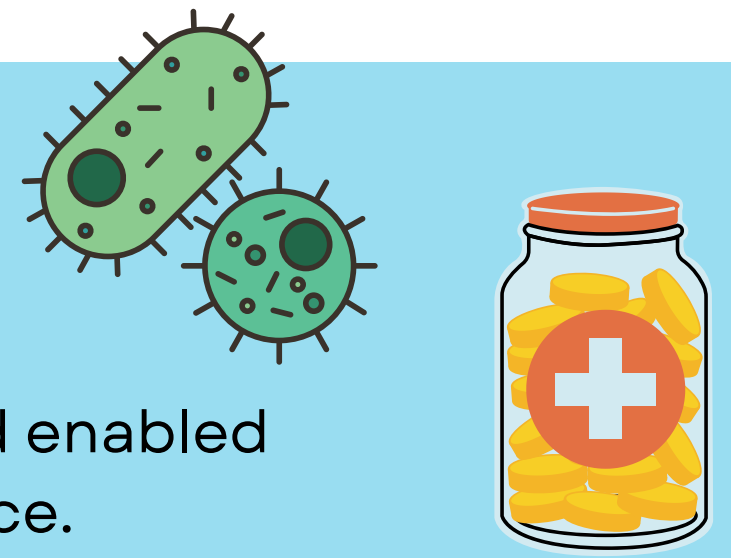


USING WHOLE GENOME SEQUENCING TO STRENGTHEN PUBLIC HEALTH SURVEILLANCE

Antimicrobial resistance is a major global public health threat. In the EU, it causes over 35 000 deaths annually, while hundreds of thousands of infections could be prevented (WHO, ECDC, 2025).

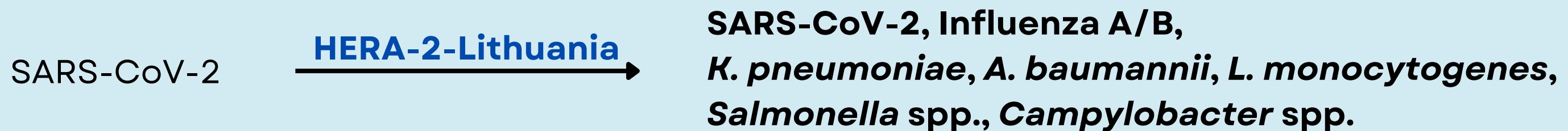
HERA-2-Lithuania strengthened public health surveillance in Lithuania and enabled more precise monitoring of infectious diseases and antimicrobial resistance.



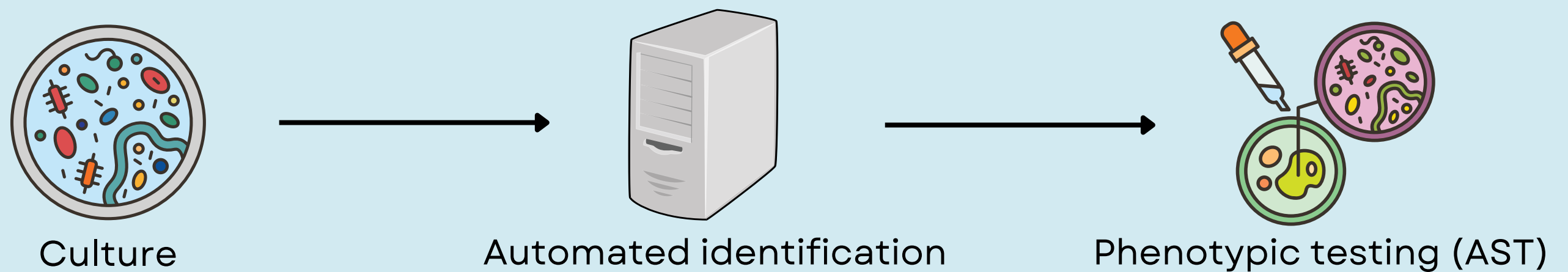
With the enhanced infrastructure, investigations now follow a clear **step-by-step workflow**.

STEP 1: Sample collection and phenotypic testing

Expanded nationwide sample collection covering new pathogens:



Phenotypic susceptibility testing is then performed according to European standards (EUCAST):



STEP 2: Molecular testing (PCR)

After phenotypic testing, targeted molecular tests (PCR) are used to detect specific **resistance genes**, such as *bla*CTX-M, *bla*KPC, *bla*NDM, *bla*OXA-48-like, etc., supporting rapid confirmation and prioritisation for sequencing.



STEP 3: Whole genome sequencing (WGS)

WGS reads the complete genetic material of a pathogen, enabling accurate identification, detection of resistance genes, and tracking of infection spread.

Expanded testing with WGS

WGS for SARS-CoV-2

Only phenotypic and PCR tests available for other pathogens



• Bacteria (priority pathogens):

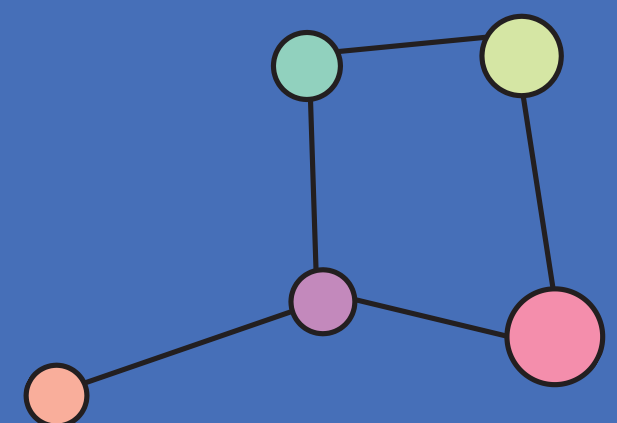
K. pneumoniae, *A. baumannii*, *L. monocytogenes*, *Salmonella* spp., *Campylobacter* spp.

• Viruses: SARS-CoV-2, Influenza A/B

STEP 4: Genomic analysis & public health action

WGS analysis is performed to:

- Determine genetic relatedness and identify variants
- Construct phylogenetic trees to map pathogen evolution
- Standardise and compare data nationally and internationally



Data are used to detect and track outbreaks, monitor AMR, adjust infection control measures, guide treatment, and support prevention through public health interventions and vaccines.