COllaborative **M**anagement **P**latform for detection and **A**nalyses of (**R**e-) emerging and foodborne outbreaks in **E**urope


mpare

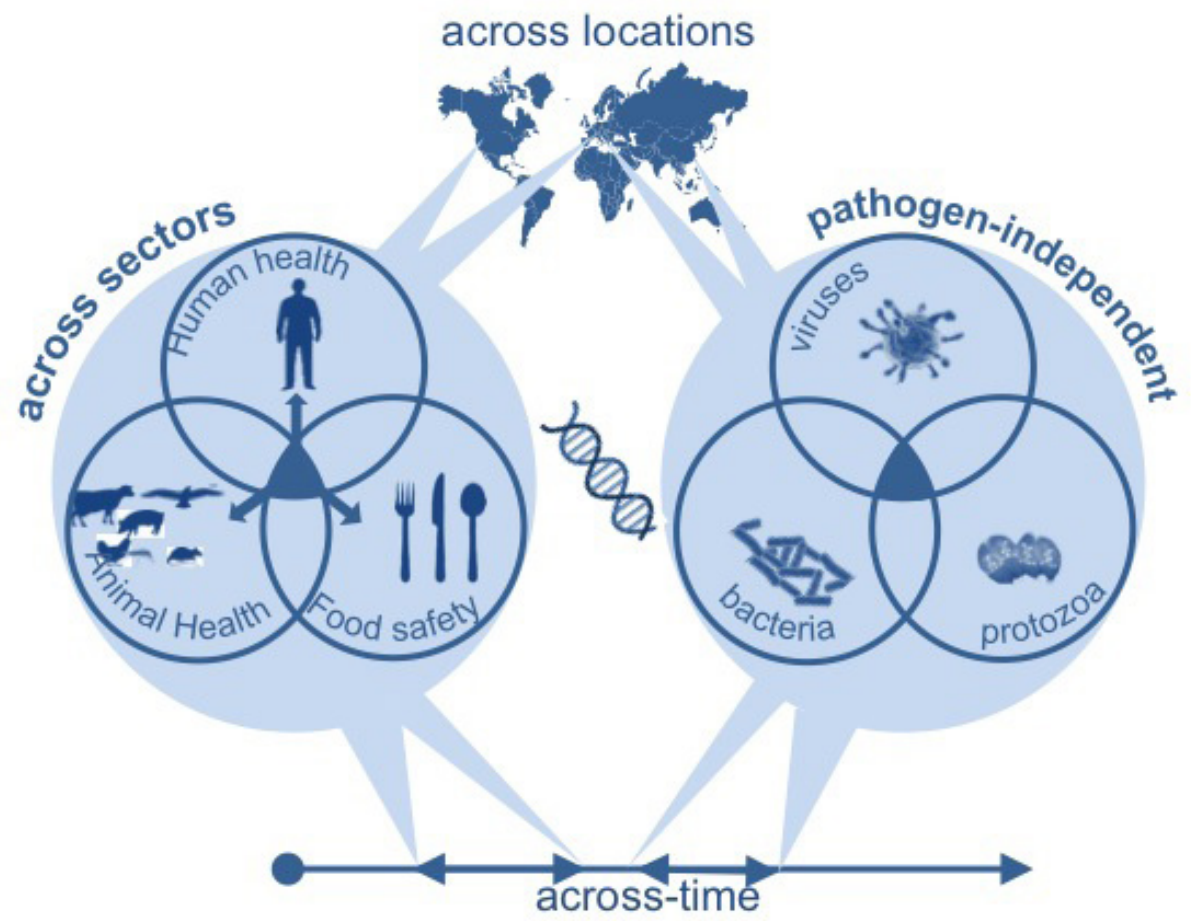

Figure 1. Genomic information as the pathogen-independent language across locations, sectors and time.

Objectives

- To improve rapid identification, containment and mitigation of emerging infectious diseases and foodborne outbreaks,
- To develop a cross-sector and cross-pathogen analytical framework and globally linked data- and information-sharing platform,
- To integrate state-of-the-art strategies, tools, technologies and methods for collecting, processing and analysing sequenced-based pathogen data in combination with associated data (clinical, epidemiological, and other), and
- To generate actionable information for relevant authorities and other users in the human health, animal health and food safety domains.

Abstract

COMPARE aims to harness the rapid advances in molecular technology to improve identification and mitigation of emerging infectious diseases and foodborne outbreaks. To this purpose, COMPARE will establish a “One serves all” analytical framework and data exchange platform that will allow real-time analysis and interpretation of sequence-based pathogen data in combination with associated data (e.g. clinical, epidemiological data) in an integrated inter-sectorial, inter-disciplinary, international “One Health” approach. The framework will link research, clinical and public health organisations active in human health, animal health, and food safety in Europe and beyond, to develop

- integrated risk assessment and risk-based collection of samples and data,
- harmonised workflows for generating comparable sequence and associated data,
- state-of-the-art analytical workflows and tools for generating actionable information for support of patient diagnosis, treatment, outbreak detection and investigation, and
- risk communication tools.

The analytical workflows will be linked to a flexible, scalable and open-source data and information platform supporting rapid sharing, interrogation and analysis of sequence-based pathogen data in combination with other associated data. The system will be linked to existing and future complementary systems, networks and databases such as those used by ECDC, NCBI and EFSA. The functionalities of the system will be tested and fine-tuned through underpinning research studies on priority pathogens covering healthcare-associated infections, foodborne disease, and (zoonotic) (re-) emerging diseases with epidemic or pandemic potential. Throughout the project, extensive consultations with future users, studies into the barriers to open data sharing, dissemination and training activities and studies on the cost-effectiveness of the system will support future sustainable user uptake.

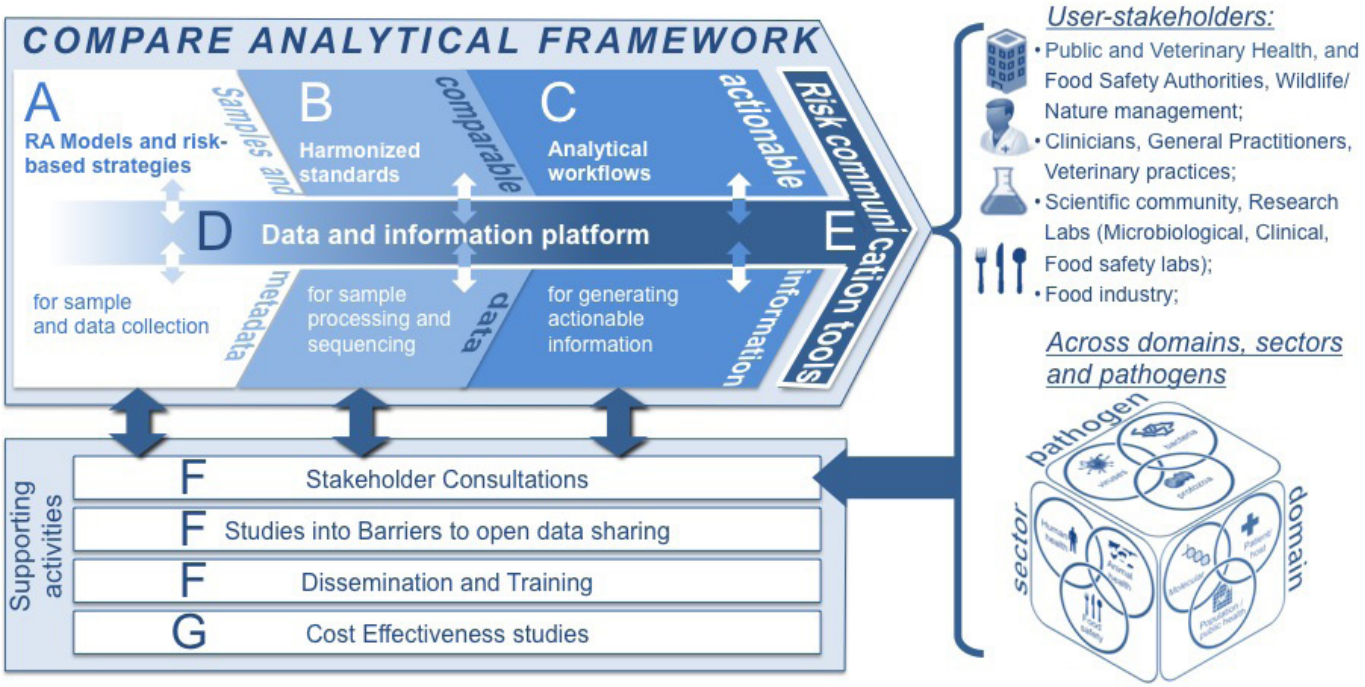

Figure 2. The COMPARE analytical framework and its main components from sample and data collection to generating actionable information for stakeholders in the human, animal and food sectors.

The COMPARE diagram

From Figure 2, we can see how the COMPARE project has been developed to serve multiple stakeholders across domains, sectors and pathogens. The text below describes the various components of the project.

A. **Risk-assessment models and risk-based sampling and data collection strategies** that enhance our capacity to detect potential disease outbreaks.

B. **From samples and associated metadata to comparable data**: harmonised standards for sample processing and sequencing to obtain high quality and comparable sequence data from metadata associated with a specimen.

C. **From comparable data to actionable information**: designing analytical workflows for turning *comparable data* into *actionable information* for addressing questions in frontline diagnostics, foodborne infections and (re-) emerging infections. “Actionable Information” is defined as information that enables users generating/receiving this information to take well-informed decisions and actions in pursuit of

- *Pathogen identification and characterization*: Pathogen identification, genotyping and phenotyping, (e.g., detection of relevant antimicrobial resistance, virulence, epidemiological markers);
- *Outbreak detection:* Detection of putative clusters by examining strain-specific clusters in time, place and host (person, animal and food);
- *Outbreak investigation*: Rapid interrogation for given molecular strains to identify the potential origin of internationally distributed clones that may result in outbreaks; analysis tools to monitor the extent of spread based on sequence diversity in relation to control measures;
- *Outbreak prediction*: Automatic analyses for predicting risk of emergence of pathogens with outbreak potential.

D. **Designing and building a common data and information platform supporting rapid sharing, integration and analysis of sequence-based pathogen data in combination with other contextual metadata**: the system will be linked to existing and future complementary systems, networks and databases such as those used by ECDC, NCBI and EFSA.

E. **Risk communication tools** will be developed enabling authorities in the human and animal health and food safety sectors to effectively communicate the results obtained with the new analytical workflows.

F. The development of the analytical framework is underpinned by a set of supporting research, dissemination and communication activities promoting the acceptance of the system and its components. These activities encompass (i) **consultations with our stakeholders** serving on expert advisory panels throughout the project to maintain a prominent focus on user needs, (ii) **studies on the barriers** (ethical, regulatory, administrative, logistical, political) to the implementation and widespread use of open-date sharing platforms, and (iii) **dissemination and training activities.**

G. COMPARE will include the development of a framework for estimating the **cost-effectiveness of the COMPARE system, including the value of safety**.

WP1—Risk assessment and risk-based strategies for sample and data collection

WP leader: Emma Snary, DEFRA/APHA (10) Emma.Snary@apha.gsi.gov.uk
co-leader: Christian Gortazar, UCLM (18) Christian.Gortazar@uclm.es

Overall task: To develop risk assessment models and risk-based sampling and data collection strategies for NGS-based analyses of foodborne and (re-) emerging infections.

1. To develop methodology for risk assessment including NGS outputs:

    1.1 To develop a generic and spatial risk assessment framework to identify which regions and species are at an increased risk of incursion and further spread of novel pathogens.

    1.2 To develop a generic food chain risk assessment framework based on NGS data.

    1.3 To develop tools for epidemiological transmission modeling and rapid spatial risk assessment.

2. To develop risk-based sampling and data collection strategies for early detection and investigation of unusual patterns of infectious disease outbreaks:

    2.1 To develop risk-based sampling algorithms and protocols for unusual clinical symptoms in humans and domestic animals in medical and veterinary practice.

    2.2 To developed risk-based sampling algorithms and protocols for early detection of emerging and re-emerging infections coming from wild or feral animals.

    2.3 To develop risk-based sampling algorithms and protocols for detection of human pathogen circulation in the absence of recognized illness.

    2.4 To develop food-level sampling strategies for surveillance as well as foodborne outbreak investigation.

Deliverables
D1.1 Automated tools for rapid assessment of key transmission parameters and rates of spread estimates (M24)
D1.2 Risk-based surveillance plans, sampling algorithms and protocols for surveillance of emerging and foodborne diseases and pathogens not covered by existing surveillance (M40)
D1.3 Generic risk assessment framework to target surveillance activities and outbreak investigations (M46)

Milestones
MS6 Common protocol drafted with target pathogens and transmission modes for WP1 and WP5 model development, 10 - DEFRA (M12)
MS7 Inventory of existing sampling and storage protocols completed, 10 - DEFRA (M12)

WP2—Harmonised standards for sample processing and sequencing

WP leader: Martin Beer, FLI (4) martin.beer@fli.bund.de
co-leaders: Simone Caccio, ISS (8) & Paul Kellam, WTSI (29)
simone.caccio@iss.it, pk5@sanger.ac.uk

Overall task: To develop harmonized analytical workflows for generation of high-quality NGS data in combination with relevant metadata for pathogen detection and typing across sample types, pathogens and domains.

1. To optimize and harmonize sample handling for NGS and related methods.

2. To develop standardized protocols for sample processing for different sample types and viruses, bacteria and parasites.

3. To develop standardized sequencing protocols for the different pathogens as well as for different purposes (surveillance, diagnostics, single isolates, metagenomics).

4. To improve sequence analyses, including novel bioinformatics tools for metagenomics, isolate typing, and de novo reference-less identification of pathogen-related sequences.

5. To develop sequence curation and storage protocols and tools.

6. To develop historic and prospective biobanks as reference.

7. To develop a scheme for ring trials and external quality assurance systems.

Deliverables
D2.1 Matrix-dependent sample handling protocols for human, animal, wildlife/vectors and food samples (M12)
D2.2 Standard protocol for sample processing (M24)
D2.3 Sequencing workflow including relevant NGS platforms (M36)
D2.4 Evaluated and documented data analysis pipeline (M24 and onwards)
D2.5, D2.6, D2.7 Testing results of molecular analytical workflow in ring trials with reference materials (M36, M48, M60)

Milestones
MS10 Performance of available sequencing platforms and protocols for COMPARE study questions reviewed, 4 - FLI (M18)
MS15 Set of core specimens prepared to be used as controls across consortium for assay comparison, 4 - FLI (M30)

WP3—From comparable data to actionable information: Analytical workflows for frontline diagnostics

WP leader: Surbhi Malhotra, UA (14) surbhi.malhotra@uantwerpen.be
co-leaders: Menno de Jong, AMC (13) & Anne Pohlmann, FLI (4)
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Overall task: To develop an analytical workflow for the use of single isolate and metagenomic NGS in human and veterinary clinical microbiology.

1. To develop general workflows for integration of NGS in clinical laboratory diagnostics.

2. To develop a framework for prediction of phenotypic antimicrobial susceptibility based on the presence or absence of genes and mutations in sequence data.

3. To develop tools for identification of hospital clusters and nosocomial transmission.

Deliverables
D3.1 Analytical workflow for clinical diagnostic application (M18)
D3.2 Prediction algorithm for antimicrobial resistance markers in sequence data (M24)
D3.3 Standardized protocols for detection of clusters of healthcare-associated infections (M42)

Milestones
MS10 Performance of available sequencing platforms and protocols for COMPARE study questions reviewed, 4 - FLI (M18)
MS17 Review completed of known genetic markers for virulence and resistance for target pathogens in WP3 and WP5, 14 - UANTWERP (M30)

WP6—Underpinning research: Frontline diagnostics using the COMPARE analytical framework

WP leader: Surbhi Malhotra, UA (14) surbhi.malhotra@uantwerpen.be
co-leaders: Menno de Jong, AMC (13) & Anne Pohlmann, FLI (4)
m.d.dejong@amc.uva.nl, anne.pohlmann@fli.bund.de

Overall task: To assess feasibility of NGS/WGS/WCS for clinical diagnostic use and hospital epidemiology.

1. To validate application of NGS for diagnostics and hospital epidemiology.

2. To test feasibility of NGS for prediction of antimicrobial resistance phenotype to guide treatment.

3. To evaluate the use of NGS for syndromic surveillance based on data from hospitalized patients.

Deliverables
D6.1 Report on NGS based diagnostics in comparison to gold standard methods (M42)
D6.2 Report on WGS and NGS based detection of antimicrobial resistance in stool samples in patients and traveler (M50)
D6.3 Reports on WGS and NGS for syndromic surveillance (M60)

Milestones
MS15 Set of core specimens prepared to be used as controls across consortium for assay comparison, 4 - FLI (M30)
MS19 Validation protocol for NGS based clinical and public health diagnostics, 14 - UANTWERP (M36)

WP4—From comparable data to actionable information: Analytical workflows for foodborne pathogen surveillance, outbreak detection and epidemiological analysis

WP leader: Eva Møller Nielsen, SSI (3) emn@ssi.dk
co-leaders: Tine Hald, DTU (1) & Anne Brisabois, ANSES (5)
tiha@food.dtu.dk, anne.brisabois@anses.fr

Overall task: To develop a general analytical workflow for population-based disease surveillance, outbreak detection and epidemiological modeling of foodborne infections.

1. To develop cross-sector and cross-pathogen methods for sequence-based surveillance for foodborne pathogens.

1.1. To develop an analytical framework for routine sequence-based surveillance of current priority pathogens.

2. To develop cross-sector and cross-pathogen methods and tools to support outbreak detection, outbreak investigations and epidemiological analysis.

2.1. To develop a framework for the application of the developed NGS and analysis tools in the epidemiological handling of and response to foodborne outbreaks in Europe.

2.2. To develop tools for source attribution based on NGS-based routine surveillance and outbreak data for foodborne pathogens (DTU).

Deliverables
D4.1 Reference sequence database based on already available datasets (M6)
D4.2 Algorithm for detection of informative (sub)types for epidemiological analysis and RA for the main foodborne pathogens (M32)
D4.3 Analytical workflow for epidemiological handling of and response to foodborne outbreaks in Europe (M48)
D4.4 Validated SA model for NGS data (M48)

Milestones
MS16 Inventory of available cluster detection algorithms finalized, 3 - SSI (M30)

WP7—Underpinning research on food outbreaks using the COMPARE analytical framework

WP leader: Eva Møller Nielsen, SSI (3) emn@ssi.dk
co-leaders: Tine Hald, DTU (1) & Anne Brisabois, ANSES (5)
tiha@food.dtu.dk, anne.brisabois@anses.fr

Objectives:

- To establish robust analytic procedures of NGS/WGS data for *Salmonella*, STEC/EHEC, *Listeria,* norovirus, hepatitis A, and *Cryptosporidium* to be able to identify epidemiologically linked isolates and differentiate these from similar unrelated isolates.
- To develop guidelines for interpretation criteria for defining clusters of disease and linking of isolates from various sources and reservoirs.
- To enable backward compatibility to important previous nomenclature (e.g. serotypes, species, MLST).
- To perform pilot studies in collaboration with global partners and networks including ECDC and EFSA.

In collaboration with WPs 3, 4 and 5:

- To evaluate analysis tools developed in WP3 and WP5 to predict phenotypic traits such as antimicrobial resistance, invasiveness and virulence.
- To improve the evolutionary reconstruction of the organisms and thus provide a rational framework for investigations into the population structure, genetic diversity, epidemiology and transmission and identification of spatial-temporal clusters.
- To provide the input for the epidemiological, source attribution and risk assessment models developed in WP4.

Deliverables
D7.1 Database of reference genomes of an epidemiologically relevant selection of each of the foodborne organisms in the pilot (M16)
D7.2 Report on NGS comparison between NGS-based analysis and reference methods for cluster detection for all pilot organisms (M36)
D7.3 Database of markers for host-association and ecophysiology (M36)
D7.4 Improved guidelines for interpretation criteria for defining clusters of disease and linking of isolates from various sources and reservoirs (M48)

Milestones
MS15 Set of core specimens prepared to be used as controls across consortium for assay comparison, 4 - FLI (M30)
MS19 Validation protocol for NGS-based clinical and public health diagnostics, 14 - UANTWERP (M36)
MS20 List of samples and metadata for WP7 studies finalized, based on task 1 criteria, 3 - SSI (M36)

WP5—From comparable data to actionable information: Additional tools for detection of and response to (re-) emerging infections

WP leader: Ron Fouchier, EMC (2) r.fouchier@erasmusmc.nl
co-leader: Mark Woolhouse, UEDIN (11) mark.woolhouse@ed.ac.uk

Overall task: To develop cross-sector and cross-pathogen methods for support of emerging pathogen identification and characterization in support of outbreak investigations and epidemiological analysis.

1. To develop an analytical framework for detection of (re-) emerging pathogens in metagenomic datasets.

2. To develop tools for rapid sequence-based detection of strain-specific clusters in time, place and host for the main emerging pathogen classes.

3. To develop tools for fast and robust phylogenetic and phylogeographic analysis.

4. To develop tools for detecting single nucleotide polymorphisms in pathogen NGS data.

5. To improve the prediction of phenotype changes related to antigenicity, drug-resistance, virulence, transmission, and other traits from nucleotide sequence data.

Deliverables
D5.1 Update of pathogen repositories for pilot and research studies (M18)
D5.2 Tools for rapid sequence-based detection of strain specific clusters in time, place and host for the main emerging pathogen classes (M30)
D5.3 Phylogenetic and phylogeographic tools for epidemiological investigations and rapid risk assessment (M30)
D5.4 Tools for detecting single nucleotide polymorphisms and analyses within and between hosts (M36)
D5.5 Methods for prediction of pathogen phenotype from genotype data and structure models (M42)

Milestones
MS6 Common protocol drafted with target pathogens and transmission modes for WP1 and WP5 model development, 10 - DEFRA (M12)
MS17 Review completed of known genetic markers for virulence and resistance for target pathogens in WP3 and WP5, 14 - UANTWERP (M30)

WP8—Underpinning research: Novel approaches to (re-) emerging disease detection and outbreak response using the COMPARE analytical framework

WP leader: Ron Fouchier, EMC (2) r.fouchier@erasmusmc.nl
co-leader: Mark Woolhouse, UEDIN (11) mark.woolhouse@ed.ac.uk

Objectives:

1. To develop and pilot early detection and surveillance of enteric pathogens and genes through strategic sampling and metagenomic analysis.

2. To develop and pilot ”hot-spot” based syndromic surveillance in animals and humans.

3. To develop and pilot early detection of surveillance of emerging zoonoses from the wildlife reservoir through strategic sampling and metagenomic analysis.

4. To develop and pilot early detection of changes in pathogen traits enhancing the risk for outbreaks and pandemic.

Deliverables
D8.1 NGS sequencing data on influenza A viruses, coronaviruses, pestiviruses, and hepaciviruses from various hosts (M36)
D8.2 Identification of key drivers of evolution of influenza A viruses, coronaviruses, pestiviruses and hepaciviruses in relation to virus emergence (M56)
D8.3 Report on results of pilot study of metagenomic pathogen detection e.g. in stool samples from healthy travelers, before and after travel (M60)

Milestones
MS13 Joint protocol for WP8 task 1 studies, 2 - Erasmus MC (M24)
MS21 Protocol for wildlife surveillance and sampling submitted to pilot sites, 2 - Erasmus MC (M36)
MS22 Review of pathogen traits associated with enhanced transmissibility completed, 2 - Erasmus MC (M36)

WP9—COMPARE data and information platform

WP leader: Guy Cochrane, EMBL (7) cocharne@ebi.ac.uk
co-leaders: Ole Lund, DTU (1) & Istvan Csabai, WIGNER (24)
lund@cbs.dtu.dk, csabai.istvan@wigner.mta.hu

Objectives:

- To create and operate the COMPARE Data Resource, workflow engine and portal.
- To create user spaces for COMPARE workflow development and pilot projects.
- To ensure the long-term sustainability of the tools developed and data generated.

An important barrier to routine application of NGS/WGS/WCS of pathogens in clinical and public health laboratories is the current capacity for bio-informatics and data management. This "big data" challenge has been recognized internationally, and calls for new solutions for data storage and rapid sharing that will be capable of handling the expected massive increase in data in the coming years. Here, we develop and pilot the core infrastructure for such future routine applications, building from the existing European ICT infrastructure that has served the needs of the wider research and public health community for the past 30 years, but linking this to frontline developments in bioinformatics and NGS/WGS/WCS. The system will support the spectrum of sequence-based analyses of relevance to pathogen detection and characterization, surveillance, outbreak detection and investigation, from single locus approaches, through whole genome methods to metagenomics studies. Data types will include contextual metadata, primary data (sequence reads), and derived data (such as genomic alignments of reads, assemblies and functional annotation). Supporting the public health, clinical, research and tools development communities, the system will be scalable and sustainable beyond the duration of funding for COMPARE. Full technical specifications will be provided to allow the system to be replicated in alternative hardware infrastructures according to future need and capacity.

Deliverables
D9.1 Hardware and cloud environment infrastructure (M12)
D9.2 COMPARE registry and data ressource component, including input and output APIs, supporting read, alignment, assembly and annotation data types (M18)
D9.3 Generic workflow engine supporting assembly and functional annotation workflows (M36)
D9.4 Integrated analytical workflows from WPs 2, 3, 4 and 5 (M48)
D9.5 Full technical specifications and publication submission (M60)

Milestones
MS8 Hardware cloud environment ready, 7 - EMBL (M12)
MS12 COMPARE registry and data ressource component ready, 7 - EMBL (M18)
MS25 Workflows from WPs 2,3,4 and 5 integrated into COMPARE platform, 7 - EMBL (M48)

WP10—COMPARE risk communication tools

WP leader: Emilio Mordini, RT (26) emilio.mordini@responsibletechnology.eu

Overall task: To design and develop appropriate risk communication tools and strategies for stakeholders involved in the process, as well as a set of management tools for authorities to handle uncertainties and available options according to the input received through the COMPARE system.

- Stakeholder analysis
- Targeted messages
- COMPARE risk communication tool box (CRCT box)

Deliverables
D10.1: Stakeholder Analysis Report including a comprehensive database, with stakeholder characteristics (M12)
D10.2: Targeted Message Report describing for each main stakeholder category timing and contents of an effective message and potential gaps or barriers in the risk communication processes (M24)
D10.3: Initial version COMPARE Risk Communication Tool box V1 (crct box V1) (M36)
D10.4: Beta version COMPARE Risk Communication Tool box V2 integrated and interoperable with the COMPARE platform (crct box V2) (M48)

Milestones
MS14 First version COMPARE RCT live, 26 - Responible Technology SAS (M24)
MS23 Beta version COMPARE RCT live, 26 - Responible Technology SAS (M36)

WP11—User consultations

WP leader: Marion Koopmans, EMC (2) m.koopmans@erasmusmc.nl
co-leader: Frank Aarestrup, DTU (1) fmaa@food.dtu.dk

Overall task: To design the COMPARE systems' analytical workflow and its main components based on the expert inputs and associated information needs of its intended future users and other stakeholders working in human, animal and wildlife health and food safety.

Deliverables
D11.1 Combined EAP report 1st cycle (M3)
D11.2 Combined EAP report 2nd cycle (M12)
D11.3 Combined EAP report 3rd cycle (M24)
D11.4 Combined EAP report 4th cycle (M36)
D11.5 Combined EAP report 5th cycle (M48)

Milestones
MS3 When all EAPs have been formally installed, 2 - Erasmus MC (M3)
MS4 When first EAP report is finished, 2 - Erasmus MC (M3)

WP12—Barriers to open data sharing

WP leader: George Haringhuizen, RIVM (9) george.haringhuizen@rivm.nl
co-leader: Jørgen Schlundt, DTU (1) jors@dtu.dk

Overall task: To identify, clarify and, as far as feasible, develop practical solutions for Political, Ethical, Administrative, Regulatory and Legal (PEARL) barriers that hamper the timely and openly sharing of data through COMPARE.

Deliverables
D12.1 Report on the legal limitations, conditions and obligations in open data sharing (task 2) (M24)
D12.2 Ethical framework and charter of principles for sharing of NGS data on European level (M48)
D12.3 Final report and recommendations on data-sharing guidelines (task 4), (M56)

Milestones
MS3 When all EAPs have been formally installed, 2 - Erasmus MC (M3)

WP13—Dissemination and training

WP leader: Frank Aarestrup, DTU (1) fmaa@food.dtu.dk
co-leader: Marion Koopmans, EMC (2) m.koopmans@erasmusmc.nl

Overall task: To ensure that relevant stakeholders of COMPARE are adequately informed about COMPARE's progress and results and have access to the training they need in order to apply the harmonized workflows, analytical tools and data resources developed and implemented by COMPARE in their pathogen detection and outbreak response activities.

Deliverables
D13.1 Stakeholder contact database (continuously updated) (M3)
D13.2 Leaflet and templates for promotional material in COMPARE corporate style (M3)
D13.3 COMPARE public website (M3)
D13.4 e-learning materials (continuously updated) (M12)
D13.5 COMPARE workshop programme (10 planned, continuously updated) (M12)
D13.6 COMPARE acknowledged publications and presentations (M60).

Milestones
MS5 When the COMPARE public website is live, 1 - DTU (M3)
MS7 When the first COMPARE workshop has been held, 1 - DTU (M12)

WP14—Cost-effectiveness framework

WP leader: Werner Brouwer, EUR (22) brouwer@bmg.eur.nl
co-leader: Nicholas McSpedden-Brown, CIVIC (25)
mcspeddenbrown@civic-consulting.de

Overall task: To develop a standardised framework for estimating the cost-effectiveness of the COMPARE system and related methods and tools, including the value of safety.

1. To identify the important elements in calculating costs and benefits of COMPARE and related methods and tools (both regarding the system itself and from a societal perspective).

2. To identify and, where necessary, develop state-of-the-art costing methodologies for the different elements in the framework.

3. To develop and apply a methodology to value safety (provided through rapid identification of pathogens through COMPARE) in several countries.

4. Using 1-3, to estimate the cost-effectiveness of COMPARE and related methods and tools using case studies.

5. Based on the results, to assess options for refining selected elements of COMPARE in view of improving the overall cost-effectiveness of the system.

Deliverables
D14.1 Framework for assessing cost-effectiveness of COMPARE in which key costs and benefits are highlighted. This will include a section on the system itself and on the wider framework (M18)
D14.2 State-of-the-art methodologies for the measurement and valuation of the elements specified in the framework. This will include a section on the system itself and on the wider framework (M30)
D14.3 A scientific paper describing the methodology and results of estimating the value of safety, with the results from several European countries (M45)
D14.4 Report on the (potential) cost-effectiveness of COMPARE, based on the case studies (scenario/pilot/retrospective studies). Each case study presented will include a section on elements related to the system and on the wider framework (M54)
D14.5 A report on the assessment of options for refining selected elements of COMPARE in view of improving the overall cost-effectiveness of the system, with recommendations (M60)

Milestones
MS11Cost Effectiveness Framework ready, 22 - EUR (M18)
MS18 Methodologies report ready, 22 - EUR (M30)
MS24 Safety data collected and analysed, 22 - EUR (M40)
MS26 CE study COMPARE reported, 22 - EUR (M54)

WP15—Management

WP leader: Frank Aarestrup, DTU (1) fmaa@food.dtu.dk
co-leader: Marion Koopmans, EMC (2) m.koopmans@erasmusmc.nl

Overall task: To implement the appropriate organizational structures and processes to ensure COMPARE's compliance to the EC Grant Agreement and the COMPARE Consortium Agreement (CA).

- To maintain the COMPARE CA.
- To implement the project management structure and decision-making processes as agreed in the DoW and CA.
- To coordinate the financial-administrative processes at project level.
- To coordinate the ethics management at project level.
- To coordinate the management of intellectual property at project level.

Deliverables
D15.1 Consortium Agreement (M0)
D15.2 Project Management manual (M2)
D15.3 Internal reporting templates (M2)
D15.4 Plan for the Dissemination and Exploitation of Results (M6)

Milestones
MS1 When the CA has been signed by all partners, 1 - DTU (M1)
MS2 GA and EB formally installed, 1 - DTU (M1)

Project-month calendar

Project month	Calendar month	Project month	Calendar month
Month 1	Dec 2014	Month 33	Aug 2017
Month 3	Feb 2015	Month 36	Nov 2017
Month 6	May 2015	Month 39	Feb 2018
Month 9	Aug 2015	Month 42	May 2018
Month 12	Nov 2015	Month 45	Aug 2018
Month 15	Feb 2016	Month 48	Nov 2018
Month 18	May 2016	Month 51	Feb 2019
Month 21	Aug 2016	Month 54	May 2019
Month 24	Nov 2016	Month 57	Aug 2019
Month 27	Feb 2017	Month 60	Nov 2019
Month 30	May 2017		

Reporting dates

Reporting period	Months	Reports	Due date
RP1	1—18	Periodic Technical/ Financial Reports	Month 20/July 2016
RP2	19—36	Periodic Technical/ Financial Reports	Month 38/Jan 2018
RP3	37—54	Periodic Technical/ Financial Reports	Month 56/July 2019
RP4	55—60	Periodic Technical/ Financial Reports	Month 62/Jan 2020
Final		Final Technical/ Financial Reports	Month 62/Jan 2020

Management bodies

- The COMPARE General Assembly (GA): the highest authority in COMPARE and the central forum for the strategic discussions in COMPARE, responsible for the overall performance of COMPARE in compliance with the EC Grant Agreement and its annexes and the COMPARE Consortium Agreement. The GA consists of the principal investigator from each beneficiary. The Coordinator of COMPARE is the Chair and the Co-Coordinator is the Vice Chair of the GA.

- The COMPARE Executive Board (EB): the central executive level coordinating body of COMPARE, responsible for the implementation of the activities as planned and budgeted in the COMPARE work packages. The EB consists of the leaders and co-leaders of the Working Groups and the Chair and Vice Chair of the GA.

- The COMPARE Working Groups: the teams responsible for the implementation of the respective work package tasks at operational level.

- The COMPARE Expert Advisory Panels: External expert advisors to the Working Groups, providing their expert opinions and feedback on the planned activities and obtained results in COMPARE.

- The COMPARE Ethics Advisory Board: External ethics advisors, providing their expert advice on the ethics management in COMPARE.

- The COMPARE Support staff: staff secretariat, providing organizational, secretarial, financial, legal and administrative support to the Executive Board and individual COMPARE partners.

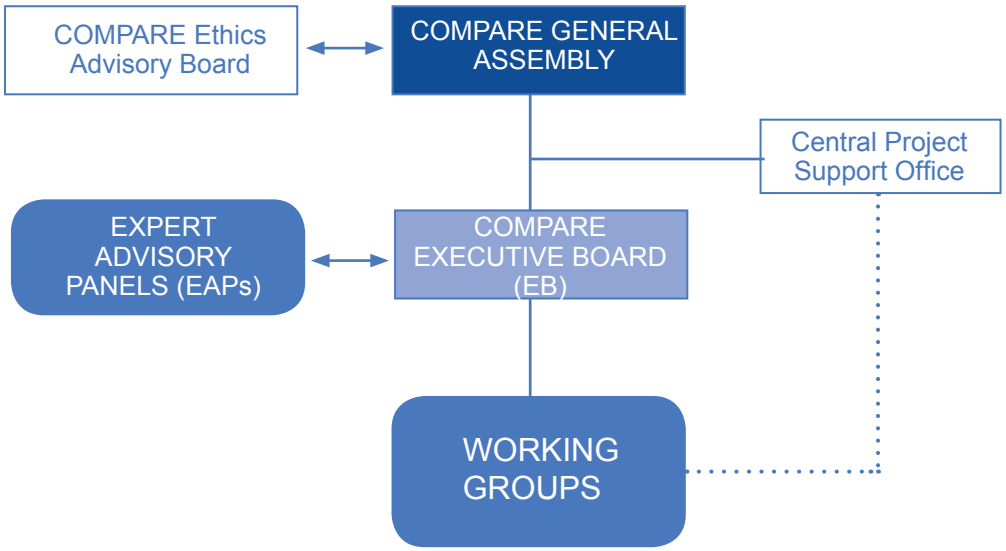

Figure 3: COMPARE Project Management Structure

Link to EU participant portal

ec.europa.eu/research/participants/portal/desktop/en/projects

NOTES

Participants in COMPARE

#	ID	PARTNER	COUNTRY
1	DTU	Danmarks Tekniske Universistet Frank Aarestrup fmaa@food.dtu.dk	Denmark
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Title

Collaborative management platform for detection and analyses of (re-) emerging and foodborne outbreaks in Europe

Acronym

COMPARE

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Coordinator

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