



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.

The project of genomic surveillance of selected infectious diseases in the Czech Republic, "HERA2CZ"

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The National Institute of Public Health is implementing a project called "Genomic Surveillance of Selected Infectious Diseases in the Czech Republic" (HERA2CZ), which is a continuation of the successful HERA project. This action represents a significant step towards enhancing the preparedness of the Czech Republic for potential threats of national or global health emergencies. Experiences from the SARS-CoV-19 pandemic have underscored the importance of genomic surveillance in public health protection. Effective public health protection cannot be achieved through partial measures limited to the national level alone. Strengthening the laboratory infrastructure of National Reference Laboratories (NRL) and improving the quality of shared data at the European level are integral components of the EU4Health strategy. These strategies aim to safeguard European citizens from the impacts of global health crises and enhance the ability of EU member states to respond effectively to cross-border health threats.

"In the Czech Republic, National Reference Laboratories (NRL) ensure preparedness by conducting diagnostic and analytical activities within their specific focus. These laboratories employ various analytical methods to determine the complete DNA sequence of the genome. High-resolution information allows precise tracking and differentiation of strains, enabling scientists to identify infection clusters and better understand the spread of diseases and the emergence of mutations. Currently, the most advanced method in use is Whole Genome Sequencing (WGS), which the National Reference Laboratory for influenza and non-influenza viral respiratory diseases utilized during the COVID pandemic and continues to use for monitoring mutations of the SARS-CoV-2 virus," explains Ms Barбора Macková, MD, the director of the National Institute of Public Health (NIPH).

WGS is employed to determine the complete DNA sequence of an organism's genome. This technique provides a comprehensive view of the genetic composition of the organism and its potential variants or mutations. Rapid and accurate identification of disease hotspots and the tracking of the spread of infectious diseases are enabled by the precision of the WGS method. This allows public health authorities to respond immediately to the occurrence of infections and trace their spread.

National Institute of Public Health

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"Cross-border collaboration and sharing WGS data allow for a faster and coordinated response to global health threats, which is a crucial step in preventing the cross-border spread of infectious diseases, protecting public health, and minimizing the economic impacts of health threats on a global scale," emphasizes Ms Jana Kozáková, MD, the head of the Center for Epidemiology and Microbiology at NIPH.

Although WGS is a highly effective method, it is more expensive and resource-intensive compared to other sequencing methods. The process of sequencing the entire genome generates a large amount of data that demands modern technological equipment and sufficient computational and analytical capacities. Managing, sharing, and storing this data require data capacity, regular system maintenance, and data security. For effective analysis and proper interpretation of data, personnel with bioinformatics expertise are necessary.

These structural requirements mentioned above may be an obstacle for smaller research facilities or local laboratories to utilize the WGS method. The identified disadvantages were partially addressed by the previous [HERA](#) project, which significantly improved the material capacity of the National Reference Laboratory for influenza and non-influenza viral respiratory diseases as well as regional sequencing centres.

The follow-up project HERA2CZ focuses on increasing the capacity of genotypic characterization within the National Reference Laboratories (NRL) of the National Institute of Public Health (NIPH) in Prague and expanding the spectrum of WGS characterization to various human pathogens – not only to SARS-CoV-2 and other respiratory viruses but also to bacterial pathogens with cross-border implications, including antibiotic-resistant bacteria. The HERA2CZ project also deals with refining methods based on whole-genome sequencing and incorporating these methods into routine genomic surveillance of selected infectious diseases.

"The project not only enhances the capabilities of monitoring infectious diseases but also strengthens the coordination and response mechanisms of public health protection systems across the European Union. By increasing capacity for WGS sequencing and refining methodology, the HERA2CZ project contributes to improving the public health protection system," concludes Ms Kozáková, MD.