



The project „Genomic surveillance of selected infectious diseases in the Czech Republic“ (HERA2CZ) is co-funded by the European Union. Views and opinions expressed are however those of the author(s) only and do not necessarily reflect those of the European Union or the European Health and Digital Executive Agency (HADEA). Neither the European Union nor the European Health and Digital Executive Agency (HADEA) can be held responsible for them.

Genomic Surveillance of Selected Infectious Diseases in the Czech Republic (HERA2CZ)

Enhancing Public Health Protection through the HERA2CZ Project

The HERA2CZ project aims to enhance the quality of public health protection and improve the preparedness of the Czech Republic for emergency health situations and pandemics such as COVID-19, or any future health crisis with potential international impact. The HERA2CZ project assists the National Institute of Public Health (NIPH/SZÚ) in increasing the capacities of the National Reference Laboratories (NRL) for whole genome sequencing (WGS) of infectious agents and expanding the spectrum of WGS characterization to various human pathogens, especially SARS-CoV-2 and other respiratory viruses, bacterial pathogens with cross-border impact, including antibiotic-resistant bacteria. WGS is a modern, precise, and time-efficient analytical method that enables rapid and accurate identification of infectious disease outbreaks, control of these outbreaks, monitoring the spread of infectious agents, and their mutations. Early detection of potential threats and a proper understanding of the spread of infectious diseases are crucial for timely responses from public health authorities.

Key Points of the HERA2CZ Project

- The HERA2CZ project addresses shortcomings in the healthcare system, particularly considering the experiences from the COVID-19 crisis.
- The main objective is to enhance the Czech Republic's preparedness for future health emergencies related to the spread of infectious diseases at national and global levels.
- Public health protection requires a comprehensive approach crossing national borders, strengthening healthcare systems, analytical capacities, implementing modern methods, and improving cross-border data sharing.

What is Whole Genome Sequencing (WGS)?

- WGS is a modern method used to analyse the complete DNA sequence of an organism's genome.
- WGS allows precise tracking and differentiation of individual strains, aiding in identifying sources of infection and understanding the spread of infectious diseases.
- The accuracy of the method makes WGS an indispensable tool for effective surveillance of the occurrence and spread of infectious diseases.
- WGS enables timely and accurate identification, monitoring, and prevention of the spread of infectious diseases in a global context.
- Cross-border data sharing through WGS supports collaboration between countries is necessary for efficient monitoring and prevention of global health threats.

National Institute of Public Health

Genomic surveillance of selected infectious diseases in the Czech Republic, HERA2CZ
Project: 101113387 — HERA2CZ — EU4H-2022-DGA-MS-IBA-1

Challenges Associated with WGS

- While WGS is highly effective, it is more resources intensive compared to other sequencing methods and requires robust technical and personnel resources. WGS generates complex data, the precise analysis of which demands specialized expertise, management, and storage, necessitating additional skilled personnel.
- Some of these challenges were partially addressed in the previous [HERA project](#).

Focus of the HERA2CZ Project

- The follow-up [HERA2CZ project](#) focuses on increasing the genotypic characterization capacity within the National Reference Laboratories (NRL) of the National Institute of Public Health (NIPH/SZÚ) in the Czech Republic and expanding the spectrum of WGS characterization to various human pathogens, especially SARS-CoV-2 and other respiratory viruses, bacterial pathogens with cross-border implications, including antibiotic-resistant bacteria.
- The HERA2CZ project further refines methods based on whole genome sequencing and incorporates these modern methods into routine genomic surveillance of selected infectious diseases.

The Project's Basic Data

Project Title (acronym):	Genomic surveillance of selected infectious diseases in the Czech Republic (HERA2CZ)
Project ID:	Grant Agreement - Project 101113387
Type of action:	EU4H Project Grants
Beneficiary:	National Institute of Public Health, the Czech Republic
Call:	EU4H-2022-DGA-MS-IBA-1
Topic:	EU4H-2022-DGA-MS-IBA-01-02
Coordinator:	Jana Kozáková, MD
Project duration	1.10.2022 – 30.6.2025



Find out more: www.szu.cz/hera2/

Acknowledgement of Funding



Co-funded by the
European Union

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