



FWD AMR.
RefLabCap

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Food- and Waterborne Diseases Antimicrobial Resistance – Reference Laboratory Capacity

FWD AMR-RefLabCap

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Provision of EU networking and support for public health reference laboratory functions for antimicrobial resistance in *Salmonella* and *Campylobacter* in human samples

- ❖ The project is run under a contract with HaDEA on behalf of DG SANTE and in close cooperation with ECDC
- ❖ 4-year project: **2021-2024**

- ❖ Contractors:
 - Statens Serum Institut (SSI)
 - Project leader: Eva Møller Nielsen, Section of Foodborne Infections

 - National Food Institute, Technical University of Denmark (DTU)
 - René Hendriksen, Research group for global capacity building

- ❖ Support countries to enhance the **validity and accuracy of surveillance data** in order to inform concerted actions against AMR at EU level and enable better **detection and control of cross border threats** to human health from AMR
- ❖ AMR in *Salmonella spp* and *Campylobacter spp* in human samples
- ❖ Participants:
 - Countries participating in the EU Health programme
 - Candidate and potential candidate countries, other funding
- ❖ Cooperation with ECDC, DG SANTE and when relevant also EFSA and EURLs in the food safety area
 - EURL-AR, -Campylobacter, -Salmonella + inter-EURL working group on NGS

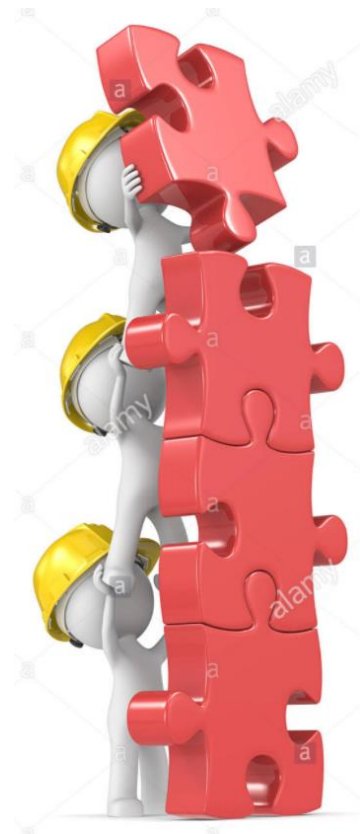
Networking and capacity building activities provided to national public health reference laboratories to improve their functions for AMR surveillance of human *Salmonella* and *Campylobacter* infections

Modernisation of methods for diagnostics, typing and AMR by using whole genome sequencing (WGS)

Activities to support the role of NRLs for public health to work with and **build capacities in the regional and local laboratories** in their own countries

Two pathogens: *Salmonella* spp and *Campylobacter* spp in humans

A specific focus on countries where capacities are less well developed



Training

Methods

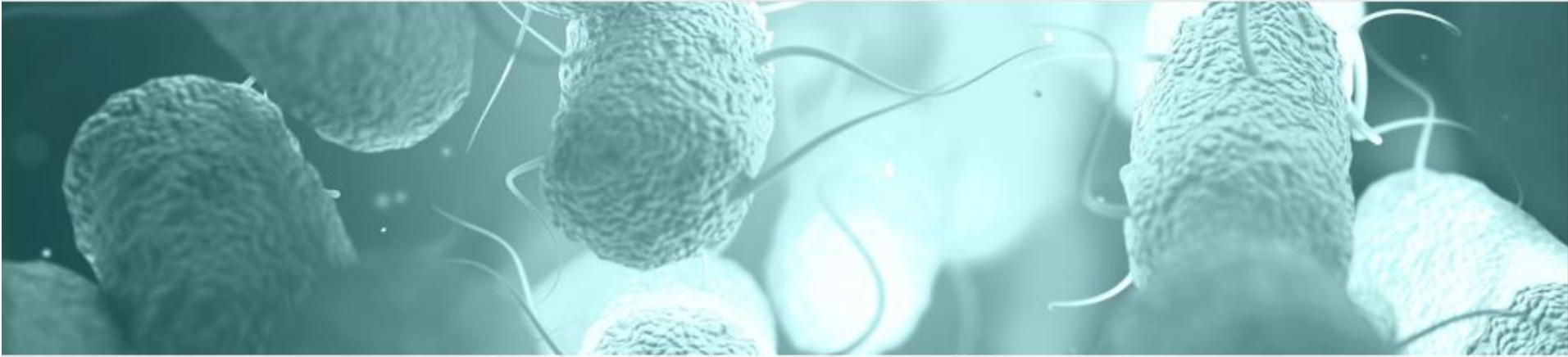
Capacity building

Networking

Network meetings, workshops, online presentations

- exchange of experience, best practice, inspiration
- discussions on NRL requirements, protocols, feedback on activities
- **complementarity with work carried out by the relevant EURLs in the food safety area**

Website: Protocols, guidance docs, training material, links



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News

[30 November – 1 December 2021 \(tentative\) – Network meeting at SSI, Copenhagen, Denmark](#)
10 September 2021

[7 September - online meeting](#)
10 September 2021

[Welcome to FWD AMR-RefLabCap](#)
12 May 2021

12 May 2021

Welcome to FWD AMR-RefLabCap



[Home](#) / [Participants](#)



Participants

Laboratories participating in the FWD AMR-RefLabCap network

Updated 8 July 2021

Albania

Institute of Public Health
Laboratory of Enterobacteriology

Austria

Austrian Agency for Health and Food Safety, Institute for Medical Microbiology and Hygiene Graz
National Reference Centre for Salmonella

Austrian Agency for Health and Food Safety, Institute for Medical Microbiology & Hygiene, Centre
for Foodborne Infectious Diseases
National Reference Centre for Campylobacter

Belgium

Sciensano
Sciensano - NRC salmonella

NRC Campylobacter - University Laboratory Brussels
LHUB-ULB - NRC Campylobacter

Bosnia and Herzegovina

Public Health Institute of The Republic of Srpska
Department of Microbiology

Bulgaria

National Center for Infectious and Parasitic Diseases
NRL of Enteric Infections, Pathogenic cocci and Diphtheria

Croatia


Croatian Institute of Public Health

43 laboratories from 36 countries

- ❖ Laboratories in 32 EU/EEA countries + EU Health Programme invited to participate
 - Participation of 38 laboratories in 31 countries
- ❖ Laboratories in 5 candidate/potential candidate countries are invited as "observers" (separate funding)
 - 5 laboratories in 5 countries
- ❖ Total of 38 laboratories in EU/EEA + EU Health Programme countries
 - 22 NRLs cover both Campylobacter and Salmonella
 - 7 NRLs of Campylobacter
 - 9 NRLs of Salmonella
- ❖ Western Balkans and Turkey (enlargement countries)
 - 5 NRLs of both Campylobacter and Salmonella

• Minimum and optimal requirements in PH NRL functions

- Recommended coverage of surveillance
- Sampling and testing frequency
- Epi-situations for isolation & referral of isolates from primary to national level
- Methodological and resource capacity and capability requirements at all levels



obs MRSA	mecA	pos	NT	32
obs MRSA	mecA	pos	NT	32
bakteriemi			NT	30
obs MRSA	mecA	pos	NT	32
bakteriemi			NT	32
bakteriemi			NT	33
bakteriemi			NT	33
bakteriemi			NT	3
bakteriemi			NT	3
obs MRSA	mecA	pos	NT	24
bakteriemi			NT	24
obs MRSA	mecA	pos	NT	28
bakteriemi			NT	32
obs MRSA	mecA	pos	NT	32
obs MRSA	mecA	pos	NT	0
obs MRSA	mecA	pos	NT	32
obs MRSA	mecA	pos	NT	32
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• Identify capacity/capability gaps in all countries

- Existing information
- Survey in network



❖ Capacity building activities for all NRLs

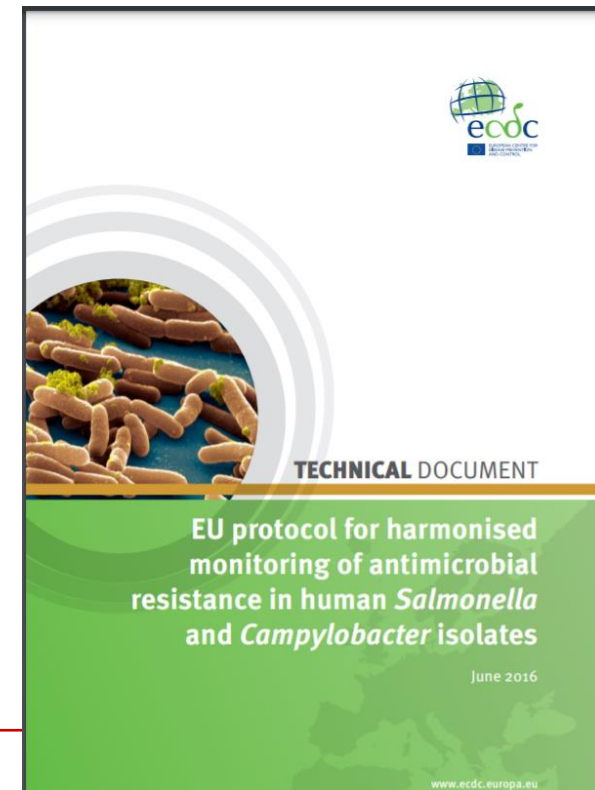
- Lab training courses
- Workshops and surveillance exercises on integrated WGS-based surveillance

❖ Tailored support to 'priority countries'

- country visits
- action plans



- ❖ **Propose optimal methodologies for AMR detection, integrated into WGS-based surveillance for cluster detection**
 - Existing guidance and literature, incl. bioinformatics and databases
 - Seek consensus experts/ECDC/EFSA/EUCAST
 - Set of common methods and standard protocols for national surveillance
 - Agreement in network
- ❖ Any relevant methodologies developed by EURLs shall be taken into account to **ensure complementarity**
- ❖ Review/amend existing EU protocol for AMR surveillance to include genetic AMR determinants




European Journal of Clinical Microbiology & Infectious Diseases (2021) 40:673–682
<https://doi.org/10.1007/s10096-020-04043-y>

ORIGINAL ARTICLE



Prediction of antimicrobial resistance in clinical *Campylobacter jejuni* isolates from whole-genome sequencing data

Louise Gade Dahl¹ • Katrine Grimstrup Joensen¹ • Mark Thomas Østerlund¹ • Kristoffer Kiil¹ • Eva Møller Nielsen¹ 

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Abstract

Campylobacter jejuni is recognised as the leading cause of bacterial gastroenteritis in industrialised countries. Although the majority of *Campylobacter* infections are self-limiting, antimicrobial treatment is necessary in severe cases. Therefore, the development of antimicrobial resistance (AMR) in *Campylobacter* is a growing public health challenge and surveillance of AMR is important for bacterial disease control. The aim of this study was to predict antimicrobial resistance in *C. jejuni* from whole-genome sequencing data. A total of 516 clinical *C. jejuni* isolates collected between 2014 and 2017 were subjected to WGS. Resistance phenotypes were determined by standard broth dilution, categorising isolates as either susceptible or resistant based on epidemiological cutoffs for six antimicrobials: ciprofloxacin, nalidixic acid, erythromycin, gentamicin, streptomycin, and tetracycline. Resistance genotypes were identified using an in-house database containing reference genes with known point mutations and the presence of resistance genes was determined using the ResFinder database and four bioinformatical methods (modified KMA, ABRicate, ARIBA, and ResFinder Batch Upload). We identified seven resistance genes including *tet(O)*, *tet(O/32/O)*, *ant(6)-Ia*, *aph(2'')-If*, *blaOXA*, *aph(3')-III*, and *cat* as well as mutations in three genes: *gyrA*, *23S rRNA*, and *rpsL*. There was a high correlation between phenotypic resistance and the presence of known resistance genes and/or point mutations. A correlation above 98% was seen for all antimicrobials except streptomycin with a correlation of 92%. In conclusion, we found that WGS can predict antimicrobial resistance with a high degree of accuracy and have the potential to be a powerful tool for AMR surveillance.

Whole-Genome Sequencing to Detect Numerous *Campylobacter jejuni* Outbreaks and Match Patient Isolates to Sources, Denmark, 2015–2017

Katrine G. Joensen, Kristoffer Kiil, Mette R. Gantzhorn, Birgitte Nauerby, Jørgen Engberg, Hanne M. Holt, Hans L. Nielsen, Andreas M. Petersen, Katrin G. Kuhn, Gudrun Sandø, Steen Ethelberg, Eva M. Nielsen

Emerging Infectious Diseases Vol. 26, No. 3, March 2020

Whole genome sequencing data used for surveillance of *Campylobacter* infections: detection of a large continuous outbreak, Denmark, 2019

Katrine Grimstrup Joensen¹, Susanne Schjørring¹, Mette Rørbæk Gantzhorn², Camilla Thougard Vester², Hans Linde Nielsen^{3,4}, Jørgen Harald Engberg⁵, Hanne Marie Holt⁶, Steen Ethelberg⁷, Luise Müller⁷, Gudrun Sandø², Eva Møller Nielsen¹

1. Statens Serum Institut, Department of Bacteria, Parasites and Fungi, Copenhagen, Denmark

2. Danish Veterinary and Food Administration, Glostrup, Denmark

Euro Surveill. 2021;26(22):pii=2001396

- Multi-disciplinary training workshops and webinars for PH epidemiologists and microbiologists
 - integration of WGS into national AMR surveillance and outbreak investigation
- EQAs of WGS-based resistome profiling
 - complement ongoing EQA schemes
 - 3 rounds for all NRLs
- Inter-laboratory ring-trials of bioinformatics pipelines for prediction of AMR



Home > Life Sciences > Medicine & Healthcare

Antimicrobial resistance – theory and methods

About this course: The course will cover the topics related to antimicrobial resistance with basic definitions and overview on antimicrobials their use and the emergence and spread of resistance. The course will guide you through the concepts and the importance of resistance spread and dissemination and how that happens. It will show you how bacteria become resistant and which mechanisms they might

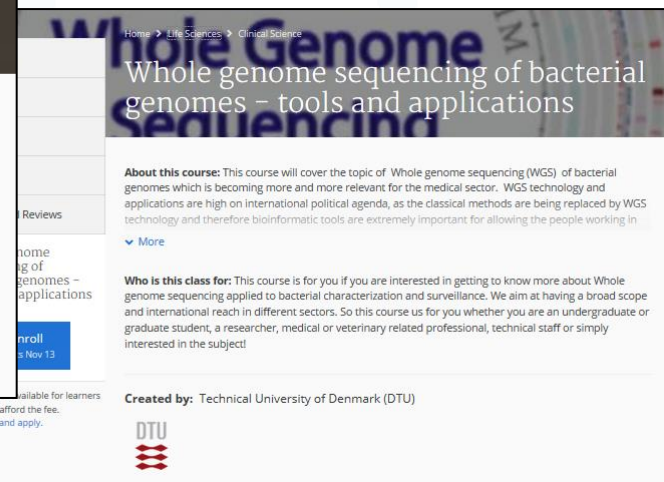
[More](#)

Who is this class for: This course is for you if you are interested in getting to know more about antimicrobials and antimicrobial resistance in bacteria. We aim at having a broad scope and international reach in different sectors. So this course us for you whether you are an undergraduate or graduate student, a researcher, medical or veterinary related professional, technical staff or simply interested in the subject

Created by: Technical University of Denmark (DTU)



Financial Aid is available for learners who cannot afford the fee. [Learn more and apply.](#)



Home > Life Sciences > Clinical Science


Whole genome sequencing of bacterial genomes – tools and applications

About this course: This course will cover the topic of Whole genome sequencing (WGS) of bacterial genomes which is becoming more and more relevant for the medical sector. WGS technology and applications are high on international political agenda, as the classical methods are being replaced by WGS technology and therefore bioinformatic tools are extremely important for allowing the people working in

[More](#)

Who is this class for: This course is for you if you are interested in getting to know more about Whole genome sequencing applied to bacterial characterization and surveillance. We aim at having a broad scope and international reach in different sectors. So this course us for you whether you are an undergraduate or graduate student, a researcher, medical or veterinary related professional, technical staff or simply interested in the subject

Created by: Technical University of Denmark (DTU)



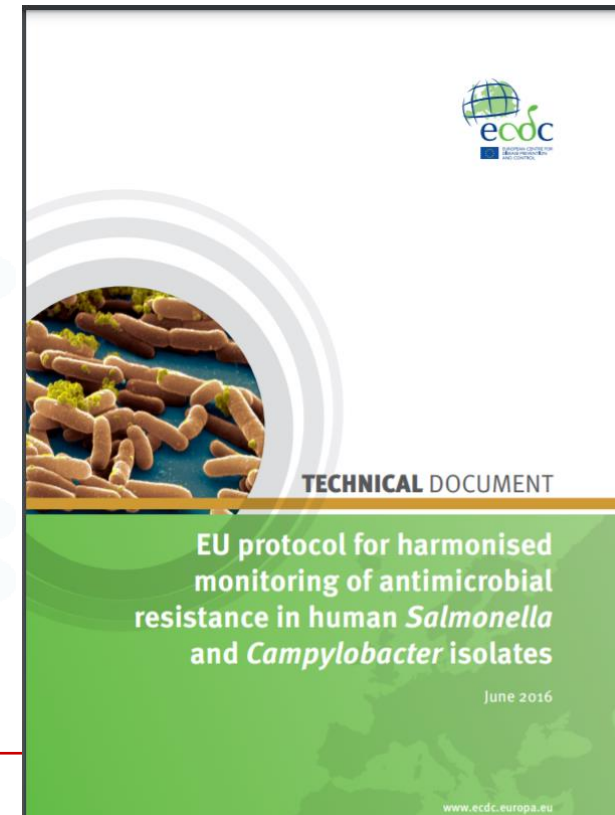
Financial Aid is available for learners who cannot afford the fee. [Learn more and apply.](#)

EQAs on antimicrobial susceptibility testing (ECDC)

- Support the implementation of the harmonized EU AST protocol for *Salmonella* and *Campylobacter* in NPHRLs
- Assess the quality of the AST data (MIC and DD methods) across Europe
- Allow evaluation of new molecular based methodologies

EQA 2020 round: 21 EU/EEA countries participated

- 13 reported disk diffusion results
- 12 reported MIC results, broth dilution or gradient strip
- 4 reported predicted results based on WGS



Support NRLs to build capacities in local/regional labs

- ❖ Support all NRLs in mapping the regional/local labs' capacities for detection and characterization of *Salmonella* and *Campylobacter*
 - Strengths/weaknesses and gaps/further needs for each country
- ❖ Support NRLs to carry out regional capacity building (≥ 16 MSs)
 - Physical and online meetings and workshops
 - Learning material
 - Ongoing individual support
- ❖ Support NRLs to establish national network of labs
- ❖ Model protocol for national surveillance of AMR in Salm/Campy
- ❖ Guidance for internal QC schemes for reference AMR testing





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