

OHEJP PROJECT OUTCOMES

BeONE

Building Integrative Tools for One Health Surveillance



October 2023

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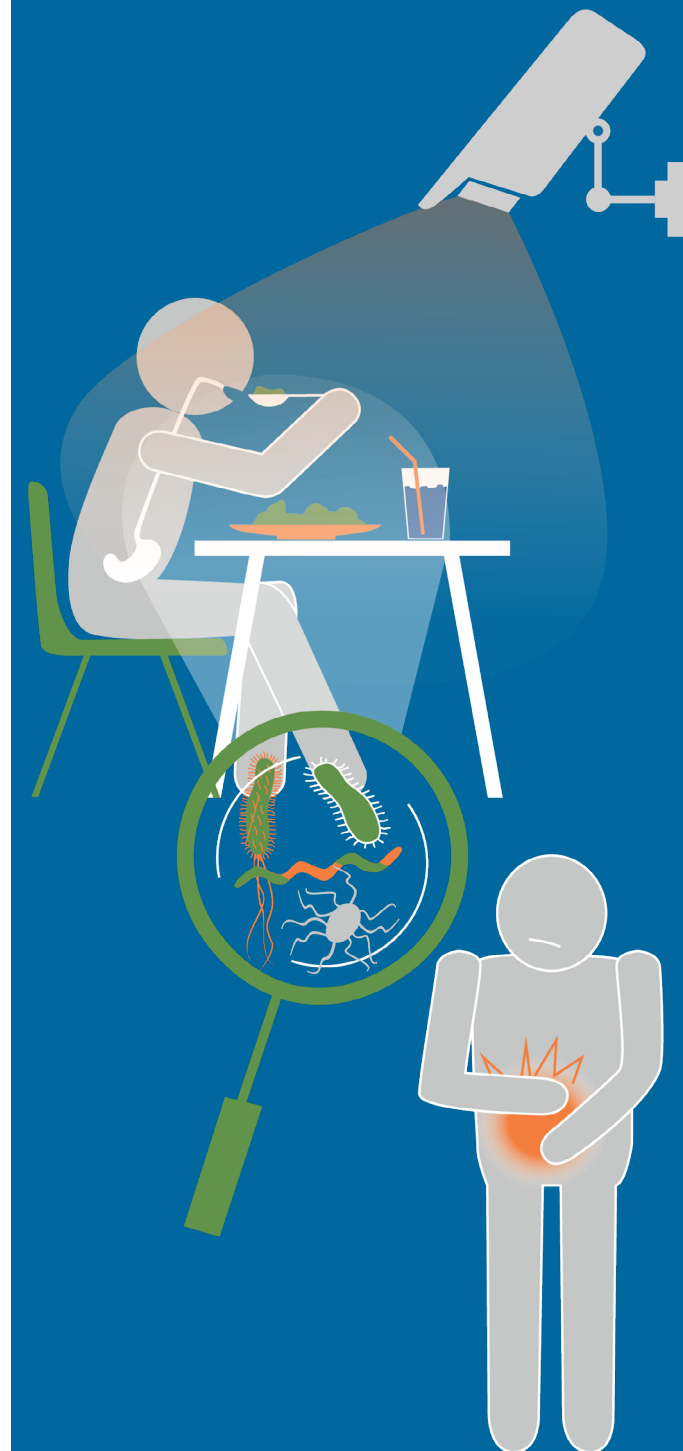
WHAT ARE FOOD AND WATER-BORNE DISEASES? HOW CAN THEIR SURVEILLANCE BE IMPROVED USING A ONE HEALTH APPROACH?

Food and water-borne diseases (FWD), also called foodborne zoonotic diseases, are caused by the consumption of food or drink products contaminated with pathogenic (disease-causing) microorganisms, that enter the body through the gastrointestinal tract ([EFSA – Topics – Foodborne zoonotic diseases](#)). The illnesses are most frequently gastrointestinal but, in some cases, can become more serious or even cause death. The most common pathogens causing FWD are *Campylobacter*, *Salmonella*, *Yersinia*, *Escherichia coli* and *Listeria* (bacterial pathogens; [ECDC Food- and waterborne diseases and zoonoses](#)). FWD are a significant and global public health threat, with over 350,000 human cases reported each year in the European Union ([EFSA – Topics – Foodborne zoonotic diseases](#)).

Systems for disease surveillance collect, analyse, interpret, and disseminate information on the occurrence of disease. The collated information can then be used to make public health decisions, for disease prevention, detection, and control as well as to monitor the evolution of diseases ([sciencedirect.com/topics/medicine-and-dentistry/disease-surveillance](https://www.sciencedirect.com/topics/medicine-and-dentistry/disease-surveillance)). In the European Union (EU), the surveillance of foodborne infections and outbreak detection is primarily handled at the national or regional level, by competent authorities for national food safety and public health. The European Food Safety Authority (EFSA) and the European Centre for Disease Prevention and Control (ECDC) then use the collated data to produce annual summary reports on zoonotic infections and foodborne outbreaks ([EFSA – Topics – Monitoring foodborne diseases](#)). In most countries, several institutions/parties are involved with more or less established collaborations, typically institutions in different sectors (animal/food/human health), as well as across disciplines, such as microbiologists, bioinformaticians, and epidemiologists.

To investigate foodborne outbreaks and pinpoint their source, the most frequently used technique is molecular typing, which identify microorganisms' strains by looking at their genetic material ([EFSA – Molecular typing](#)). Typing-based surveillance and outbreak detection are increasingly being based on [Whole Genome Sequencing](#) (WGS) of bacterial isolates, which offers high-resolution molecular typing through [single nucleotide polymorphism](#) (SNP) or whole genome/core genome [Multi-Locus Sequence Typing](#) analysis. However, despite the use of the same methodology to measure the same underlying genomic variations, inter-laboratory data exchange and comparison still need to be improved because several different [bioinformatic](#) analysis tools and schemes are being employed to analyse the data. A standardised approach is needed with a system set up to facilitate a very flexible level of data sharing, where some data can be easily shared with some (but not all) involved parties, made public or kept completely confidential, and to also give access to real-time analysis and visualisation of combined WGS-based typing data and epidemiological data. The BeONE project developed such a system for sharing data and visualising it in a dashboard.

The One Health EJP uses its unique position to facilitate a collaborative approach between institutes to deliver important multisectoral research and attain optimal health and wellbeing outcomes for humans, animals, and the environment. We bring together 44 acclaimed European scientific institutes and the Med-Vet-Net Association working together on 47 research projects to address potential and existing risks that originate at the animal-human-environment interface.





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WHAT IS THE BEONE PROJECT?

The **BeONE** project involved 13 One Health EJP partners across Europe: Animal Plant Health Protection Agency (**APHA**) and the UK Health Security Agency (**UKHSA**) in the United Kingdom, the Friedrich-Loeffler-Institut (**FLI**), Robert Koch Institute (**RKI**) and German Federal Institute for Risk Assessment (**BfR**) in Germany, the National Institute for Public Health and the Environment (**RIVM**) in The Netherlands, the National Institute of Health Dr Ricardo Jorge (**INSA**) in Portugal, the National Veterinary Research Institute (**PIWET**) in Poland, the Norwegian Institute of Public Health (**FHI**) and Norwegian Veterinary Institute (**NVI**) in Norway, the Statens Serum Institut (**SSI**) and Technical University of Denmark (**DTU**) in Denmark, and the Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise "Giuseppe Caporale" (**IZSAM**) in Italy.

With these partnerships between food safety, human, and animal health institutes, the BeONE project aimed to develop One Health surveillance integrative solutions, where molecular and epidemiological data for foodborne pathogens can be interactively analysed, visualised, and interpreted by experts across disciplines and sectors, thus contributing to a sustainable and more efficient routine surveillance.

At the beginning of the project, the need for decentralised data sharing between multiple partners, as well as a visualisation and standardisation system, was identified.

The BeONE project resulted in tools and outputs that are expected to:

- contribute to the capacity of EU laboratories to carry out routine surveillance integrating both genomic and epidemiological data,
- launch new research lines to improve food and waterborne diseases (FWD) genomic epidemiology, and
- facilitate data sharing and comparability among EU countries, international organisations, 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.





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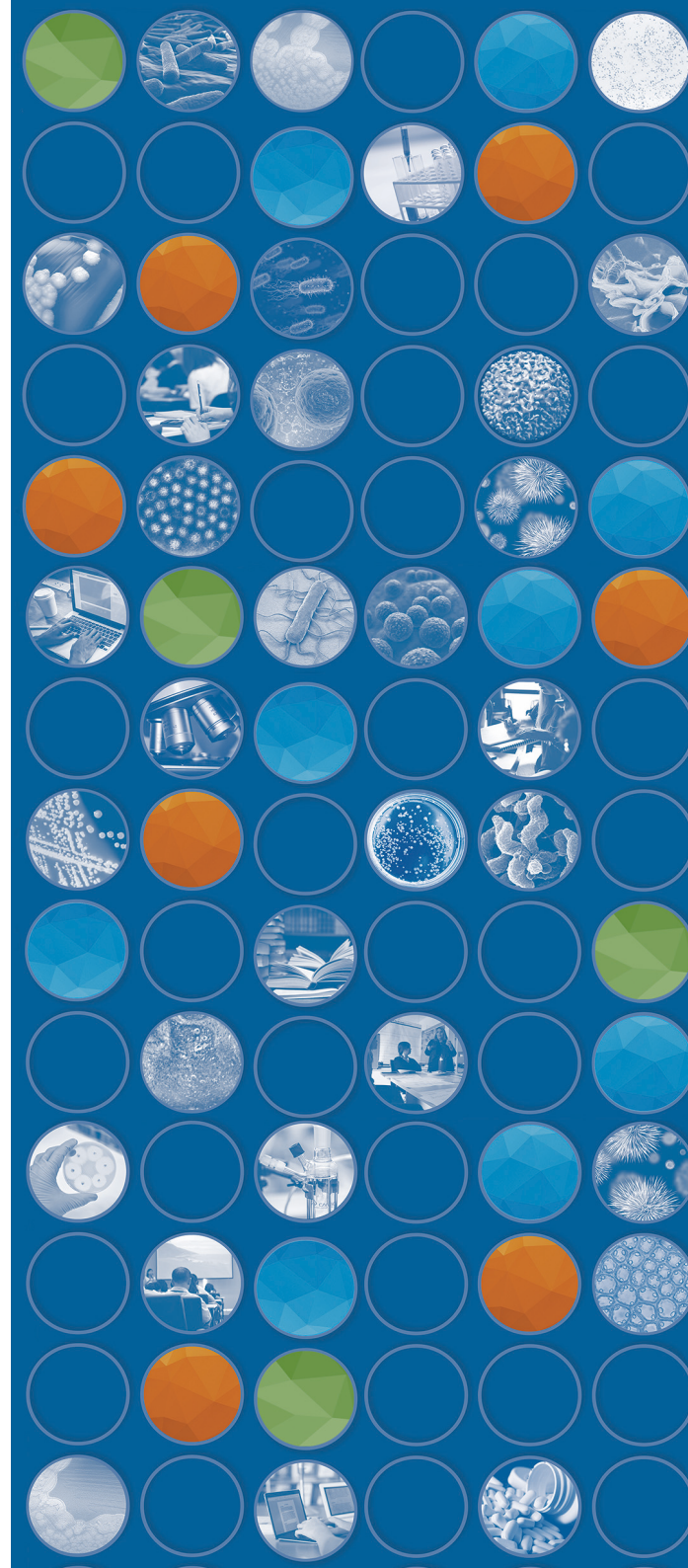
The BeONE project has helped to build a network of experts spanning different sectors to discuss different ways of doing surveillance and how best to share data between different institutes. The project compared different bioinformatics pipelines (set of software algorithms that process and analyse sequencing data) for Whole Genome Sequencing (WGS)-based surveillance, to highlight the comparability of results between different institutes.

The outcome of the pipeline comparison and differences in surveillance setup is important knowledge that can be advantageous for other future developments with One-Health surveillance setups (learn more in [Deliverable 1.3](#)). In collaboration with the [ORION](#) project, BeONE also wrote the [One Health Sequencing for Surveillance Handbook](#) that covers the main technical and practical aspects associated with the application of WGS for foodborne diseases surveillance. This document can be easily understood and applied by laboratory staff starting in the field, helping national and local laboratories to build capacity and competence on the usage of genomics methods for surveillance purposes.

[ReporTree](#), a novel surveillance-oriented bioinformatic tool, was developed by BeONE to strengthen the linkage between genomic and epidemiological data by rapidly identifying genetic clusters (set of genes with a common function) and generating surveillance-oriented reports, in a concept aligned with One Health perspectives. This tool has the potential to contribute to a sustainable and efficient public health genomics-informed pathogen surveillance. This is potentiated by ReporTree standalone open sourced release, as well as by its current integration in the BeONE Datahub/Dashboard and in the [COHESIVE Information System](#), containing solutions that can facilitate and promote (international) data analysis and sharing, cooperation and communication during routine surveillance and outbreak investigation at multi-country and inter-sectoral levels.

A [conceptual model of genomic clustering](#) and a [simulation-based algorithm](#) have been built to help and improve bacterial outbreaks detection and better understand bacterial evolution. These emphasise the need for improvement of the current method used to detect outbreaks (more flexible clustering thresholds), as well as the need for increased cooperation among the One Health sectors. Experimental studies, facilitated by the BeONE solutions, are still required to broaden the understanding of bacterial population dynamics in various niches and food-processing chains.

A harmonised data model, which is interoperable with the EFSA Data Collection Framework catalogues, has also been created by the BeONE project. Using this model and its method of files encryption, samples, and metadata (information about the genomic data) can be shared between different institutes. The [BeONE dashboard](#) has been developed for visualising both sample metadata and a phylogenetic tree (diagram that represents evolutionary relationships among organisms). A datahub has also been developed where it is possible to choose from the shared samples, make a phylogenetic tree based on these samples and visualise them in the dashboard. A server-based web application that can work directly on the database and that launches in interconnection with the





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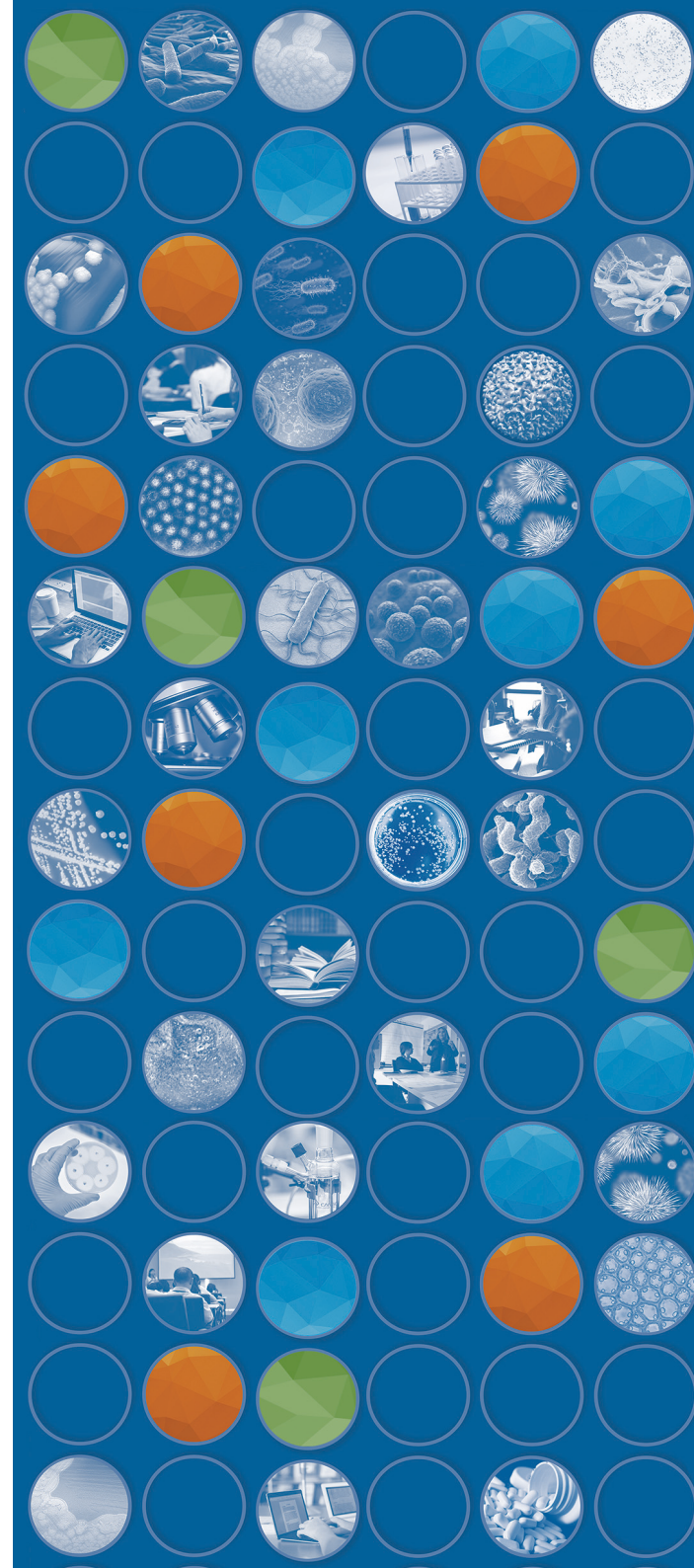


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datahub, can display output data, filter them in tables, geographically localise them on a map and show phylogenetic trees (with clustering data) in the BeONE dashboard.

The BeONE project also compiled datasets of anonymised sequencing reads and genome assemblies for four key bacterial foodborne pathogens: *Listeria monocytogenes*, *Salmonella enterica*, *Escherichia coli*, and *Campylobacter jejuni* ([consultable in Deliverable 1.2](#)). These datasets are expected to potentiate the genetic diversity necessary for certain genomic analyses, thus representing a useful asset in future surveillance- and research-oriented studies.

BeONE enables faster and easier data sharing between different institutes, animal, or human. Two institutes, BfR and FLI, already have had a national pilot for data sharing and they will continue with the data sharing after the end of BeONE. 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.





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Linde, J., Szabo, I., Tausch, S.H., Deneke, C. and Methner, U. (2023). Clonal relation between *Salmonella enterica* subspecies enterica serovar Dublin strains of bovine and food origin in Germany. *Frontiers in Veterinary Science*. 10, 1081611. DOI: <https://www.frontiersin.org/articles/10.3389/fvets.2023.1081611>

Pista, A., Silveira, L., Ribeiro, S., Fontes, M., Castro, R., Coelho, A., Furtado, R., Lopes, T., Maia, C., Mixão, V., Borges, V., Sá, A., Soeiro, V., Correia, C.B., Gomes, J. P., Saraiva, M., Oleastro, M., Batista, R. (2022). Pathogenic *Escherichia coli*, *Salmonella* spp. and *Campylobacter* spp. in Two Natural Conservation Centers of Wildlife in Portugal: Genotypic and Phenotypic Characterisation. *Microorganisms*. 10(11), 2132. DOI: <https://doi.org/10.3390/microorganisms10112132>

Mixão, V., Pinto, M., Sobral, D., Di Pasquale, A., Gomes, J. P. and Borges, V. (2022). ReporTree: a surveillance oriented tool to strengthen the linkage between pathogen genetic clusters and epidemiological data. *Research Square*. PPR552299. DOI: <https://doi.org/10.21203/rs.3.rs-1404655/v2>

Dahl, L.G., Joensen, K.G., Østerlund, M.T., Kiil, K., Møller Nielsen, E. (2021). Prediction of antimicrobial resistance in clinical *Campylobacter jejuni* isolates from whole-genome sequencing data. *European Journal of Clinical Microbiology and Infectious Diseases*. 40, 673–682. DOI: <https://doi.org/10.1007/s10096-020-04043-y>

And four more publications are under preparation.



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Each of the One Health EJP projects creates a unique Europewide network of institutes with wide-ranging expertise to achieve objectives using a cohesive One Health approach. We bring together scientific communities with expertise in medical, veterinary, and environmental health, and use integrated approaches to solve complex global issues.

The One Health EJP BeONE project worked collaboratively to achieve its aims and to produce impactful scientific outcomes, which may benefit scientists and policymakers worldwide.

- **Animal Plant Health Protection Agency (APHA), United Kingdom**
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Sofie Holtsmark Nielsen, Katrine Grimstrup Joensen, Finn Gruwier Larsen, Kristoffer Kiil, Eva Litrup, Karen Loaiza Conza, Anne Sophie Majgaard Uldall, Lars Eivind Bustamante Christoffersen, Man-hung Eric Tang, Povilas Matuskevicius, Laura Espenhain, Stefano Cardinale
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