

Update from EURL-AR

Rene S. Hendriksen

Research group of Global Capacity Building

National Food Institute, Technical University of Denmark

18th EURL-AR Workshop 2024
8th -9th October – Kgs. Lyngby, Denmark
Glassalen, Building 101



Activity: To ensure availability and use of high quality methods and high quality performance by NRLs

- Sub-activity 3.1.1.1 (Providing NRLs with details and guidance on laboratory methods)
- Updated in compliance with Commission Implementing Decision (EU) 2020/1729 of 17 November 2020 on the monitoring and reporting of antimicrobial resistance in zoonotic and commensal bacteria and repealing Implementing Decision 2013/652/EU)
 - References updated through-out the protocol stated that detection of carbapenemase producing E.coli including OXA-48 and OXA48-like producers is mandatory
 - Affecting background, contents, 1.6, 1.9, 3.1, 3.4, references, Appendix 2



Activity: To ensure availability and use of high quality methods and high quality performance by NRLs

- Sub-activity 3.1.1.3/ 4/ 5 (Providing NRLs with details and guidance on laboratory methods)
- The two MRSA PCR protocols were updated including the proper control ID strains
- MyDbFinder finalized for BioInformatic analysis
 - All should be ready for the baseline 2025 on MRSA
- Continue the updates of the protocol for short-read whole genome sequencing in addition to the development of a new WGS for long-read ONT technology
 - posted on the web pending

MRSA

[MRSA multiplex PCR-1 protocol: PCR amplification of CC398, mecA, PVL, scn and spa \(version 1.1, April 2024\)](#) (PDF document, 600 KB)

[MRSA multiplex PCR-2 protocol: PCR amplification of mecA, mecC, PVL and spa \(version 3.1, April 2024\)](#) (PDF document, 400 KB)

[Spa-typing protocol: PCR amplification and typing of spa gene \(version 2, December 2022\)](#) (PDF document, 100 KB)

[Isolation of MRSA from food-producing animals and farm environment \(version 3, April 2023\)](#) (PDF document, 600 KB)

[MLST typing](#) (PDF document, 25 KB)

MyDBFinder for MRSA

MyDBFinder for MRSA PRC PT 2024

[MyDBFinder for MRSA PCR PT 2024](#) (text document, 100 KB)

Activity: To ensure availability and use of high quality methods and high quality performance by NRLs

- Sub-activity 3.1.1.6 (Providing NRLs with details and guidance on laboratory methods)
- The EURL provided a “Freezed” version of the Resfinder database for the reporting period 2023 and 2024 including ESBL, AmpC and CP genes
 - will likely not be provided for 2025 and onwards due to lack updated ESBL, AmpC and CP genes, in ResFinder – thus the proposed discussion from EFSA

Activity: *To ensure availability and use of high quality methods and high quality performance by NRLs*

- Sub-activity 3.1.1.9 (Providing NRLs with details and guidance on laboratory methods)
- Initiate with the Veterinary Bacteriology Service, Sciensano, Belgium a voluntary linezolid resistance monitoring survey in order to assess the level of interest among the EU member states to participate in such monitoring activities



Activity: To ensure availability and use of high quality methods and high quality performance by NRLs

- Sub-activity 3.1.1.3 (Coordination and organization of inter-laboratory comparative testing)
- Trial 1 – Phenotypic AST (wrap up 2023 and launch of 2024)
 - *Salmonella*
 - *Campylobacter*
 - *Escherichia coli*
- Trial 2 – Matrix EQA (wrap up 2023 and launch of 2024)
 - Qualitative detection of ESBL and AmpC producing *E. coli* from a matrix of caecal and food samples (chicken/chicken meat)
- Trial 3 - MRSA PCR PT
 - Assessing ability to perform PCR according to PCR 1 and 2 multiplex

EQAS Reports



[The 30th Proficiency Testing, 2022 – Escherichia coli, Salmonella, Campylobacter and Staphylococcus aureus](#) (PDF document, 3.5 MB)

Activity: To ensure availability and use of high quality methods and high quality performance by NRLs

- Sub-activity 3.1.3.3 (Coordination and organization of inter-laboratory comparative testing)
- Trial 4 – DTU Genomic PT
 - Assessment of library-preparation, and WGS of six bacterial cultures
 - Results to participants released
 - on sequence quality in participants' submitted FASTQ files
 - on bioinformatic analysis to detect antimicrobial resistance (AMR) genes and mutations, and MLST

Activity: To ensure availability and use of high quality methods and high quality performance by NRLs


- Sub-activity 3.1.3.3 (Coordination and organization of inter-laboratory comparative testing)
- Trial 4 – DTU Genomic PT
 - Sequence QC data from 2021 and 2022 published

RESEARCH ARTICLE

September 2024 Volume 9 Issue 9 e00160-24
<https://doi.org/10.1128/msystems.00160-24>

Whole-genome sequencing for antimicrobial surveillance: species-specific quality thresholds and data evaluation from the network of the European Union Reference Laboratory for Antimicrobial Resistance genomic proficiency tests of 2021 and 2022

Lauge Holm Sørensen ¹, Susanne Karlsmose Pedersen¹, Jacob Dyring Jensen¹, Niamh Lacy-Roberts¹, Athina Andrea¹, Michael S. M. Brouwer², Kees T. Veldman², Yan Lou³, Maria Hoffmann³, Rene S. Hendriksen¹

Activity: *To provide scientific and technical assistance to NRLs*

- Sub-activity 3.2.2 (Conducting training courses for NRLs)

National Food Institute



30 August 2024

Invitation to the EURL-AR Training Course

On behalf of the EURL-AR team, I am pleased to invite you to the EURL-AR Training Course 2024 at DTU Food in Kgs. Lyngby, Denmark.

The training course aims to ensure harmonization in the use of Oxford Nanopore sequencing technologies in zoonotic and commensal bacteria across the EU. The course will provide you with the tools to generate and use whole genome sequence data in accordance with the EU Decision.



Course content

Members of the EURL-AR network have varying levels of expertise in WGS using Oxford Nanopore technologies and the course content will be broad to ensure that everyone gains new and relevant knowledge. The course is divided into three parts:

- 5 December 2024: Online session introducing Oxford Nanopore sequencing, one of the two most common sequencing technologies at present.
- 11-12 December 2024: Laboratory training for Oxford Nanopore sequencing (including high-molecular weight DNA extraction, library preparation, flow cell loading) at the Technical University of Denmark (DTU), Kgs. Lyngby, Denmark.
- 18 December 2024: Online session for bioinformatics analysis of Oxford Nanopore data.




Activity: *To provide scientific and technical assistance to NRLs*

- Sub-activity 3.2.4 (Coordination and organization workshops among the NRLs)
- Virtual workshop in 8th - 9th of Oct 2024

	
<p align="center">18th EURL-AR Workshop 2024 8th-9th October – Kgs. Lyngby, Denmark Glassalen, Building 101</p>	
<p>Tuesday, 8th October 2024</p>	
9:00-9:20	Welcome Meet and greet/ Introduction to the day's agenda Rene Hendriksen, EURL-AR
9:20-9:40	Update from the EURL-AR Rene Hendriksen, EURL-AR
9:40-10:15	Updates from EFSA on ongoing AMR activities Raquel García Fierro, EFSA
10:15-10:30	Update from the EU Commission Martial Plantady, EU Commission /Virtual
10:30-11:00	Coffee break
11:00-11:30	EFSA/EURL-AR Confirmatory Testing Joana Mourão, EURL-AR
11:30-11:55	2022 EUSR on AMR Raquel García Fierro, EFSA
11:55-12:20	EFSA CarbaCamp- Assessment of phenotypic susceptibility, genomic epidemiology Campylobacter from animal, food and human Elisabeth Chang, EURL-AR

Activity: *To provide scientific and technical assistance to NRLs*

- Sub-activity 3.2.5 (Work Package) (Providing information on relevant research activities to NRLs)

Microbial Genetics | Announcement


Database of all currently known mobile colistin resistance genes

Ana Rita Rebelo,¹ Rene S. Hendriksen¹

AUTHOR AFFILIATION See affiliation list on p. 2.








ABSTRACT We created a database of all currently known mobile colistin resistance genes and variants ($n = 115$). It contains accession numbers of the gene and protein sequences, mutations between the protein variants and the main proteins, and additional metadata. It is accompanied by all genetic and protein sequences as two aggregated FASTA files.

KEYWORDS colistin, *mcr* genes, gene sequences, protein sequences, database, mutations



J Antimicrob Chemother 2024; **79**: 1657–1667
<https://doi.org/10.1093/jac/dkaf161> Advance Access publication 22 May 2024

Azithromycin resistance in *Escherichia coli* and *Salmonella* from food-producing animals and meat in Europe

Mirena Ivanova¹, Armen Ovsepian ^{1,2}, Pimlapas Leekitcharoenphon ³, Anne Mette Seyfarth¹, Hanne Mordhorst³, Saria Otani³, Sandra Koeberl-Jelovcan⁴, Mihail Milanov⁵, Gordan Kompes⁶, Maria Liapi⁷, Tomáš Černý⁸, Camilla Thougard Vester⁹, Agnès Perrin-Guyomard¹⁰, Jens A. Hammerl ¹¹, Mirjam Grobbel¹¹, Eleni Valkanou¹², Szilárd Jánosi¹³, Rosemarie Slowey¹⁴, Patricia Alba ¹⁵, Virginia Carfora ¹⁵, Jelena Avsejenko¹⁶, Asta Pereckiene¹⁷, Dominique Claude¹⁸, Renato Zerafa¹⁹, Kees T. Veldman²⁰, Cécile Boland²¹, Cristina Garcia-Graells²¹, Pierre Wattiau²¹, Patrick Butaye ^{22,23}, Magdalena Zajac ²⁴, Ana Amaro²⁵, Lurdes Clemente²⁵, Angela M. Vaduva²⁶, Luminita-Maria Romascu²⁷, Nicoleta-Manuela Milita²⁷, Andrea Mojžišová²⁸, Irena Zdovc²⁹, Maria Jesús Zamora Escribano³⁰, Cristina De Frutos Escobar³⁰, Gudrun Overesch³¹, Christopher Teale³², Guy H. Loneragan³³, Beatriz Guerra³⁴, Pierre Alexandre Beloeil³⁴, Amanda M. V. Brown³⁵, Rene S. Hendriksen¹, Valeria Bortolaia^{1,36}† and Jette Sejer Kjelsgaard^{1*†}

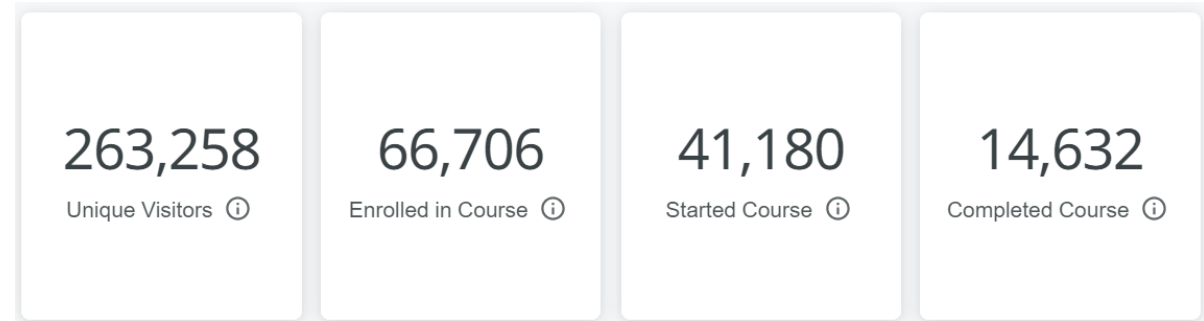
Activity: *To provide scientific and technical assistance to NRLs*

- Sub-activity 3.2.5 (Work Package) (Providing information on relevant research activities to NRLs)

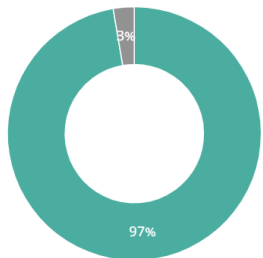
<p>Biological Hazards and Animal Health and Welfare Unit</p> 	
<p>AGREEMENT NUMBER — GP/EFSA/BIOHAW/2023/04</p> <p>TITLE — CarbaCamp</p> <p>This Agreement ('the Agreement') is concluded between the following parties:</p> <p>on the one part,</p> <p>The European Food Safety Authority (hereinafter "the Authority"), established by Regulation (EC) No 1831/2003 of the European Parliament and of the Council laying down the general requirements of food law, establishing the European Food Safety Authority and procedures in matters of food safety, as last amended, with offices on Via Carlo Magno, 4, 40138 Parma (Italy), represented by Mr Bernhard Url, Executive Director,</p> <p>and</p> <p>on the other part,</p> <p>'the beneficiary'</p>	<div data-bbox="1294 725 1431 982" data-label="Image"> </div> <div data-bbox="1457 839 1712 902" data-label="Text"> <p>BIOHAW/ASSESS</p> </div> <div data-bbox="2186 768 2323 796" data-label="Text"> <p>SENSITIVE</p> </div> <div data-bbox="2339 725 2502 959" data-label="Image"> </div> <div data-bbox="1381 1088 2109 1188" data-label="Text"> <p>Technical University of Denmark, National Food Institute (DTU Food) Kemitovet, Building 204, DK-2800, Kgs. Lyngby, Denmark</p> </div> <div data-bbox="1381 1225 1635 1253" data-label="Text"> <p>Subject: Grant award</p> </div> <div data-bbox="1381 1259 2415 1316" data-label="Text"> <p>Ref.: GP/EFSA/BIOHAW/2024/01 Data generation on Carbapenemase-producing Enterobacterales (CPEs) in the food chain in the EU/EFTA.</p> </div>

Activity: *To provide scientific and technical assistance to NRLs*

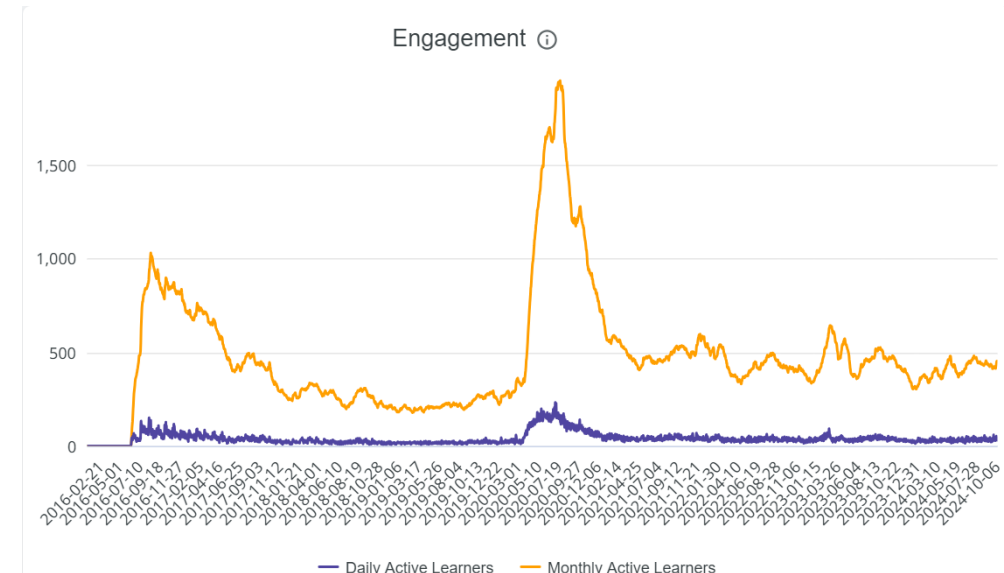
- Sub-activity 3.2.6 (Providing E-learning)
- In 2023 and 2024, the EURL has re-recorded all old videos and include videos of the practical work in recognition that many videos are more than seven years old
 - A series of new E-learning lectures and video incl. hands on antimicrobial susceptibility testing and MALDI-TOF



Likes & Dislikes ⓘ



● Likes ● Dislikes



Activity: To provide scientific and technical assistance to NRLs

• Sub-activity 3.2.7 (Confirmatory testing)

Year	zoonc	progCode	Reason	DTU no.	Ini	Dato	SMX	TMP	CIP	TET	MERO	Az	CHL	FOT	TGC	COL	TAZ	AMP	GEN	FOX	ETP	IMI	MERO	TAZ	FEP	F/C	T/C	FUT																																														
2019	E.coli	ESBL MON	AmpC	57	imha	07-10	>1024	≤0.25	≤0.015	64	≤0.03	4	≤4	≤8	2	≤0.25	≤1	4	>64	≤0.5	32	≤0.015	≤0.12	≤0.03	4	≤0.06	1/4	2/4	2																																													
							sul1			tet(A)					ampC-promoter (g.-42C>T)										ampC-prc							ampC-promoter (g.-42C>T)							ampC-promoter (g. ampC-prc							ampC-prc							ampC-promoter (g.-42C>T)																					
2019	E.coli	ESBL MON	AmpC	58	imha	07-10	>1024	>32	>8	>64	≤0.03	32	>128	32	>4	≤0.25	≤1	>8	>64	≤0.5	64	0.03	0.25	≤0.03	16	0.25	4/4	8/4	8	8	Fully agr.																																											
							sul1, sul3	dfrA12	gyrA (p.S	tet(M), tet(A)		mph(A)	gyrA (p.S	cmlA1	blaCMY-2		blaCMY-2	blaCMY-2	blaTEM-1	blaCMY-2				blaCMY-2	(blaCMY-2	blaCMY-2	blaCMY-2	blaCMY-2	blaCMY-2																																													
2019	E.coli	ESBL MON	CST-R	59	imha	07-10	>1024	>32	≤0.015	>64	≤0.03	8	≤4	≤8	>4	≤0.25	8	4	>64	1	4	≤0.015	0.25	≤0.03	1	8	≤0.06/4	≤0.12/4	32	8	Fully agree																																											
							sul1, sul3	dfrA1		tet(A), tet(M)					blaCTX-M-1	mcr-1.1	blaCTX-M	blaCTX-M-1						blaCTX-M	blaCTX-M-1			blaCTX-M-1																																														
2019	E.coli	ESBL MON	CST-R	60	imha	07-10	>1024	>32	>8	≤2	≤0.03	4	>128	>128	>4	≤0.25	8	4	>64	1	8	≤0.015	0.25	≤0.03	4	8	≤0.06/4	≤0.12/4	64	4	MS TET >64.																																											
							sul1, sul2	dfrA12	gyrA (p.S	tet(A)			gyrA (p.S	catA1	blaCTX-M-32	mcr-1.1	blaCTX-M	blaCTX-M-32	blaTEM-1B					blaCTX-M	blaCTX-M-32			blaCTX-M-32																																														
2019	E.coli	ESBL MON	CST-R	61	imha	07-10	>1024	>32	8	>64	≤0.03	>64	>128	>128	>4	≤0.25	8	2	>64	>32	4	≤0.015	≤0.12	≤0.03	2	4	≤0.06/4	≤0.12/4	64	4	Fully ag																																											
							sul1, sul2	dfrA12	gyrA (p.S	tet(A), tet(M)		mph(A)	gyrA (p.S	catA1	blaCTX-M-32	mcr-1.1	blaCTX-M	blaCTX-M	aac(3)-IId					blaCTX-M	blaCTX-M-32			blaCTX-M-32																																														
2019	E.coli	ESBL MON	AmpC FOX	62	imha	07-10	>1024	≤0.25	≤0.015	>64	≤0.03	4	≤4	128	1	≤0.25	≤1	2	>64	≤0.5	8	≤0.015	0.25	≤0.03	2	≤0.06	0.5/4	2/4	1	8	MS FOX 1																																											
							sul2			tet(B), tet(Y)			flor	ampC-promoter (g.-42C>T)										ampC-prc										ampC-promoter (g.-42C>T) (MIC close t										ampC-promoter (g. ampC-prc										ampC-prc										ampC-promoter (g.-42C>T)										
2019	E.coli	ESBL MON	AmpC FOX	63	imha	07-10	≤8	≤0.25	≤0.015	≤2	≤0.03	4	≤4	≤8	1	≤0.25	≤1	2	>64	≤0.5	16	≤0.015	0.25	≤0.03	2	0.12	0.5/4	2/4	1	8	Fully agre																																											
															ampC-promoter (g.-42C>T)										ampC-prc										ampC-promoter (g.-42C>T)										ampC-promoter (g. ampC-prc										ampC-prc										ampC-promoter (g.-42C>T)									
2019	E.coli	ESBL MON	AmpC	64	imha	07-10	≤8	≤0.25	≤0.015	≤2	≤0.03	8	≤4	≤8	1	≤0.25	≤1	4	>64	≤0.5	8	≤0.015	≤0.12	≤0.03	4	0.12	1/4	2/4	1	8	MS FOX 1																																											
															ampC-promoter (g.-42C>T)										ampC-prc										ampC-promoter (g.-42C>T) (MIC close t										ampC-promoter (g. ampC-prc										ampC-prc										ampC-promoter (g.-42C>T)									
2019	E.coli	AMR MON	CST-R	65	imha	07-10	≤8	≤0.25	≤0.015	≤2	≤0.03	≤2	≤4	≤8	≤0.25	≤0.25	4	≤0.50	2	≤0.5	2	≤0.015	≤0.12	≤0.03	≤0.25	≤0.06	≤0.06/4	≤0.12/4	≤0.25	2	Fully agr																																											
																mcr-1.1																																																										
2019	E.coli	AMR MON	CST-R	66	imha	07-10	>1024	≤0.25	≤0.015	64	≤0.03	4	≤4	128	≤0.25	≤0.25	4	≤0.50	>64	≤0.5	4	≤0.015	0.25	≤0.03	≤0.25	≤0.06	≤0.06/4	≤0.12/4	≤0.25	4	Fully agi																																											
							sul3			tet(A)			flor			mcr-1.1		blaTEM-1B																																																								
2019	E.coli	ESBL MON	AmpC FOX	67	imha	07-10	≤8	≤0.25	0.03	≤2	≤0.03	8	≤4	≤8	1	≤0.25	≤1	4	>64	≤0.5	32	0.03	0.25	≤0.03	2	≤0.06	0.5/4	1/4	1	8	Fully ag																																											
															ampC-promoter (g.-42C>T)										ampC-prc										ampC-promoter (g.-42C>T)										ampC-promoter (g. ampC-prc										ampC-prc										ampC-promoter (g.-42C>T)									
2019	E.coli	ESBL MON	ESBL	68	imha	07-10	>1024	>32	≤0.015	>64	≤0.03	4	≤4	≤8	>4	≤0.25	≤1	1	>64	1	8	≤0.015	≤0.12	≤0.03	2	16	≤0.06/4	≤0.12/4	64	4	Fully a																																											
							sul2	dfrA17		tet(B), tet(A)					blaCTX-M-1		blaCTX-M	blaCTX-M-1						blaCTX-M	blaCTX-M-1			blaCTX-M-1																																														
2019	E.coli	ESBL MON	ESBL	69	imha	07-10	>1024	≤0.25	≤0.015	>64	≤0.03	4	≤4	128	>4	≤0.25	≤1	2	>64	1	2	0.03	0.25	≤0.03	2	16	≤0.06/4	0.25/4	64	8	Fu ¹																																											
							sul2			tet(B), tet(A)			flor	blaCTX-M-1		blaCTX-M	blaCTX-M-1, blaTEM-1B						blaCTX-M	blaCTX-M-1			blaCTX-M-1																																															
2019	E.coli	ESBL MON	IMI+ and N	70	imha	07-10	>1024	≤0.25	≤0.015	64	≤0.03	4	≤4	≤8	>4	≤0.25	≤1	2	>64	≤0.5	8	≤0.015	0.25	≤0.03	2	16	≤0.06/4	≤0.12/4	64	8																																												
							sul2			tet(A)					blaCTX-M-1		blaCTX-M	blaCTX-M-1						blaCTX-M	blaCTX-M-1			blaCTX-M-1																																														
2019	E.coli	AMR MON	AmpC FOX	71	imha	####	>1024	≤0.25	≤0.015	>64	≤0.03	4	≤4	≤8	1	≤0.25	≤1	2	64	≤0.5	16	≤0.015	0.25	≤0.03	2	≤0.06	0.5/4	1/4	1	4																																												
							sul2			tet(B)					ampC-promoter (g.-42C>T)										ampC-prc										ampC-promoter (g.-42C>T)										ampC-promoter (g. ampC-prc										ampC-prc										ampC-promoter (
2019	E.coli	AMR MON	CST-R	72	ptreceived																																																																					
2019	E.coli	ESBL MON	CST-R	73	imha	####	>1024	>32	≤0.015	64	≤0.03	4	≤4	32	>4	≤0.25	8	1	>64	≤0.5	4	≤0.015	0.25	≤0.03	1	8	≤0.06/4	0.25/4	32	4	Fully agree																																											
							sul1, sul3	dfrA1		tet(A)			cmlA1	blaCTX-M-1	mcr-1.1	blaCTX-M	blaCTX-M-1							blaCTX-M	blaCTX-M-1			blaCTX-M-1																																														
2019	E.coli	ESBL MON	CST-R	74	ptreceived																																																																					
2019	E.coli	ESBL MON	CST-R	75	imha	####	>1024	>32	≤0.015	64	≤0.03	4	≤4	32	>4	≤0.25	8	1	>64	1	4	≤0.015	0.25	≤0.03	1	8	≤0.06/4	0.12/4	32	4	Fully agre																																											
							sul1, sul3	dfrA1		tet(A)			cmlA1	blaCTX-M-1	mcr-1.1	blaCTX-M	blaCTX-M-1							blaCTX-M	blaCTX-M-1			blaCTX-M-1																																														
2019	E.coli	ESBL MON	CST-R	76	imha	####	>1024	>32	≤0.015	64	≤0.03	4	≤4	16	>4	≤0.25	8	1	>64	≤0.5	4	≤0.015	0.25	≤0.03	1	4	≤0.06/4	0.12/4	32	4	MS CHL 3																																											
							sul1, sul3	dfrA1		tet(A)		mph(A)	cmlA1	blaCTX-M-1	mcr-1.1	blaCTX-M	blaCTX-M-1, blaTEM-1B							blaCTX-M	blaCTX-M-1			blaCTX-M-1																																														
2019	E.coli	ESBL MON	CST-R	77	ptreceived																																																																					
2019	E.coli	ESBL MON	ESBL	78	imha	####	≤8	≤0.25	0.5	≤2	≤0.03	8	8	≤8	>4	≤0.25	≤1	4	>64	≤0.5	4	≤0.015	≤0.12	≤0.03	8	32	≤0.06/4	0.12/4	64	4	MS NAL																																											
									qnrS1						blaCTX-M-55		blaCTX-M	blaCTX-M-55						blaCTX-M	blaCTX-M-55			blaCTX-M-55																																														
2019	E.coli	ESBL MON	ESBL	79	imha	####	>1024	>32	≤0.25	64	≤0.03	8	8	≤8	>4	≤0.25	≤1	8	>64	≤0.5	8	≤0.015	≤0.12	≤0.03	16	16	≤0.06/4	0.25/4	>64	8	Fully																																											

Activity: To provide scientific and technical assistance to the European Commission and other organisations

- Sub-activity 3.3.1 (Providing scientific and technical assistance to the EU Commission)
- Technical Specifications for a baseline survey on AMR in aquaculture animals

Approved: 2 July 2024

DOI: 10.2903/j.efsa.2024.8928

SCIENTIFIC REPORT

efsa JOURNAL

Technical specifications for a EU-wide baseline survey of antimicrobial resistance in bacteria from aquaculture animals

European Food Safety Authority (EFSA) | Marc Aerts | Sandrine Baron | Valeria Bortolaia | Rene Hendriksen | Beatriz Guerra | Anca Stoicescu | Pierre-Alexandre Beloeil

Activity: *To provide scientific and technical assistance to the European Commission and other organisations*

- Sub-activity 3.3.2 (provide scientific and technical assistance to others than EU Commission)



ONT Pipeline: Virtual Expert Elicitation

- Will bring together “users” who conduct sequencing in LMICs as part of larger capacity strengthening projects with key “providers” to share user needs with the providers and come up with a set of recommendations.
- Confirmed participants from Oxford Nanopore, Thiagen, US CDC, Institut Pasteur, University of Melbourne Peter Doherty Institute for Infection and Immunity, and WHO

international
building in

veillance System

Thank you for your attention



Prof. Rene S. Hendriksen, PhD

Head of Research Group Global Capacity Building
WHO Collaborating Centre for Antimicrobial Resistance in Food borne
Pathogens and Genomics

European Union Reference Laboratory for Antimicrobial Resistance
FAO Reference Laboratory for Antimicrobial Resistance
National Food Institute, Technical University of Denmark

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