JRP24-FBZSH9-BEONE D1.1
Workpackage 1

Responsible Partner: INSA (36)
Contributing partners: NVI (33)

GENERAL INFORMATION

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Dissemination ***Author's suggestion to inform the following possible interested parties.***	OHEJP WP 1 ☒ OHEJP WP 2 ☐ OHEJP WP 3 ☐ OHEJP WP 4 ☒ OHEJP WP 5 ☐ OHEJP WP 6 ☐ OHEJP WP 7 ☐ Project Management Team ☒ Communication Team ☒ Scientific Steering Board ☐ National Stakeholders/Program Owners Committee ☐ EFSA ☒ ECDC ☒ Other international stakeholder(s): ……………………………………………… Social Media: "One Health EJP" twitter **Other recipient(s):**

ESTABLISHMENT OF STATE OF THE ART

Introduction

Foodborne diseases (FBDs) represent an important burden for human and animal health [1]. A proper management of FBDs requires not only a good understanding of the disease, but also a fast detection and a proper response. Therefore, it is important to track the circulation of pathogens and monitor their medically relevant features. Bacterial typing is essential to monitor FBDs, and good surveillance systems are always seeking for typing methods which provide information at higher resolution. Therefore, bacterial typing methods have been evolving throughout decades according to the scientific and technological advances [2]. By providing information for each nucleotide at whole-genome level, whole-genome sequencing (WGS) technologies represent the molecular-typing technique with the highest resolution thus far [2]. For this reason, a gradual transition in FBDs surveillance from traditional methods to WGS-typing is in place [3]. In this context, the BeONE WP1-T1 aimed to establish the current state of the art within genomics methods for WGS-typing, particularly for the four target species of the project: *Listeria monocytogenes*, *Salmonella enterica*, *Escherichia coli* and *Campylobacter jejuni*. This output covers the approaches for setup, analysis, and evaluation of the remaining WPs (WP2-WP4). Given the relevance of such a topic for the scientific community and public health institutions, where this technological transition is still ongoing, this task had as ultimate goal the creation of a hands-on-oriented online handbook available for the whole community, and which can be constantly updated according to the most recent advances in the field.

The One Health Sequencing for Surveillance HandBook

1. One Health EJP collaboration

A good knowledge of the current state of the art within genomics methods for WGS-typing is a transversal need for several One Health projects. In this context, during the BeONE kick-off meeting, the partners identified that BeONE WP1-T1 objectives particularly overlapped with ORION project WP2. In fact, the ORION project, launched in 2018, aimed at establishing and strengthening inter-institutional collaboration and transdisciplinary knowledge transfer in the area of surveillance data integration and interpretation. One of the aims of this project was to do a cross-domain inventory of currently available data sources/methods/algorithms/tools that support One Health surveillance data generation, data analysis, modelling and decision support. So, in order to avoid redundancy and potentiate the output of both projects, a joint collaboration between BeONE and ORION projects arose, through the common partner NVI, culminating in a more comprehensive handbook about WGS technologies and WGS-typing methods in One Health surveillance.

2. The HandBook

The One Health Sequencing for Surveillance HandBook is available at the https://readthedocs.org platform, through the link: https://oh-sfs-handbook.readthedocs.io/en/latest/.

The handbook is currently divided in the following sections:

- "Sequencing technologies", covering technical aspects of the currently available sequencing platforms;
- "Bioinformatics methods", providing an overview of the different steps of a bioinformatics pipeline for WGS data analysis (from file formats and quality control to genome assembly);

- "Single isolate typing methods and resources", providing an overview of topics such as MLST, Serotyping, Virulence and AMR detection, among others;
- "Clustering methods and resources", covering topics such as cgMLST, SNP and allele calling, and phylogenetics;
- "Compute infrastructure", covering the computational aspects of WGS data analysis, from workflows managers to the available platforms for the analysis;
- "Species specific toolchains", providing a historical revision of the different typing methods used for *L. monocytogenes, S. enterica, E. coli* and *C. jejuni* until the advent of WGS. This section also covers the WGS data analysis specificities of each of these species, from their specific culture needs, DNA extraction protocols, bioinformatics pipelines (cgMLST and SNP-based pipelines), to their outbreak definition thresholds, medically relevant genes recognized thus far and the state of their One Health surveillance;
- "Challenges for One Health Surveillance", providing an overview of the relevance of implementing enhanced One Health surveillance frameworks, and exploring the challenges that are associated with the demanding WGS technological transition at inter-sectoral level.

BeONE and ORION projects have contributed to the writing and revision of all the above-mentioned sections. Nevertheless, each project was responsible for the structure, the development and the final content of the sections which were more in accordance with the objectives of their specific tasks. Therefore, the BeONE WP1-T1 was the leading project of the "Species specific toolchains" and the "Challenges for One Health Surveillance" sections. It is important to note that this handbook is expected to be constantly updated according to the most recent advances in the field, and because of that, its structure may suffer some alterations in the future.

Conclusions

As a joint collaboration within the One Health EJP, the BeONE project WP1-T1 has contributed to the compilation of an online HandBook covering the current state of the art of WGS-typing methods. Such a resource is expected to contribute to the success not only of the other BeONE WPs, but also, at a broader scale, to the scientific community and all the staff from public health institutions which are now transitioning between technologies.

References

1 – WHO (2020) "Food safety" (https://www.who.int/news-room/fact-sheets/detail/food-safety, last accessed on July 6th, 2021)
2 – Uelze, L., Grützke, J., Borowiak, M. *et al.* Typing methods based on whole genome sequencing data. *One Health Outlook* **2,** 3 (2020). https://doi.org/10.1186/s42522-020-0010-1
3 – ECDC (2019) "ECDC strategic framework for the integration of molecular and genomic typing into European surveillance and multi-country outbreak investigations" (https://www.ecdc.europa.eu/sites/default/files/documents/framework-for-genomic-surveillance.pdf, last accessed on July 6th, 2021)