Epidemiology

Timely data collection in order to perform epidemiological analyses is crucial to prepare for the next pandemic. The NRC data collection, among other surveillance systems, is used for **various reporting** on a national and international level (e.g. European Centre for Disease Prevention and Control). Be-HERA provides an opportunity to digitalize and enhance the NRC data collection further with data flows that are real-time and include genomic indicators such that **integrated genomic-epidemiological analyses** in a collaboration with pathogen experts (i.e. epidemiologists, microbiologists) become possible.

- Data is collected and distributed near real time
- Clinical/Epidemiological and Genomic data can be linked and analysed together
- Timely and sensitive variant/outbreak detection
- Possibility to upload FASTQ files to ENA through the system
- Improved outbreak management and investigation by enhanced data availability
- Monitoring of antimicrobial resistance profiles predicted through genomics
- Harmonised and automated bioinformatics pipelines available
- Automated uploading (system to system) and large data files possible

"Be-HERA aims to analyze data in an harmonized manner and combine data from multiple sources to detect outbreaks earlier"

"The goal is to consolidate the national digital infrastructure for monitoring infectious diseases based on both clinical/microbiological and genomic data"

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How do we strengthen Infectious Diseases surveillance for the future?

Towards a new (H)ERA:

Developments to strengthen infectious diseases surveillance and pandemic preparedness

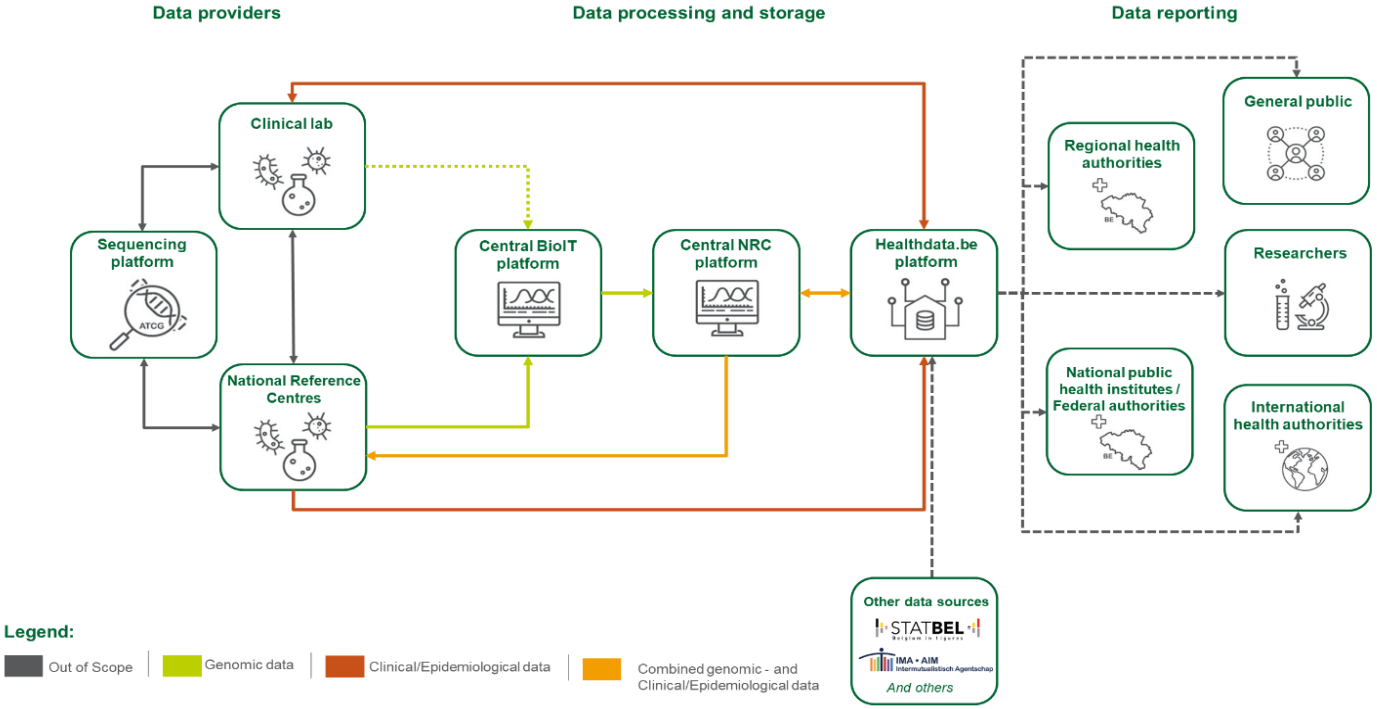
- Lessons learned from COVID-19: a high capacity, interoperable infrastructure is needed for pandemic preparedness
- Design and development of an overarching architecture to strengthen the surveillance of infectious diseases: Be-HERA
- Whole Genome Sequencing (WGS) allows for higher microbial subtyping leading to increased resolution for outbreak management
- Clinical and epidemiological data will be combined with genomic data to allow integrated genomic-epidemiological analyses

National Reference Centers for Human Microbiology (NRCs)

Today, a substantial part of clinical laboratories and NRCs have access to **whole genome sequencing** (WGS). The resolution offered by this method allows tracking of transmission dynamics, follow-up of pathogen circulation and evolution, outbreak detection, identification of known and new antimicrobial resistance determinants and investigation of vaccine evasion mechanisms. To **strengthen infectious diseases surveillance** and **pandemic preparedness**, genomic data from multiple sources should be consolidated at a national level. Therefore, **a centralized bioinformatics platform** will be established that provides tools for genomic **cluster analysis** and visualisation **combined with patient data** under strict regulations. By facilitating **analysis of patient data linked to genomic data**, an outbreak can be more easily detected and monitored. This is important to identify related cases along with potential sources, to **guide outbreak response** measures and ultimately **stop the spread of the infection**.

Laboratory Information Management System (LIMS)

To harmonize data extraction from LIMS a **conversion of the internal codes** used by NRCs to standardised international nomenclature such as SNOMED CT and LOINC codes should be performed. As a proof-of-concept for this harmonization and for the automatisation Sciensano LIMS developed new applications to import the **Data Collection Definitions (DCD)** specifications, which represent a collection of both test results, clinical and epidemiological data. These DCDs thus have been **mapped to the internal LIMS fields**. The use of **international terminology** is also required for other eHealth projects such as **FHIR Lab Results**, and hence those standardisation efforts lay the groundwork for other initiatives to come. During this current action, the Sciensano LIMS will continue to focus on **ensuring functional connectivity** for the onboarding of Sciensano NRCs as well as designing **HL7 FHIR compatibility** for the Sciensano LIMS.



BioIT

Two platforms are currently being established. Firstly, **a central bioinformatics platform** will process **pathogen genomics data**. The platform will contain all the required bioinformatics tools, pipelines, and databases for **automated, standardized, and scalable processing** to allow full genomic typing and characterization including a wide range of **genomic indicators** (*e.g.,* cgMLST, predicted antimicrobial resistance (AMR) characterization…). Obtained indicators will be fed into a centralized national molecular database that can be used to perform outbreak cluster detection based on genomic similarity of samples. Secondly, **a central NRC platform** will contain both the **obtained genomic indicators** but also on top **associated nominative and epidemiological information** about samples, which will be accessible to NRC experts by means of an intuitive visual interface using the Bacterial Isolate Genome Sequence Database application that will allow navigating all relevant information about samples and additionally provide powerful visualization possibilities to study pathogen outbreak clusters.

Healthdata.be

Healthdata.be designed and developed a **secured** platform where data can be collected and distributed in a nominative way, keeping **pandemic preparedness** in mind. All Belgian clinical laboratories can use the new technical architecture using the electronic data capturing system **HD4DP2.0** to report in a standardized way towards the newly build **Be-HERA** platform via system to system transfer (incl. use of HL7 FHIR messages) or automated CSV upload. From this Be-HERA platform, data can be distributed nominative and/or **pseudonymised** toward various end parties. The services of an **independent trusted third party** (eHealth) will be used for pseudonymization and the **end-to-end encryption** of the person identifiers towards a centralized data management and analysis platform used by researchers and surveillance teams (HD-DWH). Translation and harmonization of currently used codes and values towards international adopted terminology systems (i.e. SNOMED CT, LOINC,…) will be performed.