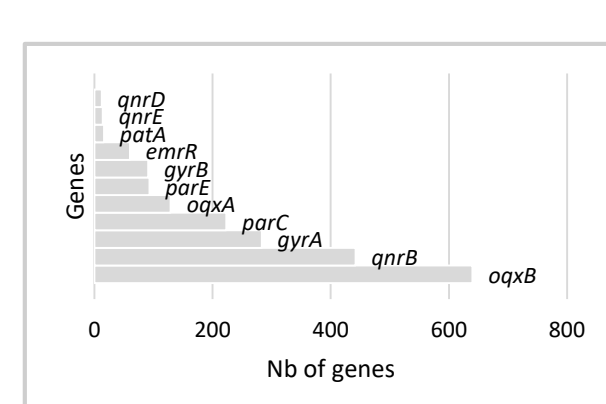
**Conclusion:** The Phyla in exDNA are dominated by Proteobacteria and Firmicutes. Phyla in **Fig. 2** represent 93.5% of the reads in exDNA, and the samples are ordered by sample data in the x axis which allow us to check if there is an alteration over time. The principal component analysis (**Fig. 3**) suggests separation between three groups: 1) soil; 2) crops; feeds, drinking water, and 3) farmers, pigs, wild animals, manure, waste water. No significant difference was detected between soil in fields with and without manure. In the wild animals compartment we detected ARG conferring resistance to ~30 antibiotic classes, where  $\beta$ -lactams, tetracyclines, aminoglycosides and fluoroquinolones are the most prevalent (**Fig. 4**). In the same compartment, we identified 11 ARG-types conferring resistance to fluoroquinolones (including episomal and chromosomal mutated gene variants) (**Fig. 5**).



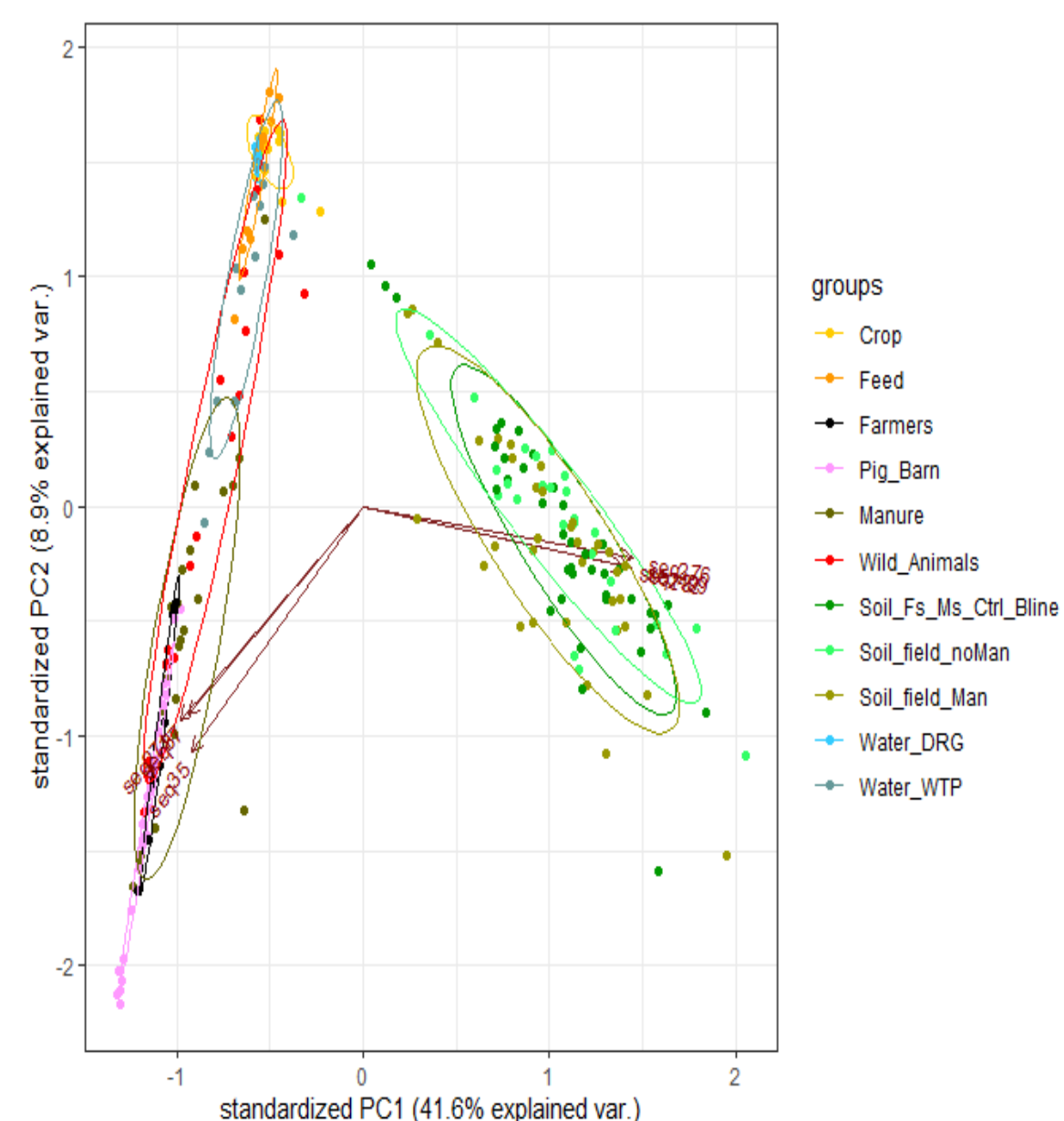
**Fig. 2. Phylum percentage in each exDNA samples, by compartment.**



**Fig. 4. Frequency of ARGs in wild animals compartment.**



**Fig. 5. Frequency of ARG-type conferring resistance to fluoroquinolones, in wild animals compartment.**



**Fig. 3. Biplot of the exDNA samples, among compartments.**

## FED-AMR Consortium

**Project Leader:** W. Ruppitsch. **WP1:** W. Ruppitsch (L); A. C. Rosel (DL). **WP2:** M. Caniça (L); A. C. Rosel (DL). **WP3:** M. Oleastro (L); S. Persson (DL). **WP4:** M. Brandtner (L); A. Gajda (DL). **WP5:** M. Chambers (L); R. La Ragione (DL). **WP6:** G. Lo Iacono (L); M. Chambers (DL)



**Acknowledgments:** This poster is part of the European Joint Programme One Health EJP. This project has received funding from the European Union's Horizon 2020 research and innovation programme under Grant Agreement No 773830.

### Other Partners:







# TOX-Detect

## Development and harmonization of innovative methods for comprehensive analysis of foodborne toxigenic bacteria

Y. NIA<sup>1\*</sup>; J-A HENNEKINNE<sup>1\*</sup>; J. MASQUELIER<sup>2</sup>; H. FRENTZEL<sup>3</sup>; D. CLERMONT<sup>4</sup>; N RAMA RAO<sup>5</sup>; K HOGEVEEN<sup>1</sup>; M. GOHAR<sup>5</sup>; T. SKJERDAL<sup>6</sup>

\* Project leaders

1. French Agency for Food, Environmental and Occupational Health & Safety (ANSES), France
2. Sciensano, Belgium
3. German Federal Institute for Risk Assessment (BfR), Germany
4. Institut Pasteur, France
5. French National Research Institute for Agriculture, Food and Environment (INRAE), France
6. Norwegian Veterinary Institute, Norway

### Introduction

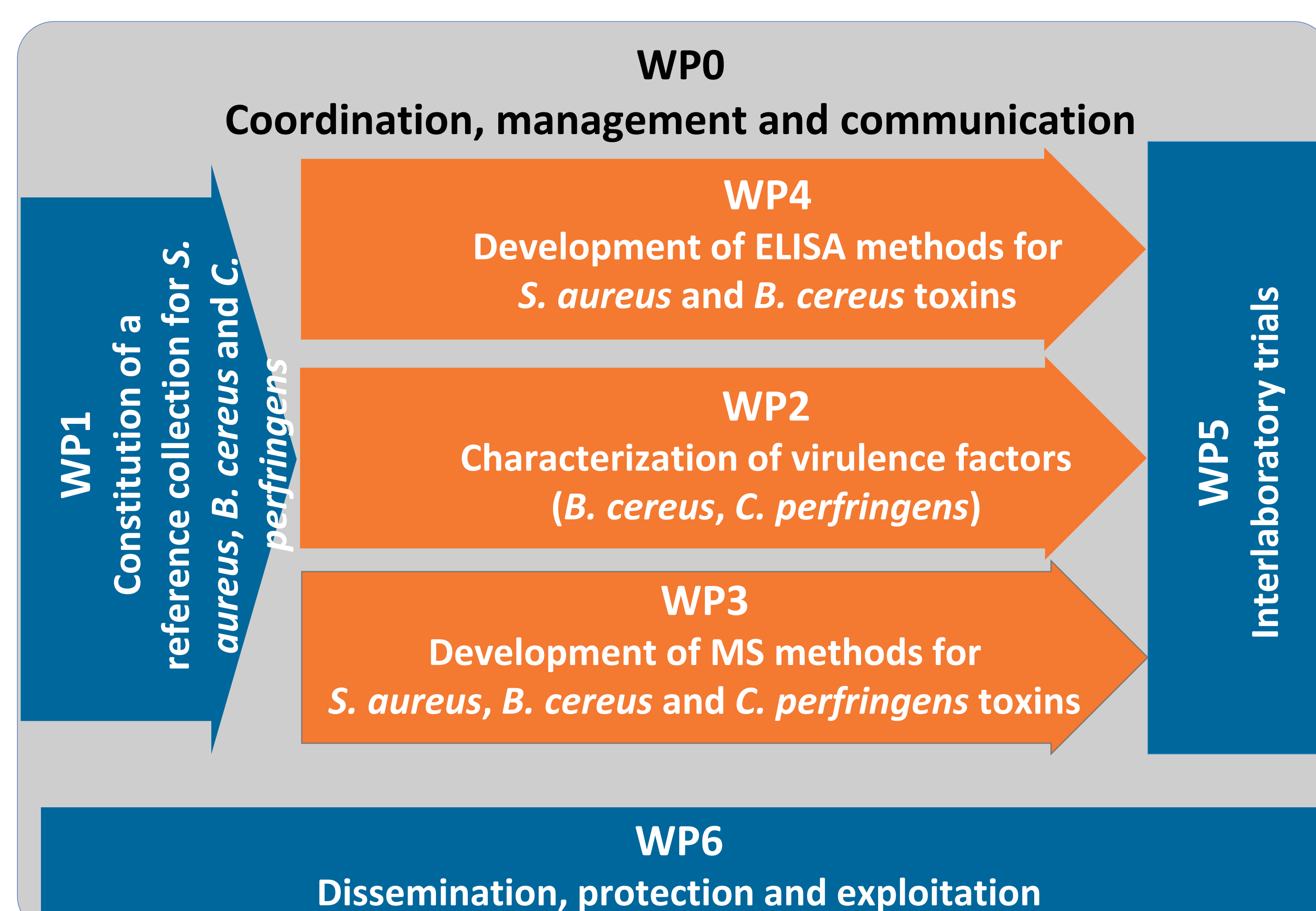
Outbreaks caused by bacterial toxins represent a major proportion of reported FBOs (thousands of cases each year). At EU level, the most frequently reported causes of food-poisoning outbreaks (FPOs) are bacterial toxins produced by *Bacillus spp.* (*Bacillus cereus*), *Clostridium spp.* (*C. perfringens* and *C. botulinum*) and *Staphylococcus spp.* (*S. aureus*). The true incidence of FPOs caused by these toxigenic bacteria is underestimated for many reasons, including misdiagnosis, under-reporting (particularly of minor outbreaks), and improper sample collection or laboratory examination. The complexity and diversity of food matrices involved in FPOs caused by bacterial toxins add to the difficulty. Moreover, FPOs caused by toxigenic 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” (90%) FPOs reported by EFSA when bacterial toxins are the causative agent.

The scientific community involved in monitoring foodborne outbreaks caused by bacterial toxins needs harmonized and innovative detection methods for this underestimated One Health issue.

### Tox-Detect project design

TOX-Detect project was designed to develop and harmonize methods to detect toxin expression and production by toxigenic bacteria across One Health pillars:

- Collating and fully characterizing a large number of toxin-producing bacterial isolates from environmental, clinical, and food samples provided by all the partner institutes
- Developing dedicated ELISA and mass spectrometry methods, and libraries for the identification of the targeted pathogens
- Harmonizing Standard Operating Procedures (SOPs) for all the targeted virulence factors and methods.



### Outputs of TOX-Detect project



**76** reference strains were selected and characterized

Strains exchanged between consortium members

**New** specific and robust **Maldi-ToF** library was developed

**10** oral presentations

**6** articles

**20** deliverables

**14** harmonized Operating Protocol transferred

**6** methods were developed and transferred

Production of **4** toxins and dedicated analytical tools

**8** transfer and inter-laboratory tests organised

Participants received the 14 operating protocols for method implementation

Participants from the **European Union Reference Laboratory** for Coagulase Positive Staphylococci (DG SANTE) network took part

### Impact of TOX-Detect project

**European Union Reference Laboratory (DG SANTE)**

**Other OH EJP projects**

Participation of 8 National Reference Laboratories to the Interlab-test: good help in absence of PT organizer

**New developed MALDI-ToF library:** EURL for CPS network decided to implement inter-laboratory validation study

EJP CARE: strains selected and characterised in WP1 were used in the OH EJP CARE project







## JRP16-ET2 Point-of incidence toolbox for emerging virus threats

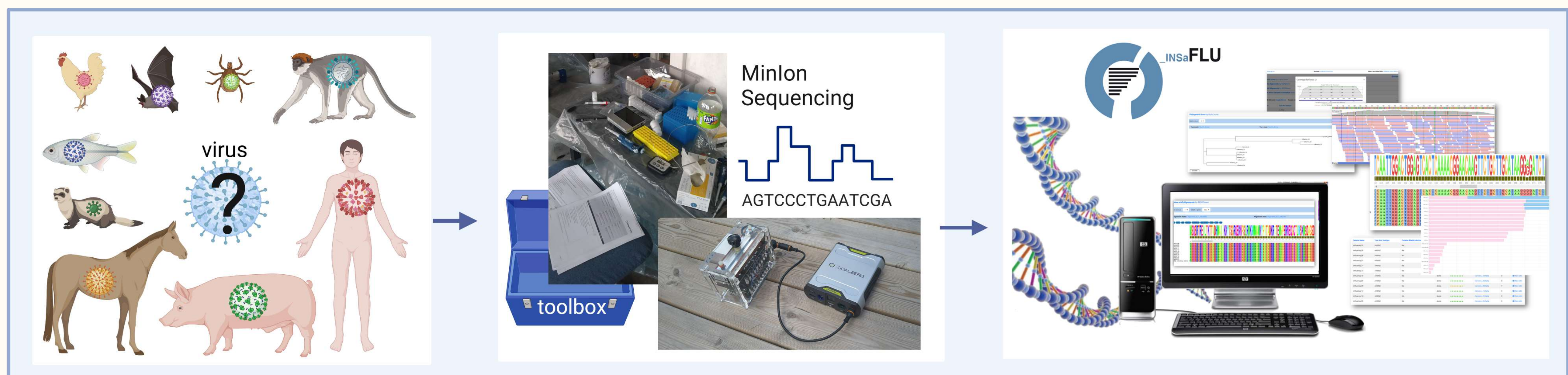


### TELEVIR Consortium

1) ANSES, France - Laurent Bigarré 2) PIWET, Poland - Artur Rzezutka, Eva Kwit 3) INSA, Portugal - Vitor Borges, Joana Isidro, Joao Dourado Santos 4) IZLER, Italy - Alessio Lorusso, Maurila Maracci 5) INIA Spain - Jovita Fernández-Pinero, Pilar Aguilera 6) UoS, UK Daniel Horton, Joaquin Prada, Guido Cordoni 7) SVA, Sweden Tobias Lilja, Mikhayil Hakhverdyan 8) NVI, Norway Øivind Øines, Carlos Goncalo das Neves 9) Sciensano, Belgium Steven Van Borm, Elisabeth Mathijs 10) SSI, Denmark Anders Fomsgaard, Katja Spiess, Morten Rasmussen, Anna Fomsgaard and other TELEVIR consortium members

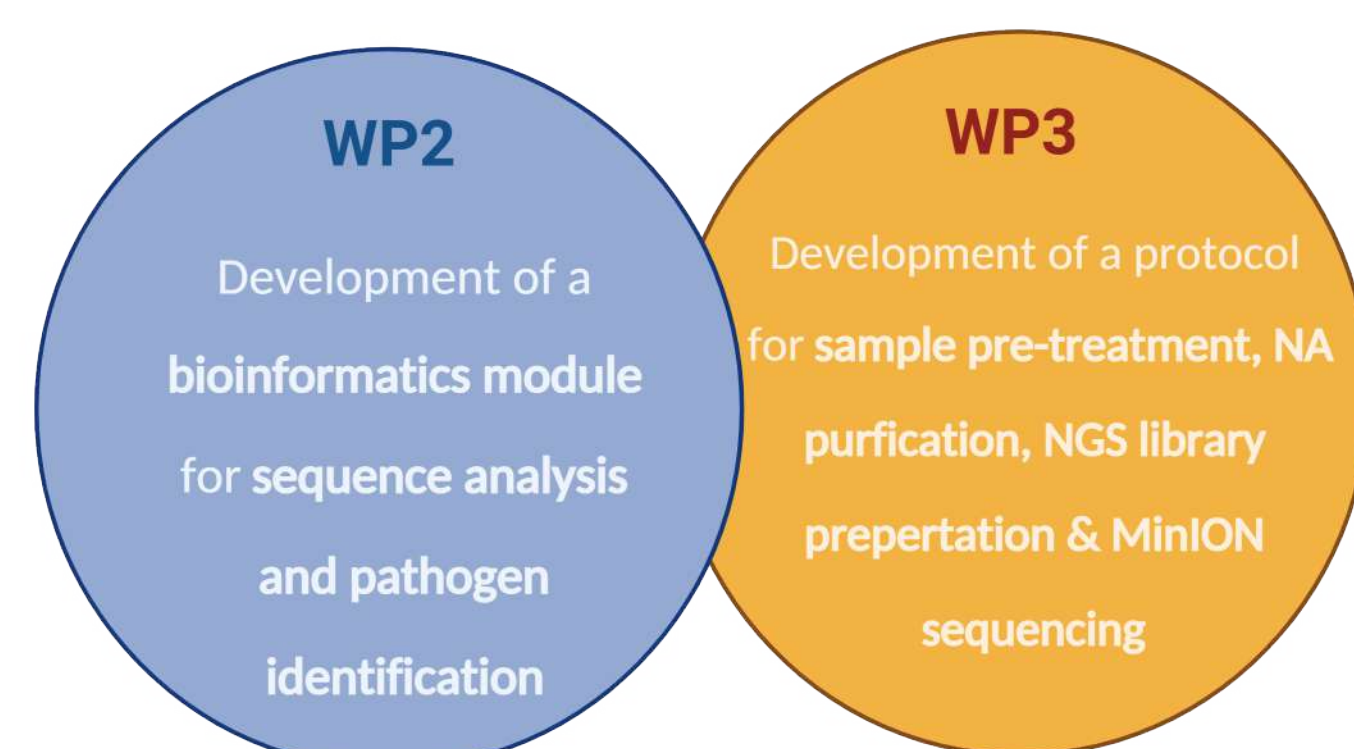


## We developed a Field-employable Protocol for Metagenomic Detection of Viruses



### INTRO / BACKGROUND

The world has been regularly facing pandemics caused by pathogens as for example SARS-CoV-2. Viruses infections of animals can lead to zoonotic events, where a virus from a non-human host is transmitted to humans. In our TELEVIR project we developed an unbiased method to detect RNA/DNA viruses. The protocol we established is relatively short and the equipment transportable (**WP3**). As such we can detect viruses in areas of the world with no laboratory infrastructure. We also provided the bioinformatics infrastructure to analyze and identify virus sequences, by developing the "INSaFLU-TELEVIR" toolkit (**WP2**).



### RESULTS

TELEVIR partners collected samples and performed field studies in Europe & Africa (**WP4**). They were trained how to use the TELEVIR toolbox developed in WP2 & WP3 at a workshop, which took place at the Statens Serum Institut (Copenhagen/Denmark) in June 2022.



The TELEVIR partners were trained how to use the point of incidence protocol in hands on teaching classes at the TELEVIR workshop. They also evaluated their sequencing results for unbiased virus detection using the INSaFLU-TELEVIR platform.



Field studies performed by the TELEVIR partners NVI and INIA in Norway and Spain. Birds can be vectors for viral diseases. In Norway feces samples were tested for Avian influenza A virus and in Spain chicken were infected with West-Nile Virus in an *in vivo* study, for later on virus detection using fresh sample material.

### METHODS

#### WP3

We established a protocol that includes simple to use sample pretreatment, nucleic acid extraction, isothermal random amplification followed by non-targeted sequencing using the Oxford Nanopore Technology system.



#### WP2

Novel features were implemented into the "INSaFLU-TELEVIR" platform, with a module for virus detection (TELEVIR).

#### This includes:

- ✓ Read quality analysis and improvement
- ✓ State of the art software
- ✓ Modular Pipeline
- ✓ Multiple Classification methods
- ✓ Multiple Viral databases
- ✓ Summary statistics and intuitive and interactive end-user reports



Field study performed by the TELEVIR partner ANSES on a fish farm in South France. Fish showed sign of unknown illness and were tested for virus infections.



Field studies performed by the TELEVIR partner IZAM on a farm in Tunisia. Diseased cattle were tested for virus infections.

### CONCLUSION

In our TELEVIR project we developed a point of incidence toolbox, that we tested as proof of concept in our field studies. We could successfully detect viruses in animals, using this metagenomic method combined with the data analysis by the INSaFLU-TELEVIR platform.

**REFERENCES** Fomsgaard et al., Improvement of field deployable metagenomics virus detection by a simple pretreatment method. Journal of Clinical Virology Plus, 2022.

**Acknowledgement** This poster is part of the European Joint Programme One Health EJP. This project has received funding from the European Union's Horizon 2020 research and innovation programme under Grant Agreement No 773830





## “Multi-centre study on *Echinococcus multilocularis* and *Echinococcus granulosus* s.l. in Europe: development and harmonization of diagnostic methods in the food chain”

### MEME Consortium

Adriano Casulli (ISS, coordinator)



#### WOK PACKAGES:

**WP1:** SAMPLING STRATEGY

**WP2:** VALIDATION of PARASITOLOGICAL and MOLECULAR ASSAYS

**WP3:** DEVELOPMENT/VALIDATION of NEW TOOLS AND PRODUCTION of EPIDEMIOLOGICAL DATA

**WP4:** TRAINING, DISSEMINATION and PROFICIENCY TESTING SCHEMES

**WP5:** SCIENTIFIC and ADMINISTRATIVE MANAGEMENT

#### WP LEADERS:



Jacek Karamon (PIWET)



Gerald Umhang, Frank Boue (ANSES)



Pavlo Maksimov, (FLI)



Adriano Casulli (ISS)



Adriano Casulli (ISS)

**MEME** is an international multicentre collaborative project that aims to fill research gaps highlighted by international agencies for the detection and control of zoonotic parasites *Echinococcus multilocularis* (Em) and *Echinococcus granulosus sensu lato* (Eg), causing alveolar echinococcosis (AE) and cystic echinococcosis (CE), respectively. MEME focuses on standardization, harmonization and validation of existing parasitological and molecular methods, and the development and comparative assessment of innovative molecular tools to detect Em and Eg in the food chain. Production of epidemiological data on the presence of Em/Eg eggs in the food chain focuses on vegetables for human consumption and on canine faeces in selected endemic countries.

#### MEME achievements were:

- The production of Standard Operating Procedures for the sampling of different matrices from naturally or experimentally infected definitive and intermediate animal hosts.
- The validation of the parasitological (Segmental Sedimentation and Counting Technique, SSCT) and molecular diagnostic (multiplex- and MC-RT-PCR) procedures to detect Em and Eg in different matrices along the food chain.
- The development and validation of new molecular tools such as: Comparison of two DNA extraction methods and two PCRs for the detection of Em in stool samples; Bayesian Analysis of three methods for diagnosis of CE in sheep; Microsatellite investigations of Eg cysts; Species detection of Eg by novel probe-based real-time PCRs; Validated method based on PCR-RFLP and multiplex PCR assay for the identification of Eg species; Identification of Eg G1/G3 by SNPs assays.
- Multicentre studies for the production of data relevant for epidemiological assessments: contamination of fresh vegetables for human consumption by eggs of Em/Eg; prevalence of Em/Eg in dog faeces).
- Quantitative assessment on the impact of human CE in Europe by means of systematic review approach.
- Molecular epidemiology studies in selected geographical areas.
- Dissemination of project results at different levels (general public, scientific community, experts, health authorities and media).

**MEME impacted on** animal health, public health and food safety sectors. Beneficiaries of scientific outputs of MEME are EU reference labs, international organizations and all decision makers.

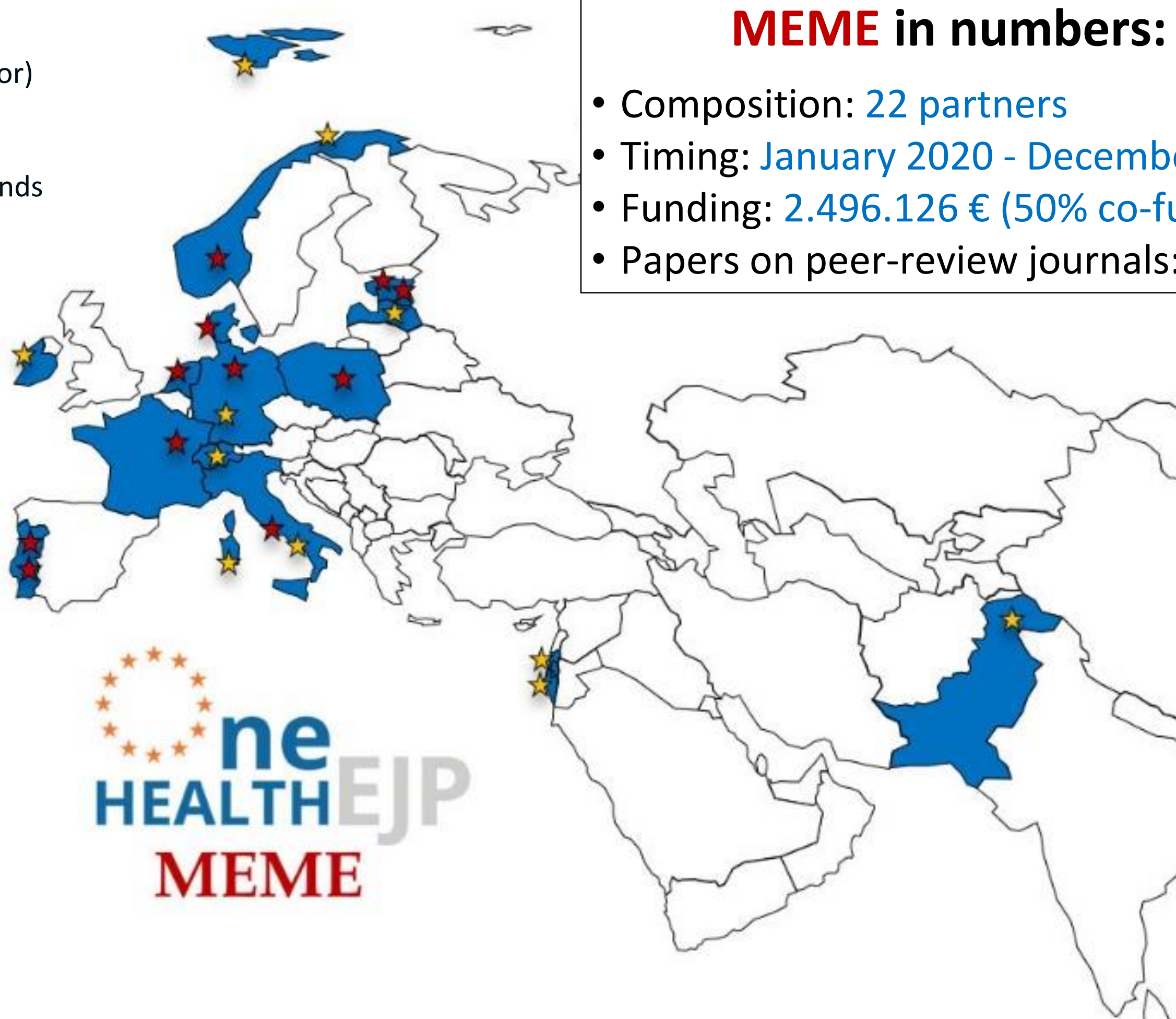
**We provided a set of molecular tools, epidemiological risk assessments and quantitative epidemiological models for the detection, surveillance and control of these parasitic infectious diseases in Europe and beyond.**

#### Funded partners:

- ISS, Italy (Coordinator)
- FLI, Germany
- ANSES, France
- RIVM, The Netherlands
- PIWET, Poland
- NVI, Norway
- SSI, Denmark
- INIAV, Portugal
- INSA, Portugal
- UT, Estonia
- VFL, Estonia
- BIOR, Latvia

#### External partners:

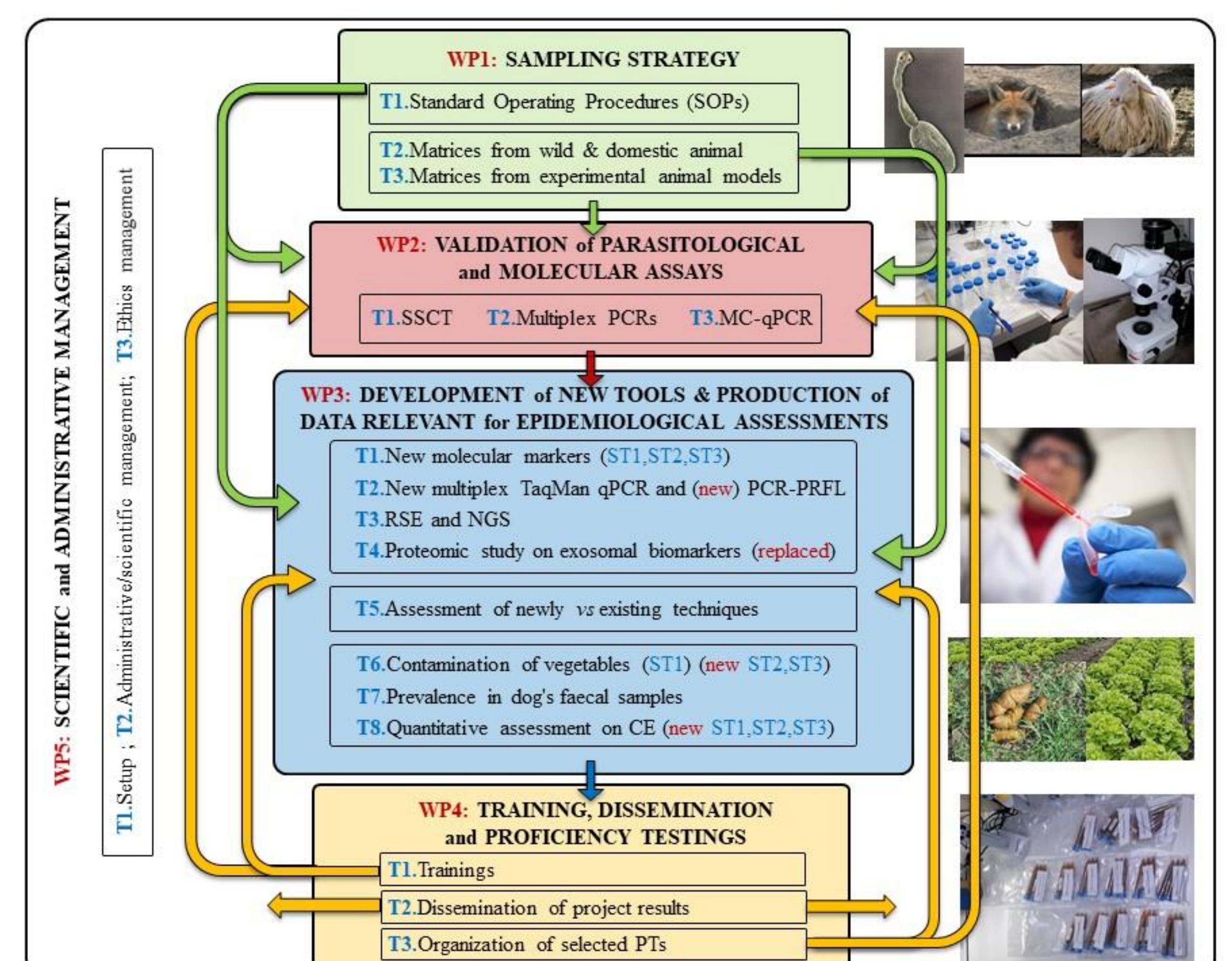
- CVRL, Ireland
- IZSS, Italy
- UNF, Italy
- UH, Germany
- IP, Switzerland
- TH, Israel
- LRUI, Palestine
- NPI, Norway
- SDAS, Norway
- COMSATS, Pakistan



#### MEME in numbers:

- Composition: 22 partners
- Timing: January 2020 - December 2022
- Funding: 2.496.126 € (50% co-funded)
- Papers on peer-review journals: 17

Countries (in blue) and centres (red star= funded partners; yellow star= external partners) participating in the MEME project.



Work Packages (WPs) and tasks (T) encompassing the MEME project (<https://onehealth.ejp.eu/jrp-meme/>).





# The OHEJP PARADISE (PARAsite Detection ISolation and Evaluation) project

Simone M Cacciò (ISS, Italy), Karin Troell (SVA, Sweden), Christian Klotz (RKI, Germany), Yannick Blanchard (ANSES, France), Marcoalle (ISS, Italy) and the PARADISE Consortium

## BACKGROUND

The PARADISE project aimed at delivering informative genotyping schemes and innovative detection strategies applicable to analysing food matrices for both *Cryptosporidium* and *Giardia*, which are important pathogens of humans, livestock, companion animals, and wildlife, with a global distribution.

## NEEDS

- Better knowledge of parasite diversity (WP2)
- New high-throughput detection methods (WP2)
- Multi-locus typing schemes with high discriminatory power (WP3)
- New sensitive methods for parasite detection and enrichment (WP4)



## ACTIVITIES

### WP2

Whole genome study of isolates of *C. parvum* and *G. duodenalis*

Experimental and *in silico* analyses of metagenomes for detection of food-borne parasites

### WP3

Development of typing schemes for *C. parvum*

Development of typing schemes for *G. duodenalis*

### WP4

Method development for pre-DNA extraction enrichment using nanobodies and aptamers

Method development for post-DNA extraction enrichment using capture probes

## OUTCOMES

Generation of hundreds of Whole Genome Sequences (WGS) from isolates of human and animal origin collected across Europe

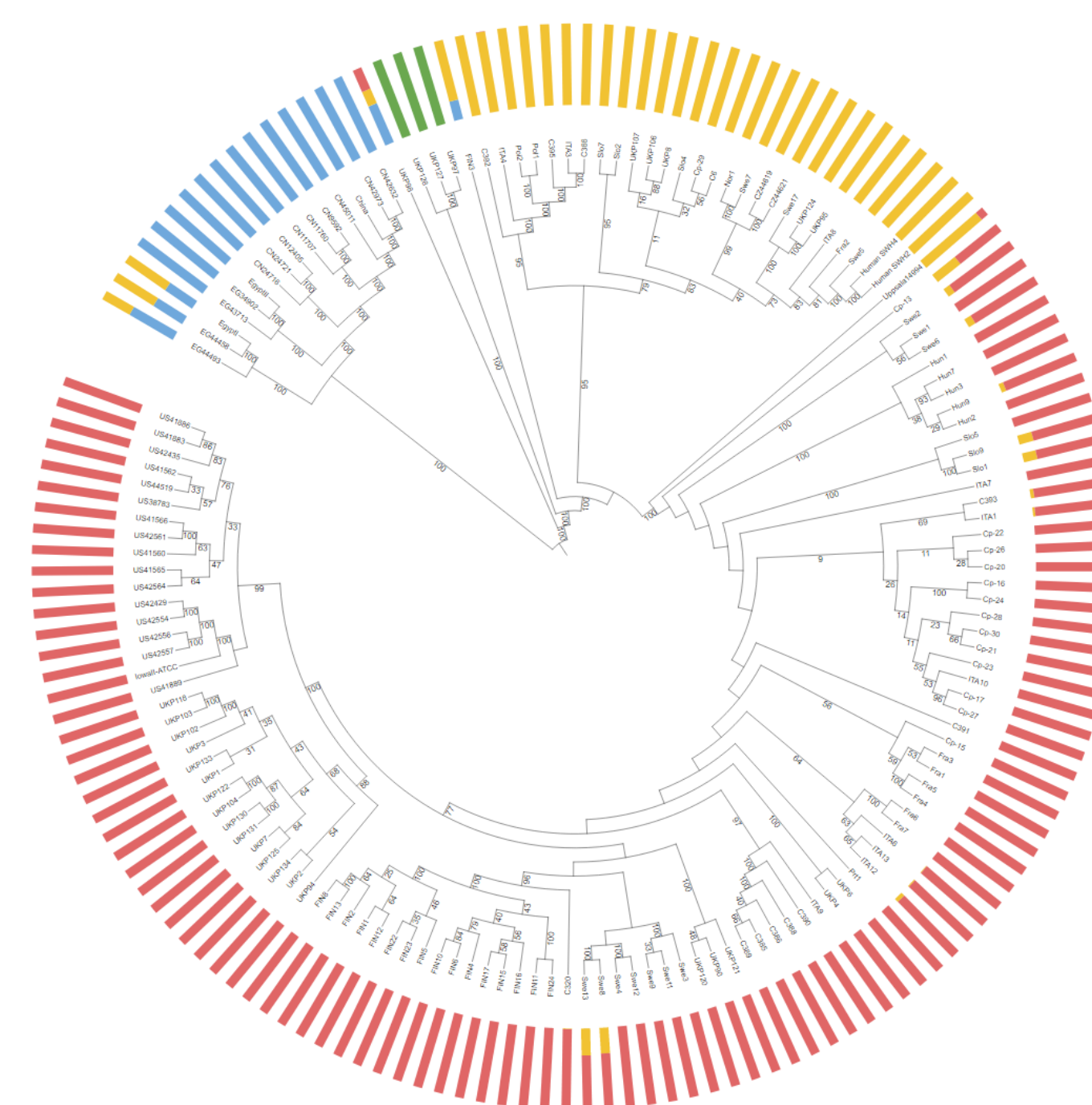
New, robust Multi-Locus Genotyping schemes for *Cryptosporidium parvum* and *Giardia duodenalis* validated and tested (SOP)

New, sensitive hybridization capture probe method for *Cryptosporidium parvum* detection validated and tested (SOP)

New reagents (nanobodies) for detection and capture of *Giardia duodenalis* cysts

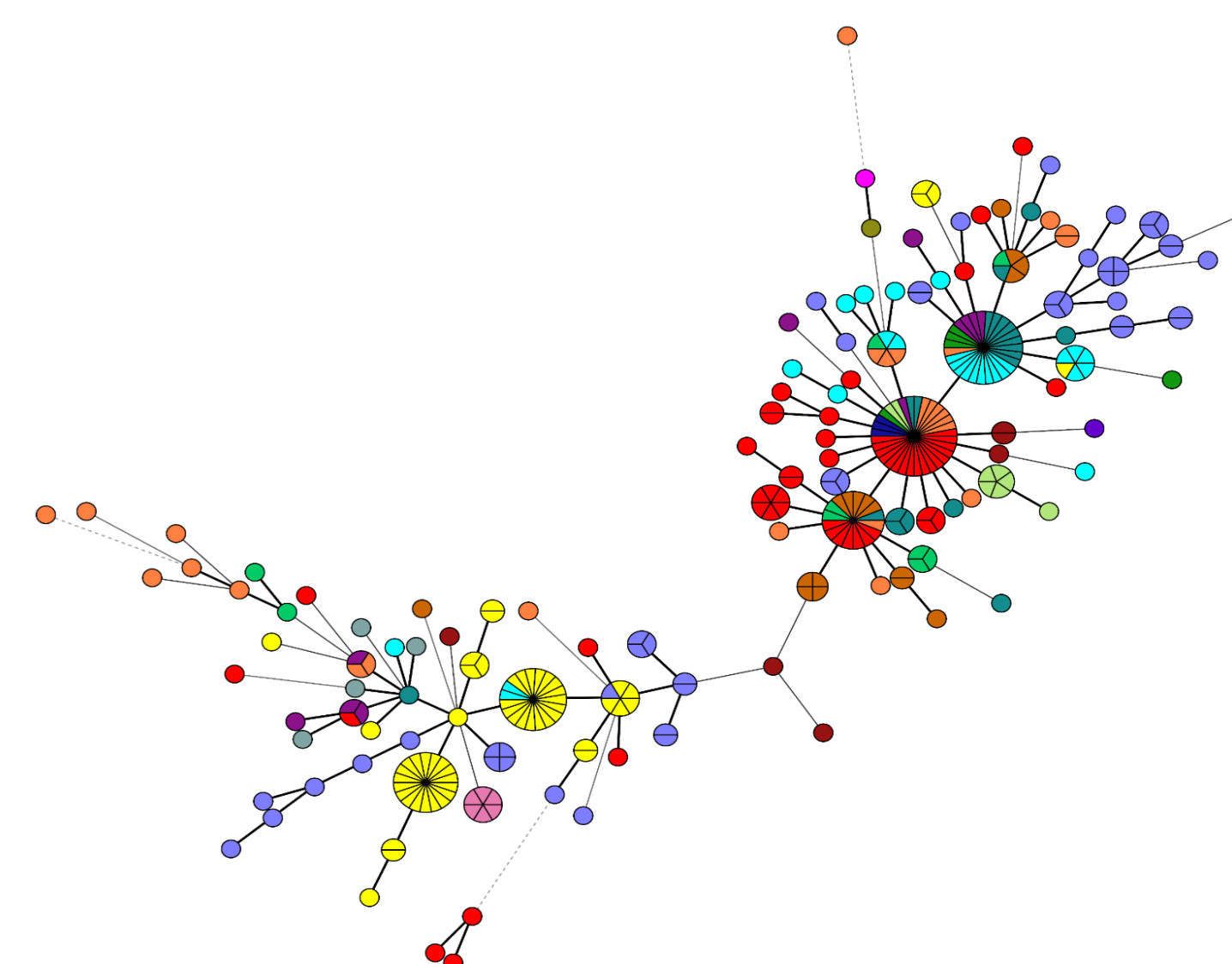
## IMPACT

WP2 : Improved knowledge of the population structure, virulence and evolution of *Cryptosporidium* and *Giardia*. Perspectives opened for functional biology studies



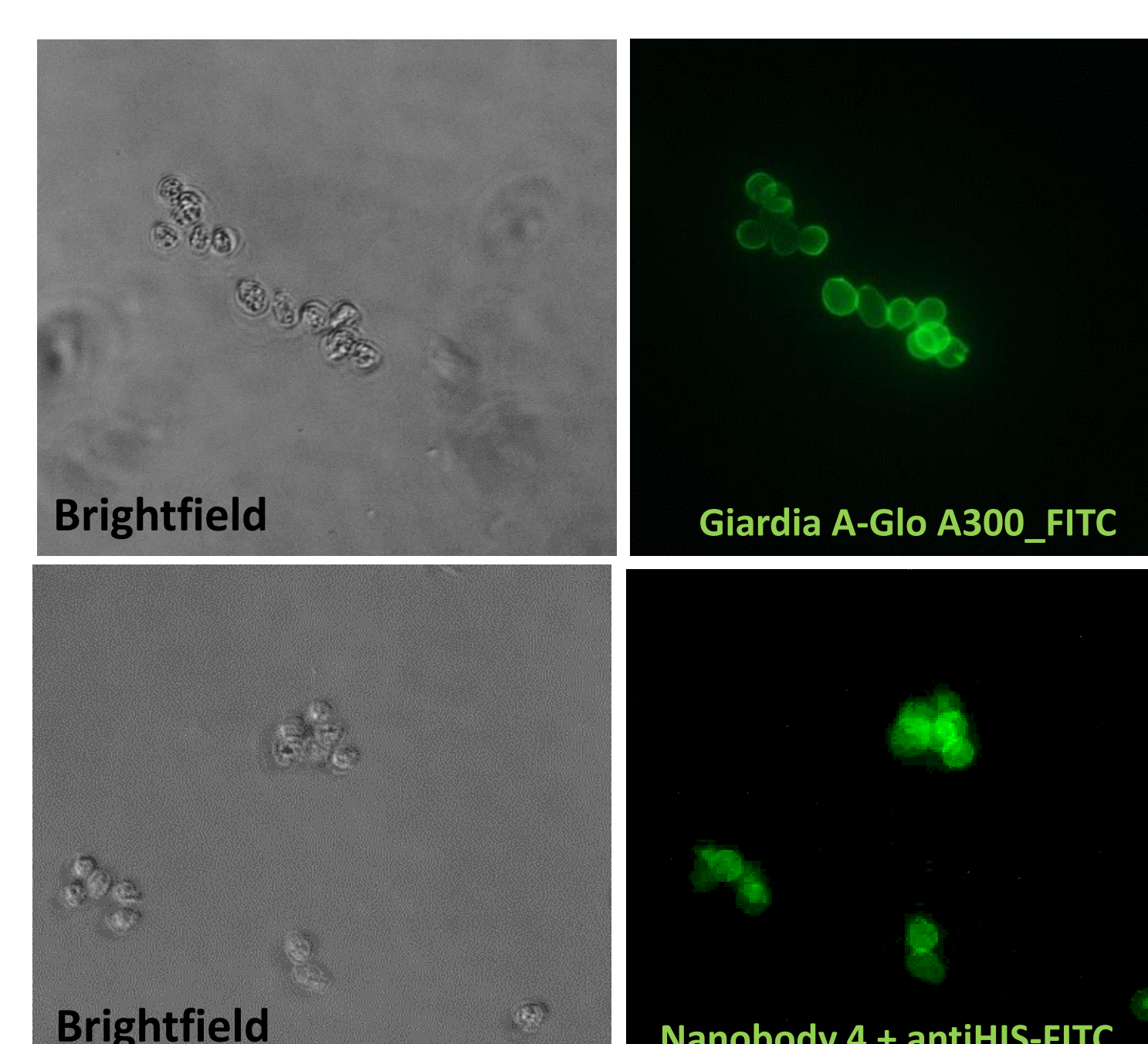
Phylogenetic tree based on genomic SNPs of *Cryptosporidium parvum* showing the presence of four clusters, three of which are comprised of European isolates.

WP3 : Improved characterization of zoonotic transmission and outbreak investigation  
Implementation by National Reference Laboratories



Minimum Spanning Tree showing the relationship among the *Cryptosporidium parvum* Multi-Locus Genotypes identified in Europe

WP4 : Improved detectability in environmental and relevant food matrices for better risk assessment, and targeted analysis of parasites in outbreaks of unknown aetiology.  
Implementation by National Reference Laboratories



Comparative immunostaining of *Giardia duodenalis* cysts WBC6 (Ass. A), obtained *in vitro*, with either the commercial antibody *Giardia* A-Glo A300\_FITC or the nanobody 4

Contact: Simone M. Cacciò [simone.caccio@iss.it](mailto:simone.caccio@iss.it) <https://onehealthejp.eu/jrp-paradise/>

This poster is part of the European Joint Programme One Health EJP.

This project has received funding from the European Union's Horizon 2020 research and innovation programme under Grant Agreement No 773830.





## WP4: Joint Integrative Projects

Karin Artursson, WP4 Leader

PMC-POC meeting 22 November



# ORION: One health suRveillance Initiative on harmOnization of data collection and interpretation

Matthias Filter, Project leader, BfR  
Fernanda Dórea, co-coordinator, SVA  
*22<sup>nd</sup> of November 2022*



# The OHS Codex

## The COLLABORATION principle

Supporting OHS  
collaboration &  
cross-sectorial  
communication

OHEJP Glossary

OHS Inspirational  
catalogue

"lessons learned"

## The KNOWLEDGE principle

Improving the OHS  
knowledge base

OH knowledge base -  
Epi

OH knowledge  
base - NGS

"lessons learned"

## The DATA principle

Supporting OHS  
data interoperability,  
integration &  
interpretation

Health Surveillance  
Ontology (HSO)

Tools to annotate  
data and meta-data

"lessons learned"

## The DISSEMINATION principle

Supporting external  
communication of  
OHS outcomes

Consensus Report  
Annotation Checklist

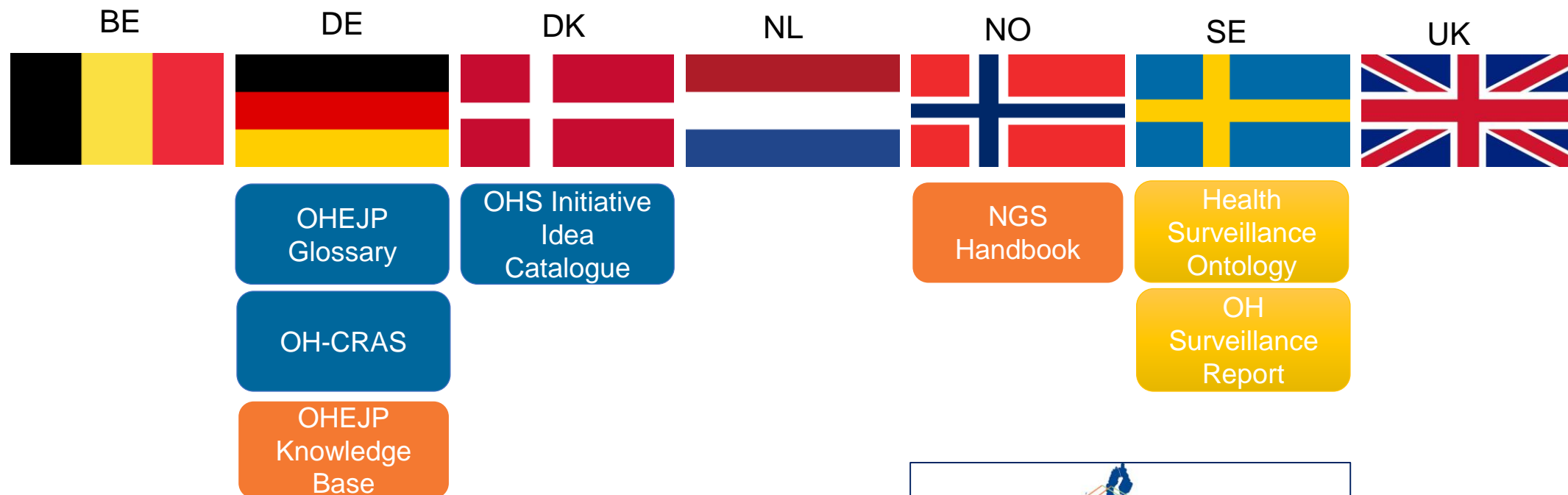
National OHS Report  
Templates

"lessons learned"

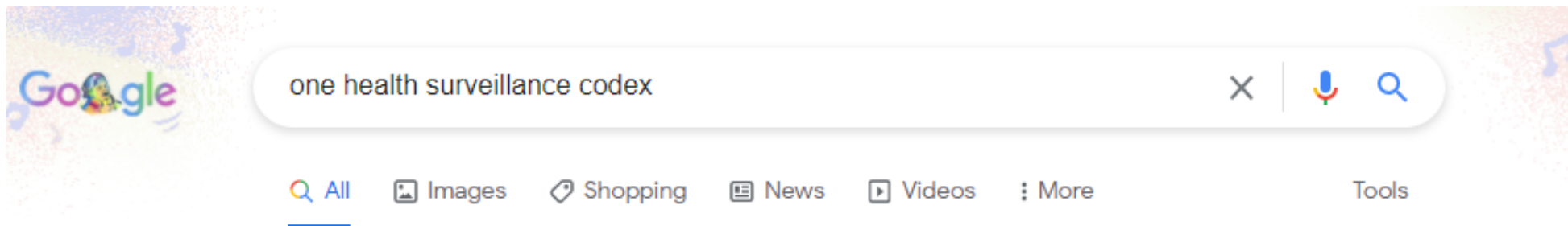
A high-level framework that supports collaboration, mutual understanding, knowledge exchange and data interoperability between OH sectors

# Impact

## One Health Pilots





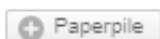


About 9 240 000 results (0,55 seconds)

To address these needs the “One Health Surveillance Codex” (OHS Codex) was established to **provide a framework for the One Health community** to continuously share practical solutions (e.g. tools, technical resources, guidance documents and experiences) applicable for national and international stakeholders from different ...



<https://www.sciencedirect.com> > science > article > pii



**One Health Surveillance Codex: promoting the adoption of ...** ✓

ⓘ About featured snippets • 🗨 Feedback

<https://oh-surveillance-codex.readthedocs.io> > latest ▾

**Welcome to the One Health Surveillance Codex Document** ✓

Welcome to the **One Health Surveillance Codex** Document: The Knowledge Integration Platform!¶ ... The OHS Codex aims at establishing a high-level framework that ...

You've visited this page many times. Last visit: 8/17/21



# The OHS Codex

## The COLLABORATION principle

Supporting OHS collaboration & cross-sectorial communication

OHEJP Glossary

OHS Inspirational catalogue

"lessons learned"

## The KNOWLEDGE principle

Improving the OHS knowledge base

OH knowledge base - Epi

OH knowledge base - NGS

"lessons learned"

## The DATA principle

Supporting OHS data interoperability, integration & interpretation

Health Surveillance Ontology (HSO)

Tools to annotate data and meta-data

"lessons learned"

## The DISSEMINATION principle

Supporting external communication of OHS outcomes

Consensus Report Annotation Checklist

National OHS Report Templates

"lessons learned"



Purpose



How it is used



Impact



Use examples



# The OHS Codex

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"lessons learned"

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"lessons learned"

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Consensus Report Annotation Checklist

National OHS Report Templates

"lessons learned"



Purpose



How it is used



Impact



Use examples

# Thank you for your attention!

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**Fernanda.dorea@sva.se**



**@OneHealthEJP**



**/company/h2020-One-Health-EJP**



**OneHealthEJP.eu**



# COHESIVE: One Health Structure in Europe



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Frits Vlaanderen, *RIVM (Netherlands)*  
Marion Gottschald, *BfR (Germany)*  
Adriano Di Pasquale, *IZS (Italy)*  
Thomas Selhorst, *BfR (Germany)*  
Rob Dewar, *APHA (United Kingdom)*  
Elina Lahti, *SVA (Sweden)*

[elina.lahti@sva.se](mailto:elina.lahti@sva.se)



# COHESIVE: One Health Structure in Europe



A five-year Joint Integrative Project, 2018-2021

AIM: Develop **sustainable One Health approaches** with respect to *signalling, assessing, responding and controlling zoonoses* at the national and regional level **within EU countries**.

**19 partners from 12 countries**

## MAIN OUTCOMES:

- 1) From signalling to response and control - integrated human-veterinary-food risk analysis structure for efficient signaling, risk-assessment, response and control of (emerging) zoonoses
- 2) A suite of software tools to support surveillance and management of outbreaks



# One Health:

## Setting up a risk analysis system for zoonoses

Get started

[About us](#)

[About this site](#)

[Funding](#)

[Contact](#)





# WHY

## A webbased guideline 'One Health: Setting up a risk analysis system for zoonoses'?

Zoonoses are a constant threat to human and animal health. A systematic cross-sectoral (One Health) approach to share signals, assess risks and coordinate the response is essential to minimise impact of zoonotic diseases.



### Goal

Support countries to set up or strengthen One Health collaboration in the area of risk analysis (signalling, risk assessment, risk management, risk communication) of zoonoses including antimicrobial resistance (AMR).



### Focus

Implementation and operationalisation of a One Health Risk Analysis System (OHRAS).



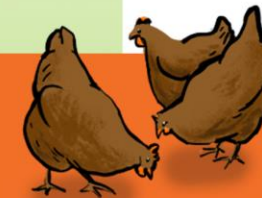
### How

Stepwise approach to implement a OHRAS tailored to each country's situation and needs.



### What

Organisation of risk analysis activities in a One Health fashion, such as signalling, risk assessment and risk management.



### Who

Professionals involved in the risk analysis of zoonoses including AMR, who would like to make a change in the One Health collaboration within their country.

### Included

Several barriers are addressed, such as the difficulty to obtain political will and to gain trust.



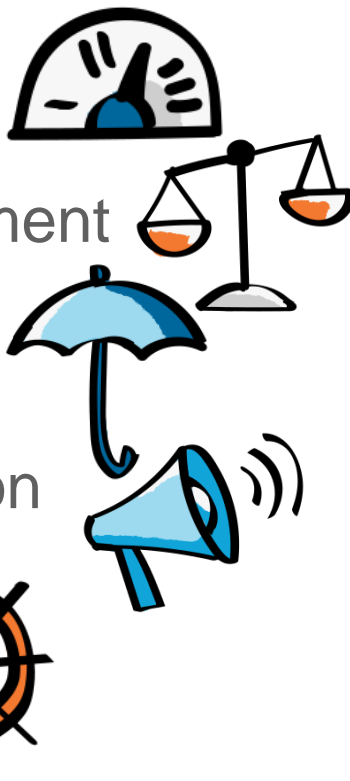




# Basis of the One Health risk-analysis system (what)

*Identified 6 activities:*

- Signalling (early warning)
- Risk-assessment
- Feasibility assessment
- Risk-management
- Risk-communication
- Governance



**Organise** the activities in  
a One Health fashion  
>>> Cross-sectoral meetings

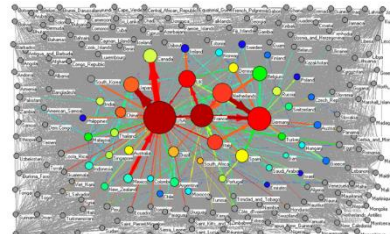




# Importance of powerful integrative software tools and interoperability in times of globalized food and feed trade

Long and complex supply chains

## Globalised trade



Large amounts of data

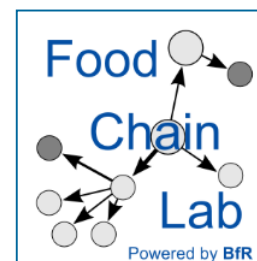
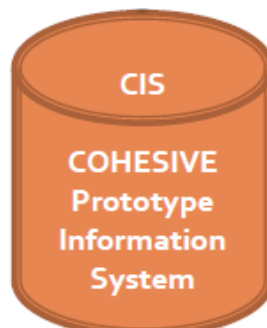
Ercsey-Ravasz M et al. (2012) PLoS ONE 7(5): e37810.  
doi:10.1371/journal.pone.0037810



**Increased complexity of risk assessment and outbreak control**

OH EJP COHESIVE developed a **suite of integrative IT tools and data formats** that are quickly available, usable and helpful in surveillance, outbreak situations and for risk assessments - **for MS and EU authorities.**

## The OHEJP COHESIVE software suite

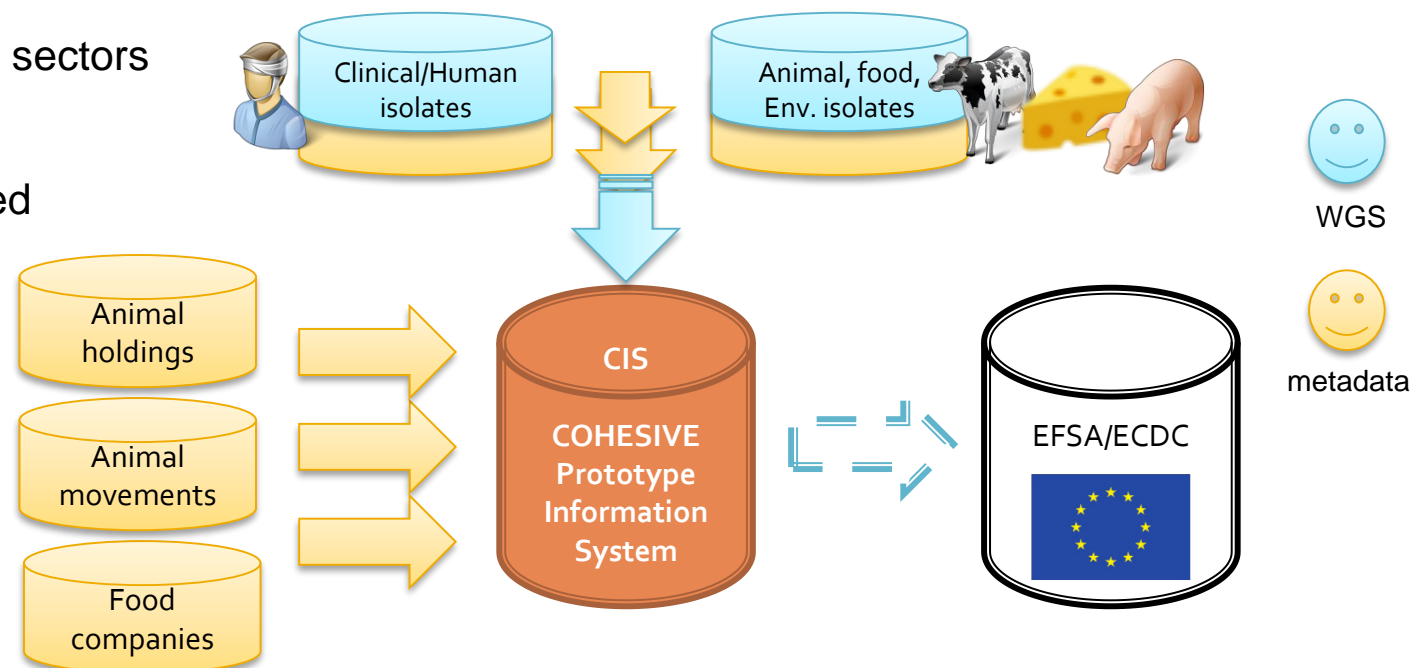


**shiny-risk**  
Risk modelling  
framework

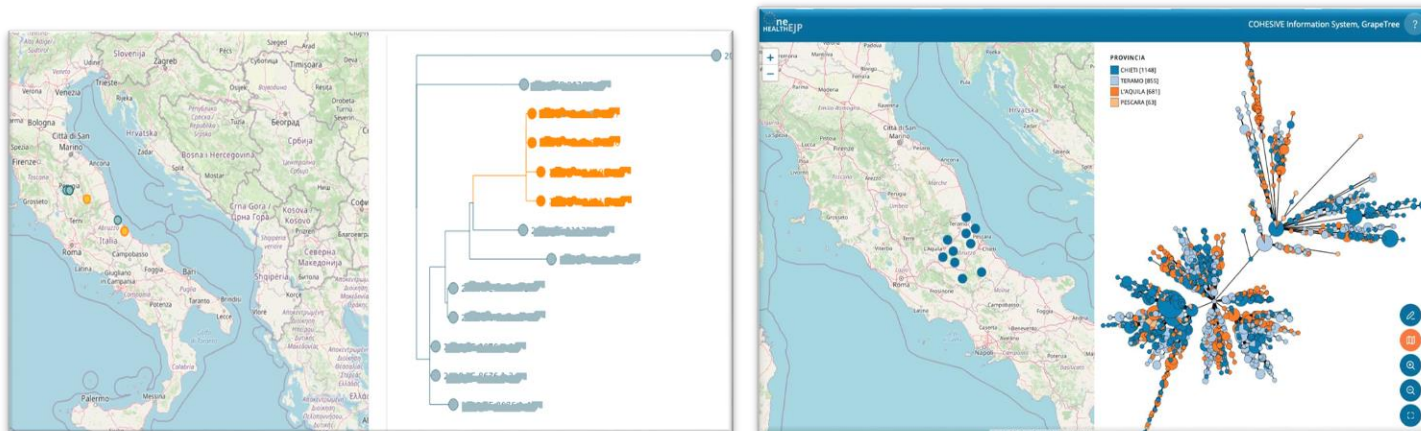


# COHESIVE prototype information system (CIS)

- integrates pathogen information, i.e. Whole Genome Sequencing (WGS) data and related metadata at country level
- facilitates data sharing between OH sectors
- CIS allows
  - (i) storing sequencing data and related metadata
  - (ii) launching bioinformatics analysis and pipelines
  - (iii) retrieving analytical results together with metadata using interactive graphical dashboards (spatial and temporal maps)
- provides EU harmonised output







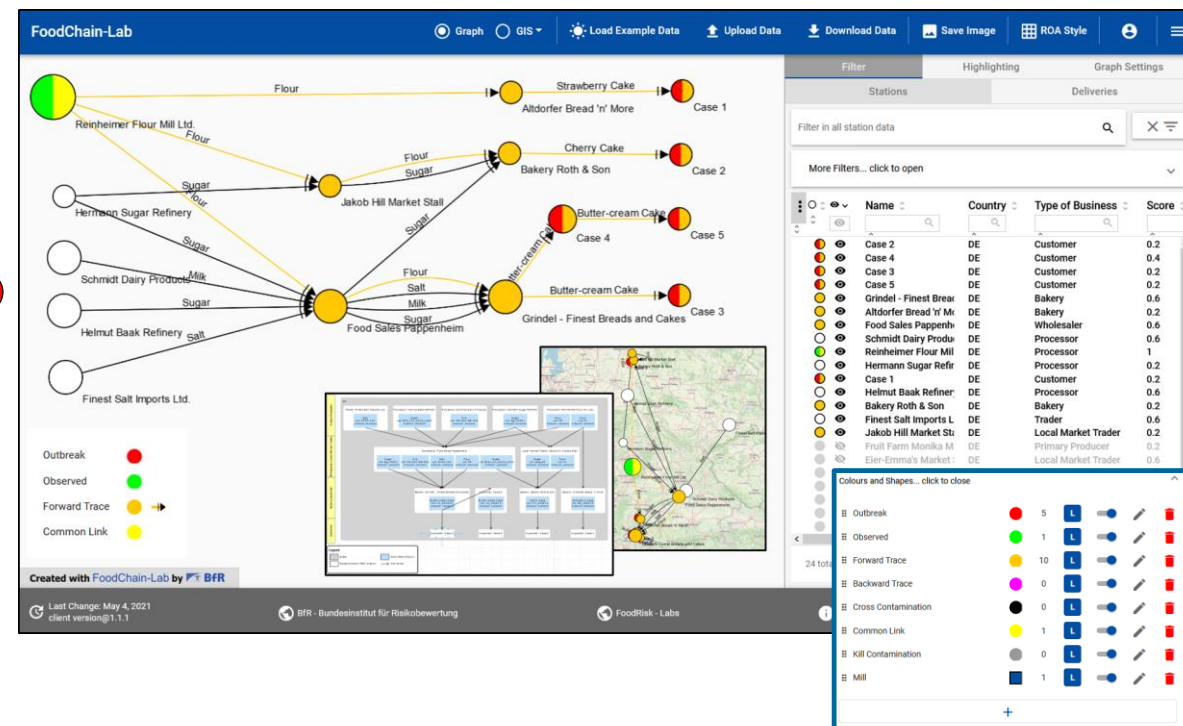
CIS Demo: <https://cohesive.izs.it/>  
 CIS Wiki: <https://cohesive.izs.it/wiki/user/>





## FoodChain-Lab

- Free open-source software (<https://foodrisklabs.bfr.bund.de/foodchain-lab/>)
- Tool to trace back and forward suspicious food items along complex supply chains to help solving foodborne crises (outbreaks, chemical contaminations)
- Available as **desktop version** and **web application**  
<https://foodrisklabs.bfr.bund.de>    <https://fcl-portal.bfr.berlin>
- Automated visualisation of FBO  and deliveries 
- Automated analysis of supply chain network to identify potential common source  of pathogen/contamination and disease cases 
- Interactive analysis, simulation of hypotheses (e.g. cross contamination)
- Helps prioritizing next investigation steps
- Reporting module e.g. for Rapid Outbreak Assessments



FCL Web integrates several modules from different projects and initiatives (**COHESIVE**, **NOVA**, **EFSA**, ...) in one tool

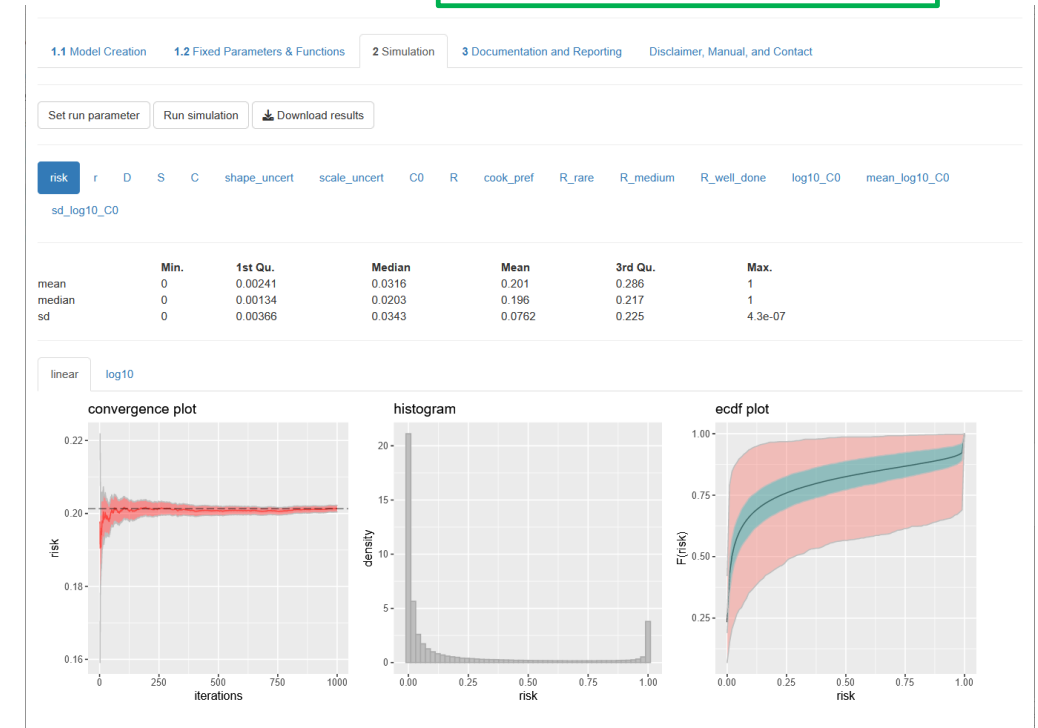
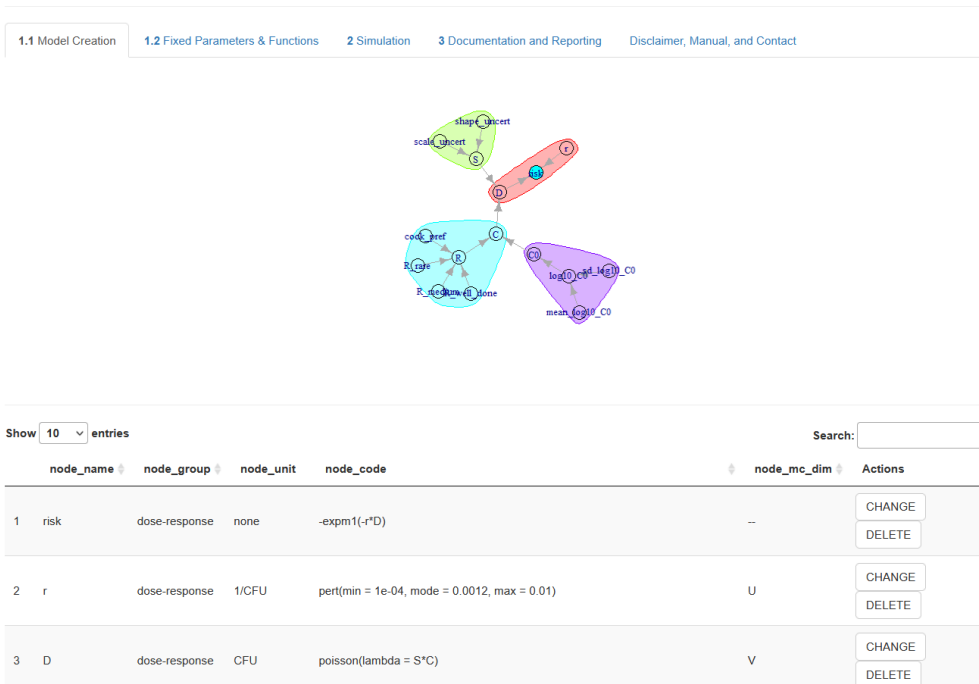




# shiny-rrisk – a web tool for quantitative risk assessment

shiny-rrisk

Risk modelling framework



## Purpose:

- shiny-rrisk is a software, and tool for state-of-the-art quantitative risk assessment modelling
- focus on transparent documentation, and reporting of results

## Impact:

- It helps modeller, and decision maker in creating transparent, well documented QRA models

## Experience:

- will be publicly available early 2023 -- <http://shiny.bfr.bund.de/apps/shiny-rrisk>



# Decision-support tool for risk assessment

Provides a range of risk assessment approaches based on the situation of its user.

Time available

Geographical specificity

Event Specificity

Data availability

Level of expertise

Hazard ID



Does this using a user-friendly, interactive decision-tree



At end-points, it provides a description of the risk assessment approach

And some linked examples of applications of these approaches and/or tools to help apply them

[GEO-SPECIFICITY] At what geographic level is your risk question?

What level of data is available?

**Qualitative disease prioritisation**

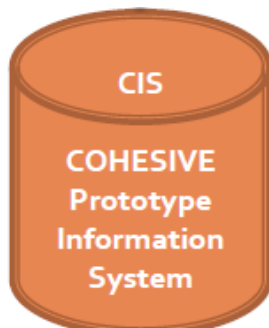
Disease prioritisation is performed in order to determine which diseases pose the greatest threat to your target country-block, country, region or area. Qualitative disease prioritisation is usually performed using a rapid risk assessment matrix, due to the large scale, need for fast results or low data availability. Estimates for each disease may need to be obtained from expert opinion or a search of published literature. Because of the need for ranking, it is difficult to avoid some form of numerical scoring system. Diseases can be ranked purely based on the final qualitative assessment, but this does not allow for fine-grained discrimination between diseases. Instead, scoring can be done using a points-based system for different aspects of each disease, which then provides a basis for ranking and prioritising diseases, as shown in the first example where a semi-quantitative system is used to rank the diseases based on their scores. The main difference between these and traditionally semi-quantitative approaches is that they are single-dimensional. The scoring of the disease determines its rank, but the different disease-specific criteria are not themselves weighted. This means these analyses can be more focussed on a single risk question than traditional semi-quantitative approaches. Exploring semi-quantitative approaches as well will help you understand which is most suitable to you. The second example, while not a prioritisation itself, highlights how different stakeholder opinions can affect the ranking of diseases. This is worth considering when parameter values rely heavily on expert opinion.

**Examples:**

- [Prioritisation of wildlife pathogens](#)
- [Stakeholder opinion in prioritisation in Quebec](#)

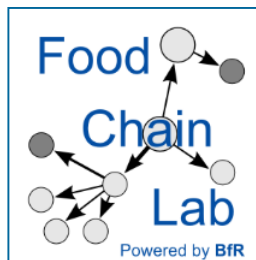


## Impact of OHEJP COHESIVE software suite



Italian national reference center for WGS of pathogens uses a variant of CIS

Several European countries tested CIS (ANSES (France), APHA (UK), RIVM (The Netherlands), INSA (Portugal))



Used by several European countries, EFSA and U.S. FDA

Integration in the production of rapid Outbreak Assessments at EFSA

Part of OHEJP simulation exercise SimEx and EFSA/ECDC crisis trainings

FAO/WHO/OIE: FCL part of Tripartite Tool Box (SISOT)

shiny-rrisk

Risk modelling framework

Applied by

- COHESIVE Partners
- German federal research institutes (BfR, FLI, ...)
- Universities
- EFSA

European Food Risk Assessment Training Programme (EU-FORA)



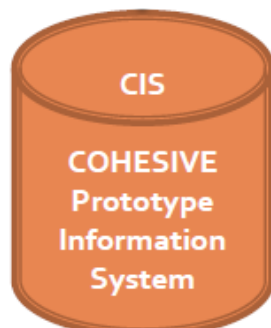
Online and publicly available to use:

- Primarily used as a training resource to familiarise new risk assessors on range of approaches available



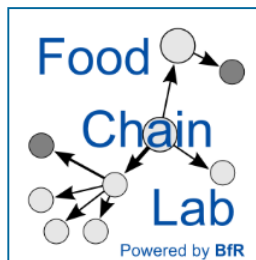
# How to further improve preparedness

Ongoing efforts to improve interoperability with main data exchange systems at EU level  
(EFSA, ECDC, RASFF and MS systems)



Contact with other relevant whole-genome sequencing (WGS) projects (BeONE, MATRIX, CARE, COVRIN and TELEVIR )

Further harmonization with EFSA WGS tool and BeONE



EFSA co-operation on

- Establishment of data standards for supply chain tracing for authorities
- Establishment of a European tracing tool ecosystem



Interoperability via harmonised model description



# Thank you for your attention!



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# Cross-sectoral framework for quality Assurance Resources for countries in the European Union

## CARE



Mia Torpdahl

CARE Project co-lead

[mtd@ssi.dk](mailto:mtd@ssi.dk)

22 November 2022





# Focus of EJP CARE

- Develop new One Health concepts for proficiency testing of laboratories, reference materials and quality/availability of demographic data for risk analysis
- 19 partners across 10 countries



# Outcomes #1

- Built up a collection of reference materials for seven foodborne bacterial pathogens
  - *Salmonella* / *Listeria* / *Campylobacter* / *E. coli* / *Staphylococcus* / *Bacillus* / *Yersinia*
- Collected and managed by 3 mBRC's based at CARE partners



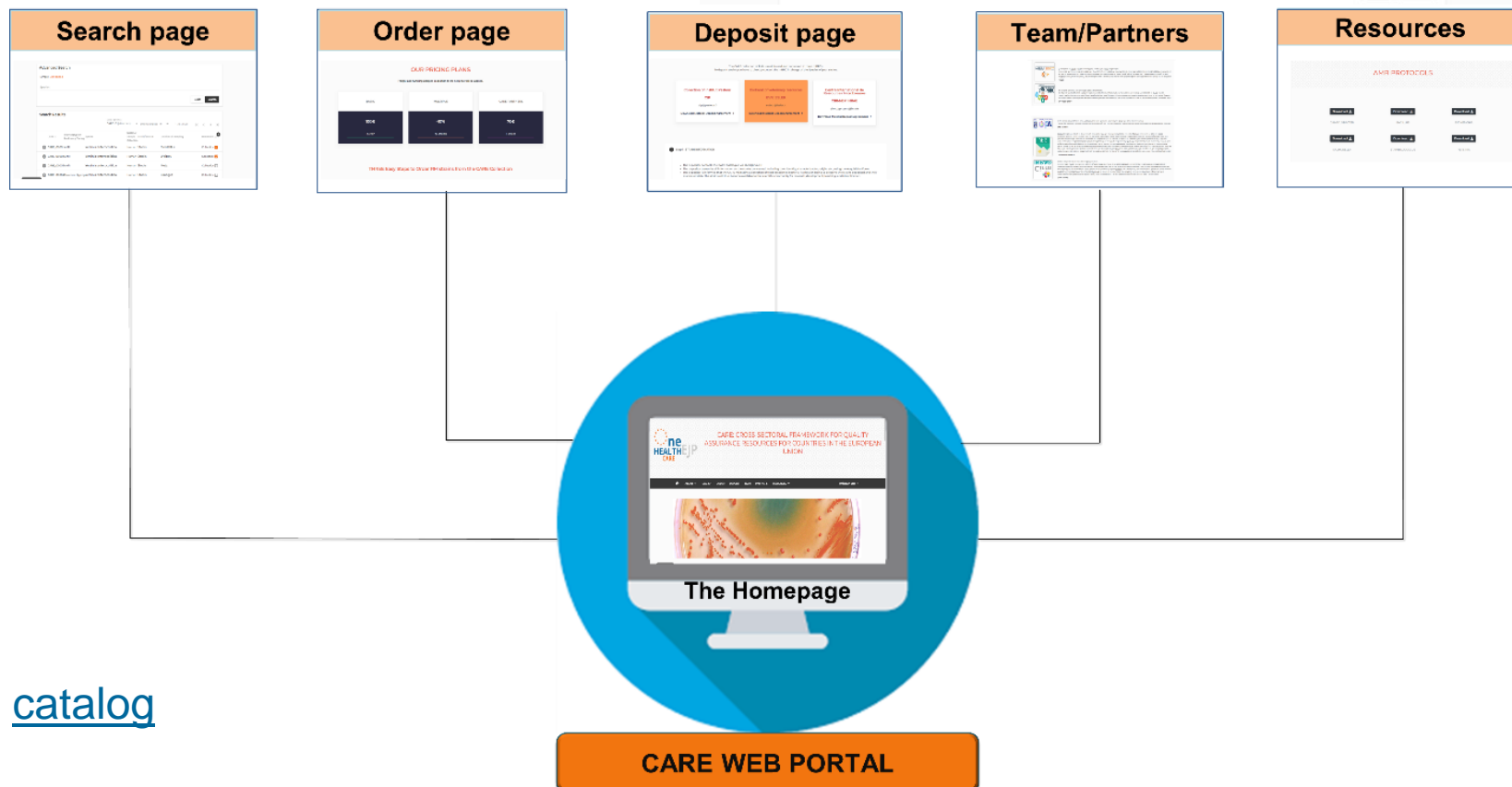
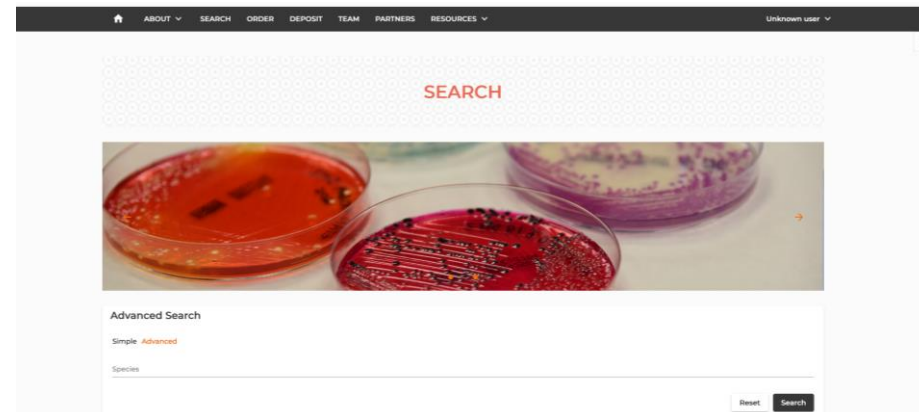




# Purpose of the CARE collection

## One health collection of well defined reference material

- ✓ Links to WGS raw data
- ✓ Date / location sampling / Sector of isolation
- ✓ Laboratory of origin
- ✓ Integration of predicted AMR / virulence genes
- ✓ Antibiofilms data



Access to the CARE catalog



# Impact of the CARE Collection

A community sharing common goals:

- Strengthening the links between food safety, veterinaries, public health agencies, research institutes
- Improving access to biological resources acquired under publicly funded schemes
- A vision of pathogen diversity circulating in the EU
- Foster the European research and innovation potential in food safety



*At which institutes are the output already in use and what are the experiences so far?*

- Providers are signing MDAs and sending strains to the mBRCs
- The 3 Microbiological Resource Centers are collecting and entering materials in their collections
- The CARE collection is growing - Difficulties sometimes encountered in the sending of strains (veto by the ministries, missing associated metadata due to national regulation, lack of harmonisation on Nagoya regulation, ...)





## Outcomes #2

- Developed a guide for accessing relevant data and models for quantitative microbial risk assessment.
- Online document

A guide for  
accessing relevant  
data and models  
for quantitative  
microbial risk  
assessment

Preface  
1 Introduction  
Hazard identification >  
2 Hazards  
3 Foods  
4 Contamination data  
5 Public health data  
Exposure Assessment >  
6 Consumption data  
7 Process model  
8 Hazard characterization  
Risk characterization >  
9 Burden of disease data  
References  
Appendices >  
A Relevant generic tools for

### Preface

This document has been prepared in the context of the EJP-OH CARE (Cross-sectoral framework for quality Assurance Resources for countries in the European Union). This document is part of WP4 : Investigate, benchmark and improve the availability and the quality of the existing data relevant for risk assessment.



This project has received funding from the European Union's Horizon 2020 research and innovation programme under Grant Agreement No 773830.



**Horizon 2020**  
**European Union Funding**  
**for Research & Innovation**

To learn more about CARE project visit <https://onehealthjep.eu/jip-care/>.





# For what purpose is the output supposed to be used?

**Our goal is to provide help to identify data/knowledge that risk assessors and data scientists need at the start of their projects.**

## Before establishing the Guide

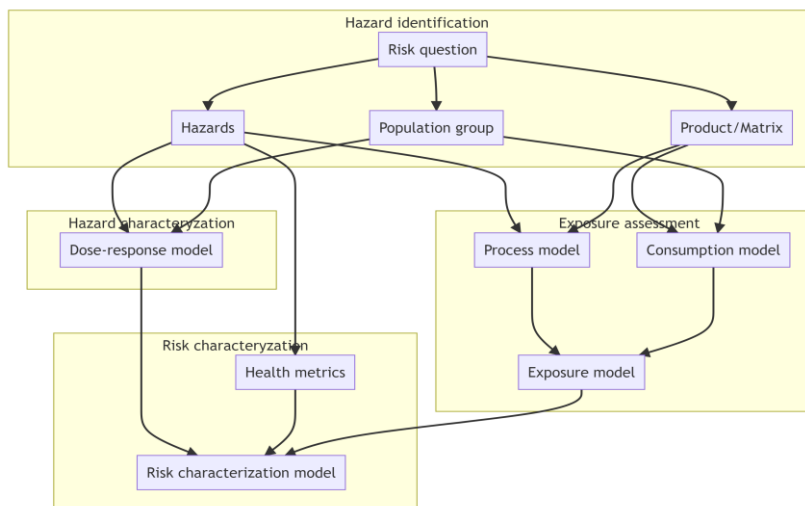
- Identified the gaps from the survey
- Contacts established with other EJPOH projects (RADAR, ORION, MATRIX, ...) or other initiatives
- Discuss with stakeholders





# How is it used?

Information for the 4 steps of risk assessment (hazard identification, exposure assessment, ...) )



For each data source

- Presentation of the scope
- Illustration of how to access

## 5.2 Surveillance Atlas of Infectious Diseases

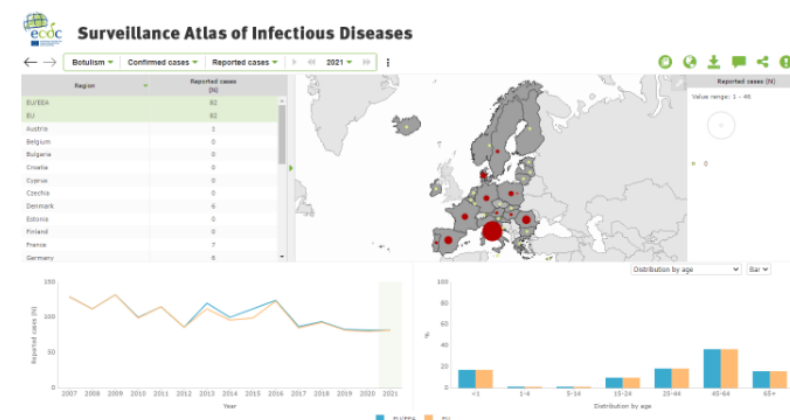
### 5.2.1 Scope

The Surveillance Atlas of Infectious is an interactive tool that allow users to manipulate aggregate EU surveillance data from The European Surveillance System (TESSy) to produce a variety of tables and maps.

### 5.2.2 Accessibility

The Surveillance Atlas of Infectious is accessible through the main page [Surveillance Atlas of Infectious Diseases \(europa.eu\)](https://surveillance-atlas.europa.eu/).

Several infectious diseases are available in the atlas and for each of them, the user can choose the subpopulation, the indicator and the years. The user then has access to tables showing the distribution of the disease according to the chosen indicator by country, year and age and a European map showing the diseases distribution according to the chosen indicator (Figure 5.1).







# Impact – what will using the output contribute to improving?

- Support the whole risk assessment community including national and international risk assessment agencies, and academic institutions.
- Identification of the relevant (high quality ) data
- Promote national partners to make their data available

At which institutes are the output already in use and what are the experiences so far?

CARE partners

EFSA MRA Network: presentation of the Guide in 2023 and discussion to use it as a reference document of the network



# Thank you for your attention!

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# One Health Harmonisation of Protocols for the Detection of Foodborne Pathogens and AMR Determinants



## OH-HARMONY-CAP

Harmonised protocols and common best practice

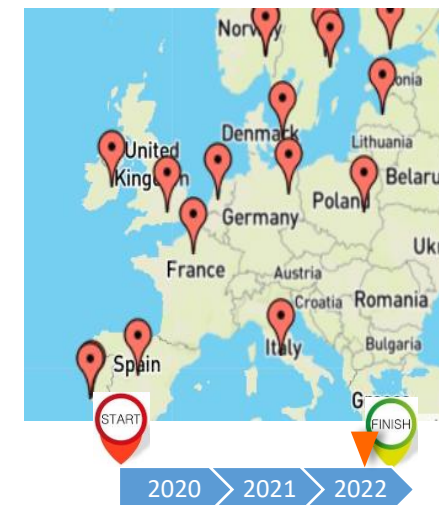
Mia Torpdahl on behalf of  
Nadia Boisen Project lead  
([nbo@ssi.dk](mailto:nbo@ssi.dk))  
(22.11.2022 Stockholm)





# Why OH-Harmony-Cap?

- Laboratory protocols and procedures are pivotal
  - Surveillance
  - Outbreak detection
- To make laboratory results comparable across OH:
  - Crucial that the same pathogens are detected and characterised
  - Harmonised approach
- Sampling and monitoring of zoonotic pathogens should follow similar guidelines
- This implies that all laboratories have similar:
  - Capabilities
  - Capacities
  - Systems for communication
- Extensive differences are documented across the EU/EEA countries



Project lead: Nadia Boisen, SSI  
Co-lead: Flemming Scheutz, SSI





# Objectives



WP2

Develop a Benchmarking  
Instrument OHLabCap

WP3

One Health laboratory interoperability  
guidance for model organisms

WP4

Design harmonised protocols  
for model organisms

WP5

Dissemination and  
Increase the EU capacity





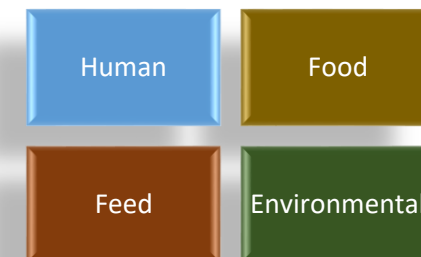
WP2

# Develop a Benchmarking Instrument OHLabCap

Overview and general description of the microbiology system in the OH-field

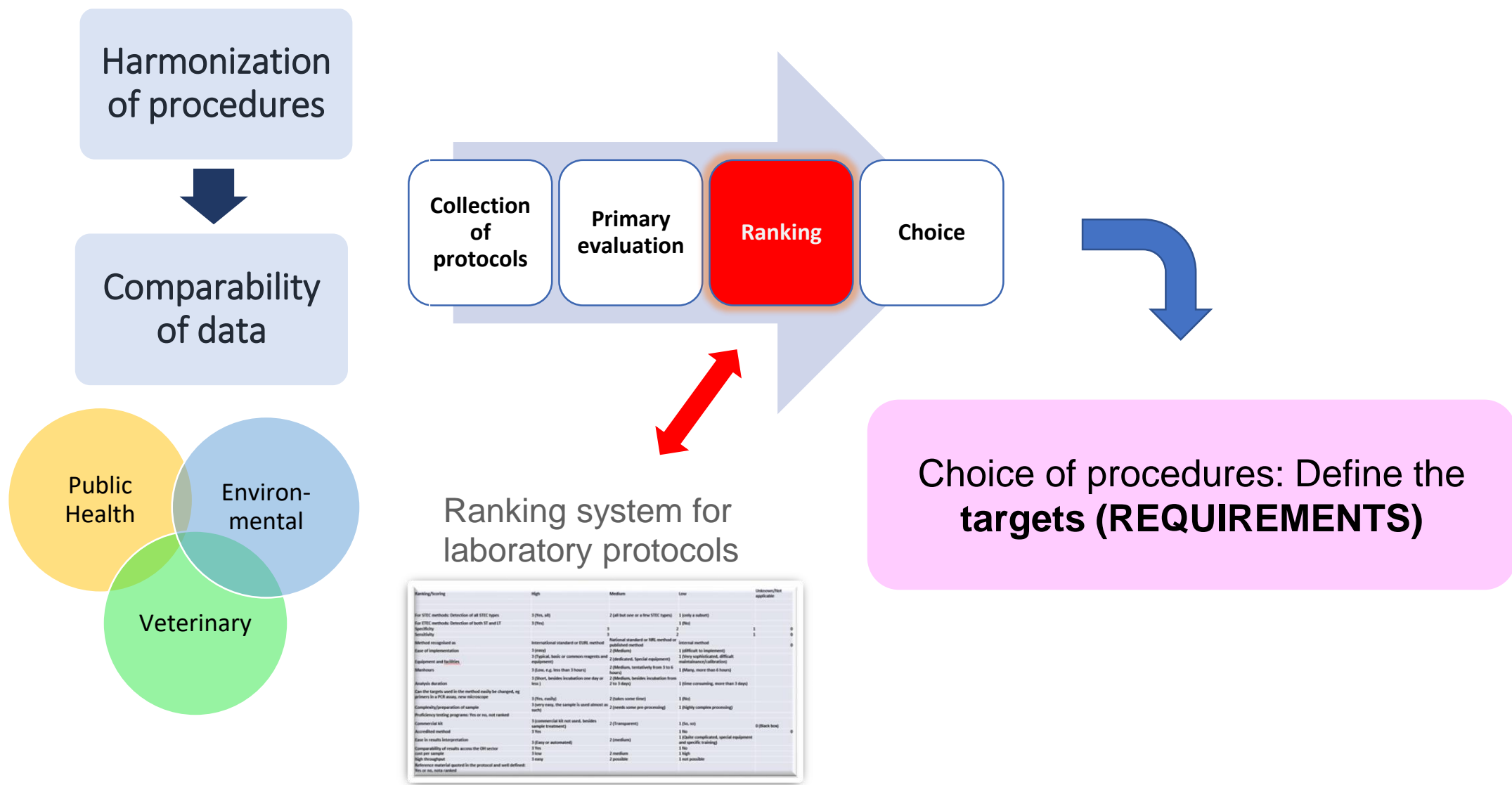
## OUTCOME #1

- **OH-HARMONY-CAP has developed** and used a tool to measure
  - Adaptability, capacity, capability, and interoperability and communication
- Responses: 25 EU/EEA countries and 122 laboratories
- Limited to
  - Six priority bacteria, five parasites and - AMR
- **Impact:** *The OHLabCap highlighted major differences across the One Health microbiological systems in place in the participating countries. Of particular concern, was the lack of accreditation and standardisation in the human clinical diagnostic laboratories*





# How to harmonise the methodology for the detection and typing of the model pathogens



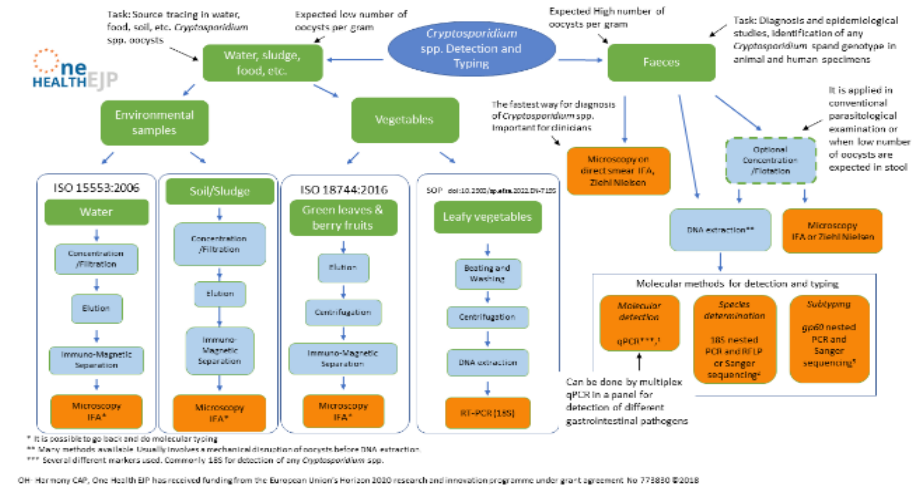
Model organisms: Shiga toxin producing *E. coli* (STEC)/enterotoxin producing *E. coli* (ETEC), *Cryptosporidium*, and AMR for *Salmonella* and *Campylobacter*

# Was Harmonisation possible?

## OUTCOME #2

Three different results based on pathogen

1. STEC/ETEC: Yes - harmonised methods
2. Cryptosporidium: No - decision tree
3. AMR: Current methods, fit for purpose



## Impact:

- The proposed harmonised procedures, if implemented, will contribute to an improvement in the standardisation of protocols for STEC/ETEC and *Cryptosporidium* spp.
- The development of new primers for the detection of STEC and ETEC related genes represents an update reflecting the current epidemiology and current knowledge of microbiology organisms
  - four new subtypes of Shigatoxin genes have been described and three of these have been published as part of the OH-Harmony-Cap project.





# Thank you for your attention!

(nbo@ssi.dk)



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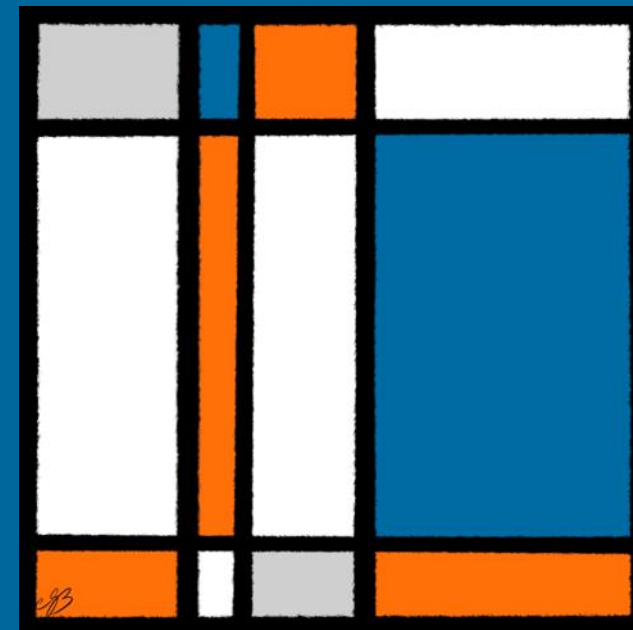
STATENS  
SERUM  
INSTITUT



OHEJP  
PMC-POC meeting  
Stockholm, Sweden  
21-22 November 2022



**JIP MATRIX**  
Outcomes for consideration  
22 November 2022



Guido Benedetti  
MATRIX PL

Statens Serum Institut



## One Health European Joint Programme

A partnership of 44 food, veterinary and medical laboratories and institutes in Europe and the Med-Vet-Net association

<https://onehealthejp.eu/>



- ▶ 19 partners
- ▶ 12 countries
- ▶ ⌚ 2020 - 2022

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dimensions  
in One Health  
surveillance

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Project

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Multi-sectorial,  
Foodborne  
pathogens,  
Emerging threats

<https://onehealthejp.eu/jip-matrix/>

MATRIX created solutions for European countries to advance the implementation of One Health Surveillance

MATRIX invites European institutes working in the animal health, public health and food safety sectors to adopt the MATRIX solutions and to further build upon them

<https://onehealthejp.eu/jip-matrix/>







# MATRIX solutions for OHS

<https://onehealthejp.eu/jip-matrix/>



## Expanding – OHS Codex: The Knowledge Integration Platform

One Health -  
EpiCap Tool

Roadmap to  
national OHS

Manual for OHS  
dashboards

Guidelines and best practices

- to develop multi-sectoral surveillance systems
- to operationalize cross-sectorial collaborations
- to design, implement, and evaluate official controls within the food sector using output-based standards

## Promoting – the Food Safety Knowledge Exchange (FSKX) Format



- For European countries (partners and non-partners) e.g. evaluating their OHS; utilizing Systems Thinking along the roadmap; developing OHS dashboards
- For OHEJP stakeholders e.g. to facilitate evaluation activities across countries and/or hazards
- SIS OT (TZG), others e.g. to support surveillance and information sharing

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# One Health - EpiCap Tool



An interactive, stand-alone tool to evaluate the capacities and capabilities for the One Health Surveillance of a specific sector and/or pathogen of choice

Benchmarking of surveillance capacities and capabilities for comparison i) with other countries for the same hazard; ii) between specific hazards within one country

Evaluating strengths and weaknesses of multi-sectoral surveillance systems and identifying opportunities for further integration

Leading partners: Agency for Food, Environmental and Occupational Health & Safety, France (ANSES) and University of Surrey, United Kingdom (UoS)



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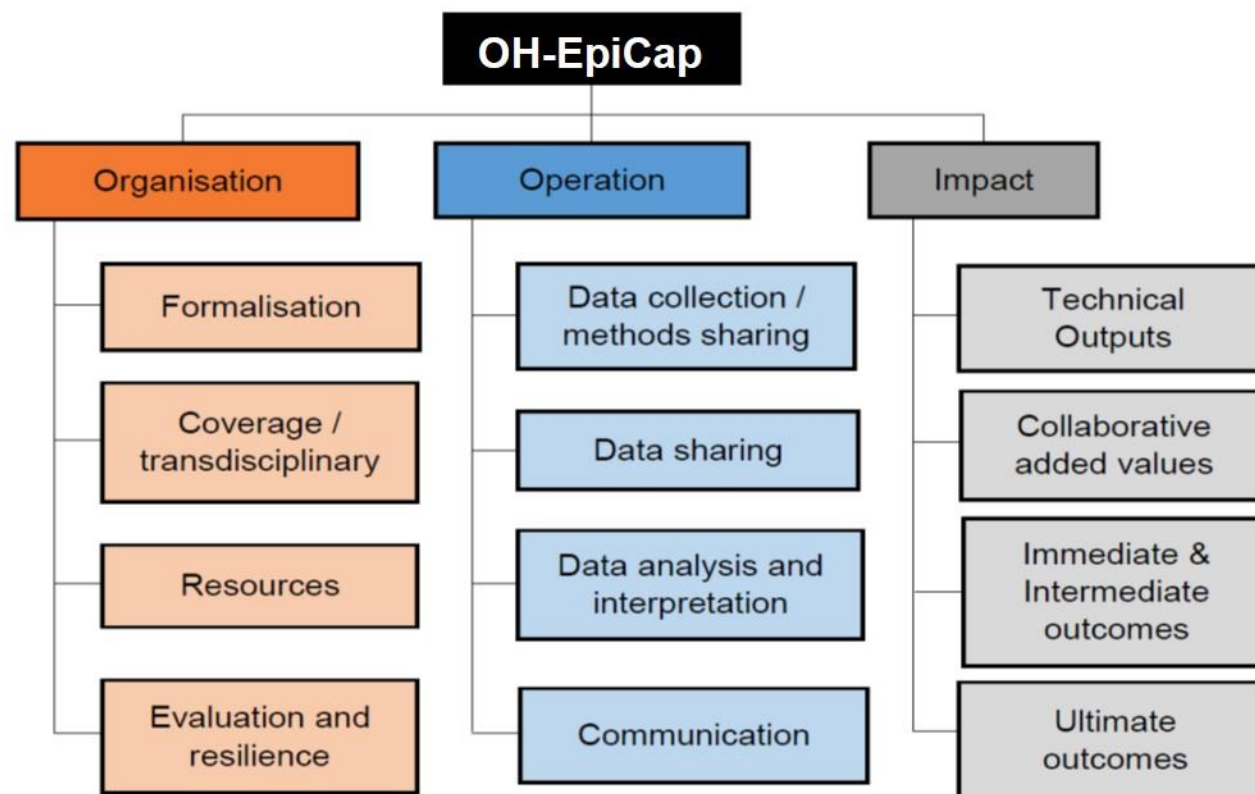


# One Health - EpiCap Tool



The tool evaluates 3 dimensions:

- Organization of One Health
- One Health in operational activities
- Impact of One Health



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# One Health - EpiCap Tool



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OH-EpiCap Tool

- About OH-EpiCap
- Instructions
- Questionnaire
- Results
- Create Benchmark File
- Benchmark
- Glossary
- Legal Information

**Important Disclaimer:**

All of the data entered in this tool is processed on your device and is not sent externally.

## OH-EpiCap Tool

**Evaluation tool for One Health epidemiological surveillance capacities and capabilities**

### About the OH-EpiCap Tool

The purpose of the OH-EpiCap tool is to develop system-specific profiles of (potential) surveillance interoperability between sectors, highlighting both strength and gaps in surveillance capacity and capabilities. The OH-EpiCap tool will allow mapping, evaluation and improvement of 'One Health-ness' using a set of standardized indicators, to allow comparison across systems, countries and hazards of interest. Countries at similar levels of 'OH-ness', including similar capacities, limitations and resources, can together form an agreement to develop a common framework for One Health Surveillance (OHS) to address zoonotic threats across borders. This will improve national OH structures, including surveillance and data analysis, while also facilitating better integration of multinational collaboration. Countries at different levels of 'OH-ness' and surveillance capacity/resources can share experiences regarding surveillance practice against the same pathogen, transfer knowledge and share ideas to improve surveillance quality and efficacy across settings.

Some of the features of the tool include:

- Evaluation of 'OH-ness' across three dimensions
- Interactive visualisation of results
- Benchmarking tool to compare to other One Health Surveillance systems

[https://onehealthejp.eu/wp-content/uploads/2022/11/OHEJP-MATRIX\\_OH-EpiCap-flyer.pdf](https://onehealthejp.eu/wp-content/uploads/2022/11/OHEJP-MATRIX_OH-EpiCap-flyer.pdf)





# One Health - EpiCap Tool

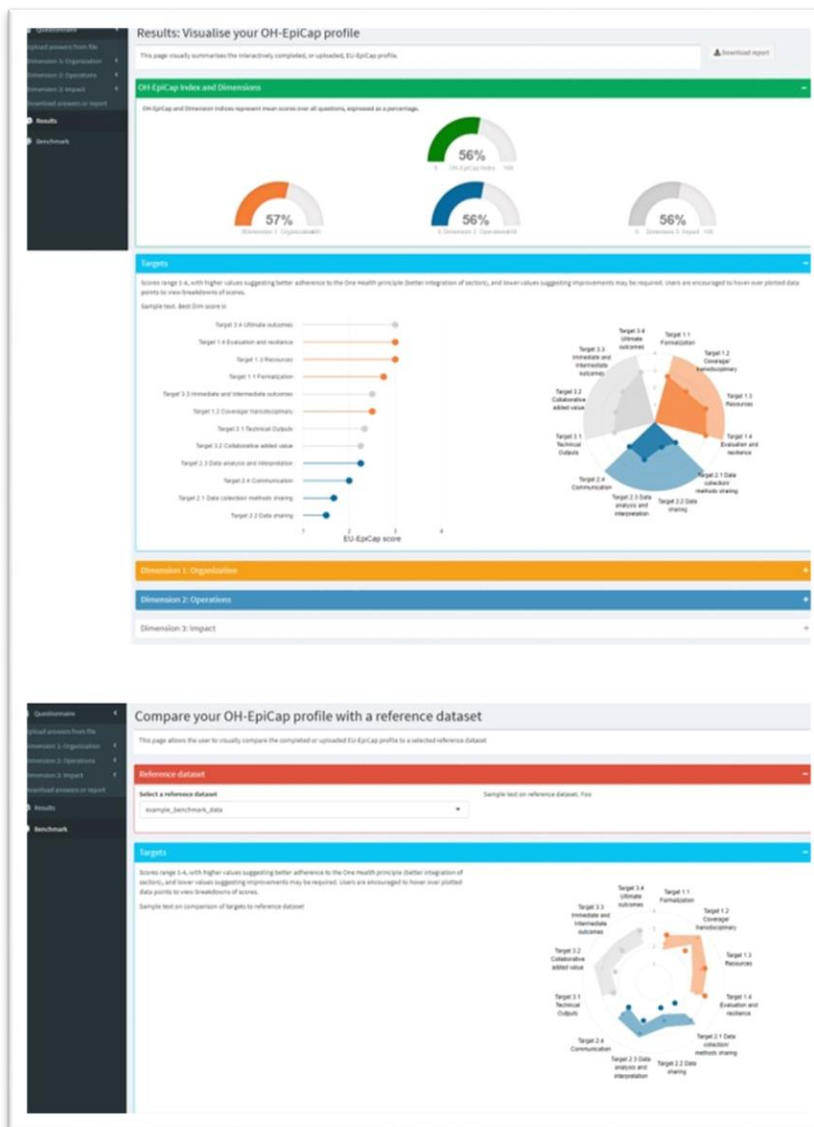


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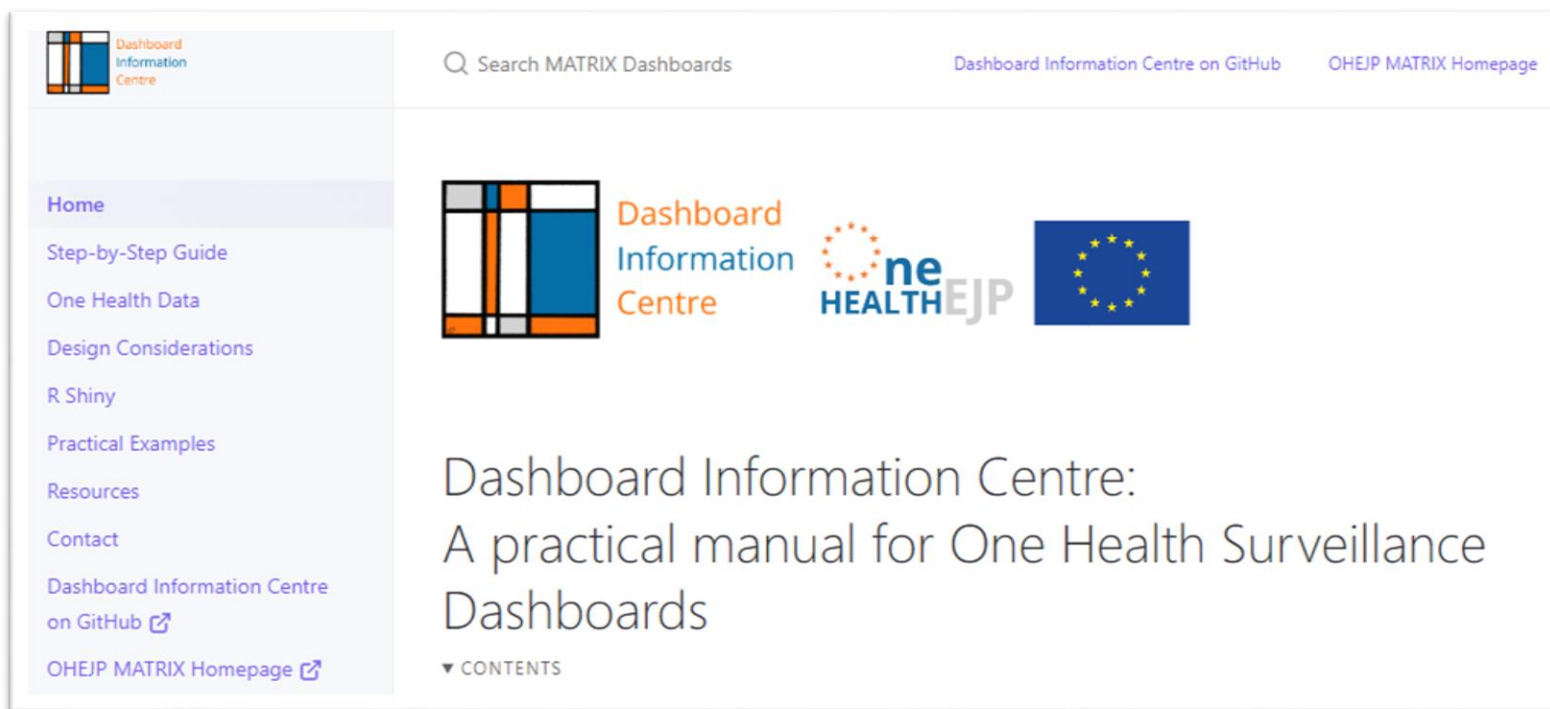
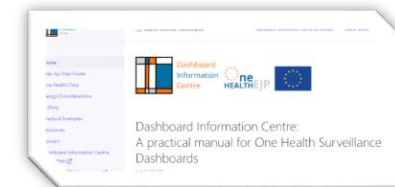
<https://onehealthejp.eu/jip-matrix/>



- For multi-sectoral surveillance system representatives
- For government / national agencies
- For European / international agencies (like EU-LabCap)
- Expert elicitation (MATRIX, EFSA, CoEvalAMR project)
- Released in fall 2022 (online application)



# Manual for One Health Surveillance Dashboards



<https://sva-se.github.io/MATRIX-dashboards/>

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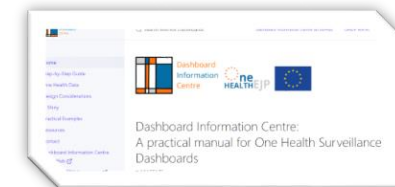
<https://onehealthejp.eu/jip-matrix/>

Leading partners: National Veterinary Institute, Sweden (SVA) & Norwegian Institute of Public Health, Norway (NIPH)





# Manual for One Health Surveillance Dashboards



An online dashboard inventory and practical manual to facilitate the design and implementation of One Health Surveillance dashboards using open source tools

The Dashboard Information Centre: a “living document” that contains an inventory of planned, ongoing and finished dashboard projects, a practical manual and a best practice guide to the development of One Health Surveillance dashboards

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surveillance

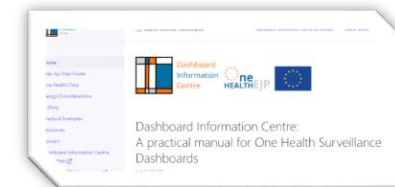
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Foodborne  
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Emerging threats

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# Manual for One Health Surveillance Dashboards



The Dashboard Information Centre covers:

- Information context and end-user considerations
- Technical and legal barriers associated with cross sector data sharing
- Pitfalls and biases of co-analysing One Health data
- A selection of the most suitable technical implementations

A “companion” when planning or developing a dashboard

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# Thank you for your attention!

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# Coronavirus Research Integration COVRIN

Prof Daniel Horton, University of  
Surrey

Prof Wim van der Poel, Wageningen  
University and Research/

November 2022





# COVRIN

## SARS-CoV2 Research Integration & Preparedness

- Drivers for Emergence and Spread, and Risk Assessment of SARS-CoV2
- Responsible Partners:
  - Wageningen Bioveterinary Research (WBVR)
  - University of Surrey (UoS)
- Contributing partners:
  - ANSES (P1), Ages (P2), Sciensano (P4), VRI (P8), Bfr (P9), FLI (P10), INIA (P16), UCM (P17), INRAe (P19), APHA, (P21), UoS (P23), ISS (P27), IZSAM (P28), IZSLER (P29), RIVM (P30), WBVR (P31), NVI (P33), PIWET (P34), INIAV (P35), INSA(36), SVA (P41), BIOR (P44).



# COVRIN

## Operational Objectives

Two main integrative research objectives:

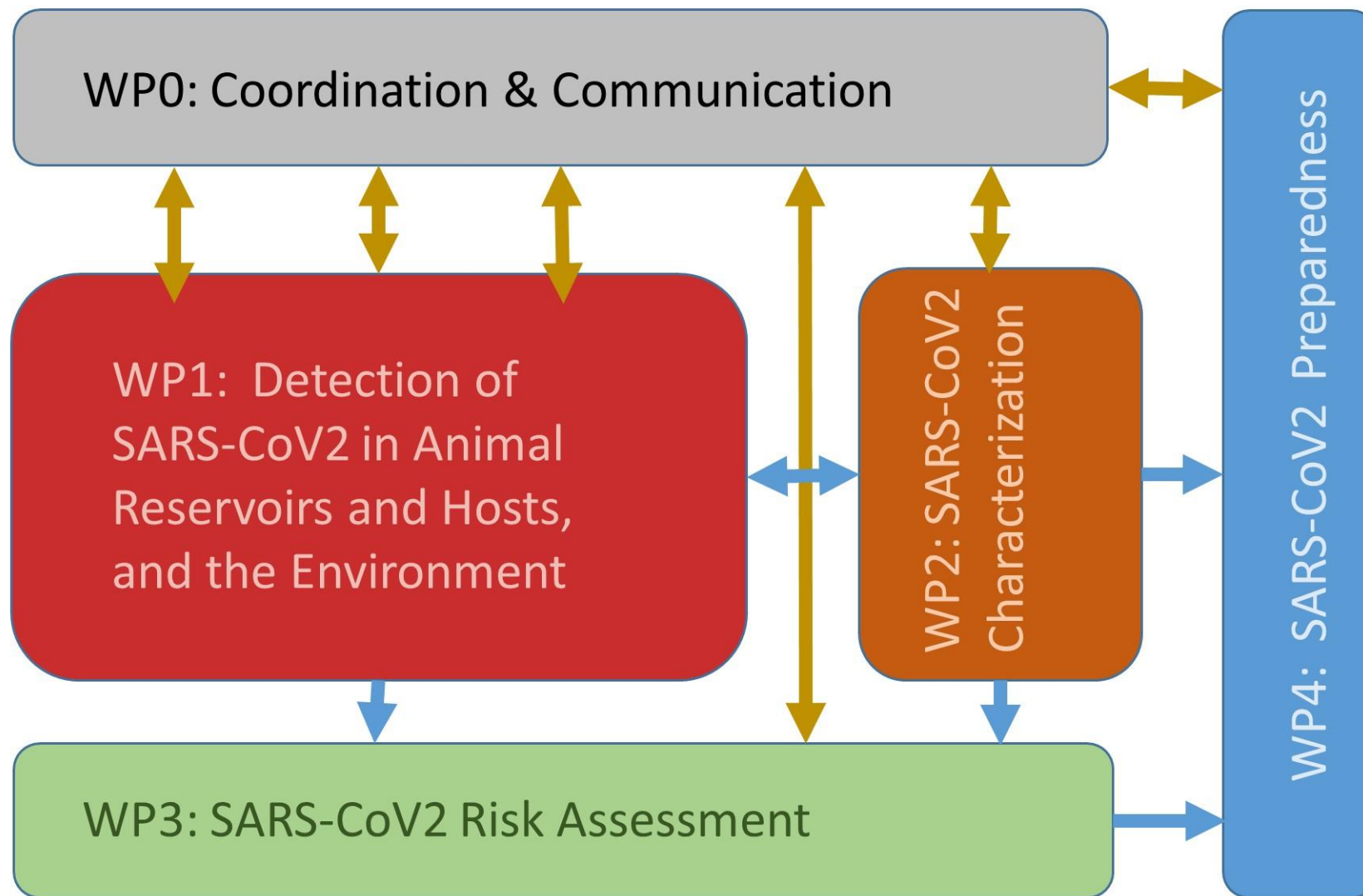
1. To identify drivers for the emergence and spread of SARS-CoV2
2. To generate data and build models for risk assessment of SARS-CoV2







## SARS-CoV2 Research Integration & Preparedness COVRIN 2.0





# COVID-19 pandemic rapid developments

- New diagnostics
- New variants
- New hosts
- New vaccines
- Environmental contamination







# WP0 Coordination and communication

## Outputs:

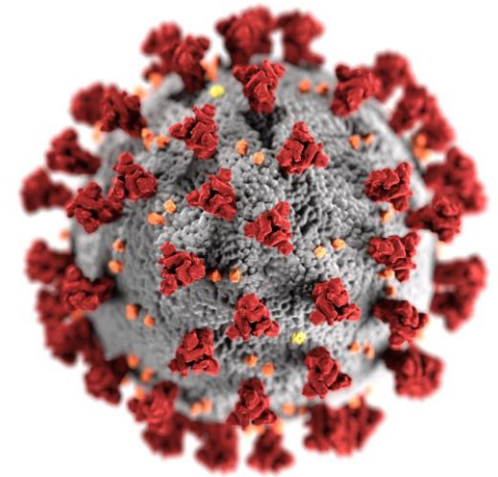
- Sharepoint for **data exchange** on EJP OH website
- Scoping review of EU COVID-19 research: database and report produced
- Stakeholder connection: joining meetings, liaison with WP5
- Kick-off March 2021, online- report available
- Mid-term meeting (June 2022 ) – hybrid, report available
- Final meeting 5/6<sup>th</sup> December 2022- *In person, Teramo, Italy*



# WP1:SARS-CoV2 detection

## Outputs:

- SARS-CoV-2 detection in animal samples:
  - Genetic, Antigen, Antibody
  - **Protocol database and comparison exercise**
- SARS-CoV-2 detection in environmental samples:
  - Infectivity assessments of virus in environmental samples; ongoing studies
  - Environmental RNA quantifications -> input risk assessment







# Case study: rapid antigen tests

- Viral loads under the hypothetical SARS-CoV-2 infectivity threshold were detected by most tests
- Saliva from various animal species did not affect the tests
- BUT VOCs B.1.1.7 and B.1.351 were less well detected

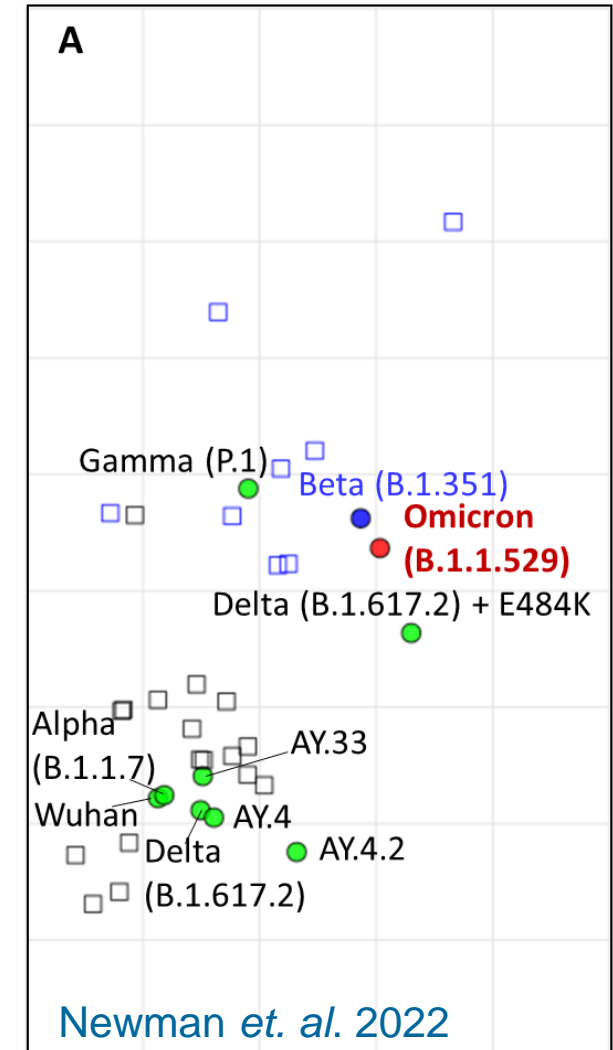


Hagag IT, Weber S, Sadeghi B, Groschup MH, Keller M. Impact of animal saliva on the performance of rapid antigen tests for detection of SARS-CoV-2 (wildtype and variants B.1.1.7 and B.1.351) Veterinary Microbiology 2021



## WP2:SARS-CoV2 Characterization Outputs:

- Next generation sequencing protocol repository set up
  - Ring trial between partners
- Cell line sensitivity->report
- Animal model protocols collated -> catalogue
- Pathology toolbox per species -> report
- Identification of antigenic site variation



Lean *et. al.* 2022





# Case study: vaccine protection in older adults

- Immunity wanes significantly over time in older adults
- Boosting works, against a broad range of variants



Newman, J., Thakur, N., Peacock, T.P., Bialy, D., Elreafey, A.M., Bogaardt, C., Horton, D.L., Ho, S., Kankeyan, T., Carr, C., Hoschler, K., Barclay, W.S., Amirthalingam, G., Brown, K., Charleston, B., Bailey, D., 2021. Neutralising antibody activity against SARS-CoV-2 variants, including Omicron, in an elderly cohort vaccinated with BNT162b2. **Nature Microbiology** 2022



## WP3 Risk assessment and surveillance: Outputs

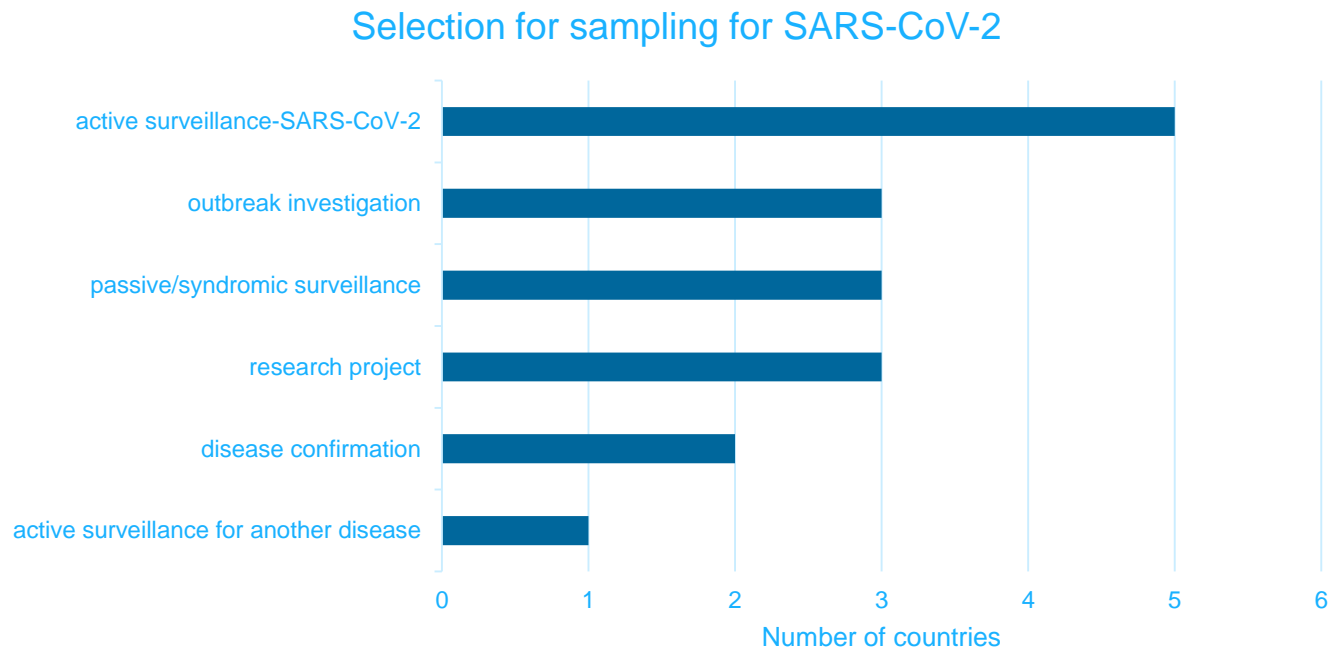
- Defined format and procedure for integration of surveillance data
  - Ongoing: collection of surveillance data
- **Evaluated** current surveillance activities
- **Analysed** risk of transmission in pets with epidemiological surveys
- Landscape survey of existing transmission models







# Case study: SARs-CoV2 sampling in Europe



- At least 10 partners undertaking sampling in animals
- METHODS vary considerably
- SPECIES biases
- Evaluation of the efficacy underway

|             |               |  |
|-------------|---------------|--|
| Title       | OHEJP         | D.3.1.2 Database on sampling on wildlife, food |
| deliverable |               | producing animals, pets, and the environment   |
| WP and task | WP3, Task 3.1 | 10.5281/zenodo.580307                          |
|             |               | 5  |



# WP4:Coronavirus preparedness

## Outputs:

- Virus host interactions
  - In vivo and in vitro studies animal coronaviruses (ongoing)
- Virus detections and isolations from wildlife species: hedgehogs, mustelids, deer.
- Tracing significant virus mutation in animal species
- Identification of newly susceptible species
- Risk assessment modelling animal coronaviruses







# Case study: assessing the risk of transmission among cats

- Estimated  $R_0 > 1$
- Cat to cat transmission is likely
- Risk of cat-human transmission remains unknown
- Risk of human to cat transmission unknown



Gonzales JL, de Jong MCM, Gerhards NM, Van der Poel WHM. The SARS-CoV-2 Reproduction Number  $R_0$  in Cats. Viruses. 2021; 13(12):2480. <https://doi.org/10.3390/v13122480>



# COVRIN impact

- Key outputs
  - Shared/Harmonized molecular tests
  - Shared/harmonized immunoassays
  - Shared/Harmonized Cell line and animal models/protocols
- Expected implementations
  - Ref lab testing procedures
  - Risk modelling approaches
- Expected impact of the research:
  - Preparedness research
  - Risk assessments and control research.
- Societal and policy impact.
  - Improved risk assessment
  - Improved health risks control





# Thank you to all COVRIN Partners

## Thank you for your attention!



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# OHEJP SimEx POC-PMC



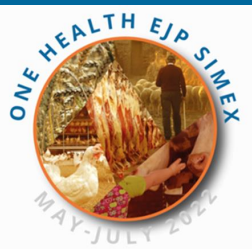
Frederico Alves  
Project Administrator  
22 November 2022





## Overall aim

*To test the **One Health capability, capacity and interoperability** of authorities in Public Health, Animal Health and Food Safety to work together*





# Scenario

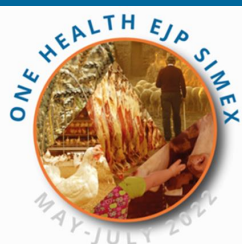
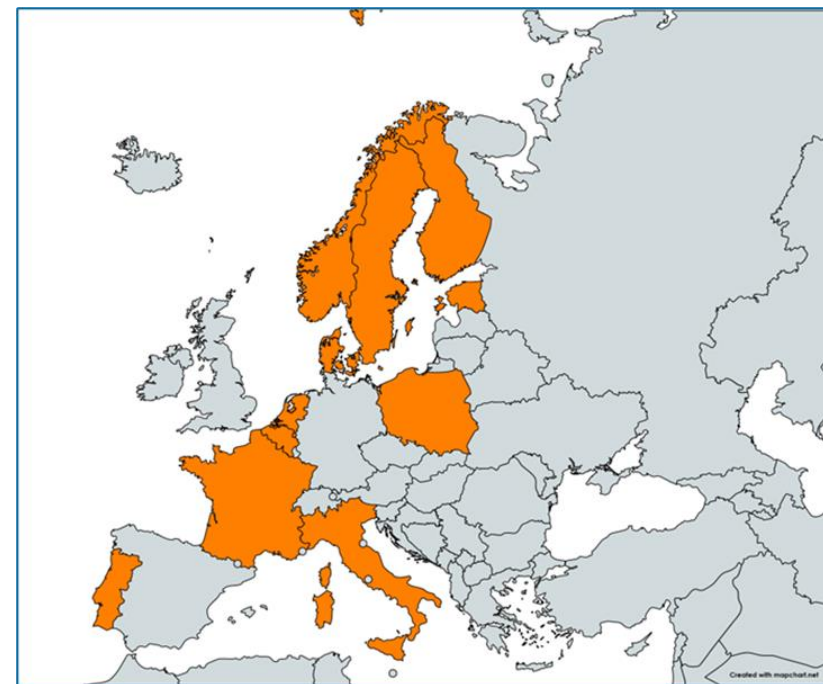
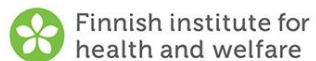
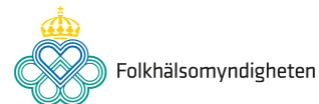
- Table-top exercise
- Salmonella *Typhimurium* outbreak at national level involving both the human food chain and the raw pet feed industry
- The scenario was designed to encourage intersectoral communication and information sharing between Public Health (PH), Animal Health (AH) and Food Safety (FS) authorities







# Participants





# Participants

- 257 participants from 11 different countries
- Participation of the relevant One Health areas:
  - 23% Animal Health
  - 35% Food Safety
  - 37% Public Health

| Country         | Institution   | Sector<br>Public Health (PH)<br>Animal Health (AH)<br>Food Safety (FS) |
|-----------------|---|--|
| Norway          | Norwegian Public Health Institute                             | PH   |
|                 | Norwegian Veterinary Institute                                | AH + FS  |
| Denmark         | DTU Food  | FS   |
|                 | DVFA  | AH + FS  |
|                 | SSI   | PH + AH  |
| Belgium         | Sciensano   | PH, AH + FS  |
| Portugal        | INIAV   | AH   |
|                 | INSA  | PH   |
| Poland          | Piwet   | AH + FS  |
| Finland         | Finnish Food Authority (Ruokavirasto)                         | AH + FS  |
|                 | Finnish Institute for Health and Welfare (THL)                | PH   |
| Sweden          | Public Health Agency of Sweden                                | PH   |
|                 | National Food Agency  | FS   |
|                 | National Veterinary Institute                                 | AH   |
| Italy           | IZSLER  | AH + FS  |
|                 | IZSAM   | AH + FS  |
|                 | ISS   | PH   |
| Estonia         | Agriculture and Food Board                                    | AH + FS  |
|                 | VetLab  | AH + FS  |
|                 | Health Board  | PH + FS  |
| France          | ANSES   | PH, AH + FS  |
|                 | Santé Publique France   | PH   |
| The Netherlands | Wageningen BioVeterinary Research, WUR                        | AH   |
|                 | National Institute of Public Health and the Environment, RIVM | PH   |





# Results

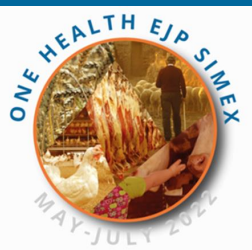
## Organization

- **>94%** satisfaction with the exercise logistics at national level
- **99%** pleased with the performance of the NEL and LEL



## Scenario

- **>95%** found the scenario relevant, **89%** felt it equally covered all sectors and **95%** thought it was in line with the objectives
- **16%** described a lack of reality in the way the outbreak unfolded





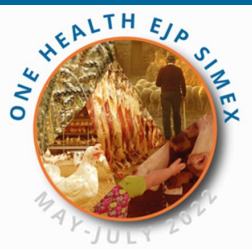
## Results: Increased Knowledge

*Focusing on collaboration, roles and responsibilities during a zoonotic outbreak and also how to use guidelines and available tools.*

- **88%** of participants improved their knowledge on their own and other sectors' responsibilities in the event of a zoonotic outbreak

*“The exercise allowed me to get to know in person some of the different stakeholders in the decision-making chain and to better understand the roles, capacities and limitations of each one of them (us).”*

*“will use the experience acquired during the exercise to improve intersectionality of real-life situations”*



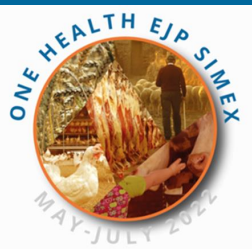




## Results: Increased Understanding of One Health and data sharing

*Focusing on understanding the benefits of a One Health perspective during a zoonotic outbreak and discussions about harmonized databases and data sharing.*

- 90% of participants claimed to have increased their understanding on the importance of data harmonization practices
- 18% feel their home institute does not prioritize the improvement of such practices
- Major Gaps:
  - Lack of political willingness
  - Cost, time and need for training in data analysis (WGS)
  - Lack of data sharing methodologies
  - Need for a common data sharing platform
  - GDPR legislation

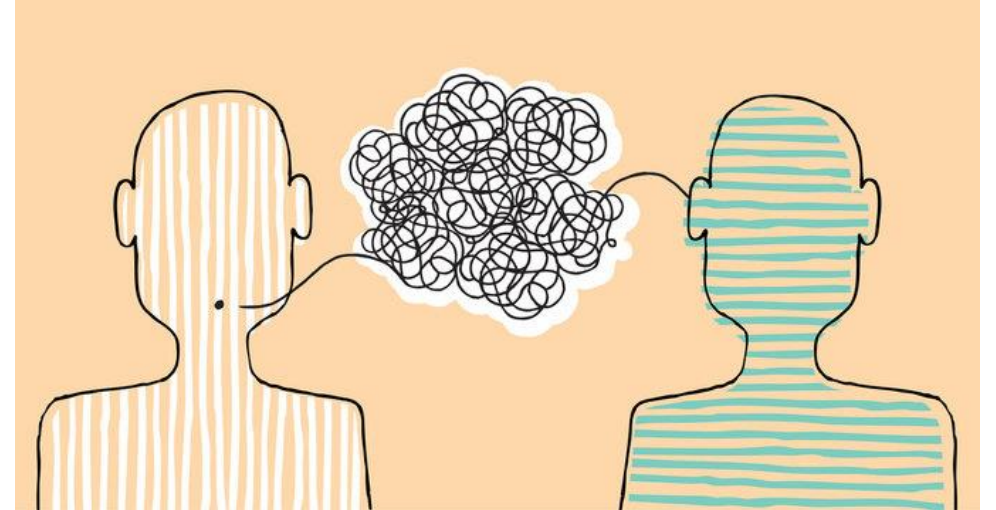




## Results: Communication

*Focusing on creating a common main message and identify different perspectives.*

- **92%** of participants claimed to have increased their understanding on the different communicational needs and target audiences
- **Major Gaps:**
  - Lack of integration of the communication team
  - Lack of a well-structured communication plan







# Recommendations for the improvement of the One Health approach to foodborne outbreaks

Create **guidelines** on One Health strategies at institutional level

Implement a routine of **meetings** between the different sectors

Implement **official communicational channels** between institutes

Improve **coordination** between regional and central authorities

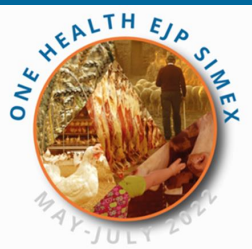
**Harmonize typing methods** and reinforce interlaboratory network

Strengthen the link with human and veterinary medicine practitioners

**Training** in genomic data analysis and **WGS**

Implement common data collection and **data sharing platforms**

Create **communication plan** for outbreak situations





## Final Conclusion

- 94% felt encouraged to pursue a One Health approach and try to work closer with other sectors in a future outbreak situation!
- What's next? **IMPLEMENTATION!**







# Dissemination

- 6<sup>th</sup> December, 13:00h-16:00h CET
- OHEJP WP5 Dissemination Series
- Highlight good practices and the major gaps
- Recommendations for the improvement
- [simex@sva.se](mailto:simex@sva.se)



**One Health EJP**  
**Joint SimEx/Dissemination Workshop**  
**A One Health Simulation Exercise as a roadmap for future foodborne outbreak preparedness**

**Date:** 6th December 2022, 13.00 - 16.00 CET

**Location:** Virtual, free to attend event

Further information [here](#)

Organised by OHEJP **Work Package 5** in collaboration with OHEJP **Work Package 4**, this dissemination workshop is a tool to disseminate research outcomes to policy and decision makers at the national, European and international level. These workshops focus on applicability, and are tailored to provide useful information to those involved in coordinating practical implementation and those involved in wider strategic future plans.



@OneHealthEJP



ONE Health EJP

#OneHealthEJP #OHEJPDissemination

# Thank you for your attention!

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[simex@sva.se](mailto:simex@sva.se)



@OneHealthEJP



/company/h2020-One-Health-EJP



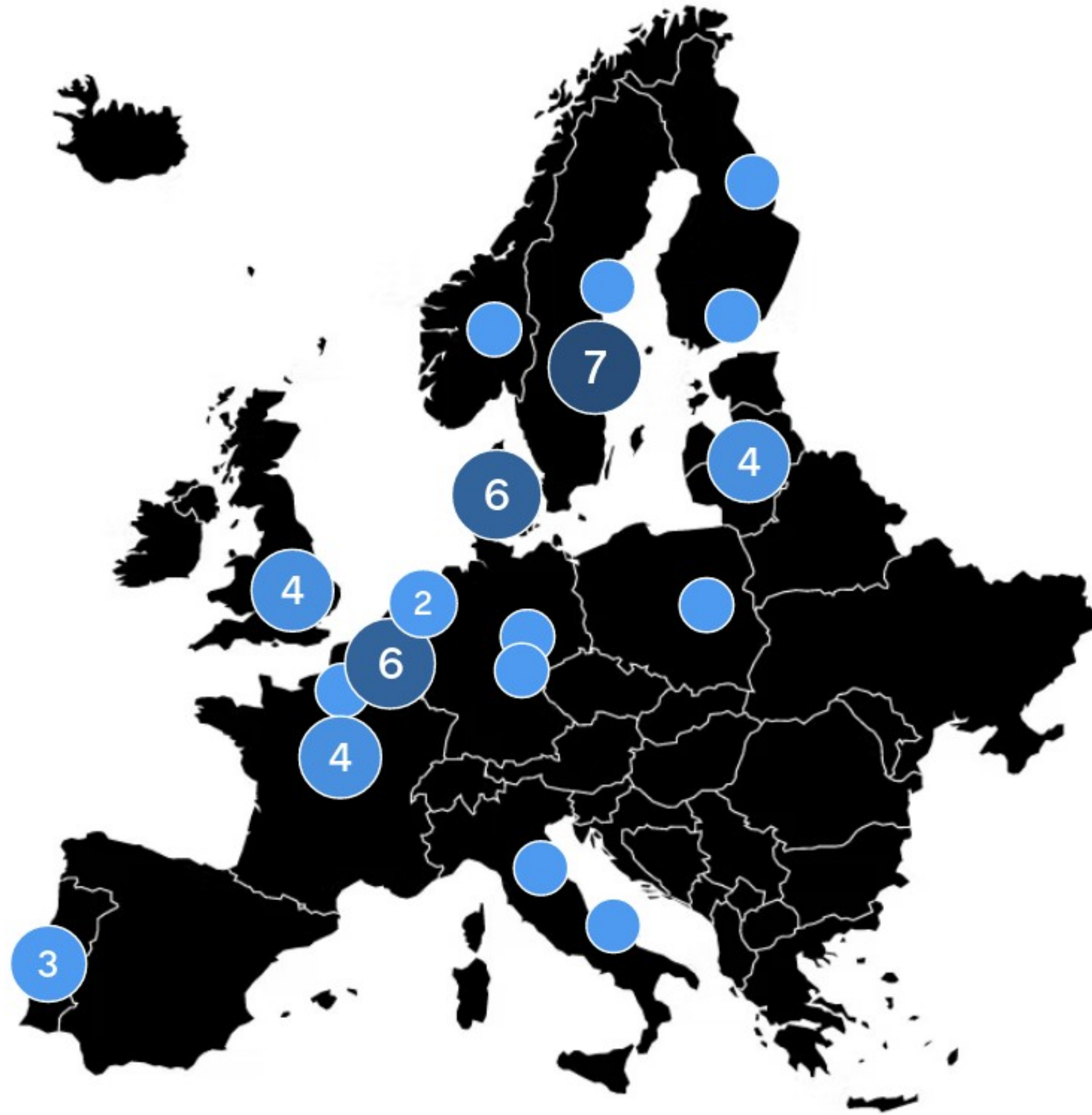
OneHealthEJP.eu



# What did you get from the One Health EJP?

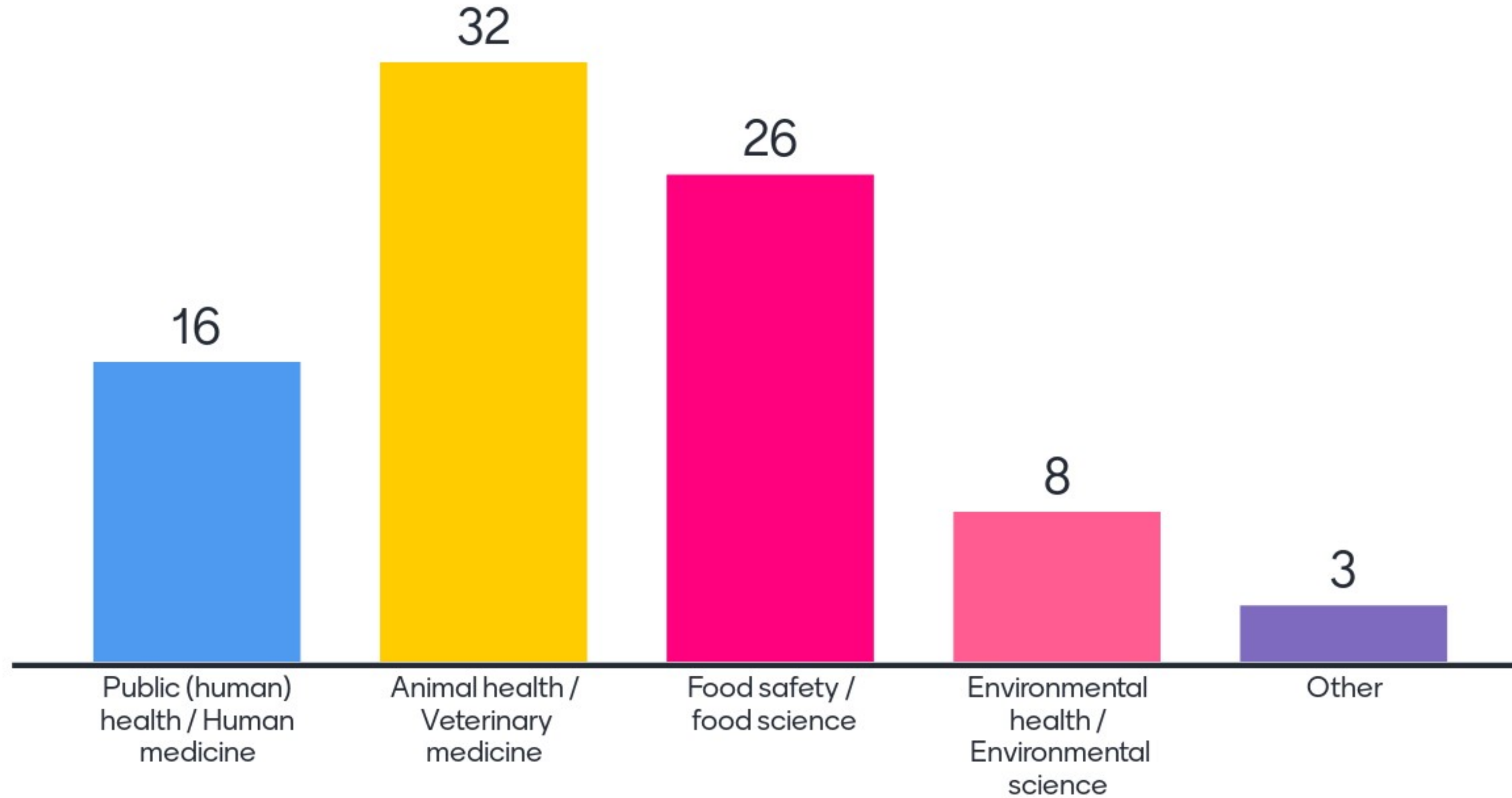


# Where (in Europe) are you from? (workplace)

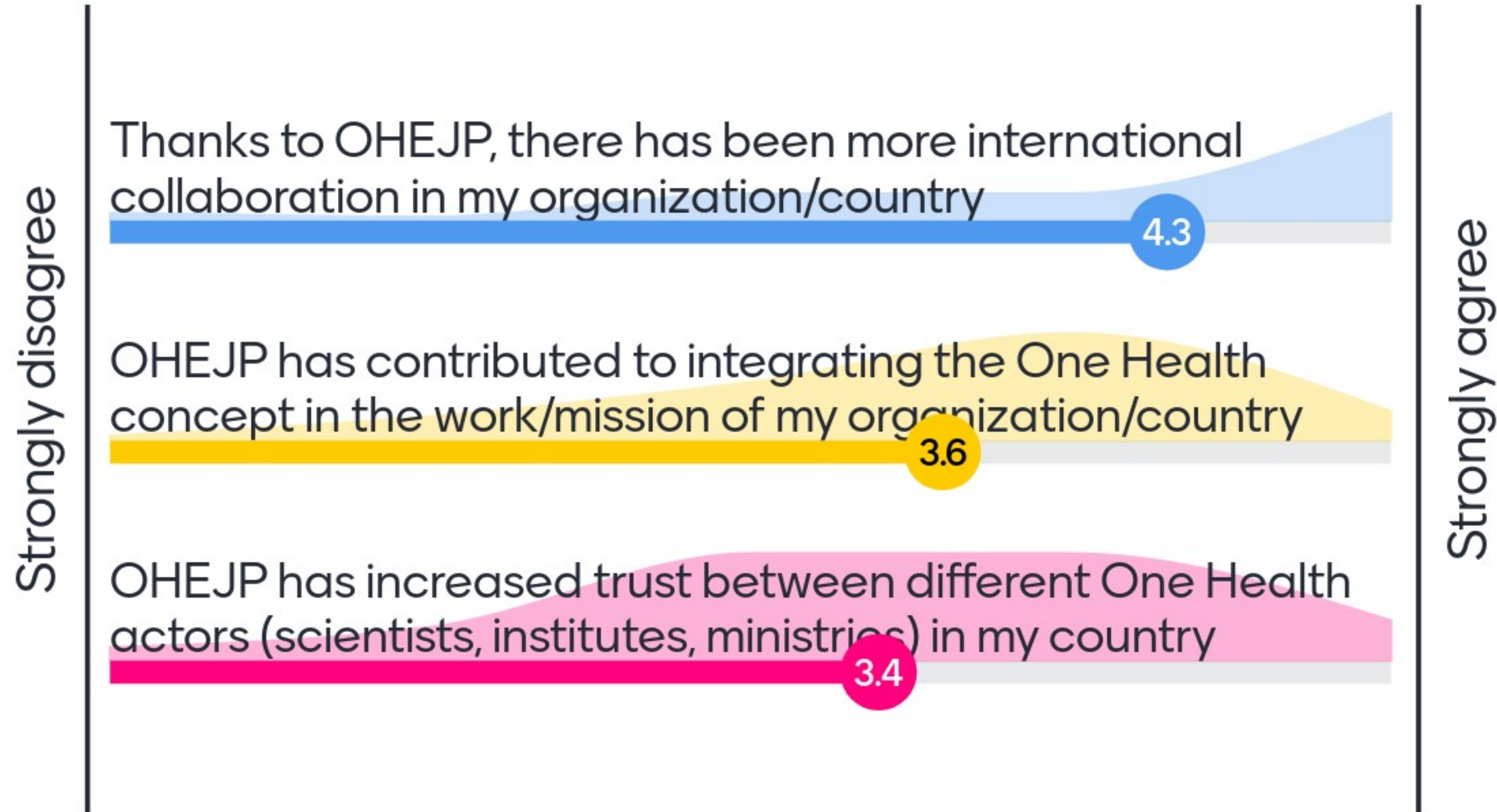




# Which is the main focus of your organization?

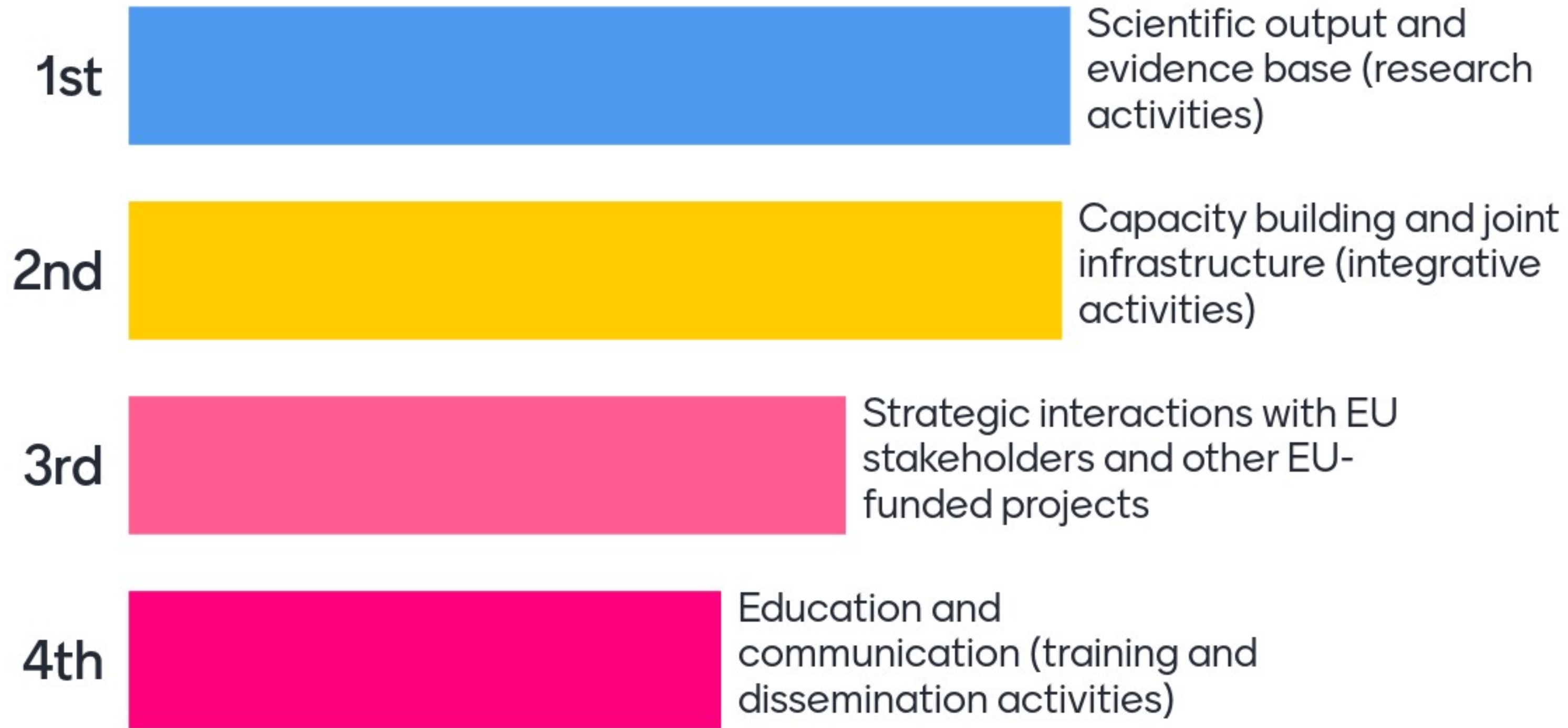


# Impact of OHEJP on my organization/country

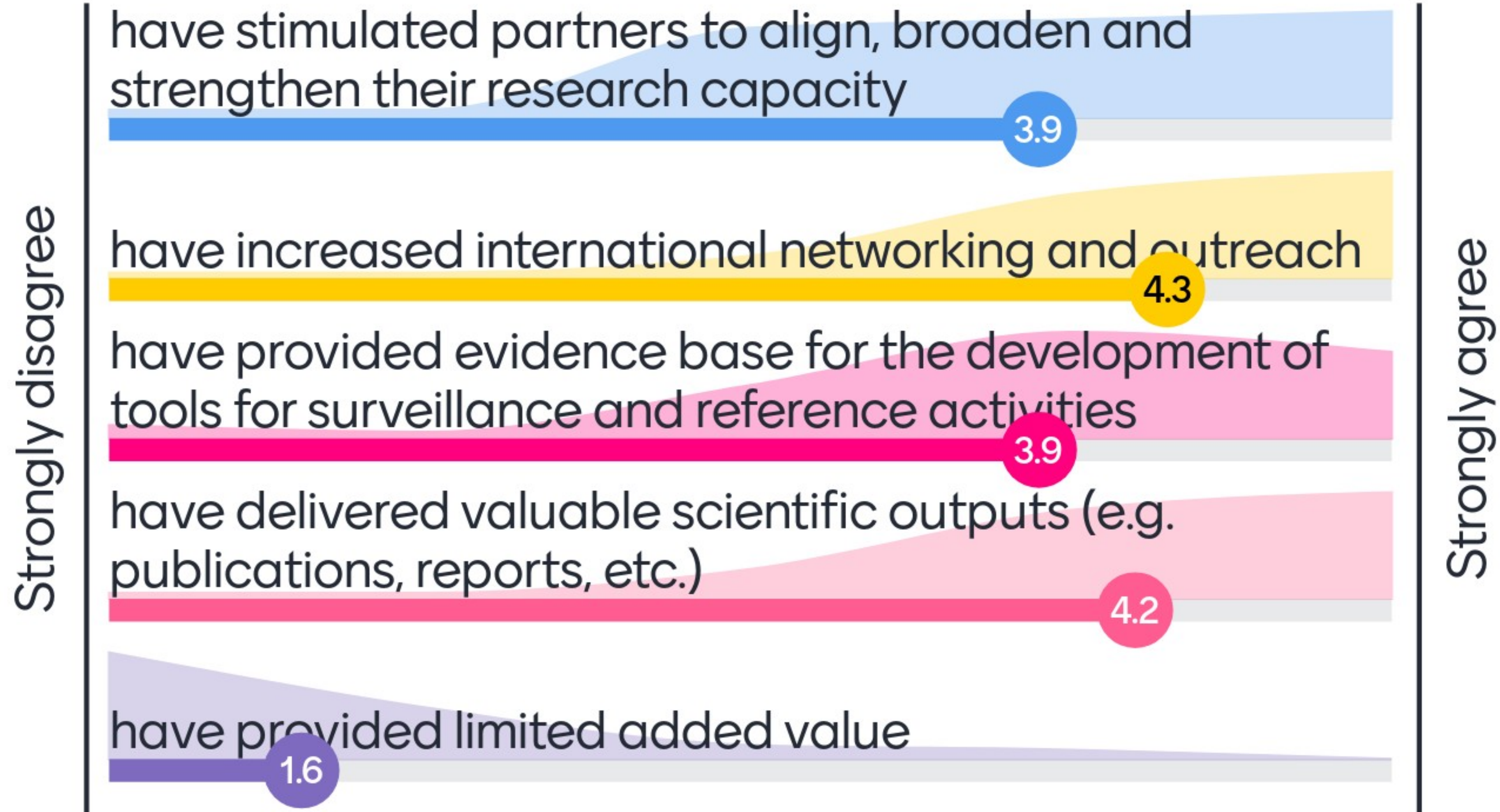




# Where did OHEJP make the biggest difference?

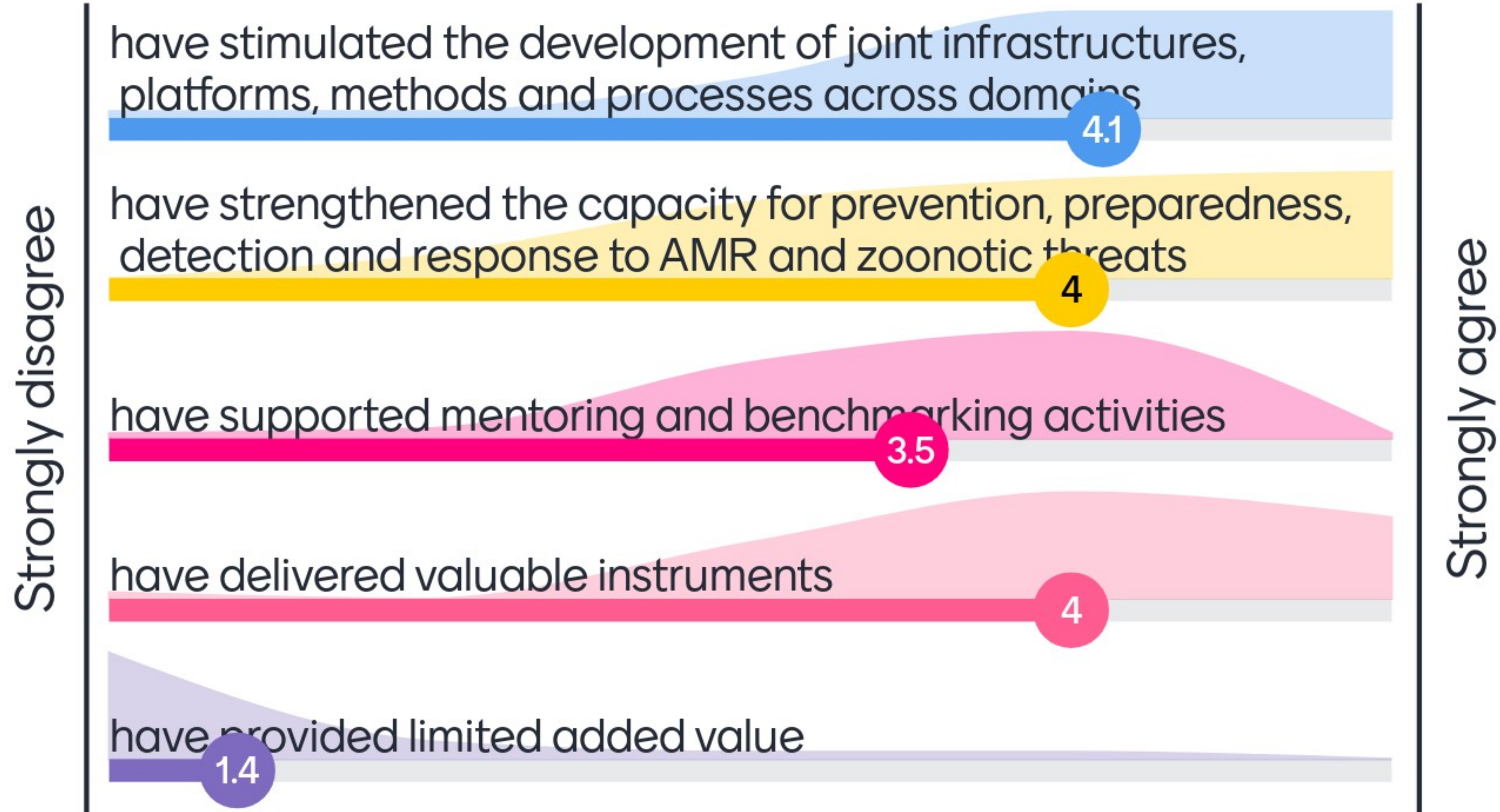


# The research activities (JRP)...



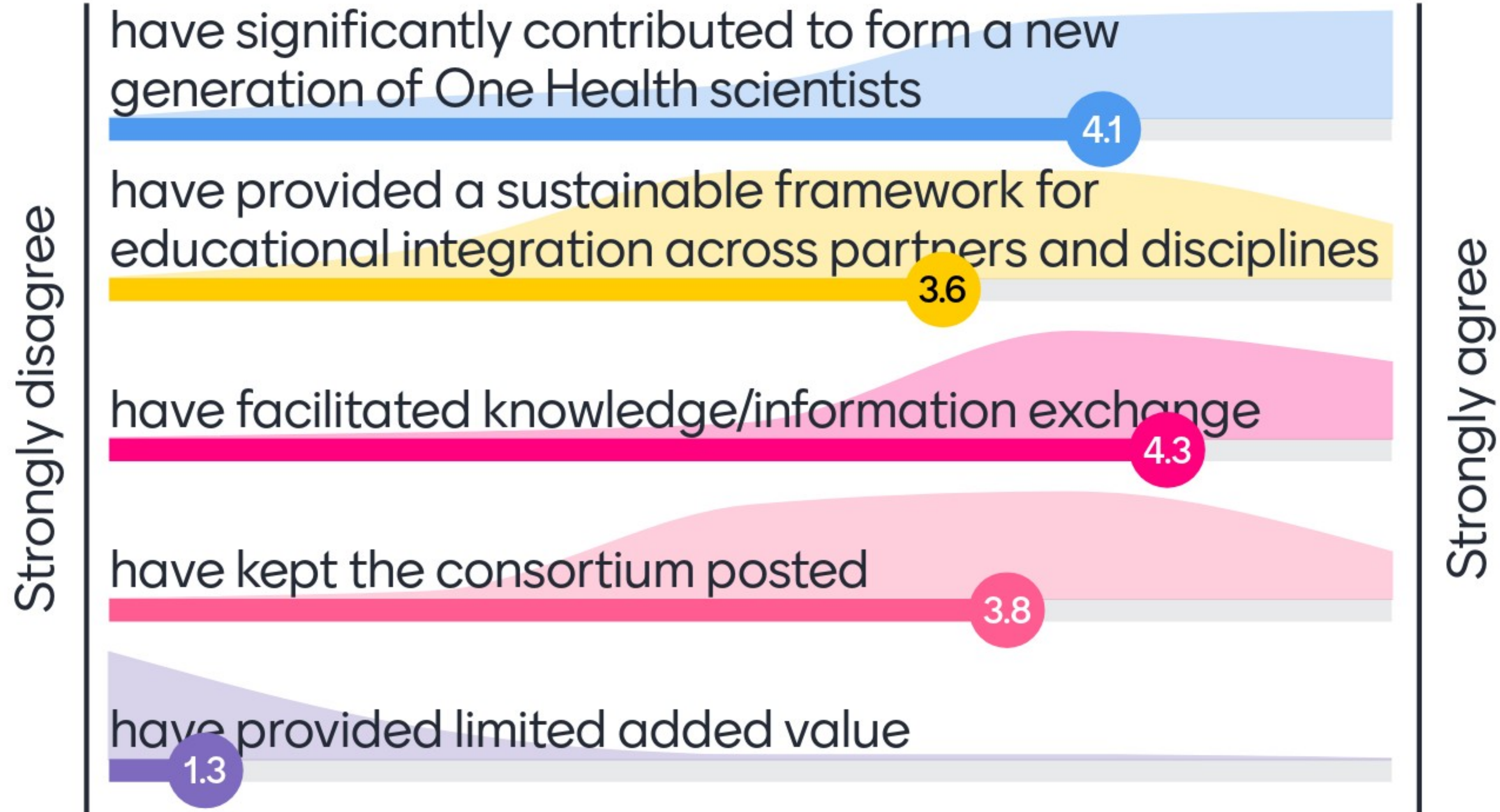


# The integrative activities (JIP)...





# The training and dissemination activities...





# The main legacy from OHEJP



An extended and consolidated international One Health network



A positive learning curve for cross-sectorial collaboration

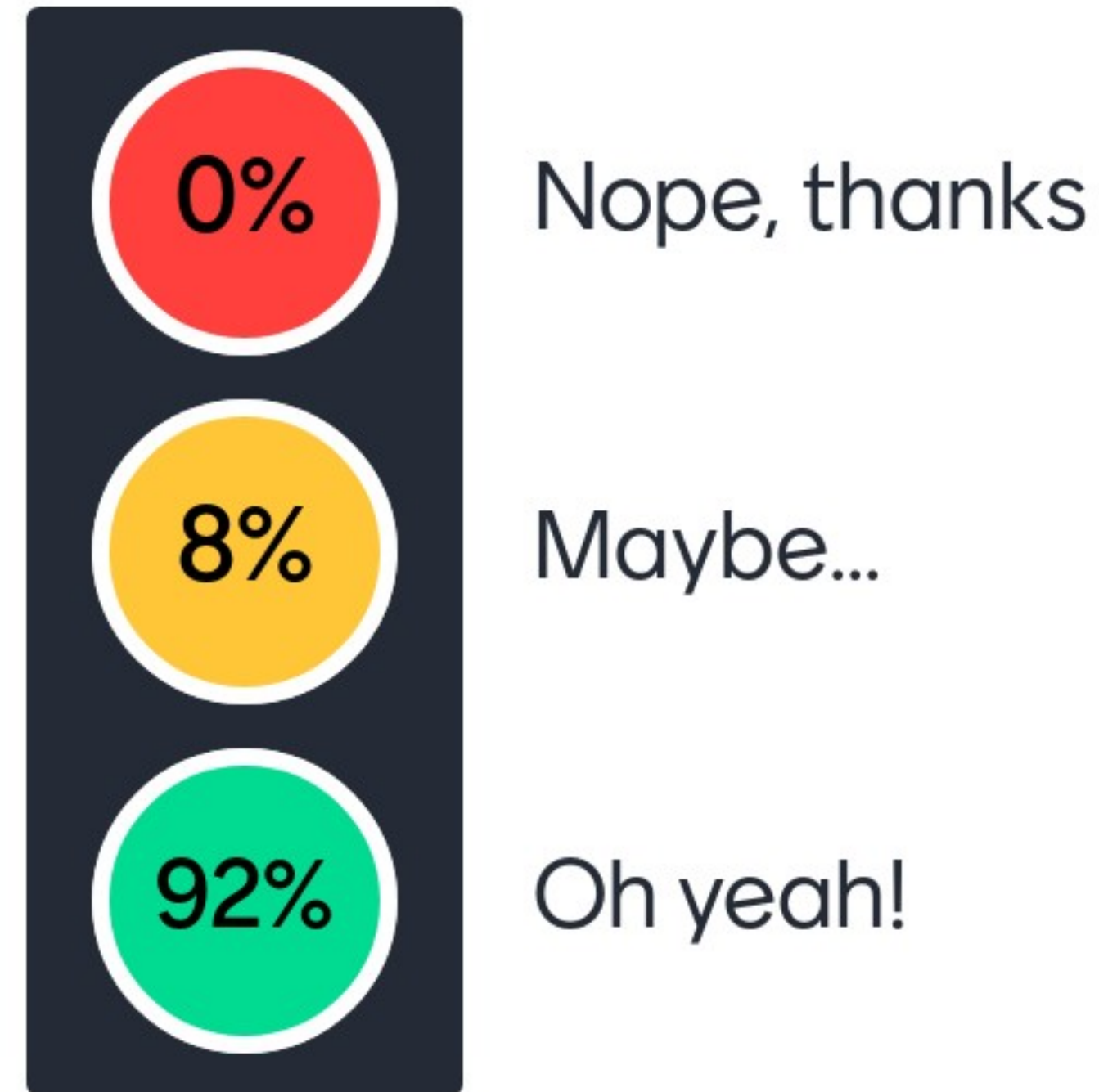


Alignment with national and EU stakeholders



Orientation towards uptake and impact

# I want to be there for OHEJP 2.0!





# What would you like to see in OHEJP 2.0?

