

From genome to public health

How Latvia strengthened its capacity to detect and track dangerous pathogens



EU4Health Project No. 101113261 (WGS-NMRL-Latvia)

National Microbiology Reference Laboratory (NMRL)

Riga East University Hospital (REUH)



**Co-funded by
the European Union**



About the project and its implementer

This brochure provides a brief and accessible overview of the WGS-NMRL-Latvia project, its objectives, achievements and next steps. The project built on the foundations established by the 2022 HERA project, thereby strengthening and making sustainable the existing whole-genome sequencing (WGS) and real-time PCR (RT-PCR) capacity.

Project profile

Programme	EU4Health, implemented by HaDEA (European Health and Digital Executive Agency)
Grant Agreement No.	101113261
Duration	36 months (1 July 2023 to 30 June 2026)
Project budget	EUR 1,229,858, including EUR 962,485 in European Union funding
Lead beneficiary	Riga East University Hospital (REUH)
Implementer	Riga East University Hospital National Microbiology Reference Laboratory (NMRL)
Previous phase	HERA support, Contract No. ECDC/HERA/2021/014 ECD.12229 (2022)

Project in numbers

182 TB DATA STORAGE	36 MONTHS PROJECT DURATION
5000+ SEQUENCED ISOLATES	1 HOMEPAGE FOR MEDICAL AND CARE STAFF

What is the NMRL?

The NMRL is Latvia's nationally designated National Microbiology Reference Laboratory. It operates across the country and fulfils a national public health mission: monitoring infectious diseases, investigating outbreaks and supporting laboratory-based decision-making in healthcare.



Project objectives

The overall objective of the project was to continue and deepen the work initiated under the previous HERA project implemented during the COVID-19 pandemic: to strengthen, improve and further develop laboratory processes across all stages of genomic sequencing, namely sample preparation, sequencing itself and data analysis.

Specific objectives

- ✓ Ensure the sustainability of project results against future threats and establish infrastructure enabling a rapid response to new or other diseases.
- ✓ Promote the integration of genomic methods into routine disease surveillance and outbreak preparedness and response.

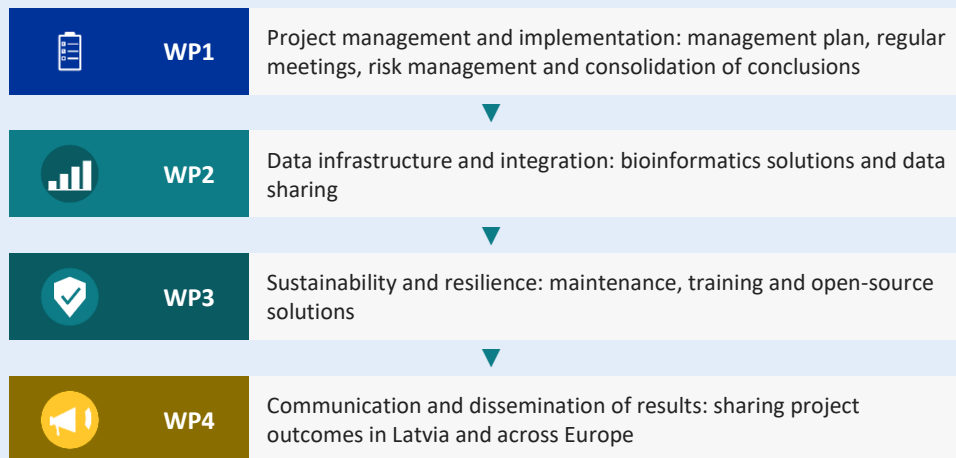


To achieve these objectives, work was organised across three areas: data infrastructure, sustainability and resilience, and communication and dissemination. These areas are described in more detail on the following page.



Project structure

The project was divided into work packages (WPs). Each work package covered a distinct area of project implementation, ranging from equipment to communication with the public.



The project has significantly strengthened Latvia's public health infrastructure by enabling more effective infectious disease surveillance and response. By integrating advanced genomic technologies into routine practice, the project aims to improve pathogen detection and monitoring, support outbreak investigations and ensure preparedness for future public health threats. At the same time, this initiative contributes to broader European efforts to strengthen health security and coordination among Member States.



Key achievements (1/3)



Equipment and computing capacity

The laboratory's computing and storage capacity was expanded to approximately 182 TB, with the addition of a GPU accelerator card and a new high-performance computing cluster. A new MiSeq i100 Plus sequencer was acquired for short-read sequencing, while the PacBio Vega platform was selected for long-read sequencing and is currently being validated for routine use.

For sample preparation, the Tecan DreamPrep automation platform was further developed, and additional equipment was acquired, including a DNA extraction system, homogenisers, thermoshakers and other auxiliary tools.



Bioinformatics solutions

Standardised, reusable analysis workflows (Ardetype, nmrl-mycopipe-nf, nmrl-metapipe-nf) were implemented for bacterial, tuberculosis and metagenomic data processing, and a web platform was created for authorised users to access typing and resistance analysis results.





Key achievements (2/3)



Surveillance and outbreak investigation

The new capacity delivered tangible results in practice. The NMRL identified a multi-hospital outbreak of *Klebsiella pneumoniae* ST147, leading to a joint report prepared with the Centre for Disease Prevention and Control of Latvia (SPKC) and the Ministry of Health. The outbreak was also referenced in the European Centre for Disease Prevention and Control (ECDC) 2025 report on Latvia.

- ✓ The spread of NDM-1 resistance gene-carrying *Acinetobacter baumannii* across a hospital network was characterised.
- ✓ A cross-border *Salmonella* Enteritidis outbreak in the Baltic States linked to egg products was mapped.
- ✓ An international external quality assessment was completed, confirming the laboratory's competence.



Cross-border and European cooperation

Latvian genomic data and expertise have been integrated into the European surveillance networks EurGenNet and EpiPulse, as well as reporting flows to ECDC / EARS-Net, GLASS and the European Nucleotide Archive (ENA).



Latvian genomic data are now visible and usable across Europe!



Key achievements (3/3)



Sustainability

Sustainability is ensured through open-source, version-controlled analysis workflows, a database replicated across three independent locations, and cooperation with national academic research networks and the GÉANT network. Continuous training of laboratory specialists and engagement of regional laboratories are also ongoing.



Communication and dissemination

Project results were presented at international congresses (ECCMID/ESCMID Global, BALM, ESM). Posters presenting NMRL research received 1st and 3rd place awards at the BALM-2026 congress, and an invitation was received to present a poster at ESCMID Global 2026.

A bilingual brochure and infographic booklet, a video and a national press release republished by several media outlets were also produced for the public.

A website for healthcare professionals was developed: <https://laboratorija.aslimnica.lv/>



1st and 3rd place at the BALM-2026 congress

 Scientific impact

The project strengthened the NMRL's position as a recognised participant in European molecular surveillance networks, demonstrated by co-authorship of publications in *Eurosurveillance*, contributions to ECDC rapid risk assessments and international recognition at congresses.

 Public impact

Public-facing materials made complex sequencing processes understandable to a broader audience, increasing awareness of how molecular surveillance helps protect public health.

Overall, the project contributed to Latvia's epidemiology moving from a descriptive approach towards high-precision analytics. This represents a lasting, systemic change in the country's public health landscape.





Challenges and lessons learned

Areas for further development identified during the evaluation:

- ✓ Continue validation of the new PacBio Vega long-read platform for routine use.
- ✓ The planned automated data exchange with the National Health Service (NVD) and the Centre for Disease Prevention and Control of Latvia (SPKC) was delayed because dependent national projects were cancelled or launched later than planned. Prerequisites, including LOINC data structures, have been prepared for future integration.
- ✓ Expert review remains necessary until full automation is achieved.
- ✓ Further communication and explanation of genomic surveillance for non-specialists are needed.

Importantly, none of these challenges or areas for further development diminish the project's main achievements; rather, they define the agenda for continued progress.





Conclusions and next steps

Overall, the project can be considered effective and impactful: the main objectives were achieved, and several long-term integrations will continue beyond the end of the project.



What happens next



Validation of the PacBio Vega long-read platform and transition to the new computing environment in routine work.



Harmonisation of clinical reporting across different pathogen groups.



Expansion of automated data exchange with NVD and SPKC as soon as national platforms are further developed.



Application of the DiaLab data extraction solution in other laboratories using the same system; this could cover the majority of bacterial isolates tested nationwide.



Links with other EU and national initiatives

The project results, including open-source analysis workflows, data exchange solutions and accumulated expertise, are ready for use in other EU-funded actions and national health systems, including ECDC-coordinated European surveillance networks (EurGenNet, EpiPulse) and future EU4Health- and HERA-supported projects in other Member States.



Towards broader use of genomic methods across Latvia



Find out more

Project materials

At the end of the project, a final evaluation report (D3.1) and other project deliverables were prepared:

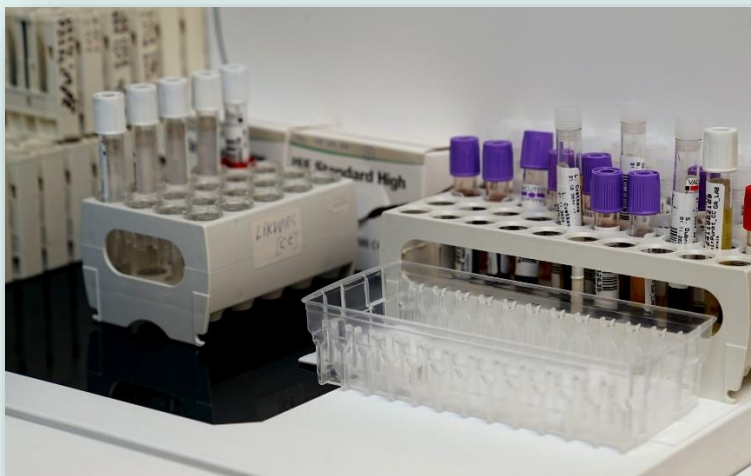
- D2.1: Bioinformatics solution
- D2.2: Data sharing process
- D2.3: Sequencing data flow
- D3.1: Evaluation report
- D4.3: Communication and dissemination report

These materials are available from the project coordinator and at Riga East University Hospital.

More about the project

aslimnica.lv: [RAKUS Eiropas sadarbības projekti](#)

[WGS-NMRL-Latvia](#)





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