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COMPARE Quick Facts

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Funding	€20 million (approximately)
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Contents

Note from Coordinators

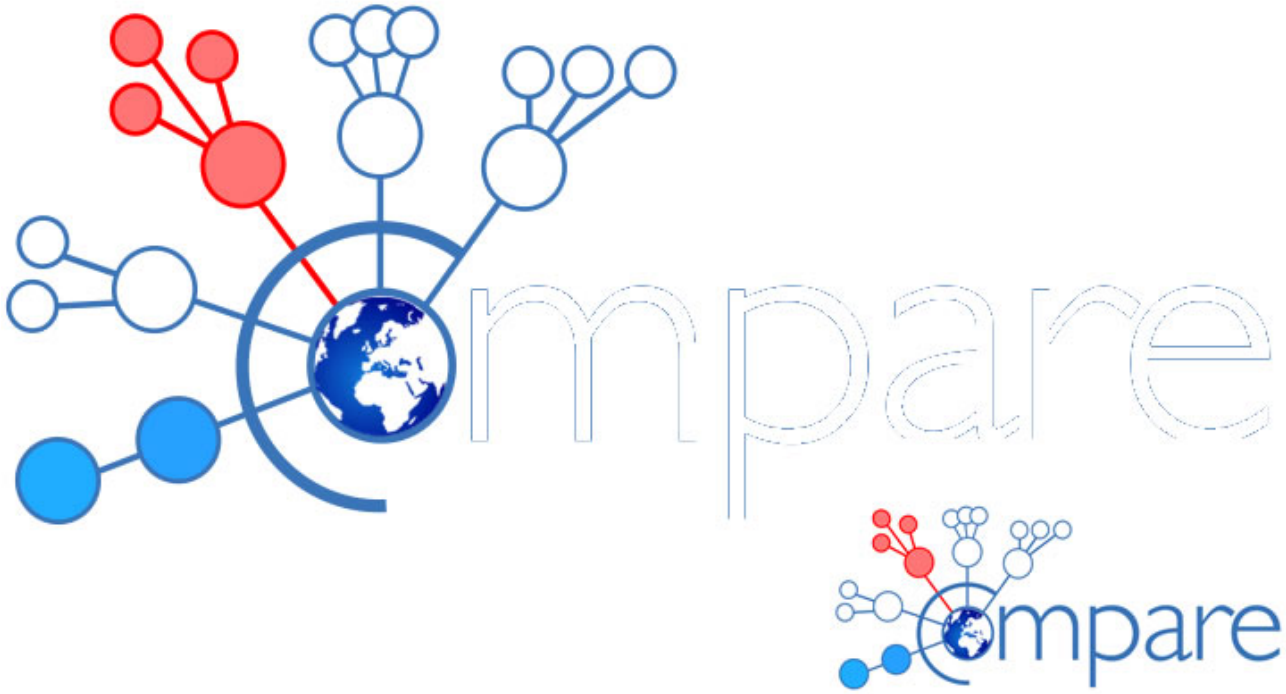
COMPARE has now been running for almost three years. We have during the first years experienced successes and failures, progress and delays, confusion and understanding, and multi-partner collaboration across the network. We have also experienced the difficulties of working across disciplines and of combining and creating infrastructures for the future with high-impact research.

A lot of the outcome has been great. This not only is reflected by the number and impact of the scientific publications, but also by the development of guidelines (SOPs) for sample and data collection, sample handling and data-generation as well as suggestions and tools for data analysis. This will provide assistance for laboratories outside of the consortium.

The sharing of data, as well as getting local analytic pipelines to run smoothly on servers with multiple users has taken a lot of effort, and a first version of a working datahub for bacteriological data is operational. A second datahub enabling the automated analysis of viral metagenomic data is ready for testing and demonstration at the annual meeting in March 2018. With the progress here, as well as the overview provided of legal and other barriers, and the economic consequences and benefits, we do feel that we are getting close to a situation where we can provide guidance for the EU and beyond in how, when and why to combine next generation sequence information with epidemiology for more rapid and precise outbreak detection of infectious diseases.

Our internal “test project” that has been developed to combine all these efforts and bring the different disciplines together is the global urban sewage project. We are now in the phase of the project where we can start to harvest the scientific benefit of working as a consortium which spans different disciplines, and see teams converging around collaborative studies envisioned at the start of COMPARE.

The great strides that were achieved in the first two years, and the hurdles that were overcome (maybe with a bit of pain) brought the Consortium even closer together for the common goal. But with the completion of year 3 just on the horizon, COMPARE is coming upon another growing pain: moving our work and results beyond the Consortium and testing the waters beyond the comforts of our partners. Sharing the results of our pilot projects, expanding the use of a standard SOP, linking pipelines and workflows, and inviting an outside stakeholder to develop and participate in a pilot. In the coming year, COMPARE partners will work with the European CDC on such a pilot, which includes the use of a functional datahub for sharing and analysis of data. All of these activities will provide input for a longer-term sustainability plan, which we will need sooner than later, as time – as always – is flying.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WP1 – Risk assessment and risk-based strategies for sample and data collection

In WP 1, a generic framework for the risk assessment is being developed. The work in Workpackage 1 focuses on asking

- Where might NGS be best applied in routine surveillance?
- How can NGS data improve our risk assessment outcomes?
- Under which scenarios should we apply NGS – which samples should we take and how many?
- Can we bring together risk specialists within public health, animals, wildlife and food?

For risk based sampling, a decision support algorithm has been developed that guides the choice of samples for different scenarios, ranging from routine surveillance in the absence of disease, to sampling during outbreaks. The algorithm covers human, livestock and wildlife disease problems, and is currently being validated by inviting comments from COMPARE partners from specific case studies. It also has been used to develop a protocol for a pilot study with an external network of infectious disease specialists from GEOSENTINEL.

For the risk assessment work, steady progress is being made with the first microbial risk assessment and spatial risk assessment case studies now being completed. These models have been parameterized for *Listeria monocytogenes* in ready to eat foods using machine-learning techniques and Lumpy Skin Disease transmitted through trade and livestock movements. Peer review publications are being prepared for submission, led by partners DTU and APHA.

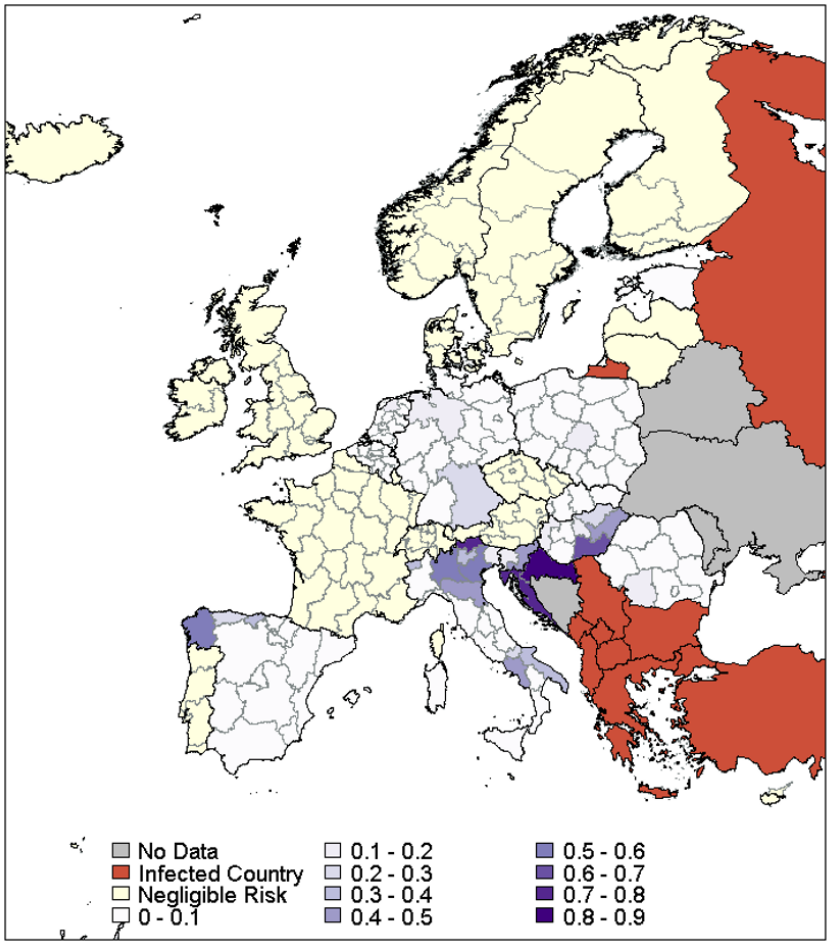


Figure1. Generic spatial risk assessments; regional mean probability of infection of Lumpy Skin Disease in 2016.

The data collection has already begun on the next case studies within our tasks with partner FLI collaborating with the second case study for the spatial risk assessment which will focus on a disease with a wildlife reservoir component, Zika virus and *E. coli*.

We have provided public access to emerging outputs from WP1 with a specific webpage devoted to Epidemiological Datasets now available in the Library area of COMPARE website. Here you can access the searchable catalogue of open-source models or modelling frameworks that can be readily used to investigate an outbreak situation and soon the inventory of harmonized sampling and storage protocols and soon.

In the near future, we will provide a database of diseases and their standard sampling protocols via the COMPARE website as well.

WP2 – Harmonised standards for sample processing and sequencing

Workpackage 2 is addressing the harmonization of standards for sample handling as a basis for other tasks in the COMPARE project.

During the recent period, efforts were made to draft and finalize Milestone 15 led by FLI. The milestone is a list of core specimens compiled by the partners of COMPARE. The samples are available to test and evaluate sample processing workflows, for example, across the COMPARE consortium. The MS15 document can be downloaded from the Milestone folder on the COMPARE Share site.

After development of sample processing protocols, WP2 is now especially focused on executing ring trials to evaluate the metagenomic sample processing pipelines that have been developed. The GMI Virus Proficiency Test, organized by RKI, was recently finished and a final detailed report will come in Deliverable 2.5 (due in M36). The next ring trial will be on food metagenomics and partners UNIBO, DTU, FLI and ISS are organizing it. Preliminary tests have been conducted regarding how the ring trial will be executed.

A standard sample processing workflow has been in use in-house at FLI and was validated for different matrices and different pathogens (viruses, bacteria, parasites). This sample processing workflow will soon be released as the standard procedure for sample processing (SOPs). Additional validation of the process has been undertaken during the ring trials (both previous and future).

Future work for WP2 includes additional ring trials and pilots for testing and comparing methods, including the protocols shared between partners. Workpackage partners will also to further improve the metagenomics workflow through comparative bilateral studies. In addition, there is more work to be done in curating the collection of protocols from partners and working to develop ‘core methods’.

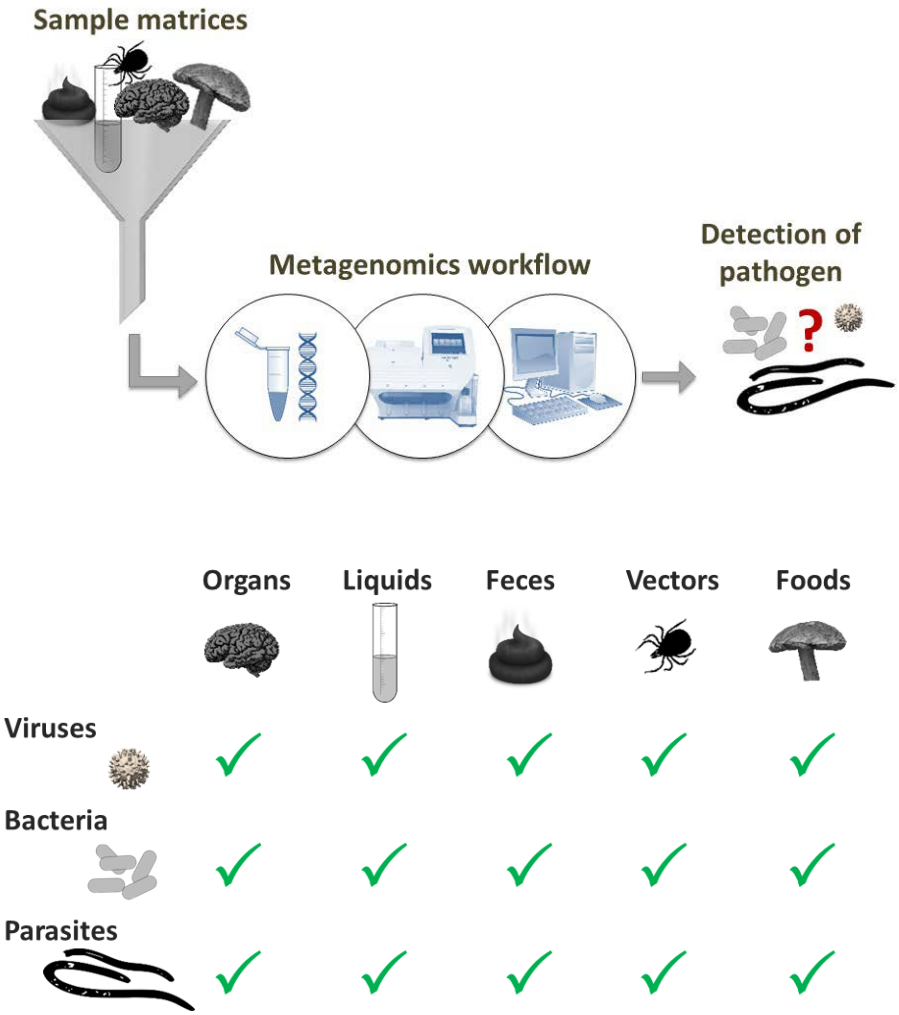


Figure 2. Overview of the "one serves all" analytical framework (above), and matrix/pathogen combinations that were successfully tested (below).

WP3/6 – Frontline diagnostics

In Workpackage 3/6 the objectives are to develop an analytical workflow for the use of single isolate and metagenomic NGS in human and veterinary clinical microbiology and to assess the feasibility of NGS/WGS/WCS for clinical diagnostic use and hospital epidemiology.

The WP3/6 has organized itself into 'Work Bundles', and the current achievements of the Work Bundles are described below.

As part of Work Bundle 1 ("Pathogen typing"), the bacterial whole genome sequencing pipeline (BacPipe) is being tested by various partners. A publication for this pipeline is under review. Work continued on the phylogenetic snapshot of the worldwide population of mcr-1-carrying *E. coli* isolates. To develop this snapshot, whole genome sequences and plasmid sequences were collected from previously published data.

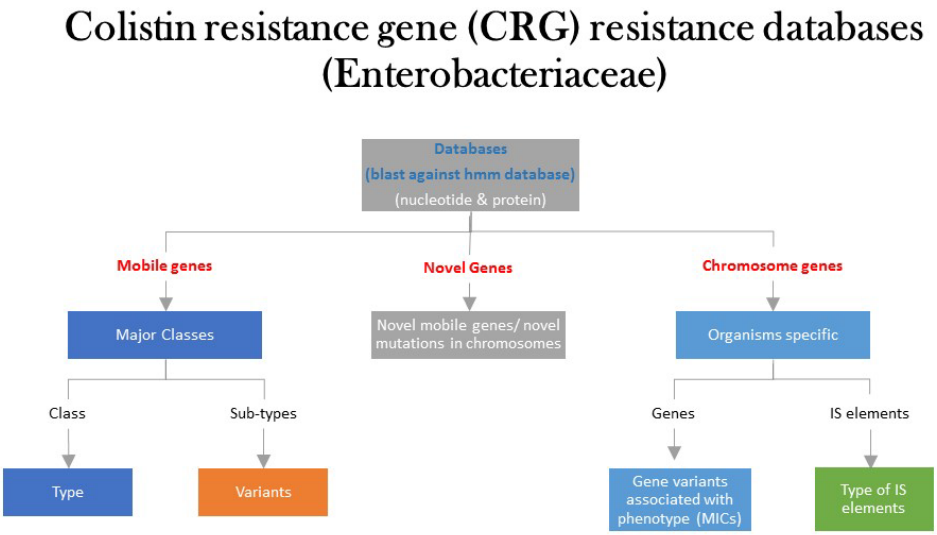


Figure 3. Algorithm for colistin resistance gene database for Enterobacteriaceae.

Regarding Work Bundle 2 ("AMR prediction from WGS data"), the data collection and literature-based association has been ongoing for colistin resistance gene hidden Markov models (HMM) database for Enterobacteriaceae for phenotype and genotype association (UA). The first focus will be *K. pneumoniae* because, based on literature and our data, it indicated that >60% CR due to mgrB modification. Machine-learning approach for prediction of antimicrobial resistances using whole genome sequences continues. Genomes are being provided by partners and the data are being stored at EMBL/ENA. The team has decided to follow three different approaches to machine learning simultaneously. The team is looking to gather a total of 1000 *E. coli* genomes. The work will also be expanded to the prediction of AMR for additional antibiotics (azithromycin) and microorganisms (*Salmonella enterica* non-Typhi).

For Work Bundle 3 (“In-hospital transmission”), from a May 2017 surgery ward outbreak of VRE, 17 isolates were collected. The isolates were phylogenetically very closely related, 11 strains showing less than 10 SNP differences between each other across the entire genome. Approaches for integration of the WGS workflow as a routine surveillance tool during hospital outbreaks in the AMC are being explored.

In Work Bundle 4 (“Diagnostic metagenomics for pathogen detection”), the shot-gun metagenome studies of feces from swine with diarrhea (FLI) analysis will be continued. In addition, a metagenomics analysis tool for clinical samples (MetaPipe) is being developed. This pipeline is for microbiologists and researchers with limited computational experience. It will be fully automated and will include screening for AR genes, IS, transposons, phage, plasmids and taxonomical diversity. For viral metagenomics, the SLIM and RIEMS pipelines, developed by EMC and FLI, respectively, are being incorporated into the COMPARE VM to prepare for automated analysis following data upload to a datahub. This process will be validated through the WP8 sewage virome project, and subsequently be tested for clinical applicability.

WP4/7 – Foodborne pathogen surveillance, outbreak detection and epidemiological analysis

Workpackages 4 and 7 are focused on developing and validating cross-sector and cross-pathogen methods for sequence-based analysis within surveillance, outbreak investigation, epidemiological analysis, and source attribution of foodborne pathogens.

During this period, there was a focus on planning Deliverable 4.2 (Algorithm for detection of informative (sub-) types for epidemiological analysis and RA for the main food-borne pathogens) and Milestone 16 (Inventory of available cluster detection algorithms), both were completed in this reporting period. Milestone 16 gives an overview of five algorithms representing distinct types of mathematical methods to determine spatial, temporal or spatio-temporal clusters, which could be used for disease outbreak monitoring. It highlights pro and cons for each method when applying them to WGS data. Milestone 16 also feeds into Deliverable 4.2, which gives an overview of how to apply whole genome sequencing data within different areas, to provide meaningful data for epidemiological analysis and risk assessment. Deliverable 4.2 can be used as a document that can continuously be updated to include new knowledge and experiences reached through COMPARE.

During the workpackage face-to-face meeting, a lot of discussion took place about epidemiological tools and analysis, as well as the use of WGS data for bacterial analysis. The WP4/7 team was joined by representatives from WP 9 (Clara Amid and Nicole Silvester, EBI) to inform about and gather ideas about the Pathogens Platform.

Figure 4. Participants of the WP4/7 face-to-face meeting in Weybridge, UK, April 2017.

The Source Attribution Study that is part of the WP4/7 (WP4 task 2.2) is coordinated by DTU and a benchmarking study with several partners was initiated aiming at exploring different approaches and models for source attribution based on *Salmonella Typhimurium* sequencing data. Datasets from four countries (Denmark, France, Germany and England) will be investigated.

It was decided to have separate work plans and activities for the virus-focused work. For this, a cross-WP working group on genomics was developed, in collaboration between IFREMER, RIVM, DTU, FLI, EBI and EMC. The working group has agreed to the following:

- develop agnostic protocols for random-primed sequencing of the RNA and DNA virome directly from clinical samples (RIVM lead),
- conduct a systematic assessment of available workflows for analysis of metagenomics data (RIVM lead),
- develop and validate protocols for virome analysis from stools and sewage (EMC-lead),
- analyze sewage-contaminated food (IFREMER lead),
- work on data analysis workflows in a COMPARE datahub (EMC-EBI-DTU), and
- develop visualization tools (EMC-EBI).

A study was performed using the plethora of data from NoroNet, and the study showed that currently used protocols that target short sequences rarely include the main antigenic epitopes on the viral capsid, which will become important in view of ongoing vaccine development. These short sequences are also not ideal for tracing foodborne outbreaks. Thus, this study contributed to Deliverable 4.2 and Milestone 16 as it provides a foundation for future studies on norovirus outbreaks and the use of tools for source attribution, it also highlights the need for sustained norovirus surveillance using NGS technologies.

WP5/8 – Detection and response to (re-) emerging diseases

The focus for this Workpackage is on harnessing the potential added value of NGS for emerging disease detection and research. The unique opportunity from the H5N8 outbreaks pushed these Workpackages (and the Consortium) to evaluate the methods and abilities to share data, analyse data and work across disciplines. With the recent re-emergence of avian influenza virus in The Netherlands, the network again is discussing updating the sequence based tracking of viruses. Currently two variants of influenza H5N6 appear to circulate that differ in the internal gene sets.

Work on the global collection of H5N8 influenza A virus genome sequences has continued for phylogeographic analyses and a second manuscript for publication later this year. Other components of the H5N8 pilot projects (SNP detection) are reaching completion.

With regards to other outbreak investigations; a collection of three papers on the genomics and epidemiology of the Zika virus was published in the 15 June 2017 edition of Nature and two papers on Crimean-Congo haemorrhagic fever (CCHF) and one on Ebola virus have also been published. In a cross-workpackage collaboration, cluster analysis was done on norovirus genome sequences from high-risk patients with chronic norovirus infection. This work has been published.

Further, Workpackage 8 has made good progress with the sewage projects and a good start with the wildlife sampling project. The urban sewage sample set is being completed and a plan for mining of the combined datasets (bacterial and viral metagenomes) will be discussed during a face-to-face meeting in Paris, planned for January 2018. Visualisation tools are being developed to allow interactive data mining for non-bioinformaticians (Figure 5).

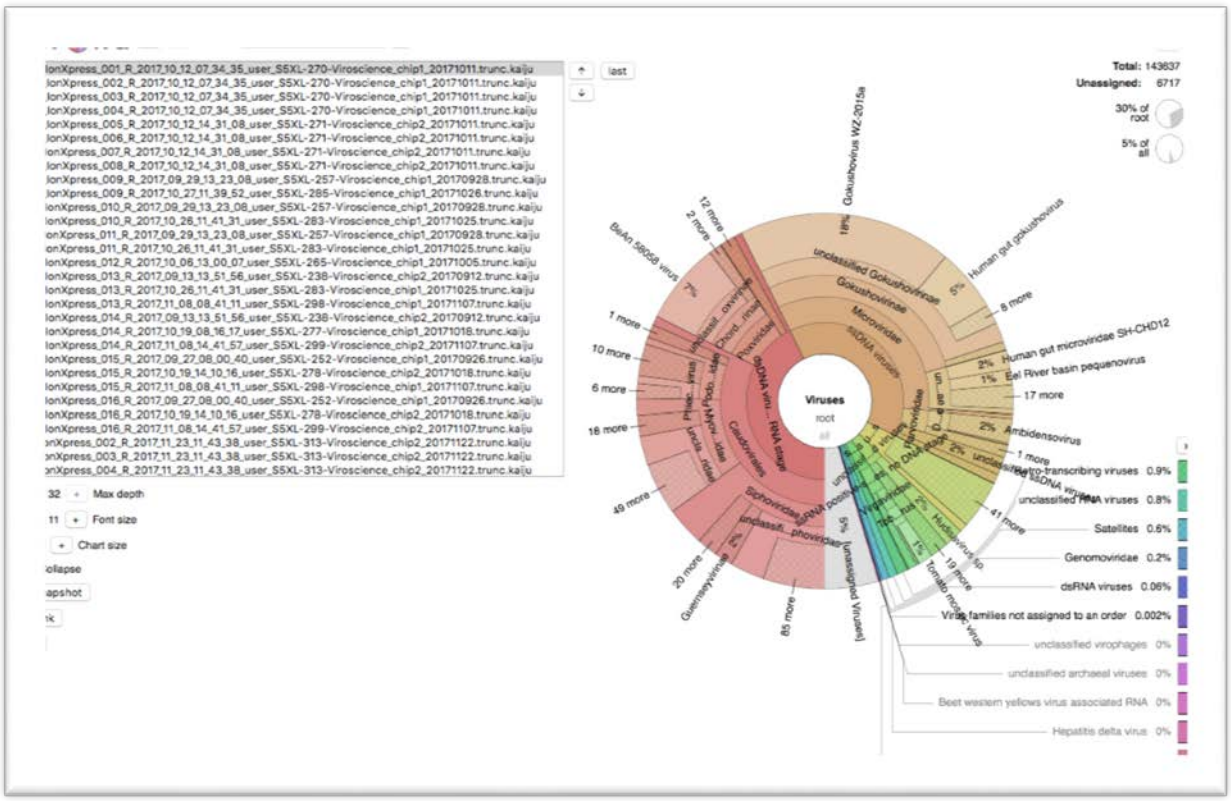


Figure 5: Interactive data exploration of the virome of a sewage sample from the global urban sewage project (courtesy David Nieuwenhuijse, ErasmusMC).

Because wildlife health centres (WHCs) are important strategic sampling sites for endemic wildlife and border inspection posts (BIPs) for exotic wildlife, we will determine the suitability of sampling protocols (working with Workpackage 1), protocols for handling and processing of samples (Workpackage 2), and analyses of obtained data for routine surveillance, epidemiological investigations, and rapid risk assessment (Workpackages 1 and 5) for at least one representative WHC and BIP in each participating country. The initial part of the task will involve retrospective NGS analysis of known cases of wildlife morbidity and mortality, where the primary cause has been established to be of viral, bacterial, or protozoal origin, and where suitable samples of tissue, respiratory excreta, feces, blood, and/or arthropod vectors are available. Several cases involving viral and bacterial infections have already been proposed.

The University of Cambridge (Partner 16 UCAM, along with Erasmus Medical Center, EMC, and University Clinic Bonn, UKBonn) was offered a unique opportunity to examine ancient human DNA specimens for evidence of pathogens. Highly parallelized software was used for processing >120 billion DNA sequencing reads. Ancient viruses were found and an initial manuscript was submitted for publication (Nature).

Importantly, this work provides a first real-world opportunity to investigate how the behavior of various bioinformatics algorithms is affected by the presence of (partial and complete) ancient exogenous viral sequences, in particular, phylogeny (analysis of evolutionary rates and origins), sequence matching, and recombination tools. Although these datasets were not included in the original proposal, they are expected to contribute substantially to improvements in tools and research projects proposed under WP5/WP8.

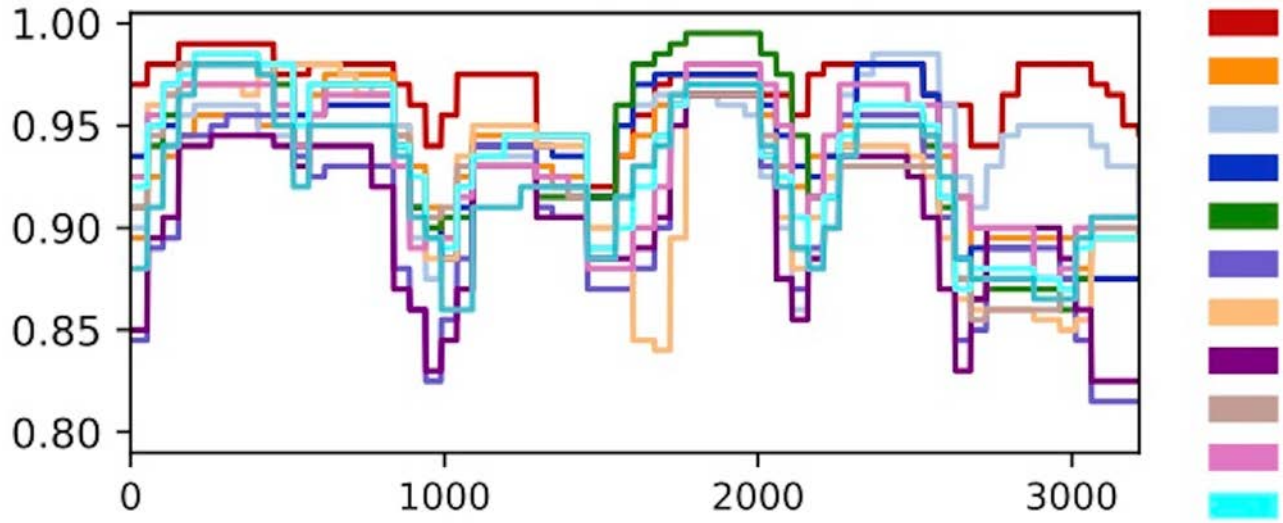


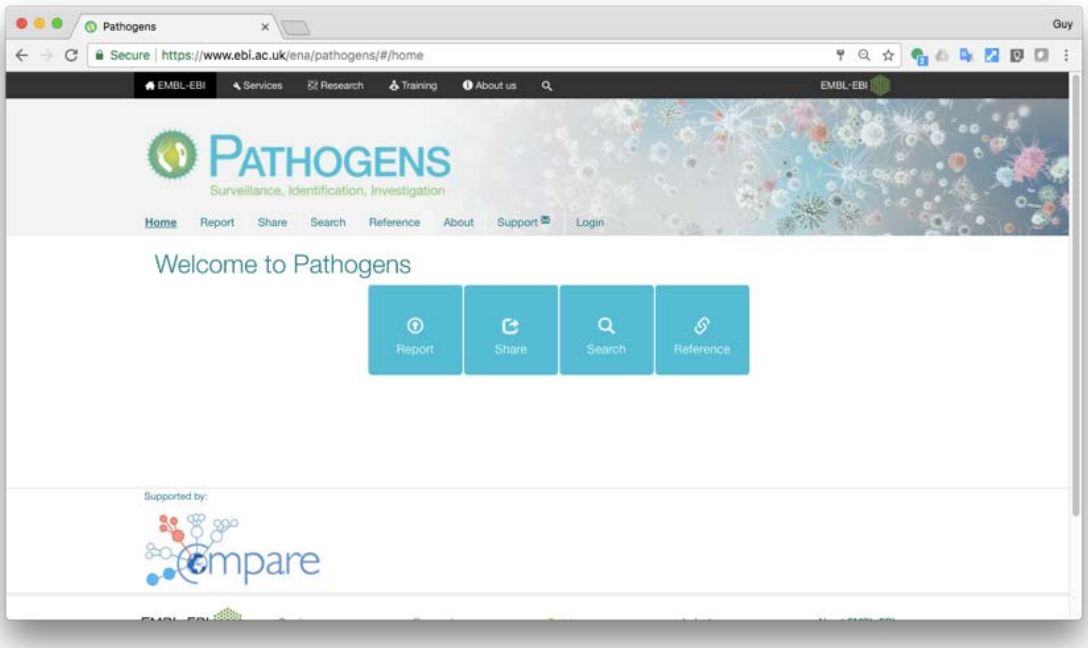
Figure 6. Snapshot of virus recombination detection (Terry Jones, U of Cambridge). Graphic from a forthcoming publication.

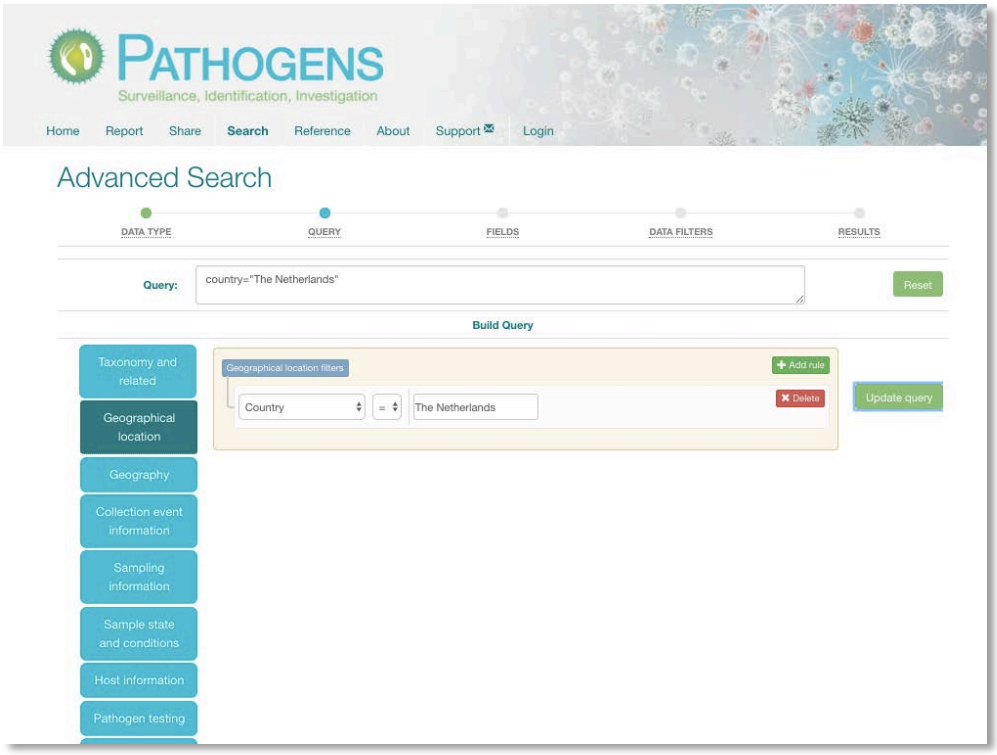
WP9 – COMPARE platform

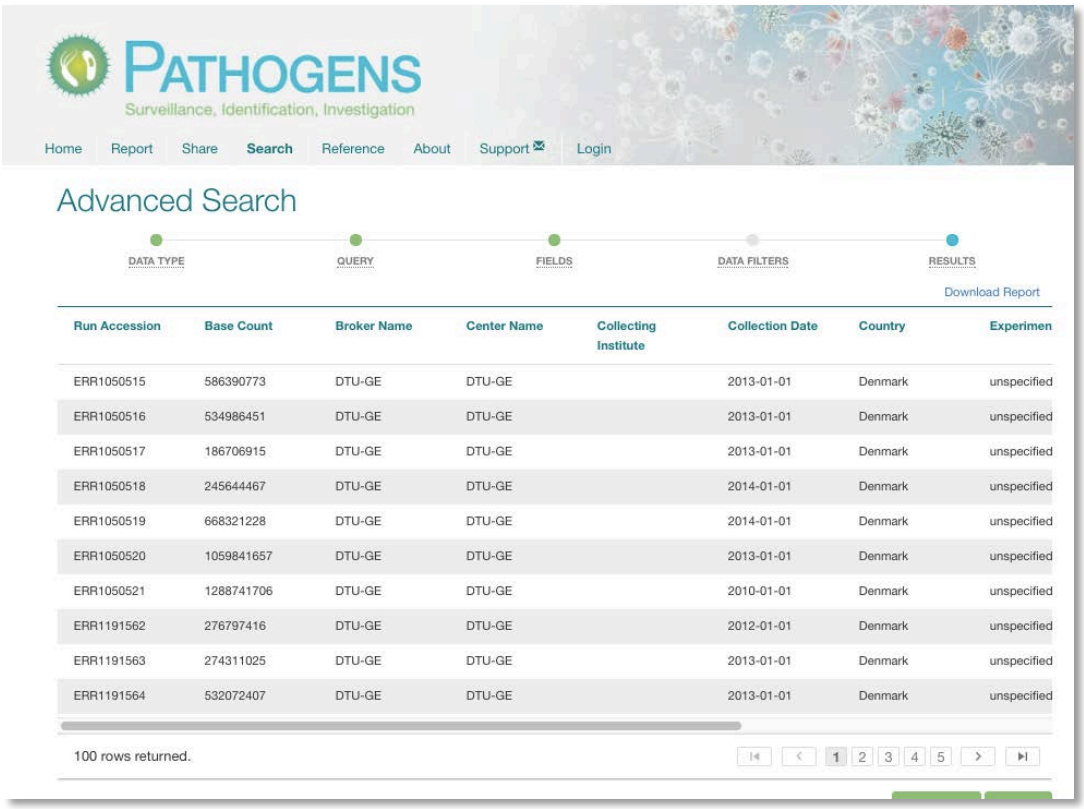
Rapid sharing and analysis of pathogen genomics data is central to COMPARE, and in WP9, they have built the informatics to enable this. During the reporting period, partners in Workpackage 9 continued to develop and provide technology and support for an increasing number of users who are engaged in describing, sharing and analysing pathogen sequence data. Major products include the Pathogen Data Portal (www.ebi.ac.uk/ena/pathogens; see Figure 7), which has been launched into full production and includes a new search interface providing comprehensive discovery across public and authorised pre-publication confidential data.

Accompanying the Pathogen Data Portal is a software application for the efficient download of data files. We have made a number of improvements to the Notebook system, which allows exploratory access to COMPARE data for those with bioinformatics skills; enhancements include options for deeper customisation, better management systems for the sharing of projects and improved performance.

On the support side, we have provided additional data hubs for a growing user base, such as the data hub supporting the AMR working group, for which we have provided data validation, reporting and access support. Finally, ongoing development sees us working towards data brokering in the DTU suite of tools, improvements to the SLIM viral analysis workflow and the connection of Notebooks to the Pathogen Data Portal, to allow easy launch for users.







Figures 7a-c. Screenshots from the Pathogen Data Portal (home page, search page, search results).

WP10 – Risk communication tools

Workpackage 10 is designing and developing the appropriate risk communication tools and strategies for COMAPRE stakeholders. Workpackage 10 has completed extensive inventory on stakeholders to the COMPARE platform, and has developed a message mapping tool that was demonstrated at a recent General Meeting.

In the reporting period, Workpackage 10 activities still focused on the message map exercise, which was further enriched through the incorporation of feedback received during the workshop on Risk Communication held in conjunction with COMPARE General Assembly 2017. The workshop was convened in early March, and offered the possibility to test both the first version of the Message Map Excel spreadsheet V.1 and the software for text analysis LWC2015 ("Linguistic Inquiry and Word Count"), which analyses texts extracting 80 different variables. We plan to use LWC2015 as a tool for the assessment and self-assessment of risk communication texts.

In preparation for the workshop, we also administered online to workshop participants the psychometric scale Domain-Specific Risk-Taking (DOSPERT). We received 37 complete answers, which allowed us to sketch a collective risk-taking profile for this group in five content domains: financial, health/safety, recreational, ethical, and social decisions. Results allowed us to better interpret the outcomes of the workshop, which we incorporated into the message map tools.

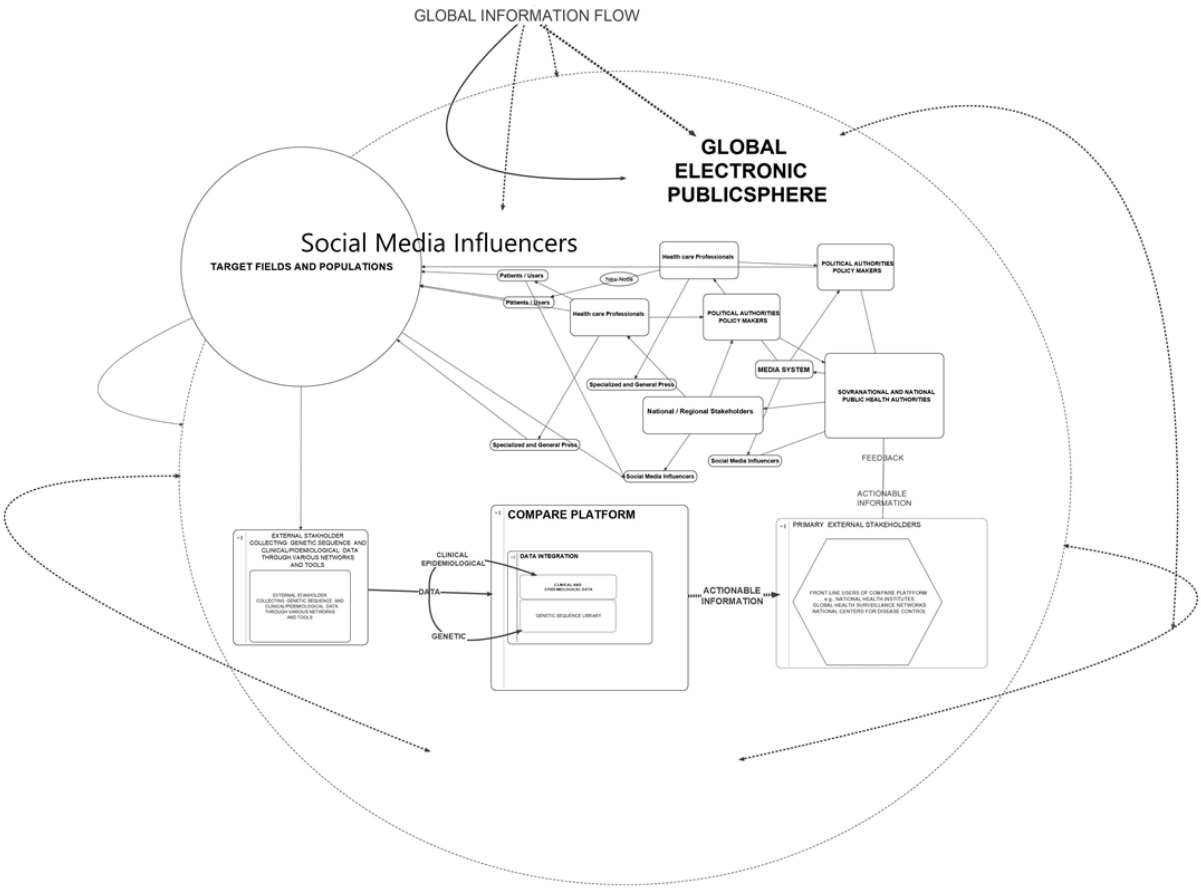


Figure 8. Graphical outline of the COMPARE Risk Communication Model.

In the spring, we produced two advanced versions of Message Map Excel spreadsheet (V.2) linked to the stakeholder spreadsheet (V.3), and an advanced version (V.4) of Message Map templates. Major efforts were also devoted to defining the first version of the COMPARE Risk Communication Model, including 1) principles, 2) working outline, and 3) charts and mind maps.

Our most recent efforts were devoted to collecting, revising and selecting the huge amount of material produced in all of Task 10.2 (about 2.000 pages) and summarizing it into a comprehensive report, for Deliverable 10.2, which includes the main findings of Task10.2. In the reporting period, we have also edited, published, and disseminated 12 issues of the COMPARE Risk Communication Bulletin

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WP11 – User consultations

The third round of the COMPARE Expert Advisory Panel (EAP) meetings was held during the annual COMPARE meeting in Rotterdam, the Netherlands (1-3 March 2017). In particular, EAP members were encouraged to participate in the workpackage (WP) meetings and the cross-WP workshops on Barriers or Risk Communication providing their expert advice and perspectives on the topical discussions.

At the end of the second day of the General Meeting, a COMPARE Executive Board and EAP member meeting was held. During this meeting, the EAP members provided feedback to the Executive Board on the progress of the project and strategic choices made by COMPARE thus far. In total, 13 EAP members attended this meeting: 2 from EAP Domestic Animals, 1 from EAP Barriers, 1 from EAP Databases and Tools, 5 from EAP Food Safety, and 4 from EAP Public Health. The purpose of the meeting was to receive feedback, hear suggestions and take an inventory of impressions from what the EAP members have heard so far at the General Meeting. A report has been made (Deliverable 11.3) and shared with the EU, consortium members and EAP members.

The EAP members who provided feedback through the Executive Board and EAP session at the annual meeting have raised many points that have been discussed and followed up by the COMPARE consortium in the past months. Examples include better and more vigorous use of the COMPARE ShareSite, and actively alerting the EAP members about information available on the share site, in close collaboration with WP15.

Further strengthening of the collaboration between Workpackage 12 (Leader George Haringhuizen) and WP11 (especially with the EAP Barrier members) took place. The goal of this collaboration is to globally discuss the implications of the Nagoya Protocol and other international treaties, and draft a document on guiding principles for global and open data sharing to be shared and discussed with members of the Global Microbial Identifier consortium and the conference of parties, amongst others. In addition, the WP12 in-depth study on ownership barriers to data sharing, for which WP11 and WP12 closely collaborated, has been submitted for publication. This survey aimed to identify the barriers for data sharing that are related to the ownership of data and regulations assigning ownership of data. Results from this survey were presented during the YOUNG COMPARE and the COMPARE General Meeting.

WP12 – Barriers to open data sharing

The focus is on understanding barriers to the development of COMPARE, in terms of legal, ethical, administrative and other considerations that may play a role.

The Workpackage 12 team in collaboration with RIVM, Erasmus MC and VU University, submitted a research article for publication in a peer-review journal, regarding the investigation of ownership barriers to the sharing of microbial genetic resource in a timely and open-access manner. Besides investigating barriers and the causes of barriers, through a root-cause analysis, the article also analyzes and discusses the impact of these barriers in infectious disease surveillance and control, and the further development of medical innovations.

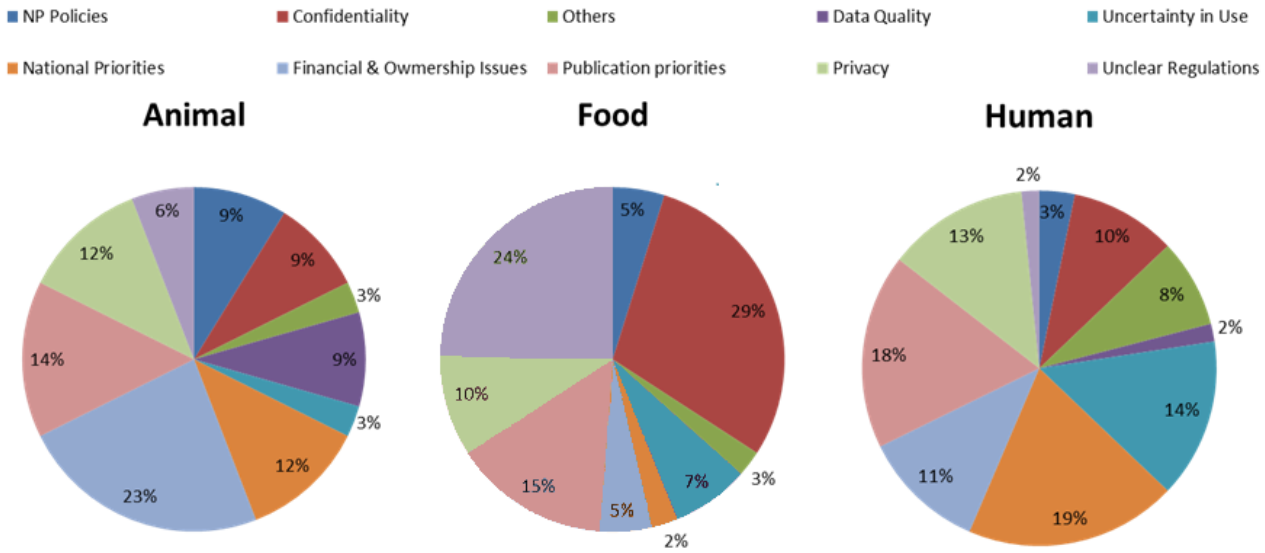

Figure 9. Results from the in-depth study on ownership barriers to the sharing of microbial genetic resource in a timely and open-access manner: frequency in which some of the barriers (most referred) were mentioned considering the stakeholders' domains (food, animal and human).

The WP12 team was involved in two presentations for the COMPARE Consortium: one at the Young COMPARE meeting, with the exposition of the poster: *Four main reasons why people will not share Microbial Genetic Data in COMPARE* (M.Y. van Roode, C.S. Ribeiro e.a., COMPARE/RIVM/Erasmus MC/VU University, February 2017); and another at the COMPARE annual meeting.

At the annual meeting, WP12 members conducted a workshop in the form of group discussions about political, ethical, administrative, regulatory and legal (PEARL) barriers to the sharing of genetic data from pathogens, as identified on the research activities of WP12 during the previous years. The workshop consisted of discussions about concrete case studies where decisions on data sharing in different situations needed to be made. In the workshop, participants were able to learn about the different challenges in data sharing, to expose their ideas and opinions, to learn the opinion of others and to engage on group deliberations about the steps forward to the overall sharing of microbial genetic resources.

In addition, members of WP12 performed this workshop for other audiences to get an overview about the same subject matter from different stakeholder groups: firstly, at the 10th GMI Meeting (16-18 May in Mexico); and secondly, at The Netherlands National Institute for Public Health and the Environment (RIVM). The WP12 team, with the contribution of the COMPARE coordination team, has been strategically liaising with other partners in order to promote the workshop performance at different organizations not yet reached, such as national surveillance centers, research institutes, global disease networks and supranational organizations involved on the sharing of NGS-data from microorganisms.

Deliverable 12.1 was finalized. This deliverable consists of a report to the EC and the COMPARE Consortium, listing the identified non-technical barriers for the sharing of microbial genetic data in COMPARE. Besides providing an inventory of barriers, the report also explains, analyzes and describes them within the relevant context.

WP12 continues to collaborate with other EU-funded projects under the umbrella of COMPARE and the knowledge production of the workpackage. In April 2017, the WP12 team shared with the partners of the EU project EVAg expertise about the Nagoya Protocol and its potential impact for microbial repositories. For that, an opinion paper was prepared and an oral presentation shared. On 24-25 October 2017, WP12 was invited by the WHO Biobanking working group to an expert consultation on material and data sharing in times of global crises. Finally, the WP12 leader provided juridical advice for the COMPARE coordination team for the performance of the ECDC/COMPARE Pilot Project.

WP13 – Dissemination and Training

Members of the COMPARE Consortium share their experiences and results from COMPARE at conferences and workshops all over the world. The Coordinators of COMPARE share their numerous presentations where they talked about COMPARE:

- Future Health Threats Initiative, Brussels, Jan 2017, Emerging and Re-Emerging Disease Outbreaks
- Bioinformatics Center, Germany, March 2017, Towards NGS based disease detection: The COMPARE project
- DTU Commemoration, Denmark, April 2017, Honorary Doctorate
- COMPARE demo for ECDC, Denmark, May 2017,
- Congres Albert Heijn over voedselveiligheid en –hygiene, Rotterdam, May 2017, Voedselveiligheid en bacteriele infecties: oorzaak en gevolg
- EURL biological risks and WGS meeting, Brussels, May 2017, Possible contributions of COMPARE tools and datahubs to NGS based developments across EU
- EFFORT Annual Mtg, Bulgaria, Jan 2017, COMPARE update
- University of Greifswald, Micobime Research, Germany, Jan 2017, COMPARE update
- Danish Veterinary Association, Denmark, March 2017, COMPARE update
- Copenhagen University, March 2017, COMPARE and NNF antibiotic resistance project
- ECCMID Meeting, Austria, April 2017, COMPARE update
- Sludge Flok Meeting, Wastewater Association, Denmark, May 2017, COMPARE and Sewage Surveillance
- British Embassy, Denmark, June 2017, AMR issues in Europe
- AMR One Health, Norway, June 2017, COMPARE and One Health
- ELIXIR AMR Node, Denmark, June 2017, COMPARE Interest

Regarding Training, COMPARE is providing e-learning options that can be accessed online via the COMPARE portal. So far, the course on whole genome sequencing of bacterial genomes - tools and applications is available. An introduction to Metagenomics will be available soon (early 2018).

Members of the COMPARE Consortium continue to publish manuscripts in peer-reviewed scientific journals. These are reported via the public website. IN this last reporting period, there are four articles in *Nature* (3 in *Nature* and 1 in *Nature Ecology and Evolution*).

The COMPARE Twitter account (@CompareEurope) shares related news about COMPARE and from the project partners.

Figure 10. COMPARE becomes EU Research Results Header for the week! Twitter account (@CompareEurope)

WP14 – Cost-effectiveness framework

COMPARE can potentially bring about huge benefits through a variety of mechanisms such as earlier detection of disease outbreaks but also through increased research output. However, quantifying and valuing the benefits is often more challenging than quantifying the costs. Workpackage 14 has the aim to quantify costs and benefits of the COMPARE system and will develop methods to value the benefits of COMPARE.

Workpackage 14 delivered its second deliverable, which presents the work conducted 'to identify, and where necessary, develop state-of-the-art costing methodologies for the different elements in the [cost-effectiveness] framework' in line with Specific Objective 2 and related Task 2 of WP14. The deliverable also contains a literature review of studies that have estimated the value of safety, which serves as starting point for our approach to value safety in several countries (Task 4).

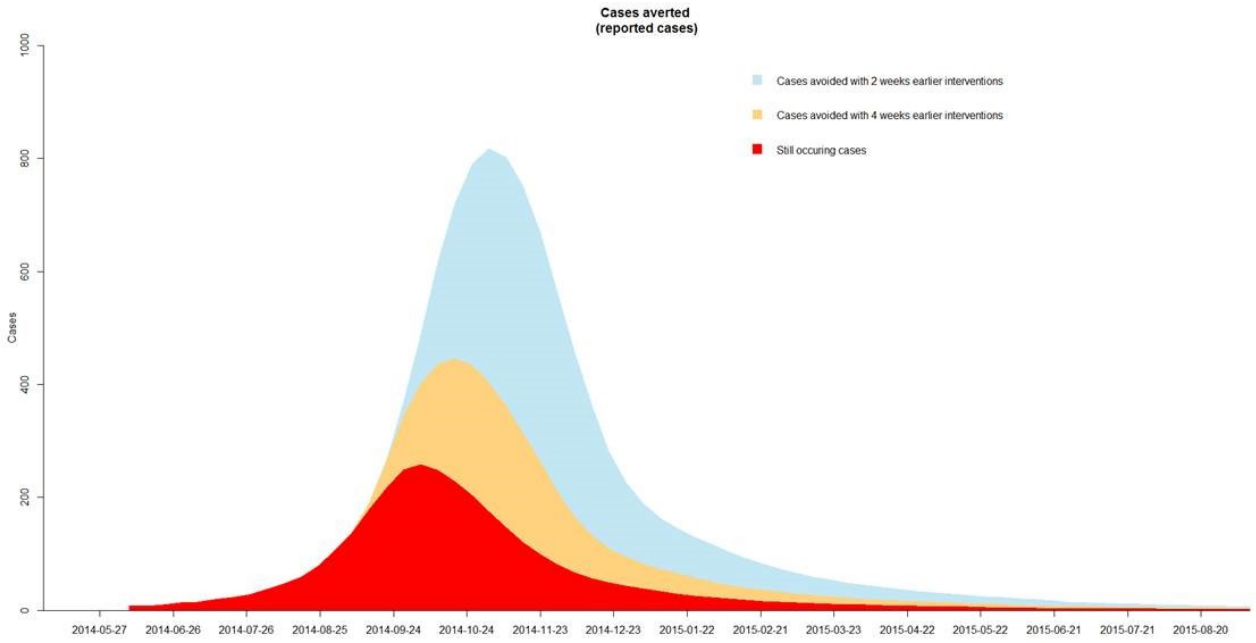

Figure 11. Number of cases averted because of earlier interventions in the Ebola outbreak in Sierra Leone.

Partner 22 (Erasmus Universiteit Rotterdam, EUR) finalized the case study of the costs and benefits of early detection in case of an Ebola outbreak. EUR also began a second case study, which aims to explore the cost of implementation of WGS in a surveillance system and compare the estimates to the health benefits needed to reach a cost-effectiveness threshold. For this case study, they made contact with the Dutch National Institute for Public Health and the Environment and foresee contacting the WHO. Finally, EUR finalized the literature on the value of safety and started developing the questionnaire on how we estimate the value of safety.

Partner 25 (Civic Consulting) has continued working on the selection of case studies and the related methodology. They have also conducted interviews with the Microbiological Laboratory of the Danish Veterinary and Food Administration and the FDA's Genome Trakr Network, which are both expected to be the focus of a case study.

Furthermore, they are discussing the possibility of conducting case studies with the Friedrich-Loeffler-Institut and Animal and Plant Health Agency. Lastly, they are in the process of contacting the Public Health England Salmonella Surveillance Network. In parallel, they have been consolidating initial data on the costs and benefits from the interviews and literature review to use as a basis for preparing detailed questionnaires for the case study institutions.

WP15 – Management

The appropriate organizational structures and processes have been put in place to respond to the EC's as well as partners' needs and to ensure COMPARE's compliance with the EC Grant Agreement and the COMPARE Consortium Agreement.

COMPARE submitted an Amendment to the Grant Agreement to reflect the changes that have occurred in the Consortium. The Amendment came into force on 19 October 2017.

During the next period, efforts will focus on submitting the Second Reporting Period Technical and Financial Reports (due 30 January 2018).

COMPARE Partners