
Image: Needpix

## HIGHLIGHTS

- The incorporation of plasmid data into genomic surveillance systems can add greatly to a more comprehensive understanding of AMR spread.
- There are large differences in technical capacity between EU veterinary and public health institutes.
- Harmonize, build and test long-read sequencing capacity at each institute.
- Provide an excellent dataset to benchmark public and in-house developed tools for MGE typing.
- Enhance our insight in dominant MGEs which are driving resistance among commensal and pathogenic Enterobacteriaceae in Europe.

# FULL FORCE: supplying a technological toolbox and hands-on training in SMRT sequencing.

> ***Monitoring of AMR should go hand in hand with monitoring of mobile genetic elements."***
>
> *Pieter-Jan Ceyssens*

Surveillance of antimicrobial resistance (AMR) is an essential governmental tool to develop empirical therapeutic guidelines, to design intervention and infection control policies, and to direct research agendas. However, current surveillance practices fall short in grasping the two distinct mechanisms of the continuous flux of AMR genes: clonal versus horizontal transmission across species and reservoirs.

Consensus is growing that dynamics of horizontal gene transfer, i.e. mediated by **plasmids and other mobile elements**, have to be taken into account in risk assessments. The potential danger is not only associated with antimicrobial and biocide resistance genes, but also with toxin-antitoxin modules, virulence and resistance genes which might co-select and cause a plasmid to persist and spread, long after antimicrobial treatment has stopped or even in complete absence of selection pressure.

Although an increasing emphasis is put on genomic-based surveillance, these mobile elements remain very difficult to reconstitute from short-read sequence data due to their chimeric, modular and repetitive nature. This complexity can often be resolved by long sequence reads. Although several veterinary and public health laboratories have strong interest in this technology, many **struggle with its technical implementation**, resulting in a wide knowledge gap between (and even within) countries.

The FULL-FORCE consortium will broadly introduce long-read sequencing in EU veterinary and public health institutes. We will harmonize, build and test each institute's long-read sequencing capacity. We will apply this knowledge on six study cases which will greatly profit from MGE sequencing, incl. samples isolated in the context of national surveillance programmes, EFFORT and ARDIG projects. This will be followed up by detailed investigation of prominent MGEs, and by applying this knowledge to modelling efforts of AMR dynamics in closed production systems. At the same time, high-quality MGEs sequencing will provide an excellent dataset to test the performance of public and in-house developed tools for MGE typing, and to study associations between AMR genes and MGEs in metagenomic datasets from the EFFORT project.

**For further information contact Pieter-Jan Ceyssens**

One Health EJP has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 773830.