



---

**Deliverable D-JIP2-4.2.3**  
**Workpackage JIP2-WP4**  
**Data platform to facilitate**  
**risk-analysis and**  
**outbreak control**

Responsible Partner: BfR

Contributing partners: IZS-AM, FHI/NIPH,  
IZSLER, FLI, FOHM/PHA, ISS



This deliverable is part of the European Joint Programme One Health EJP. This project has received funding from the European Union's Horizon 2020 research and innovation programme under Grant Agreement No 773830.



## GENERAL INFORMATION

European Joint Programme full title	Promoting One Health in Europe through joint actions on foodborne zoonoses, antimicrobial resistance and emerging microbiological hazards
European Joint Programme acronym	One Health EJP
Funding	This project has received funding from the European Union's Horizon 2020 research and innovation programme under Grant Agreement No 773830.
Grant Agreement	Grant agreement n° 773830
Start Date	01/01/2018
Duration	60 Months

## DOCUMENT MANAGEMENT

Deliverable	Integration and analysis of epi-data from 4.1 → WGS-Epi module and selected features from IA-1, WP2, WP3
WP and Task	JIP-WP4: Data platform to facilitate risk-analysis and outbreak control; T2: Development of a platform-independent tracing framework ST3: Integration of surveillance and outbreak data into the software platform for analysis
Leader	BfR
Other contributors	IZS-AM, FHI/NIPH, IZSLER, FLI, FOHM/PHA, ISS
Due month of the deliverable	M42
Actual submission month	M47
Type <i>R: Document, report</i> <i>DEC: Websites, patent filings, videos, etc.</i> <i>OTHER</i>	DEC, R
Dissemination level <i>PU: Public</i> <i>CO: confidential, only for members of the consortium (including the Commission Services)</i>	PU

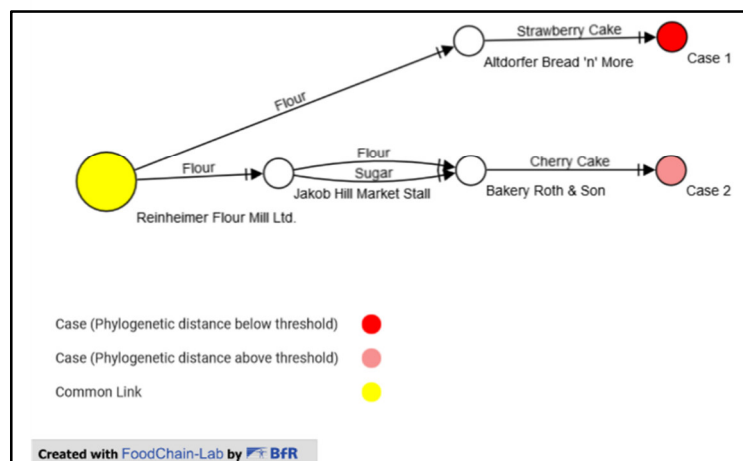
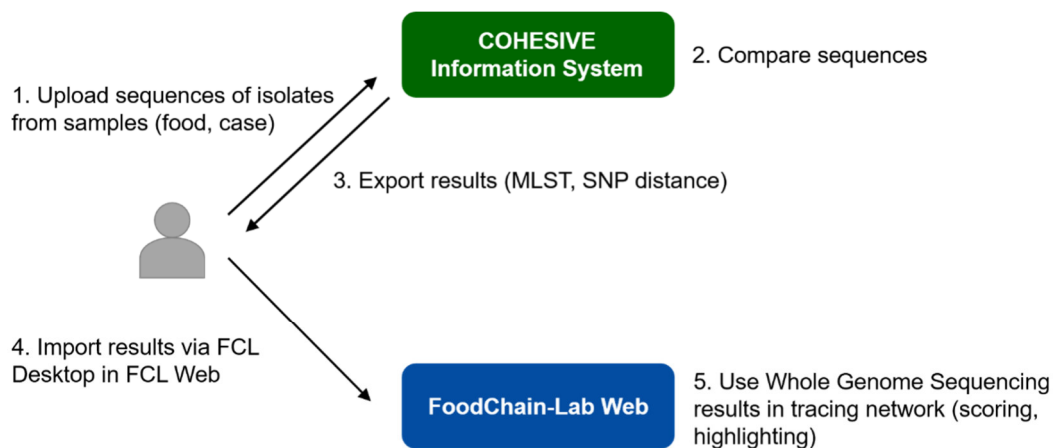


# INTEGRATION OF SURVEILLANCE AND OUTBREAK DATA INTO THE SOFTWARE PLATFORM FOR ANALYSIS

*Birgit Lewicki, Marion Gottschald, Jakub Fusiak, Marco Rügen, Alexander Falenski, Valentina Caldarelli, Iolanda Mangone, Adriano Di Pasquale, Annemarie Käsbohrer, Armin Weiser*

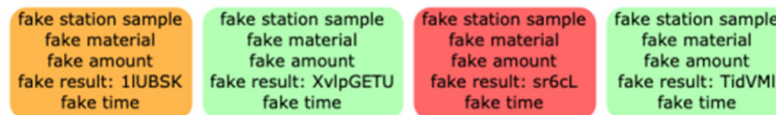
In **subtask 3**, additional meaningful surveillance and outbreak data/tools were integrated in the FoodChain-Lab web application (FCL Web, <https://fcl-portal.bfr.berlin/>) for analysis purposes. As a requirement analysis, data needs with regard to cases, samples and animal movement were clarified with public and veterinary health institutes during workshops.

One task was to connect FCL Web with the COHESIVE Information System (CIS) from WP4.1, a system to integrate pathogen information (e.g. Whole Genome Sequencing (WGS) data) from public health, animal health and food safety surveillance at Member State level (<https://doi.org/10.5281/zenodo.5482421>). To achieve this, a CSV-based data export for MLST and SNP distance data from CIS was developed. MLST and SNP distance data are imported into FCL Desktop to match phylogenetic with tracing data and then the dataset is transferred to FCL Web. With that, WGS results can be used in FCL e.g. by setting a lower weight for disease cases whose samples have – compared to the outbreak strain – a phylogenetic distance which is higher than the pathogen-specific threshold. Hence, cases with a higher phylogenetic distance have a lower rank in the score calculation in FCL. The phylogenetic distance can also be visualised in the supply chain network via different colors. For the future, an API is envisioned to optimize data exchange between FCL and CIS.





A data format for sample and case data was developed in JSON to receive the respective information from an EFSA data extraction tool for RASFF notifications. It is possible to display sample results (color code for confirmed (red) or probable (orange), not associated with outbreak (green); sample material, amount and timing) of cases, products or companies within the reporting module of FCL Web.



Case and sample data visualisations from CIS and from the EFSA tool were tested in the framework of case studies.

In EJP NOVA, a likelihood model developed to analyse spatial distribution of disease cases, whole sales data and country-specific geospatial information on municipality level to identify potential causative food items for subsequent lot-specific tracing in foodborne disease outbreak investigations. The model was then improved and transformed from R into Webassembly to increase usability, performance, security and sustainability (<https://doi.org/10.5281/zenodo.5497430>). In the framework of EJP COHESIVE, a webcomponent was developed based on the Webassembly model to integrate the NOVA likelihood model in FCL Web. It is already available in FCL Web on a local test system. Integration into the official FCL Web is in preparation. It is envisioned to continue the work on the NOVA likelihood model in FCL Web in upcoming projects e.g. by displaying the flow of goods on a map.

Additional tracing tools with varying purposes are going to be connected to FCL Web via a common data format – the Universal Tracing information eXchange format which will be developed in the framework of a current project cooperation between BfR and EFSA. Those tools are: 1) a comprehensive EFSA tool for guided and structured manual data extraction from unstructured RASFF notifications, 2) the Rapid Alert Supply Network Extractor (RASNEX) tool developed by BfR (<https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0254301>) for automatic data extraction of relevant tracing information from RASFF notifications using pattern recognition, 3) a web-based data entry mask for local food safety officers with on-site plausibility checks and access to curated data via catalogues developed by the German Federal State NRW. As a result, a comprehensive interoperable tracing tool workflow will be available for the One Health community on the local, national and European level.

The Deliverable D-JIP2-4.2.3 consist of this report and the FoodChain-Lab web application (<https://fcl-portal.bfr.berlin/>) with implemented additional surveillance and outbreak data/tools.