



IMAGE: PXHERE

TAKE-HOME MESSAGES

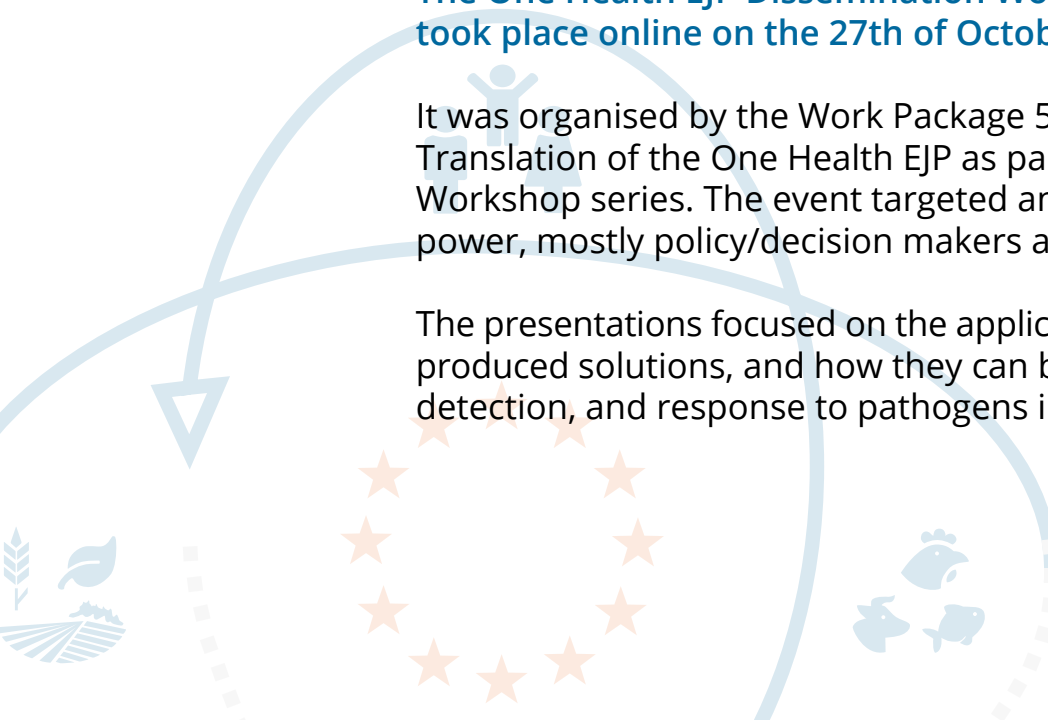
- Metagenomic techniques provide considerable advantages over current standard techniques, for example they are unbiased, allow simultaneous detection of different pathogens, are culture-independent and are applicable to different matrices.
- Challenges and limitations include the need of large databases and technical expertise, as well as EU General Data Protection Regulation (GDPR) issues.
- Results from metagenomic analyses have to be interpreted correctly, and require clear and transparent communication.
- The apparent trend in Europe is that metagenomic techniques are entering the routine work of reference laboratories.

One Health EJP Dissemination Workshop Series: METAGENOMICS

The One Health EJP Dissemination Workshop on Metagenomics took place online on the 27th of October 2021.

It was organised by the Work Package 5 (WP5) Science to Policy Translation of the One Health EJP as part of the Dissemination Workshop series. The event targeted an audience with decisional power, mostly policy/decision makers and risk managers.

The presentations focused on the applicability of One Health EJP produced solutions, and how they can benefit the prevention, detection, and response to pathogens in One Health settings.



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One Health EJP Dissemination Workshop Series: METAGENOMICS

...the advantages of using metagenomic techniques in a One Health setting were highlighted.

Introduction

Steven van Borm, Sciensano
One Health EJP project [METASTAVA](#)

Steven van Borm introduced the audience to the basic definition of metagenomics, “the study of genetic material directly obtained from (environmental) samples”, and clarified which questions can be answered using metagenomics. Metagenomic tools can be applied to the environmental, industrial, and clinical field, making their use optimal for One Health practices.

The speaker took us then through a full metagenomic workflow, highlighting the technical requirements and the expertise needed.

He highlighted the advantages of using metagenomic techniques in a One Health setting. These techniques require, for example, no prior isolation of the pathogen or knowledge of the pathogen in the sample, minimising the risk of detection bias. The large amount of data obtained, however, presents some challenging aspects in relation, for example, to the ethics of detecting unwanted pathogens (e.g. HIV in clinical specimen), or to the validation of the organisms being really present in the sample. Other challenges include costs and the need for sharable databases, raising technical as well as GDPR issues. A number of One Health EJP projects mined the potential of metagenomics by applying it in a number of settings at the human/animal/food/environment interface (for example [DiSCoVer](#), [FARMED](#), [FULL-FORCE](#), [MAD-Vir](#), [MedVetKlebs](#), [MEmE](#), [METASTAVA](#), [PARADISE](#), [RaDAR](#), [TELE-Vir](#), [TOXOSOURCES](#)).

...several applications of metagenomics for One Health in the areas of antimicrobial resistance (AMR), food/feed chain safety, discovery of emergent viral threats, and in diagnostics were presented.

After this introductory talk, several applications of metagenomics for One Health in the areas of antimicrobial resistance (AMR), food/feed chain safety, discovery of emergent viral threats, and in diagnostics were presented. These presentations provided a snapshot of the work that is being conducted in the One Health EJP consortium, using metagenomics.

Antimicrobial Resistance Identification

Saria Otani, DTU
One Health EJP projects [FARMED](#) and [FULL-FORCE](#)

One of the challenges of infectious disease surveillance is finding a method that allows real-time observation of trends in pathogens presence, including virulence and antimicrobial resistance (AMR) genes. By collecting and analysing samples from wastewaters throughout the world, Saria Otani introduced DTU work on sewage wastewater, and demonstrated that sewage sampling is a reliable surveillance methodology for both pathogens and AMR detection. For this aim, a novel method of sampling and sequence analysis was developed, coupled with bioinformatic tools that facilitate the understanding of AMR dynamics globally.

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Food/Feed Chain Safety

Sigrid De Keersmaecker and Florence Buytaers, Sciensano

One Health EJP project [FARMED](#)

Sigrid De Keersmaecker and Florence Buytaers took us through issues linked with the safety in the food chain, a process which goes “from farm to fork”. In this context, metagenomic techniques can support investigation of foodborne outbreaks, and detection of unwanted genetically modified microorganisms (GMM) and related AMR genes in microbial fermentation products. This is faster than, or sometimes even not achievable with, conventional methods, and unbiased, not requiring prior isolation. EFSA called for proofs of concepts of metagenomic use for outbreak investigation, source attribution and risk assessment of foodborne microorganisms, therefore paving the way for a possible future routine use.

Discovery of Emerging Viral Threats

Anders Fomsgaard, SSI

One Health EJP projects [MAD-Vir](#) and [TELE-Vir](#)

Anders Fomsgaard presented two metagenomic tools for virus surveillance and detection of emerging virus threats: the Panvirus Micro-Array and a novel metagenomic field test based on whole genome sequencing. These tools allow the unbiased detection of viruses from a number of matrices and have the advantage of identifying co-infections. They were used in Denmark to detect the source of SARS-CoV-2 outbreaks that involved both human and mink transmission, events which had major public health, economic and political consequences. In addition a previously unknown Alphacoronavirus was detected in Danish bats using metagenomic methods.

Diagnostics

C. Rune Stensvold and Pikka Jokelainen, SSI

One Health EJP projects [PARADISE](#), [TOXOSOURCES](#), [MEmE](#);

Steven van Borm, Sciensano, One Health EJP project [METASTAVA](#)

Metabarcoding relies on detection and differentiation of - typically - ribosomal genes using next-generation sequencing. Rune Stensvold and Pikka Jokelainen presented a platform already applied for testing clinical samples and piloted for surveillance, allowing the simultaneous detection and differentiation (typically to species level) of bacteria, parasites and fungi.

Steven van Borm closed the session by presenting his work on metagenomic methods' standardisation, validation and quality control, and the steps to follow to move from research to diagnostics in a One Health perspective. For this aim, guidelines for [diagnostic metagenomics](#) were set in a reference document.

Conclusions

Simone Cacciò, ISS

One Health EJP project [PARADISE](#)

The presentations of the workshop exemplified the use of metagenomics applied to food chain safety, AMR detection, pathogen discovery, and diagnostics. In the final talk, Simone Cacciò summarised the key take-home messages, highlighting in particular the applications and possibilities of metagenomic approaches, their limitations, the challenges to overcome, and the steps to take to overcome the challenges.

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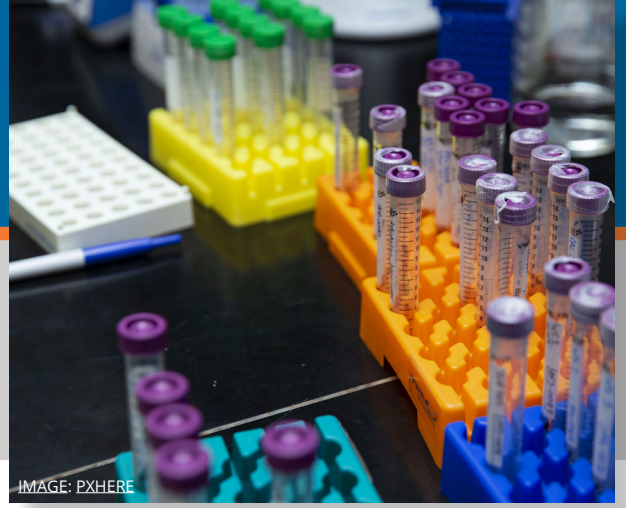


IMAGE: PXHERE

One Health EJP Dissemination Workshop Series: METAGENOMICS

The speakers generally agreed on the growing need to share data across sectors and countries, while the EU General Data Protection Regulation (GDPR) has been identified as a major challenge.

Discussion

Moderated by Pikka Jokelainen, SSI, and Annemarie Käsbohrer, BfR
One Health EJP WP5 Science to Policy Translation

The discussion initially focused on the scenarios where metagenomic techniques offer a sensible advantage over conventional methods. Metagenomic approaches allow the detection of many possible pathogens at once therefore saving time and efforts, something particularly important in the case of co-infections. Metagenomic-based methods were seen as an additional support to current standard methods for diagnostic use. Similarly, in the food sector, metagenomics can be applied where traditional methods fail, supporting, for example, faster resolution of the origin of an outbreak. Consensus was that the benefits of application of metagenomics depends on the question to be answered.

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The audience was interested in the interpretability of the data from the perspective of the policy makers, and how to minimise issues potentially arising from metagenomic results. The speakers agreed that in case of an unexpected result, confirmation is crucial. Moreover, it was highlighted that metagenomic techniques are not functional assays, meaning that when a gene of concern is detected (for example an AMR gene) additional tests are needed to investigate its functionality. The shared understanding of these factors requires a clear communication.

Clear and transparent communication between scientists and policy makers was overall an important point identified during the discussion between the audience and the speakers.

Clear and transparent communication between scientists and policy makers was overall an important point identified during the discussion between the audience and the speakers.

The speakers also stressed the need of capacity building initiatives and of sharing the knowledge across laboratories. The sharing should go hand in hand with harmonisation of methods, ideally across countries and sectors - an endeavour brought forward by the One Health EJP.

The workshop was closed with the forecast that it is just a matter of time until metagenomic techniques become more incorporated alongside the current standard detection methods in reference laboratories.



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