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Deliverable

13.2 Leaflet and templates for promotional material in COMPARE corporate style

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Contents

Deliverable Description

In WP 13, Dissemination and Training, Task A2 is titled Producing and distributing promotion materials applying consistent COMPARE identity and visibility. Deliverable 13.2 is the leaflet and templates for promotional material in COMPARE corporate style.

COMPARE has developed and applied a ‘corporate identity’ that will be applied in all internal and external communications of COMPARE. The COMPARE identity includes a logo (see upper left-hand corner of this page) and standard colour schemes and font types, as demonstrated in this document. These standards have been used to develop templates for presentations, Deliverables, general document papers, posters, and a two-page leaflet describing the project (See Annex 1). Additional types of templates will be designed based on the standards as needed.

Templates can be found on the COMPRE website for download (http://www.compare-europe.eu/Library/COMPARE-templates), from the COMPARE Share Site for download, or from the Project Office (compare@food.dtu.dk).

The corporate identity is also used in internal documents and reports, such as meeting notes and Workpackage Snapshots (see Deliverable 15.3, Internal reporting templates). The COMPARE corporate identity is also visible online and in social media; via the website (www.compare-europe.eu) and the COMPARE Twitter account (@CompareEurope).

Besides the presence online and in social media, COMPARE will be identified when the lead investigators speak at national and international conferences, seminars and symposia via the presentation template, use of logo and financial support statement (‘This work was supported by the European Union’s Horizon 2020 research and innovation programme, COMPARE, grant agreement No. 643476.’). At these professional gatherings, many of our stakeholders are also present. The lead investigators will leverage this to the benefit of raising awareness of COMPARE at these stakeholder events by presenting COMPARE and its results and added value to public and veterinary health and food safety.

Annex I. COMPARE Leaflet

The following is the COMPARE leaflet.

COllaborative Management Platform for detection and Analyses
of (Re-) emerging and foodborne outbreaks in Europe

COMPARE is a multidisciplinary research network that is set up with the common vision to become the enabling analytical framework and globally linked data and information sharing platform system for the rapid identification, containment and mitigation of emerging infectious diseases and foodborne outbreaks. The system sets out to integrate state-of-the-art strategies, tools, technologies and methods for collecting, processing and analyzing sequence-based pathogen data in combination with associated (clinical, epidemiological and other) data, for the generation of actionable information to relevant authorities and other users in the human health, animal health and food safety domains.

Next Generation Sequencing (NGS) used for *Whole Genome Sequencing* (WGS) or *Whole Community Sequencing* (WCS or metagenomics) enables generating the complete genomic information from the isolate or sample independent of both the **sector** (public health, veterinary health, food safety), and **the type of pathogen** (viruses, bacteria, parasites). The outputs (sequence data) provide one common language that can be exchanged and compared **between laboratories and over time,** in combination with other associated data defined here as **“metadata” including contextual data** (e.g. data on sample type and process, clinical, microbiological, epidemiological and other data) **primary data** (raw sequence reads) and **derived data** (e.g., genomic alignments of reads, assemblies and functional annotation data sets). COMPARE aims to harness the rapid advances in these technologies to improve identification and mitigation of emerging infectious diseases and foodborne outbreaks.

To this purpose, COMPARE will establish a “One serves all” analytical framework – as depicted in the figure on the following page– showing the different components of the COMPARE Analytical Framework.

For more information about the project please contact:
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- Prof. dr. Marion Koopmans of Erasmus MC: m.koopmans@erasmusmc.nl

COMPARE runs from 1 December 2014 to 30 November 2019. The consortium has been awarded EUR 20 million funding under the European Commission’s Horizon 2020 programme.

The COMPARE consortium consists of the following members:

Technical University of Denmark
Erasmus University Medical Center
Statens Serum Institute
Friedrich Loeffler Institute
Agence nationale de sécurité sanitaire de l’alimentation, de l’ environnement et du travail
Robert Koch-Institut
Istituto Superiore di Sanita
European Molecular Biology Laboratory
Animal and Plant Health Agency/DEFRA
Rijksinstituut voor Volksgezondheid en Milieu
Universitaetsklinikum Bonn
University of Edinburgh
Universiteit Antwerpen
Academisch Medisch Centrum Universiteit van Amsterdam
University of Cambridge
Universidad de Castilla- la Mancha
Artemis One Health Research bv
Aristotelio Panepistimio Thessalonikis
Tierärztliche Hochschule Hannover
Erasmus Universiteit Rotterdam
Fondation Mérieux
Magyar Tudomanyos Akademia Wigner Fizikai Kutatokozpont
Institut Français de Recherche pour l’Exploitation de la Mer
Responsible Technology
The Australian National University
Leibniz Institut Deutsche Sammlung von Mikroorganismen und Zellkulturen
Civic Consulting
University of Bologna
Wellcome Trust Sanger Institute

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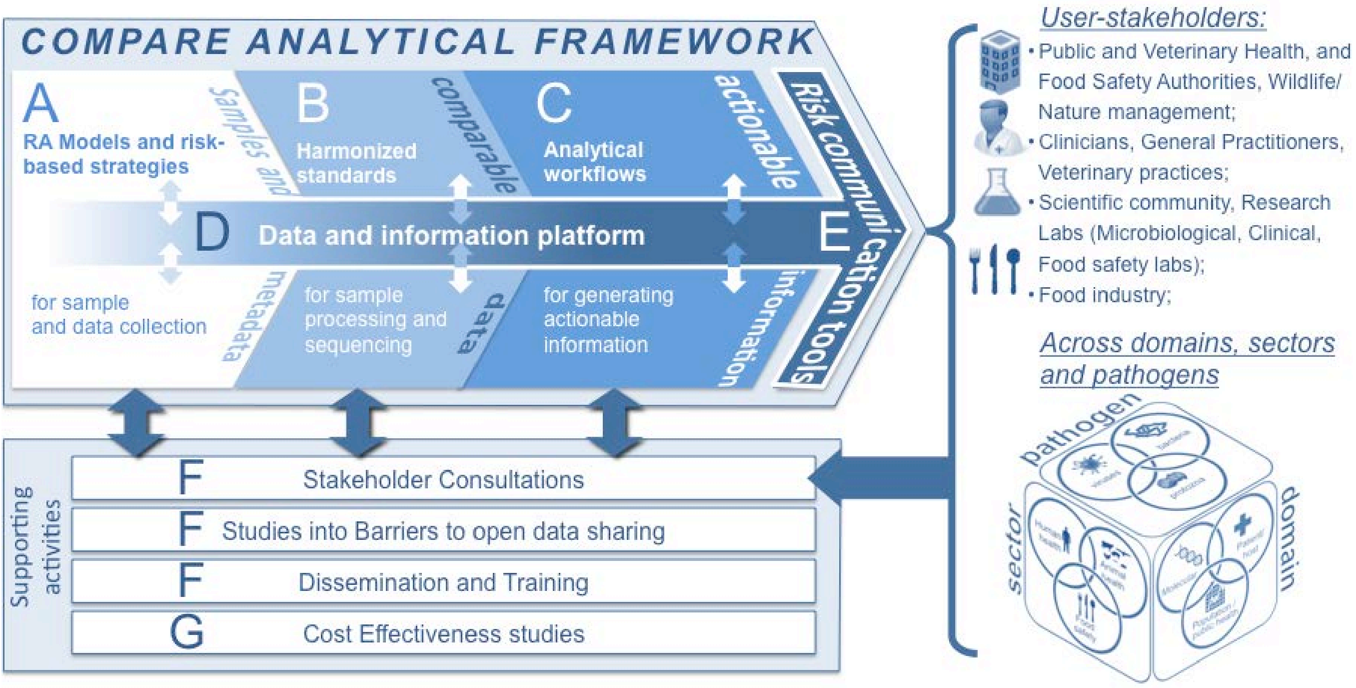

A. **Risk-assessment models and risk-based sampling and data collection strategies** that enhance our capacity to detect potential disease outbreaks;

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 and 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, food-borne 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 extend 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, (iii) **dissemination and training activities;**

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

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Annex 2. Presentation Template

The following is an example of the COMPARE presentation template in use.

COllaborative Management Platform for
detection and Analyses of (Re-) emerging
and foodborne outbreaks in Europe

Closing the Kick-off meeting

This project has received funding from the *European Union's Horizon 2020 research and innovation programme* under grant agreement No 643476.

What are our challenges

- What needs solutions?
  - External interactions
    - Scientifically
    - Politically
    - Communication
  - Cluster analysis
  - Internal interactions
    - Economy
    - From biology to IT and back again

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