FWD AMR-RefLabCap

Update on current EQAs of AST on Salmonella and Campylobacter

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First network meeting
30 November 2021

AGENDA

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- ECDC EQA-AST on Salmonella and Campylobacter organized by Statens Serum Insitut
- Presentation of the set-up
- Accumulated results 2018-2020 – DD and MIC
- DNA based results – 2020 (EQA-AST6)
- Conclusins
- Questions

Objectives/aims of the ECDC EQA

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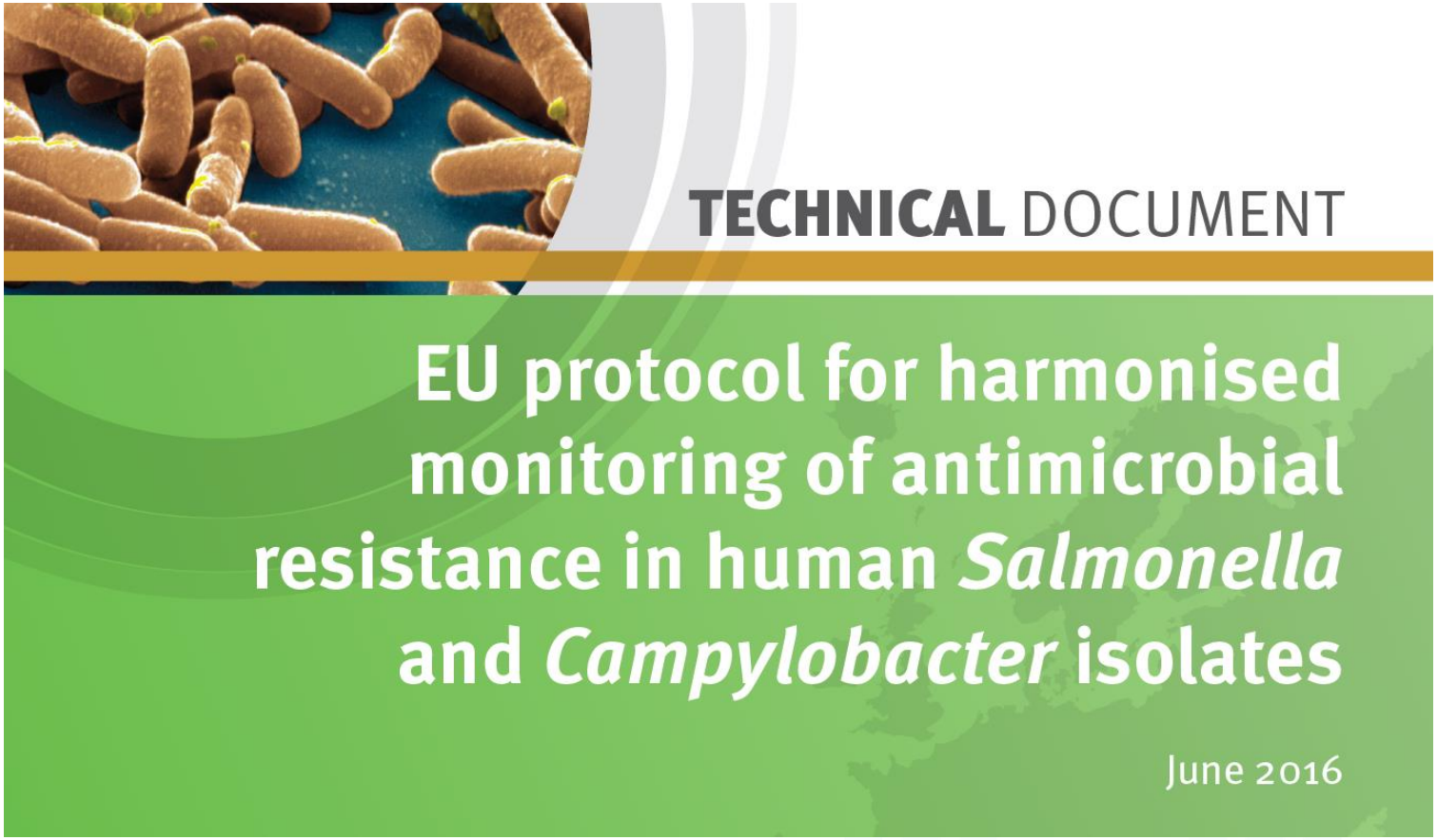
Aims:

- support the implementation of the harmonized EU AST protocol for *Salmonella* and *Campylobacter*
- To asses the quality of the AST data obtained using MIC and/or DD methods in NPHRLs across Europe
- allow evaluation of new molecular based methodologies (WGS, PCR etc.)
- evaluation of serotyping of Salmonella and species identification of Campylobacter

Objectives:

- identify common laboratory problem(s)
- assess the overall comparability of routinely collected AST results from European NPHRLs

Protocol



https://www.ecdc.europa.eu/sites/default/files/media/en/publications/Publications/antimicrobial-resistance-Salmonella-Campylobacter-harmonised-monitoring.pdf

Participation – and organisation

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Laboratories in the FWD-Net from EU/EEA and laboratories from “enlargement” countries invited to participate – most laboratories accepts the invitation

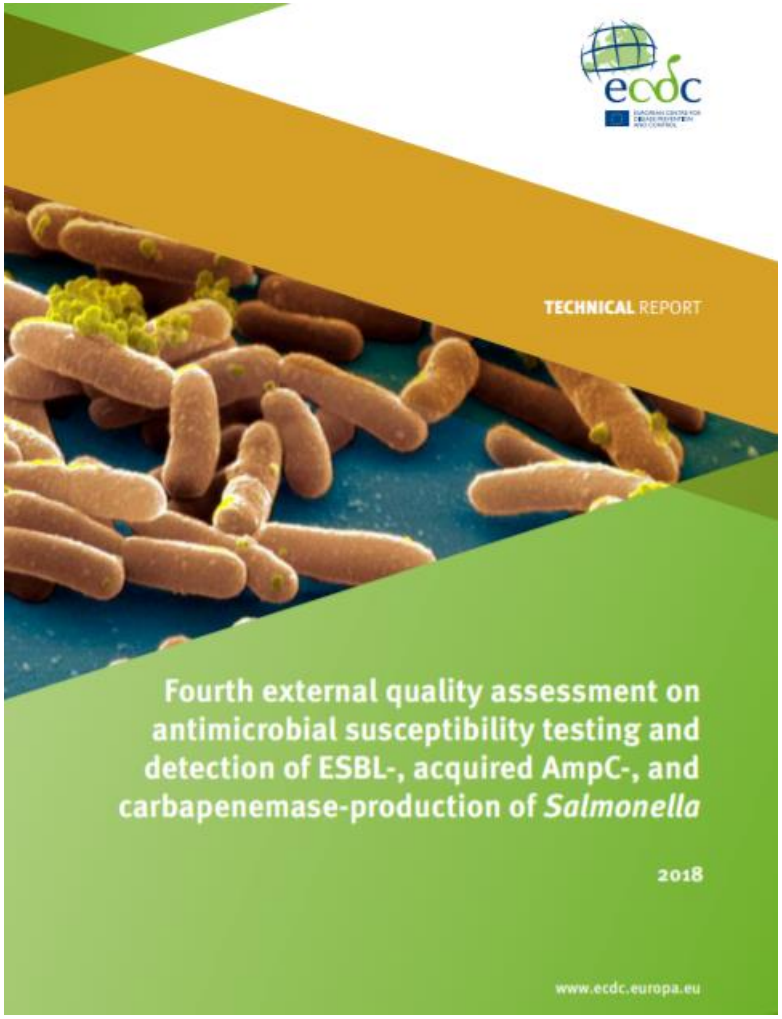
Salmonella

- Eight strains for AST testing - DD and/or MIC
- Possible to report ESBL-, acquired AmpC-, and carbapenemase status both pheno- and genotypes
- Possible to report predicted results (WT/NWT) from molecular analysis
- Possible to report serotyping results

Campylobacter

- Five strains - AST testing and species determination
- Possible to report DD and MIC results
- Possible to report predicted results (WT or NWT) from molecular analysis

EQA-AST – FEEDBACK AND REPORTING



Individual feedback provided to all participants

Salmonella: MIC results within +/- one dilution difference and DD results within +/- 3 mm difference from the expected results are evaluated as correct

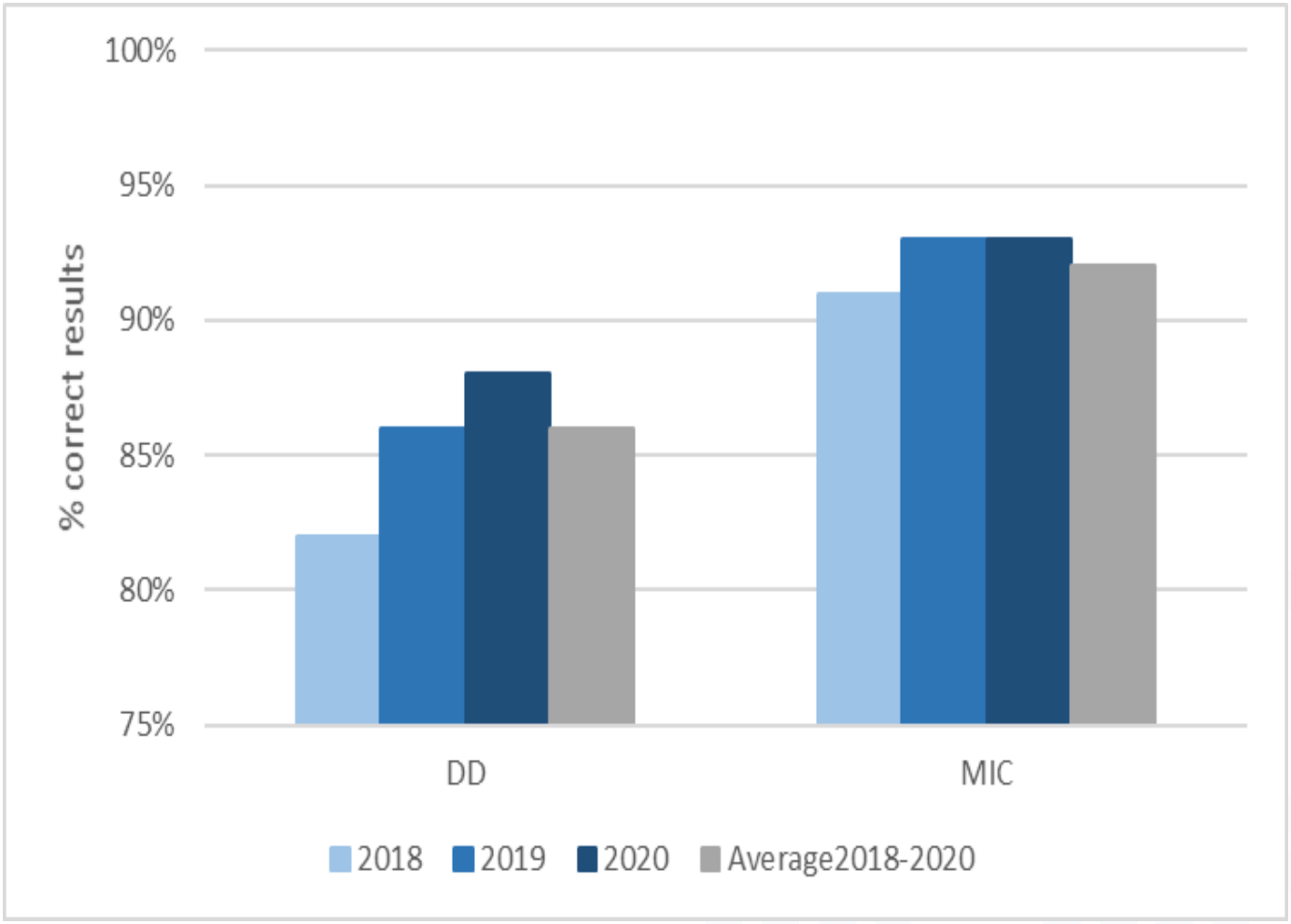
Campylobacter: MIC results within +/- one dilution difference and DD results within +/- 4 mm difference from the expected results are evaluated as correct

ESBL/AmpC/carbapenemase pheno- and genotypic results evaluated case by case

Predicted genotypic results evaluated against phenotypic qualitative results using ECOFF's

Report summarizing the results of the EU/EEA countries are produced

Overview of correct results using DD/MIC for Salmonella from 2018-2020 – all participating laboratories



Overview of results using DD/MIC for Campylobacter from 2018-2020 – all participating laboratories

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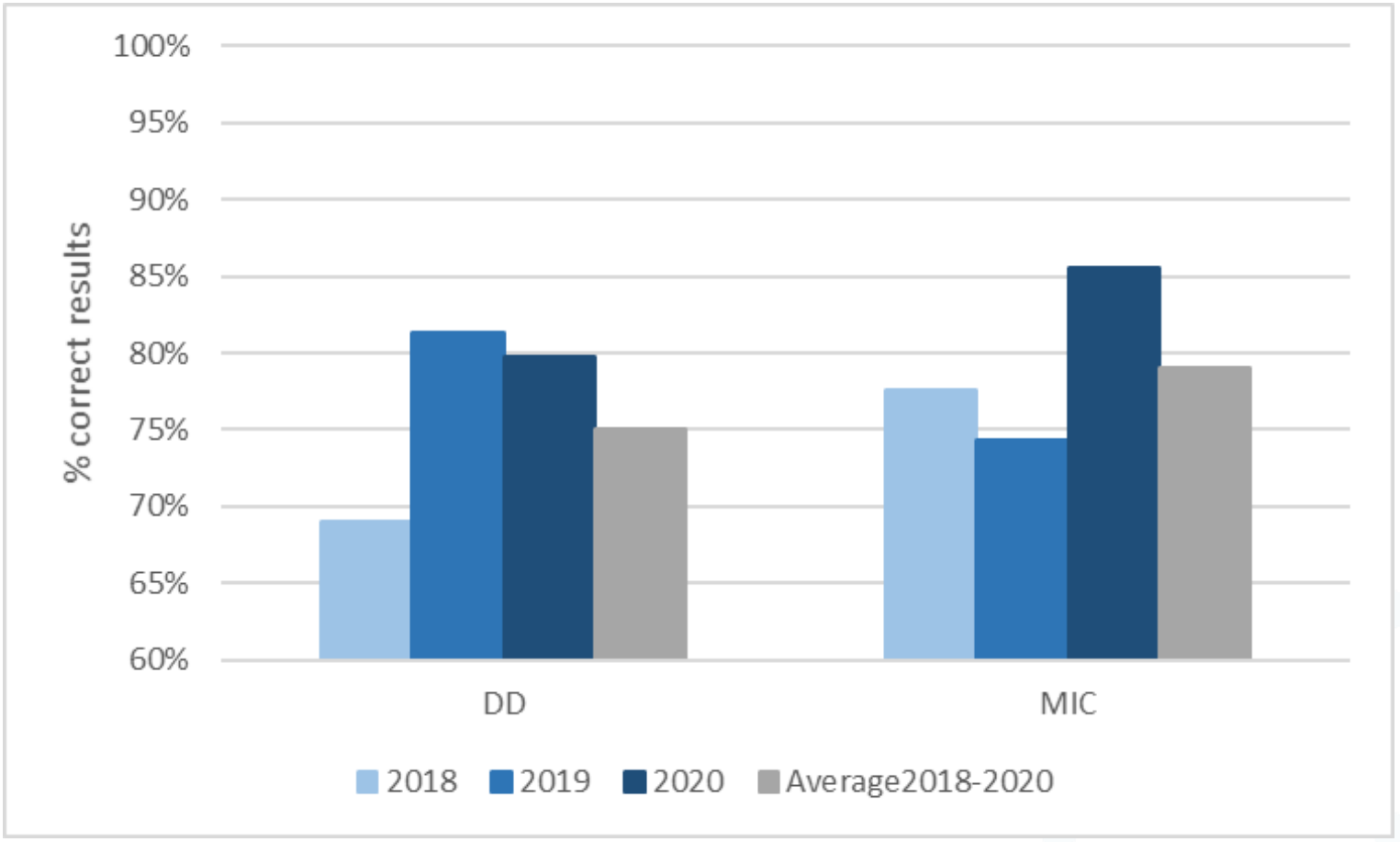

MIC: CORRECT RESULTS FOR *SALMONELLA* 2018-2020 BY LABORATORY (BOTH MBD AND GS RESULTS)

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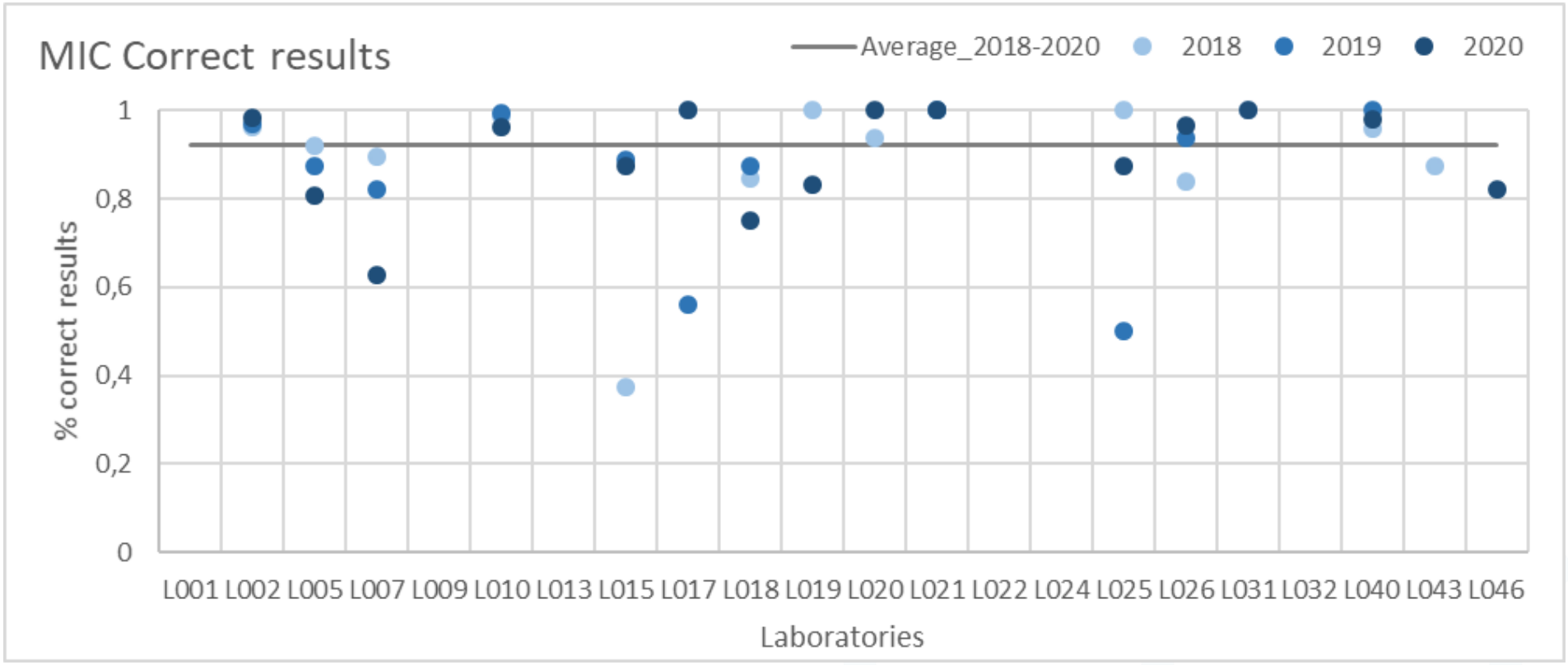

DD: CORRECT RESULTS FOR *SALMONELLA* 2018-2020 BY LABORATORY

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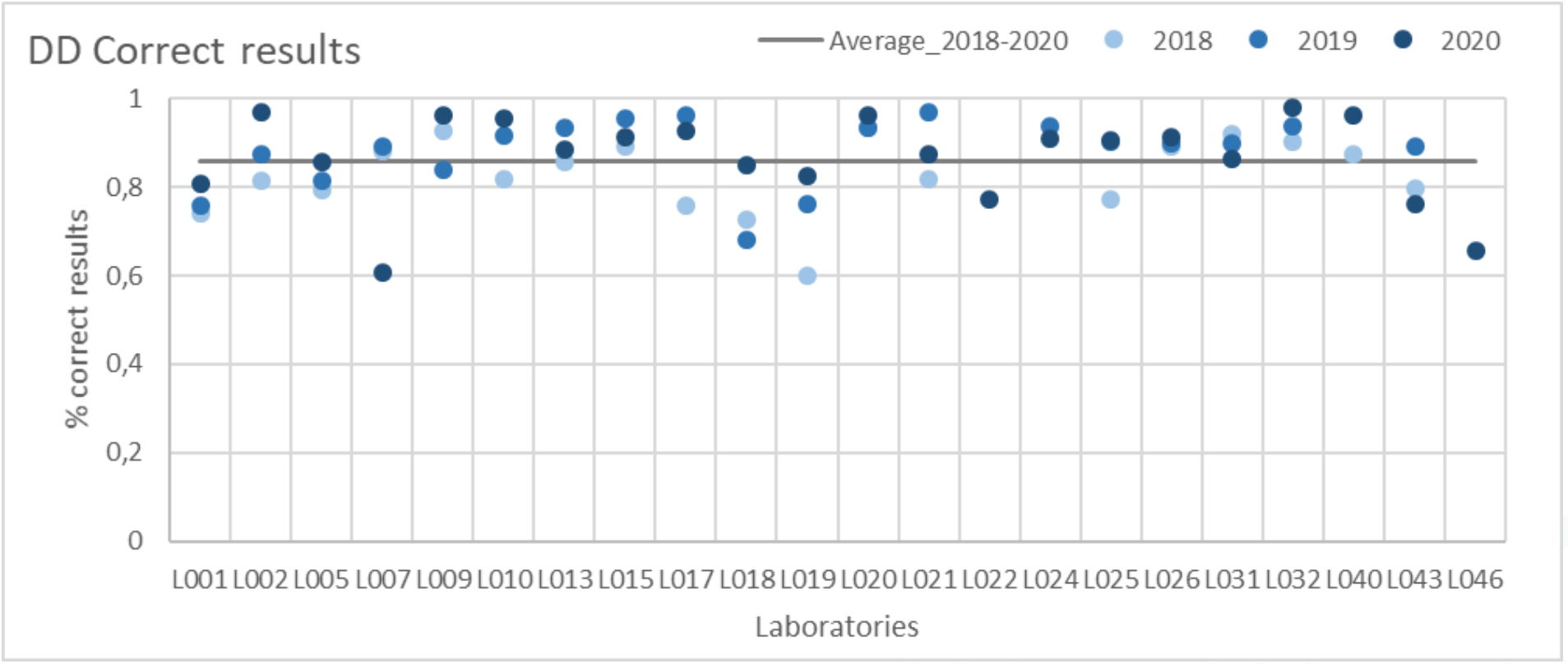
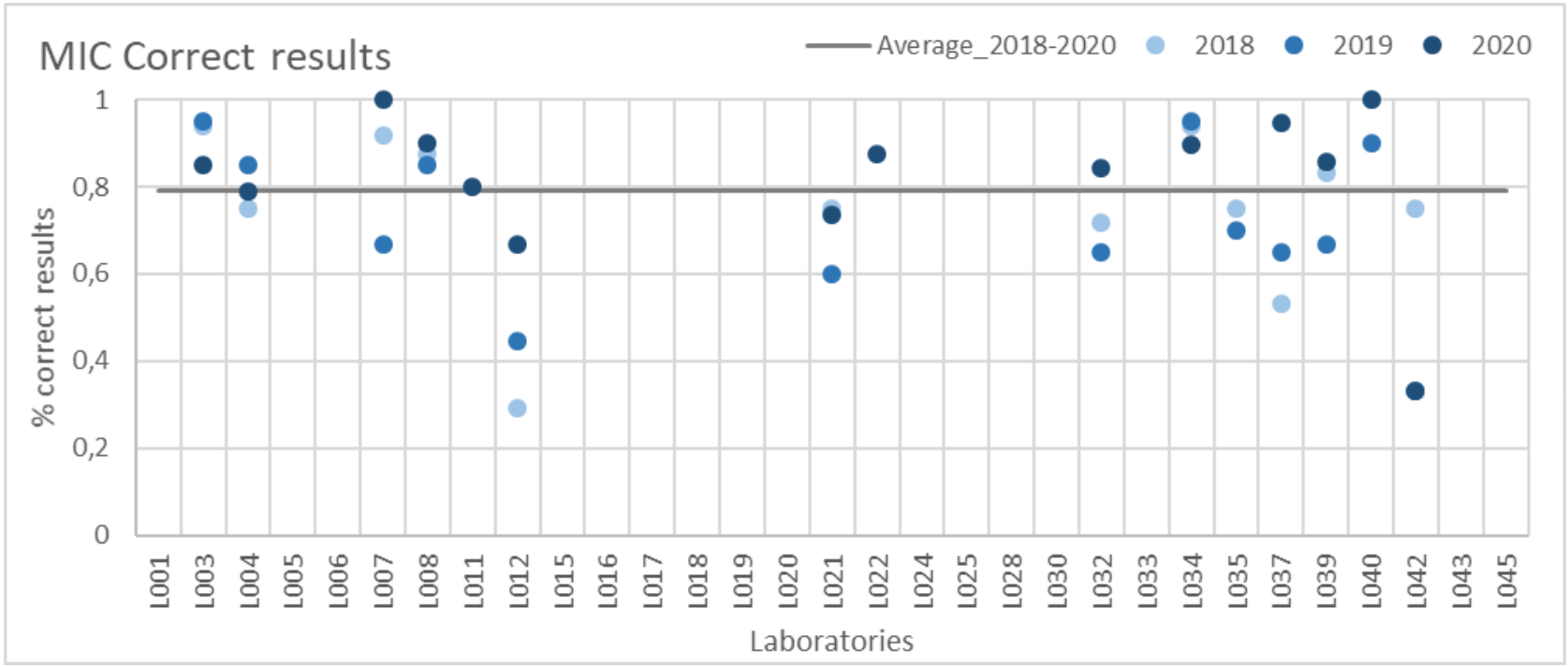


MIC: CORRECT RESULTS FOR *CAMPYLOBACTER* 2018-2020 BY LABORATORY (BOTH MBD AND GS RESULTS)



DD: CORRECT RESULTS FOR CAMPYLOBACTER 2018-2020 BY LABORATORY

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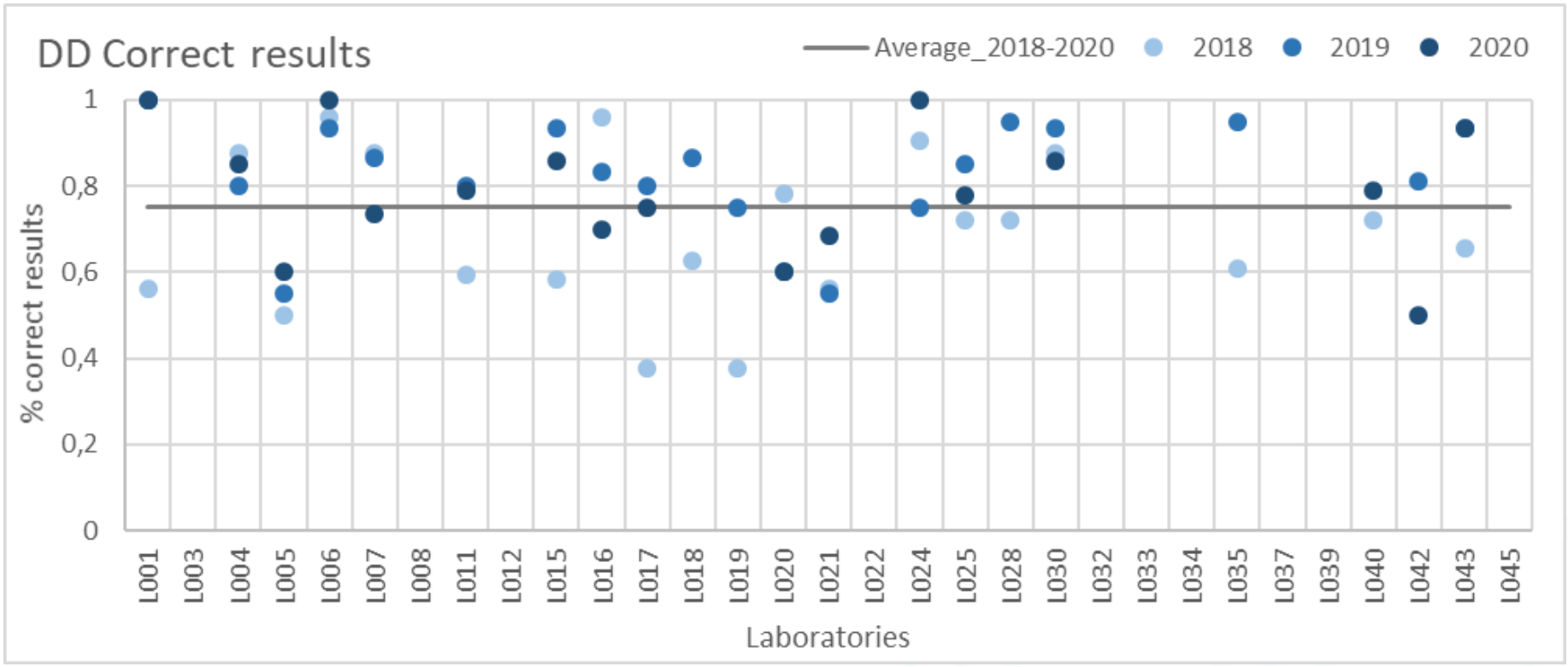

EQA6-AST Genotypic characterization of ESBL-, acquired AmpC,and carbapenemase genes

Strain	Expected genotype	Method used for genotype prediction	Genotype predicted (number of laboratories)
S20.0005	CTX-M9/65*	WGS	CTX-M-65 (6)
		PCR/sequencing	CTX-M-65 (1)
		PCR	CTX-M-9 (3)
		PCR	CTX-M positive (1)
		In house Luminex assay	CTX-M-9 group (1)
		PCR	CTX4 (1)
		Total	13
S20.0006	blaCTX-M-55	WGS	CTX-M-55 (6)
		PCR/sequencing	CTX-M-55 (1)
		PCR	CTX-M (4)
		PCR	CTX1,CTX2 (1)
		In house Luminex assay	CTX-M-15 (1)
		PCR/sequencing	CTX1,CTX2
		Total	14
S20.0006	CTX-M-9	WGS	CTX-M-9 (6)
		PCR/sequencing	CTX-M-9 (2)
		PCR	CTX-M9 (3)
		PCR	CTX-M (1)
		PCR	CTX4 (1)
		In house Luminex assay	CTX-M9 (1)
		Total	14
C20.0008	CTX-M-123	WGS	CTX-M-123 (6)
		PCR/sequencing	CTX-M-123 (1)
		PCR/sequencing	CTX-M-128 (1)
		PCR	CTX-M-9
		PCR	CTX-M (3)
		PCR	CTX2 (1)
		In house Luminex assay	CTX-M-15 (1)
		Total	14
Grand total			55

Approximately half of the laboratories report results.

Generally the laboratories are able to identify the correct genes

Results reflects that there is no standardized method available

WGS applied by 6 laboratories – all reporting correct

PCR and PCR in combination with sequencing is also working

*both results correct

EQA6-AST (2020) SALMONELLA PREDICTED PHENOTYPES FROM WGS – DATA FROM 6 LABORATORIES

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Predicted phenotypes from WGS data by antimicrobial					
Antimicrobial	**Correct**	**Incorrect**	**Incorrect NWT**	**Incorrect WT**	**Total**
Ampicillin	40				40 (100%)
Azithromycin	20	4	4		24 (83%)
Cefepime	16				16 (100%)
Cefotaxime	46	2		2	48 (96%)
Cefoxitin	32				32 (100%)
Ceftazidime	14	2		2	16 (88%)
Chloramphenicol	24				24 (100%)
Ciprofloxacin	36	4	4		40 (90%)
Colistin	22	11	8	3	33 (67%)
Ertapenem	24				24 (100%)
Gentamicin	23	1	1		24 (96%)
Meropenem	48				48 (100%)
Nalidixic acid	16	4	3	1	20 (80%)
Sulfamethoxazole	24				24 (100)
Temocillin	7	1	1		8 (885)
Tetracycline	35	3		3	38 (92%)
Tigecycline	8				8 (100%)
Trimethoprim	24				24 (100%)
Total	459	32	21/241	11/250	491 (93%)

EQA-AST6 (2020) CAMPYLOBACTER PREDICTED PHENOTYPES FROM WGS – DATA FROM 4 LABORATORIES

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Predicted phenotypes from WGS data by antimicrobial					
	Correct	Incorrect	Incorrect NWT	Incorrect WT	Total
Ciprofloxacin	15	5	3	2	20
Erythromycin	16	4	4		20
Tetracycline	9	6	6		15
Gentamicin	7	13	1	12	20
Total	47	28	14/37	14/38	75

Conclusions

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- The NPHRL are participating in the EQAs
- The quality of the AST data from the laboratories are constant
- Some laboratories performs better than others – there is a best practice
- Dilution based methods superior to diffusion based
- The data produced in the different countries are comparable
- More laboratories could deliver DNA based results
- Synergy to this project

THANK YOU FOR YOU ATTENTION

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