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COMPARE Quick Facts

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Project period	01 December 2014 – 30 November 2019
Funding	€20 million (approximately)
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Contents

Note from Coordinators

As we are completing our fourth year in the project and entering into the final year, we can see some of our work coming to fruition, giving results and insights; but also identifying questions and issues that still remain to challenge us.

The world of data still expands, not just with more sequence data becoming available due to more sharing, the cost of sequencing reducing or the availability of machines increasing; but with additional metadata available. In addition, there is useful information available that can be linked to the metadata to explain certain situations, issues or phenomena.

The next question for COMPARE is how do we exploit these data, this amount of data, and this connection of data? There are opportunities to push the COMPARE concept to explore how the COMPARE platform can use, connect and exploit the data that are available to us and the alternate data we can gather via citizen science projects, internet search data mining and database linking.

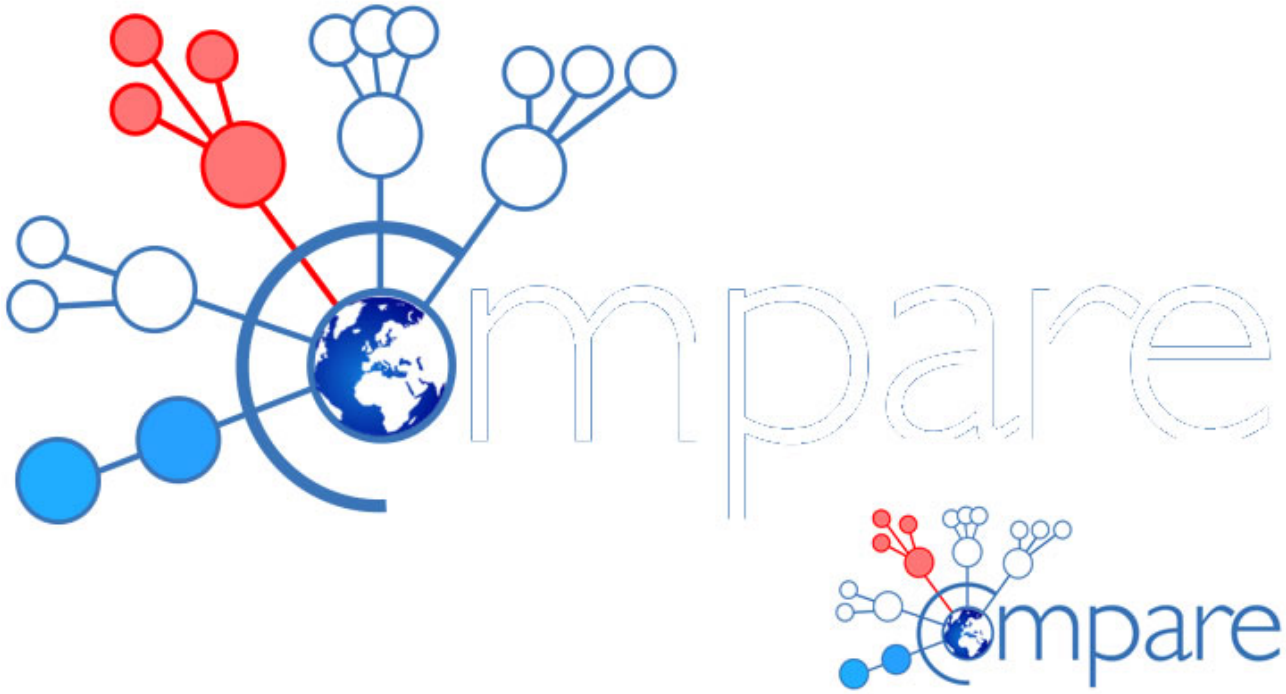
COMPARE is also very aware that the landscape for this type of research is evolving as well. Large companies are interested in data mining as well, and exploring new ways of gathering information, such as using drones for mosquito species identification, or using whole genome sequencing technologies not to find where contamination of their products happened, but to prove that their product could not be contaminated.

But, with all the talk of data mining, data sharing and open sources; we are very aware that governments, national versus regional versus international regulations and the court system will have a strong influence on how these data will be used, shared and exploited. We must pay attention to all developments and questions regarding the Nagoya Protocol. COMPARE is active in sharing its knowledge, research and opinion regarding the Nagoya Protocol, and we will continue this work through the end of the project.

COMPARE has just completed a pilot project with the ECDC and EFSA regarding the COMPARE platform and data sharing, storage and analysis. We are looking forward to possibly expand the pilot as well as develop a pilot with food industry partners. In addition, our pilots are also looking at the cost-effectiveness of sequencing versus plate culture techniques.

In the final year of COMPARE, we will continue to disseminate our results and findings, through workshops, scientific articles, conferences and other presentations. But we also find that though it is a 'final year', we are not finished. More work and research needs to be done to develop the **'one serves all'** analytical framework and data exchange platform that allows for real-time analysis and interpretation of sequence-based pathogen data in combination with associated data.

The COMPARE vision still holds true, with steps made towards the horizon.



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.

Overall the work in the tasks is progressing to the final phases; finalizing the different pathways and tools and preparing manuscripts to disseminate the methodologies developed.

Within the risk assessment tasks, a number of risk pathways and case studies have now been completed. In Task 1.1, the Lumpy skin disease manuscript has been accepted and available online at *Transboundary and Emerging Diseases.* The wild animal movement pathway is now completed and applied to the case study of African swine fever. Similarly, the generic framework is now complete for the food trade, bird migration, vector flight and human transportation pathways. For Task 1.2, the case study *E. coli* manuscript has been submitted. Work has started on *Listeria monocytogenes* exposure assessment using NGS data linking with another EU project (ListAdapt) and a collaboration with the University of Bologna. Finally, within Task 1.3, the manuscript has been submitted for the global sewage dataset and work started on integrating UK livestock movement databases into the COMPARE framework.

For the risk-based sampling and collection protocols, the combined package of tools developed in Tasks 2.1 to 2.3 (flowchart, database with protocols, syndrome based sampling protocol, metadata checklist and background document) are being tested and validated by 30 different disease experts from the human, domestic animal and wildlife health sector, using scenarios based on past disease outbreaks and practical pilots are underway in the field. For Task 2.4, the Global Foodsource Identifier (GFI) has been developed which is a social networking site for outbreak investigations and allows access to shared datasets and analytical tools.

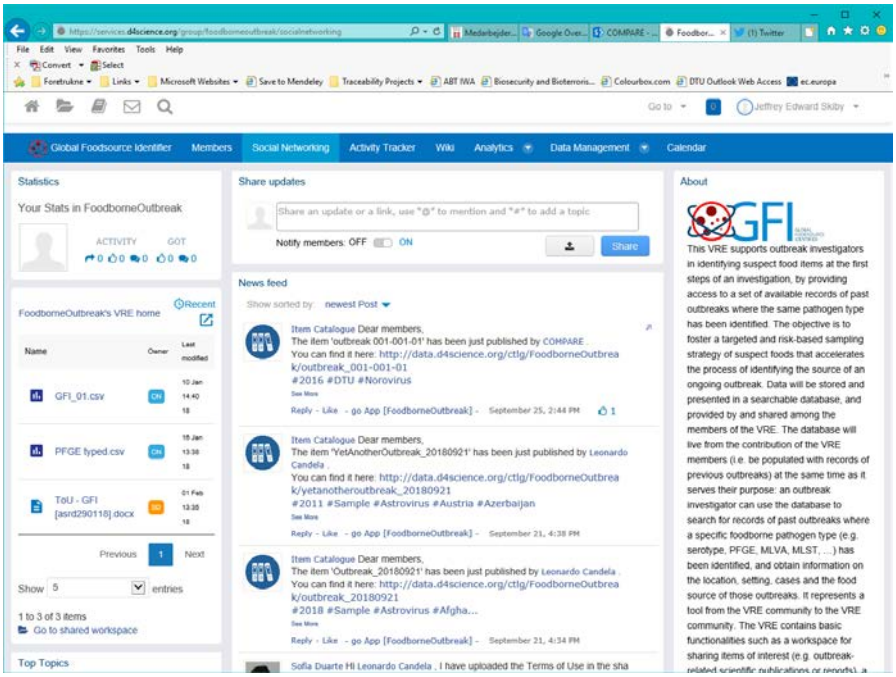


Figure 1. Global Foodsource Identifier (GFI) – a shared virtual research environment to assist with outbreak analysis.

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 reporting period, many protocols, collected, tested and validated by WP2 partners, have been uploaded to the public COMPARE website (http://www.compare-europe.eu/library/protocols-and-sops) for dissemination. The COMPARE-branded protocols are either Laboratory Operating Procedures (LOPs, used at least by the provider, but as yet not validated in detail) or Standard Operating Procedures (SOPs, validated in detail and already published, in some cases validated for different matrices and different pathogens).

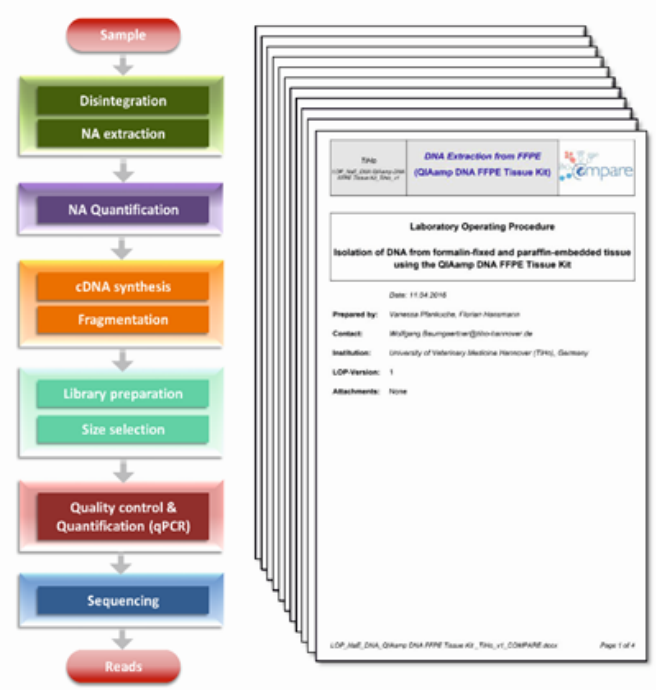


Figure 2. Generic process for sample processing and sequencing.
LOPs and SOPs are now published on the COMPARE website, www.compare-europe.eu

WP2 continues the validation of sample processing workflows using ring trials (RT).
1) The GMI Virus Proficiency Test (Deliverable D2.5) with a dry and a wet lab part organized by RKI was finished in 2017. A manuscript summarizing the dry lab part is ready for submission.
2) The RT on food metagenomics was organized, prepared and executed during the reporting period. A complex mock community containing bacteria, viruses, parasite and fungi was spiked in a sample of salmon. The outcome will be reported as Deliverable D2.6 (due November 30, 2018).
3) The next RT is already planned and will be conducted in the next reporting period to be reported as Deliverable D2.7 (due November 30, 2019). Subject of that RT is the handling and processing of difficult material like formalin-fixed parafine-embedded samples.

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.

In Work Bundle 1 (WB1), some analytical frameworks for routine sequence-based identification and characterization of pathogens have been developed and benchmarked. These include RIEMs metagenomic workflow, BacPipe whole genome sequencing workflow, VirSaDB database for *Staphylococcus aureus* virulence factors, refRank for reference genome selection, SNPfilter for alignment-based SNP-filtering in NGS analyses, and ISR database for *Clostridium difficile* ribotype detection.

In WB2, in order to predict phenotypic susceptibility, three approaches are being developed: a machine-learning approach for prediction of fluoroquinolone-resistant *Escherichia coli*, Hidden Markov-Model (HMM) for prediction of colistin-resistant Klebsiella pneumoniae, and network-based machine learning for antimicrobial resistance prediction.

In WB3, a number of in-hospital transmissions and outbreaks have been studied, including outbreaks of VRE, carbapenem-producing *Enterobacter cloacae*, longitudinal *Enterococcus faecium* and *C. difficile* utilizing phylogeny methods, and Structured COalescent transmission tree inference tool etc. Whole genome sequencing and bioinformatics strategies were utilized for polyclonal outbreak scenarios analysis of ESBL Klebsiella pneumoniae (Figure 3).

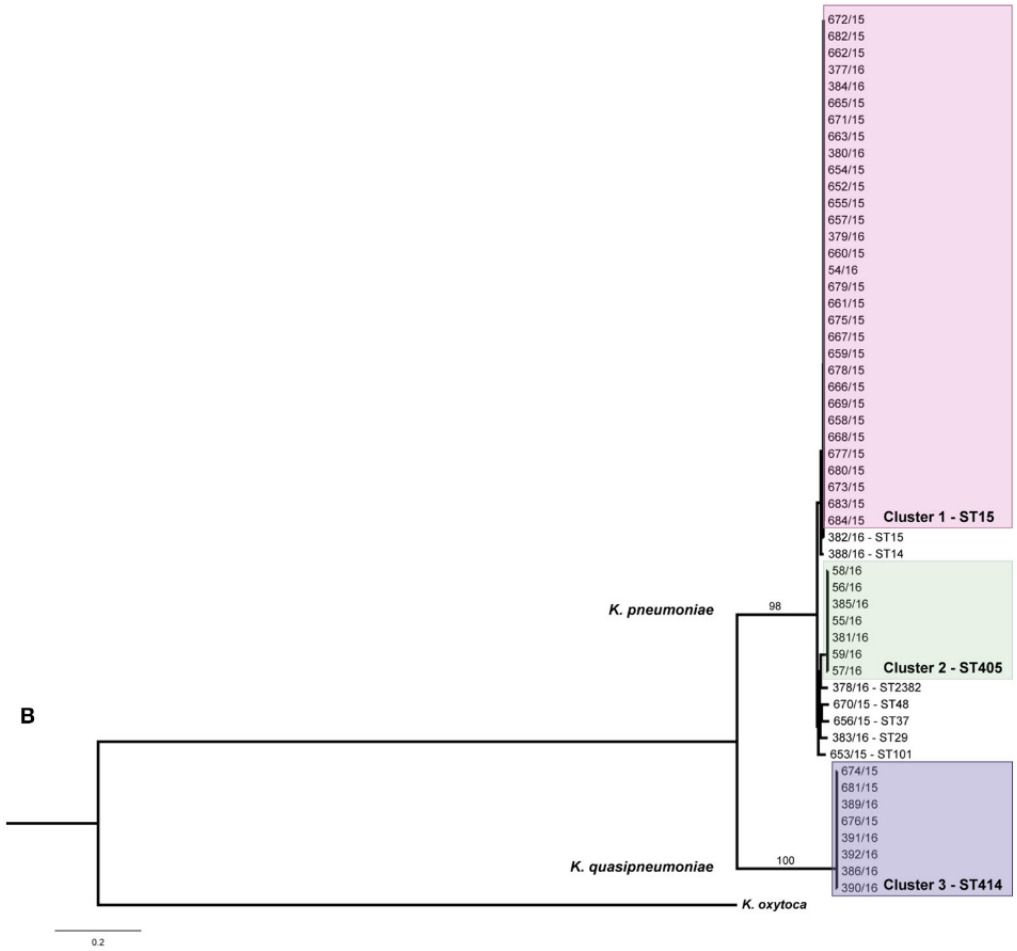


Figure 3. Phylogenetic relationship of sequenced isolates. The maximum likelihood tree was calculated based on 468,250 SNPs filtered after mapping to the reference genome. K. oxytoca KONIH1 was included to root the tree. Values on branches display to support values (100 bootstraps). The three outbreak clusters are depicted by coloured boxes. Isolates 680/15 and 684/15 originated from the same patient.

The metagenomics approach has been applied to detect pathogens from feces of swine with diarrhea, from stool samples of diarrheal patients, to detect viral respiratory infections in children, and to analyze the changes in the nasopharyngeal bacterial microbiome after viral upper respiratory tract infection (WB4). Efforts have been made to develop internal controls for metagenomics sequencing. A study has been conducted to evaluate the performance of metagenomics in comparison with semi-quantification of urine culture for establishing clinically relevant bacterial growth in urine.

In WP6, NGS was applied in laboratory diagnosis for three arboviral strains (one phlebovirus, one West Nile virus and one Crimean-Congo hemorrhagic fever virus) causing CNS infections. 16S metagenomics was applied in samples from ”known” and ”unknown” cases as a pilot study to evaluate the feasibility of metagenomics analysis in the clinical diagnostic laboratory. In order to study the feasibility of NGS for diagnostics in the clinical laboratory, a pilot study to assess the cost-effectiveness of NGS in the laboratory is being conducted. Protocols and workflows are being developed in attempt to shorten the turnaround time of NGS in clinical microbiology.

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.

The COMPARE project and European Centre for Disease Prevention and Control (ECDC) initiated a pilot project where WP4/7 and WP9 were especially active. The project concerns the sharing of whole genome sequence data between European public health laboratories and ECDC for the purpose of real-time data sharing and faster detection and response to multi-country foodborne outbreaks. The pilot included genome sequences of Salmonella enterica and 9 member states participated. The project will be evaluated in September.

APHA staff has worked on assessing appropriate methods for outbreak detection using WGS data, and comparing detection performance against standard non-WGS data, to help inform strategies. The informed strategies may differ in contexts where WGS is currently heavily biased and non-random compared with a future situation where sequencing is completed as standard. APHA has also been gathering UK data and analyzing source attribution methods for four different WGS outcomes to identify an efficient standardized method.

ANSES staff has worked on developing statistical methods and guidelines for delineating related from non-related isolates using WGS data applied to four Salmonella outbreaks. ANSES was involved in the construction of a representative genome dataset from four member state datasets to analyze the genetic evolution of Salmonella monophasic variant S. I 4,[5],12:i:-

The benchmarking study in WP4 Task 2.2 aiming at exploring different approaches and models for source attribution based on Salmonella Typhimurium sequencing data is progressing. Metadata are shared on the COMPARE share site and raw data are analyzed for resistance genes, plasmid replicons, MLST type and phylogeny using the CGE tools ResFinder, PlasmidFinder, MLST 2.0 and CSI Phylogeny and core-and whole-genome MLST using BioNumerics. Source attribution models are still being explored and developed using machine-learning methods, network analysis and Bayesian modelling.

Figure 4. WP4/7 participants at the F2F meeting, 22-23 May 2018, Robert Koch Institute, Wernigerode, Germany.

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.

The collection of genetic sequences of avian influenza viruses from both poultry and wild birds from different countries around the world into a common, open access database, GISAID, continued (Global consortium for H5N8 and related viruses, moderated by UEDIN, FLI, EMC). Following the intercontinental epidemic of H5N8 HPAIV in the winter of 2014-2015 reported on previously, there was an epidemic of H5N8 HPAIV and some reassortants in the winter of 2016-2017, with infection of many wild birds and poultry holdings in Europe. It is intended to repeat a global analysis for this epidemic. Subsequently, in the winter of 2017-2018, there was another such epidemic, but with far fewer cases. The involvement of raptors, such as buzzards, eagles, and falcons, in these epidemics, was prominent and will be investigated further and the involvement of white-tailed eagles was reported by FLI. A manuscript of linkage between Dutch and Korean H5N6 strains is in preparation (APHA-EMC).

UCAM, EMC, and UK-Bonn/Charité have collaborated on the publication of two papers on ancient viruses. 1) Ancient human parvovirus B19 in Eurasia reveals its long-term association with humans (PNAS Jul 2018) and 2) Bronze and Iron Age human hepatitis B viruses (Nature May 2018). Two additional papers on ancient viruses are anticipated. Work has been done on a computational method to separate NGS sequencing reads in cases of double infections. Consensus sequences made in cases of double infections can be highly misleading, giving a blurred picture of viral evolution and distorting the topology of phylogenetic trees. Our program is being evaluated against six suspected double HBV infections and against simulated datasets.

UCLM published an innovative meta-omics approach integrating metatranscriptomics and metaproteomics to characterize bacterial communities in the microbiota of the vector Ixodes ricinus. We observed that the metatranscriptomic approach together with metaproteomics provided better characterization of tick bacterial microbiota by increasing bacteria identification and support for identified bacteria with putative functional implications. During this report period, UCLM has also published the first characterization of *Culicoides imicola* microbiota and the impact of biotic and abiotic factors on these microbial communities. These results contribute to characterizing the role of the microbiome in insect adaptation and its utility in predicting geographic expansion of Culicoides species with potential implications for the control of vector-borne diseases. Raw metagenomic reads for the *C. imicola* and proteomic data for host identification are deposited in the Dryad repository [doi:10.5061/dryad.mr401g7].

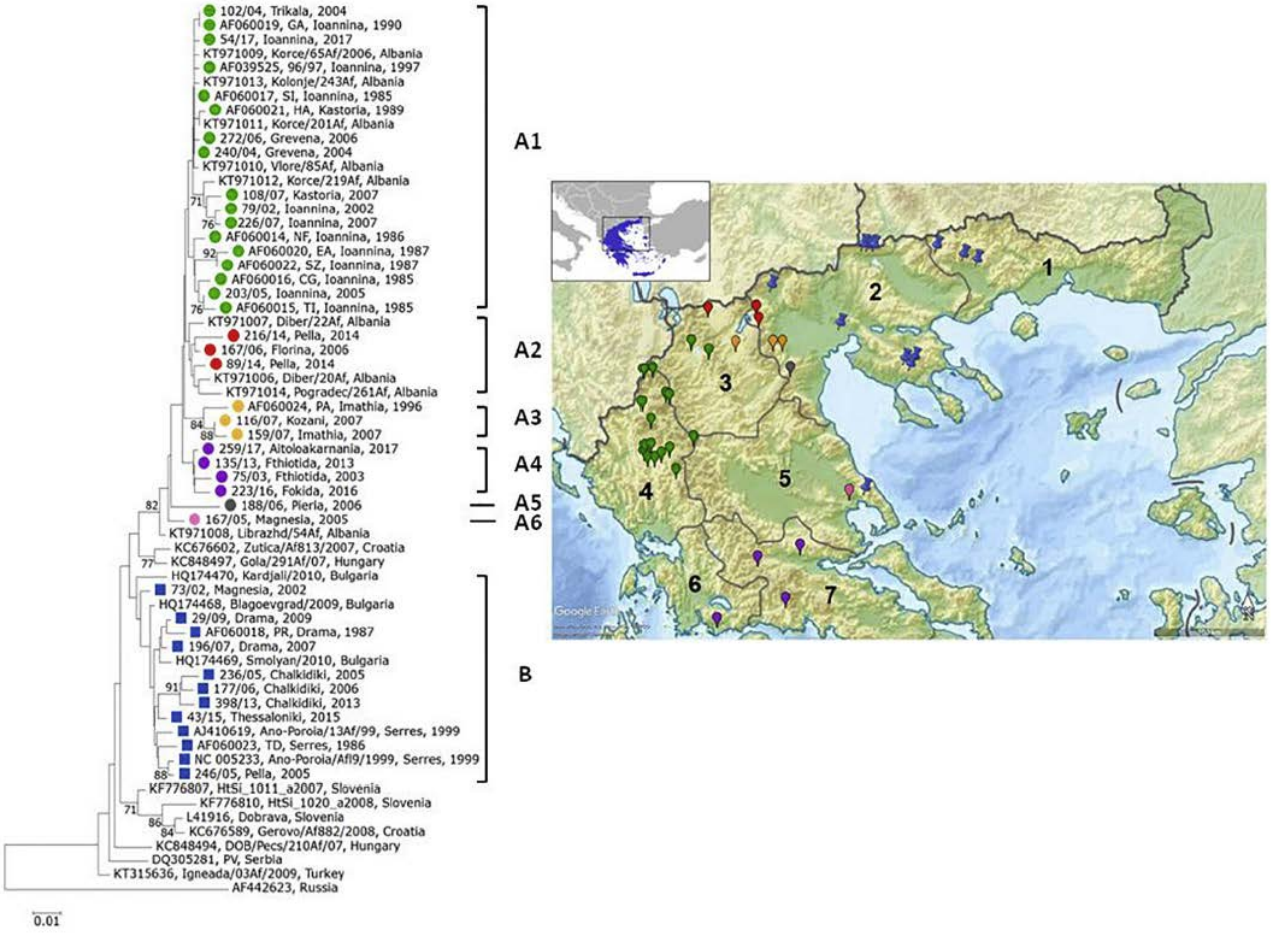
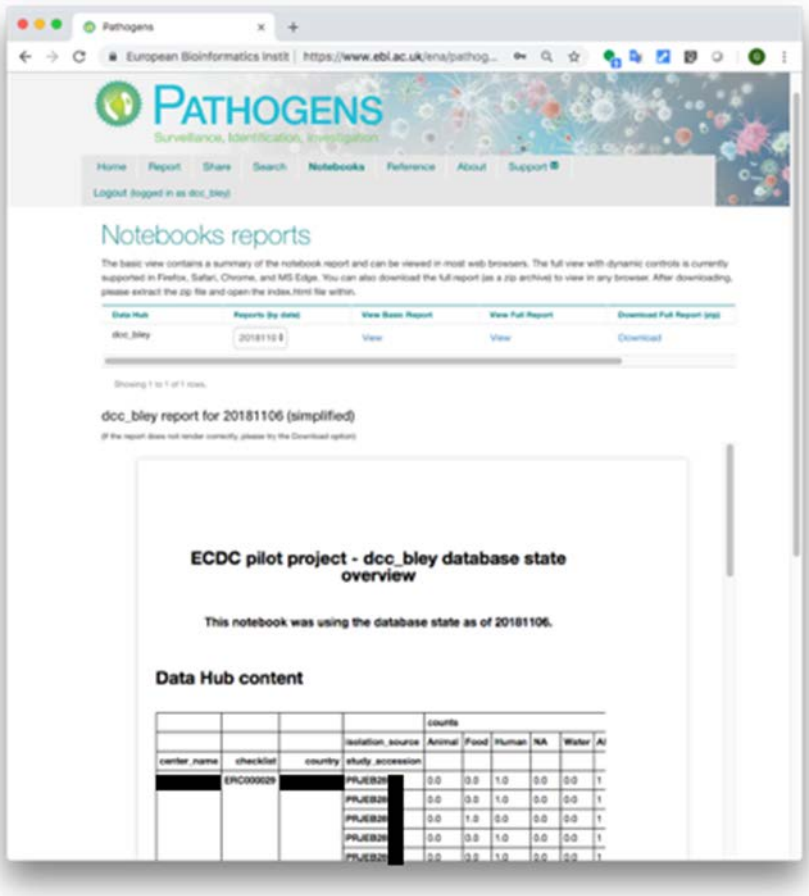


Figure 5. AUTH sequenced and performed phylogenetic analysis in relation to geographic distribution of Dobrava-Belgrade hantaviruses detected in clinical cases in Greece. Above shows the phylogenetic clustering and geographic distribution of DOBV in Greece.

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.

We have continued to provide and support the COMPARE platform across its broad range of application areas. Our datahubs provide a center point for a number of initiatives within COMPARE, including AMR, global sewage and food metagenomics. During the reporting period, we have taken the Pathogen Portal (https://www.ebi.ac.uk/ena/pathogens/home) to full life-cycle support across COMPARE data operations, spanning data reporting, sharing, search and visualization. The last of these components is provided by the Notebook system. Here, working closely across partner sites, we have integrated directly accessible Notebooks into the web site and supported rapid cycles from statements of datahub user requirements, though Notebook design and launch in the system (Figure 6). A particular focus of our work has been the ECDC/EFSA pilot, in which we have provided datahubs for the testing of upload, sharing and analysis. This support has driven rapid extension of functionality in relevant areas, such as for internal analysis process tracking systems and the addition of cgMLST to the CGE analysis workflow. Finally, our methods development work can seen the KMA publication and further work towards the Evergreen publication.



Figures 6 Screenshot of summary Notebook view within Pathogen Portal (some fields redacted as data are under pre-publication confidentiality).

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.

In the period from March 2018 to August 2018, WP10 has made advances in the following areas:

The message map, which was finalized and fully integrated with the dynamic stakeholder list, and enriched by linking it to a collection of 64 narrative examples, related to narrative paradigms and master storyboards, is in progress to be turned into an electronic format, to be used as an operational tool by communicators. The goal is to provide communicators with sample stories that could be used both to capture audience reactions to information and the impact on people of news about epidemics and preventive measures (including fake news), and to shape tailored message based on a narrative framework. To our best knowledge, the COMPARE message map is the first and sole risk communication tool today available, explicitly designed within a narrative framework and inspired by narratology theories.

The COMPARE Tool Box is now in progress. It is now hosted in the domain https://www.riskcommunication-compare.eu/ , where it can be already accessed by COMPARE partners.

We are also pursuing the development of specific tools, including those initialized in the previous period (i.e., Stakeholder dynamic list; Narrative Paradigm Generator; Risk Communication Ecosystem; Message Templates; Additional Templates; Digital Trust Model, Persuasion Matrix). We are also developing a downloadable app to guide communicators to create risk communication campaign based on COMPARE Message Map.

Finally, Workpackage 10 is organizing a dissemination event, the Vaccines, Anti-vax, and Health Communication Workshop for 26-27 October 2018, near Pordenone, Italy. The rationale of the workshop is to address vaccine hesitancy and refusal, which are complex phenomena, indubitably due also to disinformation, scientific illiteracy, and medical quackery. Yet, medical education, correct information, prosecution of charlatanism are not enough, although essential. Why do so many educated people, even apparently scientific literate, distrust vaccination and believe in unbelievable conspiracy theories concerning vaccines? The crisis of trust, involving scientific expertise and health communication, demands a more in-depth analysis and this is the main aim of the workshop, which will also have a public session involving general practitioners and health professionals. The workshop will be held under the sponsorship of the Italian Ministry of Health and the Medical Association of Pordenone, it will provide CME credits to its participants (in Italian only).

Spadaro: *Piazza Mercatello during 1656 plague* (San Martino Museum - Naples)

26-27 OCTOBER 2018

VACCINES, ANTI-VAX, AND HEALTH COMMUNICATION

Participants

- **Gerardo D'Amico**, scientific writer and journalist, vice editor-in-chief, RaiNews24, Rome
- **Elena Fattori**, vice-president of the Standing Committee Food and Agriculture of the Italian Senate, Rome
- **Alberto Garcia**, UNESCO Chair on Bioethics and Human Rights, Rome
- **Donato Greco**, past-Director of the Laboratory of Epidemiology and Biostatistics of the Italian National Institute of Health, Roma
- **Guido Lucchini**, Chairman of the Medical Association of Pordenone, Pordenone
- **Alessandra Martini**, European Commission. Research & Innovation DG, Unit RTD.E.3. Fighting infectious diseases and emerging epidemics
- **Emilio Mordini**, COMPARE Risk Communication, Responsible Technology, Paris
- **Giorgio Mustacchi**, Professor Emeritus of Medical Oncology, University of Trieste, Trieste
- **Andrea Rubin**, Sociologist, "Observa Science in Society", University of Salerno, Salerno
- **Giorgio Simon**, Managing Director, Local Health Authority of Pordenone, Pordenone
- **Fabrizio Turoldo**, Professor of Moral Philosophy, University Ca' Foscari, Venice

COMPARE (*Collaborative management platform for detection and analyses of (re-) emerging and foodborne outbreaks in Europe*) is funded by the European Commission H2020 Programme (Grant n. No. 643476)

Friday 26 October
(internal session)

How to talk to patients, journalists and policy makers

Arrival and registration
14:00 – Opening
14:15 – Informal Presentations
16:00 – Roundtable
19:00 – Closing
19:30 – Business Dinner
21:00 – Fireplace talks

Saturday 27 October
(public session)
Working language Italian

Vaccination and autism: what makes a hoax successful?

09:00 – Opening
09:30 – Roundtable moderated by Gerardo D'Amico
10:30 – Coffee
11:00 - Questions and Comments
12:30 – Conclusions
12:45 – Informal talks and refreshments
13:30 – End of the workshop

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26-27 ottobre 2018

There are no fees. Participation in the internal session is only by invitation, participation in the open session is restricted to health professionals. Advance registration is necessary. Please send an email to compare@responsibletechnology.eu providing your name, main qualification and affiliation.

Figure 7. The Vaccines, Anti-vax, and Health Communication Workshop held 26-27 October 2018, near Pordenone, Italy, organized by Workpackage 10.

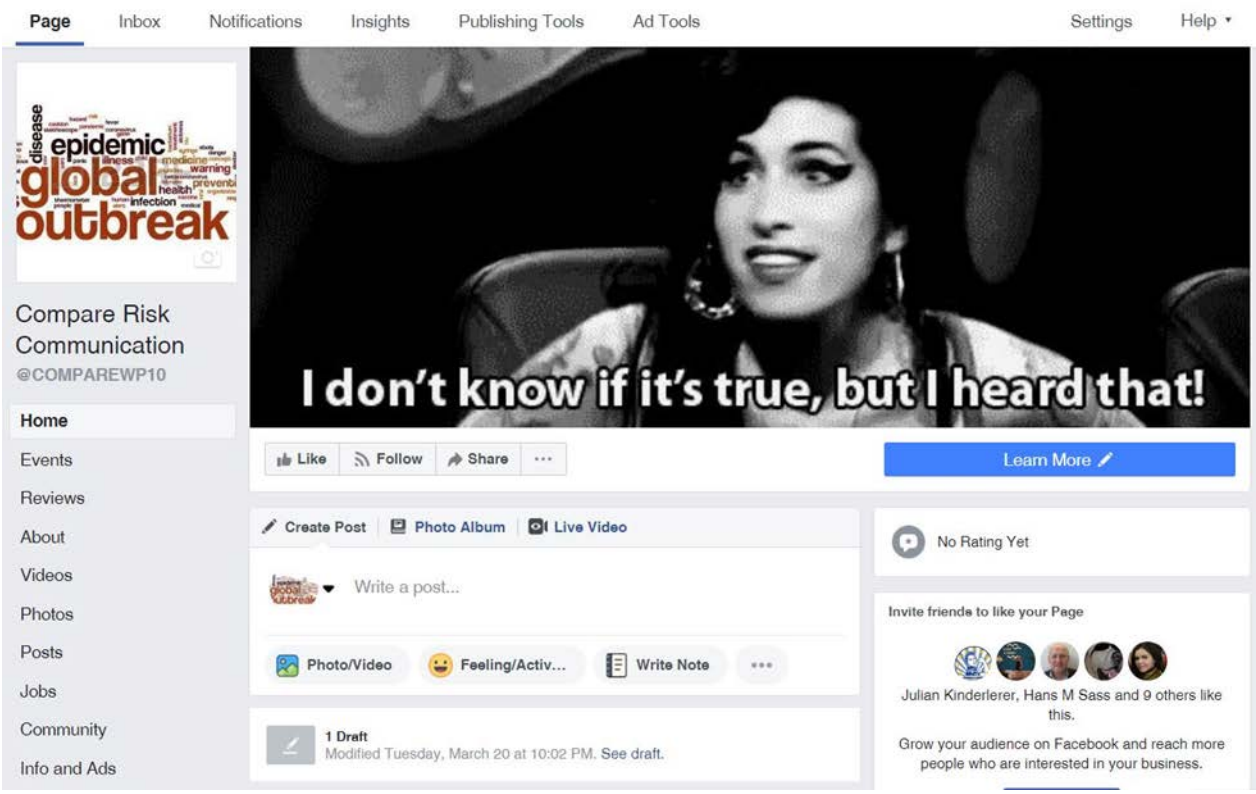

Figure 8. FACEBOOK COMPARE Risk Communication page.

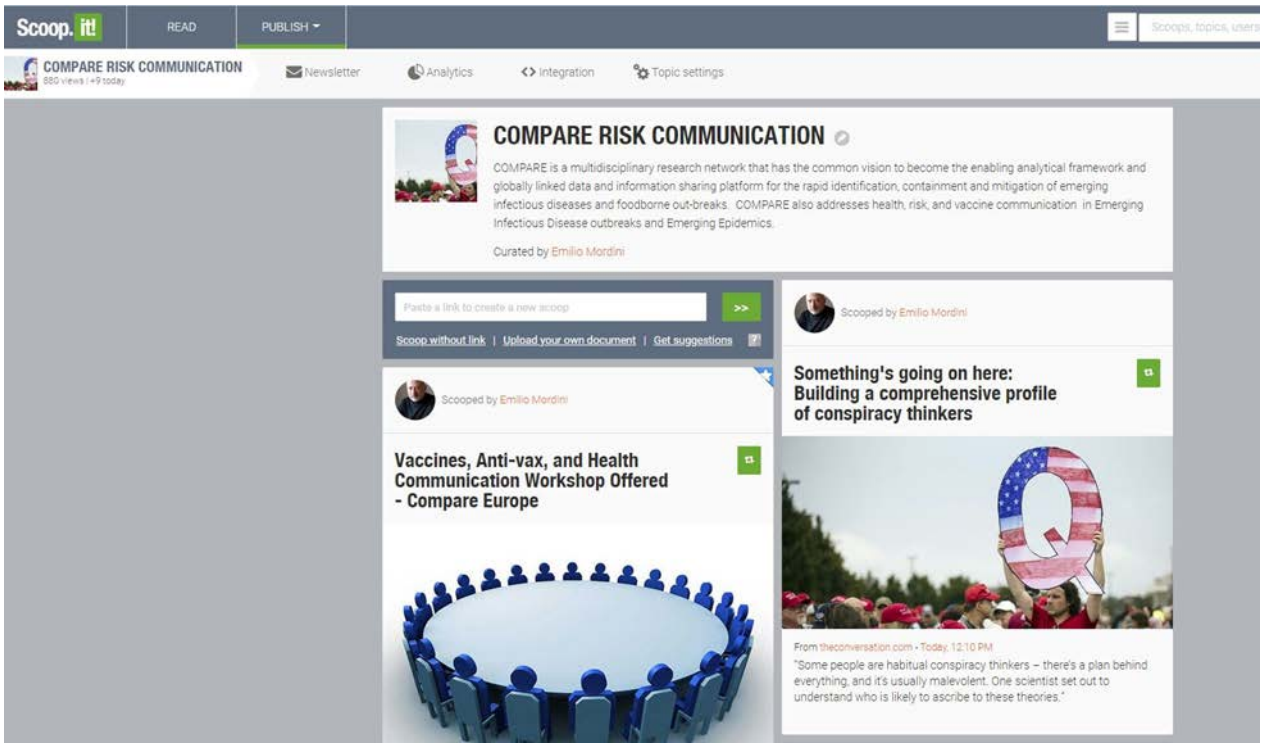

Figure 9. SCOOP.IT! page.

WP11 – User consultations

The fourth round of the COMPARE Expert Advisory Panel (EAP) meetings was held during the annual COMPARE meeting at the Technical University of Denmark (DTU) in Lyngby, Denmark. The members of the EAP were invited and encouraged to attend the COMPARE meeting (28 February, 1 and 2 March 2018). In particular, EAP members were encouraged to participate in the WP meetings and cross-WP meeting on Barriers 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 on March 1, 2018. During this meeting, the EAP members were invited to provide their feedback to the Executive Board on the progress of the project and strategic choices made by COMPARE thus far. In particular, the plan for the development of the COMPARE sustainability plan was presented and EAP members were invited to give feedback on this plan. In total, 18 EAP members attended this meeting: 2 from EAP Domestic Animals, 4 from EAP Barriers, 7 from EAP Food Safety, 1 from EAP Wildlife, 1 from EAP Clinical Health, and 3 from EAP Public Health. In addition, two members of the Ethics Advisory Board (EAB) attended this meeting.

Furthermore, during the COMPARE meeting, a working group session on data sharing was held by the WP12 team and EAP members. In total, 9 EAP members attended this session, the majority representing the EAP Barriers (4 members), 3 from EAP Food Safety, 1 from EAP Domestic Animals, and 1 from Public Health.

A deliverable report (D11.4) was submitted summarizing abovementioned EAP meetings in April 2018. Meanwhile in August, preparations have started for the final round of EAP meetings.

Currently, there are two pilots with members from the EAP:

- ECDC/EFSA pilot WP4/7, 9 and 12
- CDC-Guangdong China with WP5/8

A pilot with the food industry is currently being discussed between the COMPARE management team (Marion Koopmans, WP11 leader and co-coordinator, and Frank Aarestrup, coordinator).

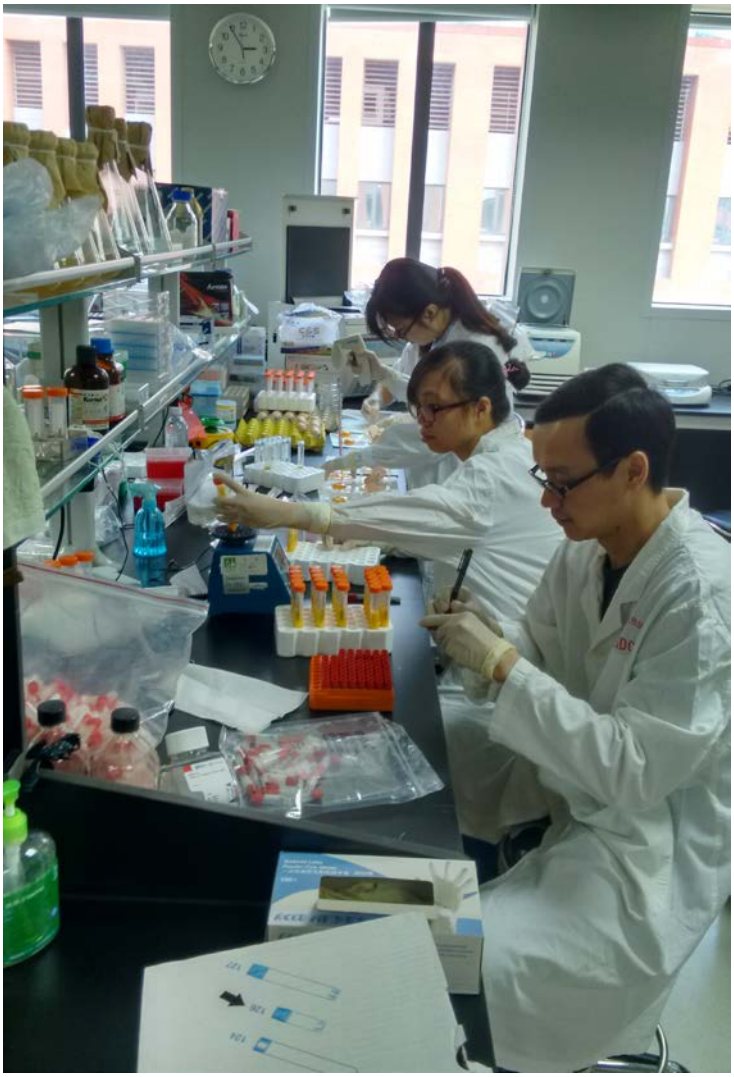

Figure 10. Lab work from the pilot with CDC-Guangdong China and WP5/8.

Preparations are being made for the involvement of EAPs in the sustainability plan of COMPARE, amongst others through a questionnaire.

Besides the above-mentioned Barriers meeting during the COMPARE General Meeting, the barriers work of WP12 in collaboration with the EAPs will be a continuous effort. The joint WP11 and WP12 study into ownership barriers to the sharing of microbial genetic data was published this May in PloS One: https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0195885. Marion Koopmans (WP11 leader) is co-author on a paper with George Haringhuizen (WP12 leader) on the Nagoya Protocol, currently under review. In addition, a study into barriers and enablers to the sharing of outbreak-related data during the MERS epidemic in Arabian Peninsula, with particular focus on Qatar, is currently ongoing. The study is funded by Wellcome trust but could provide insights useful for COMPARE, and involves some of the international organizations also represented in the EAPs.

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.

During the reporting period, the WP12 working group continued to work on Deliverable 12.2: developing a charter of principles and ethical framework for the COMPARE community. Two main activities were so far performed: (1) field research to assess the main issues related to data sharing according to different stakeholders and possible/ perceived solutions, through interactive workshops; and (2) a literature review to obtain contextual insights and assess developed knowledge from relevant literature. An oral presentation about the work performed in WP12 so far and the planning for the next year was given by the WP leader at the COMPARE Executive Board meeting on 6 September 2018, at Schiphol, Amsterdam.

In accordance with Tasks 4, 5 and 6, WP12 developed, and was active on the negotiations with the partners of the Salmonella pilot project (ECDC and EFSA), an agreed Confidentiality Agreement (CA) and Terms of Reference (ToR) for participating EU Member States and the other stakeholders involved. In addition, WP12 was involved in the development of the evaluation questionnaire for the pilot project, by proposing questions in relation to the developed agreements (CA and ToR), and the level of engagement of Member States on this development.

As case studies and for real-time information gathering and the sharing of knowledge and experience gathered by our research, internationally relevant meetings have been attended on the topic of data sharing and public health. In April 2018, WP12 was present at the GMI 11 Meeting, Geneva, Switzerland, in which we presented a poster titled “Pathogen sequence-databases under the Nagoya Protocol: What can we learn from biobanks in view of the future of health protection?”. In addition, an oral presentation was given by the WP leader on the global sharing of NGS data, especially concerning the recent developments within the international political and legal context, and the impact of those for the timely sharing of pathogen isolates and genomic data. In May 2018, WP12 attended the ZIKA Symposium in Marseille, France, where the aforementioned poster was again presented, in addition to two oral presentations. The first presentation, from the WP leader, elaborated on reflections about ethical and legal considerations for global ZIKA virus research, and possible ways of improving global cooperation in such context. The second presentation, by the WP researcher, elaborated on challenges and opportunities for data sharing in public health emergencies, with a final reflection on key aspects for improving such efforts.

Lastly, the WP12, in collaboration with the COMPARE leadership, finalized a policy (concept) paper regarding the future of the sharing of pathogen genetic resources in relation to the most recent legal and political global developments in the field. The paper is an assessment of how biobanks and culture collections have been dealing so far with the sharing of pathogen isolates and sequence data under the norms of sovereignty rights of countries and the international treaty Nagoya Protocol (to the Convention of Biological Diversity). Furthermore, we reflect on if/how such models can be adapted to include genomic sequence data for existing databases, as COMPARE, and ultimately how they can be improved as an attempt to facilitate the sharing of pathogen genetic resources, so important for outbreak and epidemic control, response and research. This paper has been submitted for publication in a scientific journal, and is currently under revision.

WP13 – Dissemination and Training

Members of the COMPARE Consortium share their experiences and results from COMPARE at conferences and workshops all over the world.

Regarding Training, COMPARE is providing e-learning options that can be accessed online via the COMPARE portal. There are three e-learning courses available from the COMPARE website currently:

- Whole genome sequencing of bacterial genomes - tools and applications
- Metagenomics applied to surveillance of pathogens and antimicrobial resistance
- Antimicrobial resistance - theory and methods

Members of the COMPARE Consortium continue to publish manuscripts in peer-reviewed scientific journals. These are reported via the public website. There are more than 125 research articles that acknowledge COMPARE support.

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

Figure 10. COMPARE Tweets. 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 has finished collecting and analyzing data from the questionnaire to estimate the value of safety in six European countries. Results from this study suggest that people are willing to pay €22.70 per household per month on average for an early warning system for infectious diseases and foodborne outbreaks aiming to increase the safety of citizens. This work is relevant for Task 4 (Develop and apply a methodology to value safety in several countries). Furthermore, EUR has finalized a review on economic evaluations of pandemic outbreaks which is relevant for Task 2 (Identify and where necessary develop state-of-the art costing methodologies for the different elements in the framework) and Task 6 (To assess options for refining selected elements of COMPARE in view of improving the overall cost effectiveness of the system.) One of the conclusions of this review is that economic evaluations so far have not looked at health system type of interventions focusing on disease surveillance. EUR has started working in collaboration with EMC on a case study aiming to describe the policy options related to mitigating and/or preventing disease outbreaks resulting from utilizing surveillance data from NGS and real-time sharing of that data compared with traditional testing methods with and without data sharing. As an illustrative case study, we will use data from an ongoing study in Guangdong aiming to improve emerging disease detection and influenza A surveillance by sequencing full genomes of poultry, eggs and other pets at local markets.

Civic Consulting has completed or is in the process of completing data collection for the cost-effectiveness case studies with four institutions so far: the Friedrich-Löffler-Institut (DE), the Istituto Zooprofilattico Sperimentale della Lombardia e Dell'Emilia Romagna (IT), Public Health England, and the Animal and Plant Health Agency (UK). The four case studies conducted so far cover both routine surveillance activities as well as outbreak situations, and the pathogens concerned include avian influenza (FLI, APHA) as well as various foodborne diseases, notably Salmonella and Listeria (PHE, IZSLER). Detailed cost data have been collected for all four case studies for the use of WGS as well as the next-best conventional method(s), and suggests that key factors influencing costs include the batch size for processing, the professional staff time required for the bioinformatics analysis, and the degree of automation in sample processing. Qualitative data has been collected regarding the benefits of using WGS at the institutional level. We are also exploring potential approaches for further quantifying the benefits of WGS, e.g., regarding the detection of more and smaller clusters, the detection of 'slow-burn' outbreaks, or ex-post assessments of potential cases averted, in partnership with our case study institutions.

Further potential case studies are currently being pursued in the United States (the FDA's GenomeTrakr), Argentina (Instituto Nacional de Enfermedades Infecciosas), Belgium (University of Antwerp), Canada (Public Health Agency Canada), and concerning the MinION (in cooperation with EUR). Interviews were also conducted with the International Livestock Research Institute (ILRI) in Kenya, but the institution was determined to be unsuitable for a case study due to the lack of routine surveillance activities.

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.

An Amendment to the Grant Agreement was submitted to the EC regarding the work from Workpackage 5/8 and the gain of function activities.

As was mentioned under Workpackage 4/7 and 12, a pilot project with eh ECDC and EFSA was negotiated and performed. The pilot project is currently being evaluated by the participants and the ECDC7Steering Committee.

The Consortium continues to submit deliverables. The COMPARE public website maintains a list of those Deliverables accepted by the EC and available for public dissemination.

The COMPARE General Meeting 2019 is planned for 27 February – 1 March 2019. It will be held at the technical University of Denmark campus. The Young COMPARE research event will be held 26 February 2019.

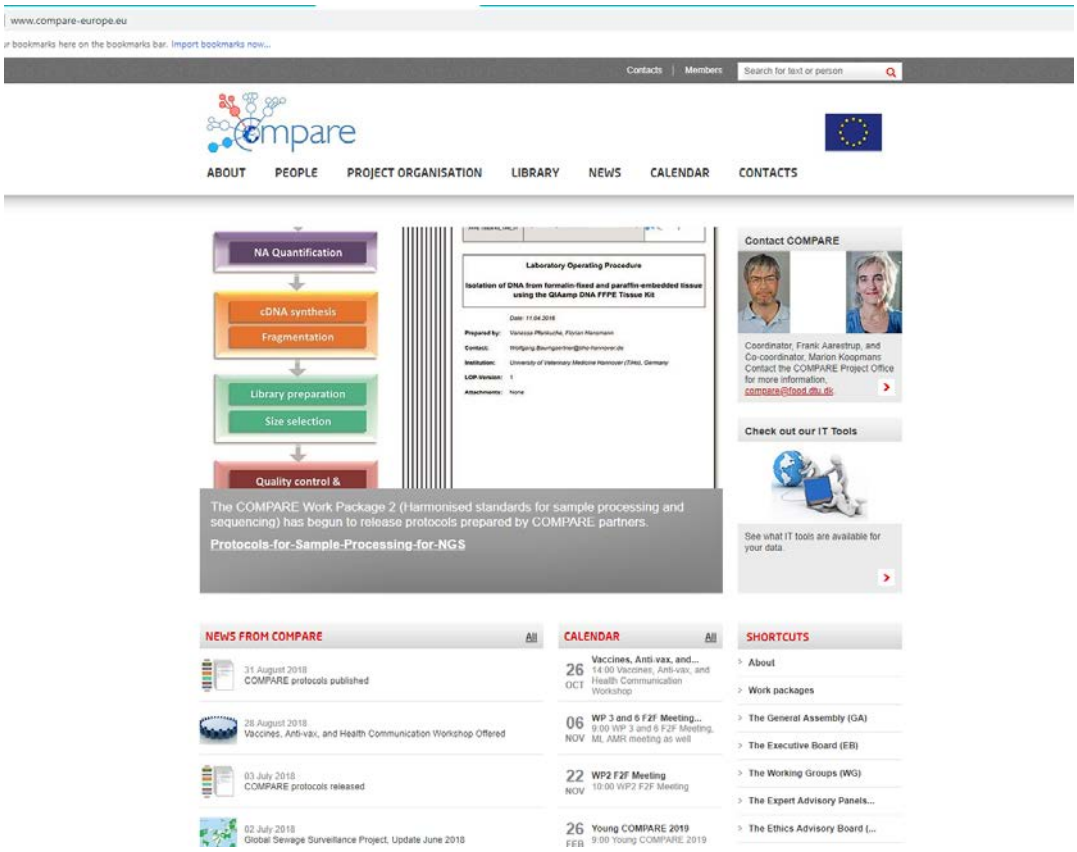

Figure 11. COMPARE public website.

COMPARE Partners