

EQAS 2019 FOR SELECTIVE ISOLATION OF *E. COLI* WITH PRESUMPTIVE ESBL, AMPC PHENOTYPES OR CARBAPENEMASES FROM MEAT OR CAECAL SAMPLES

Matrix EQAS 2019

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Description of the ESBL/AmpC Matrix EQAS

- Sent out September 2019 – result database delayed
 - **5 pork meat samples**
 - M-5.1 ESBL + AmpC *E. coli* (CMY-2; CTX-M-27)
 - M-5.2 ESBL *E. coli* (TEM-1B; CTX-M-32)
 - M-5.3 ESBL *E. coli* (CTX-M-2)
 - M-5.4 Carbapenemase *E. coli* (OXA-162)
 - M-5.5 Susceptible *E. coli*
 - **3 cattle caecal samples**
 - M-5.6 ESBL (+ AmpC) (TEM-1B; CARB-2)
 - M-5.7 AmpC *E. coli* (Upregulated AmpC)
 - M-5.8 Carbapenemase (NDM-1)

Participants

- 35 participating laboratories
 - Some handle only meat or caecal samples
- One dataset per country included in evaluation
 - 31 sets of data included from 30 countries

Challenges in this round of Matrix EQAS

- **M-5.4**
 - 5 of 31 participants did not isolate the carbapenemase producing strain from the meat sample
- **M-5.5**
 - 9 of 31 participants isolated a presumptive carbapenemase (n=7), ESBL (n=1) or other phenotype (n=1) isolate from a meat sample spiked with a susceptible *E. coli*.
- **M-5.7**
 - Phenotypical ESBL + AmpC, genotypical ESBL
- Some difficulties in prediction of ESBL or ESBL + AmpC or AmpC phenotypes

Interpretative criteria – Matrix EQAS protocol

<i>Antimicrobials for E. coli</i>	MIC (mg/L) R is >
<u>Cefepime, FEP</u>	0.125
<u>Cefotaxime, FOT</u>	0.25
<u>Cefotaxime + clavulanic acid (F/C)</u>	0.25
<u>Cefoxitin, FOX</u>	8
<u>Ceftazidime, TAZ</u>	0.5
<u>Ceftazidime+ clavulanic acid (T/C)</u>	0.5
<u>Ertapenem, ETP</u>	0.064*
<u>Imipenem, IMI</u>	0.5
<u>Meropenem, MERO</u>	0.125
<u>Temocillin, TRM</u>	>32*

*Tentative ECOFF

Six laboratories did not apply the interpretive criteria for F/C & T/C

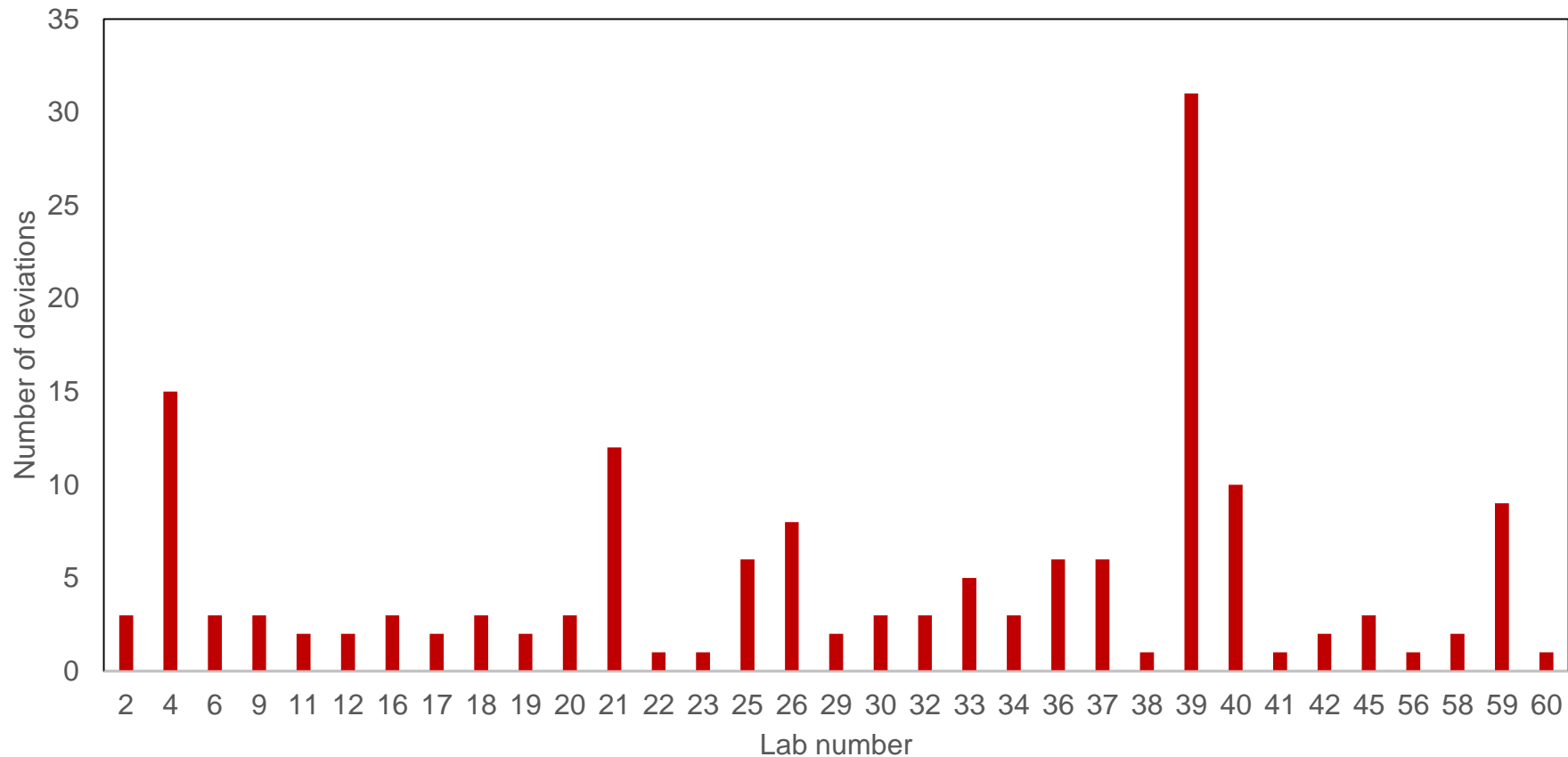
The overall performance of ESBL/AmpC isolation and identification, 2019

Isolation of ESBL/Carb/AmpC from samples		Correctly classified samples	
Number of test performed		Correctly classified samples	
N	%	N	%
248	100	232	94
Number of expected negative tests		Number of correctly identified negative tests	
N	%	N	%
31	12.5	22	71 %
Number of expected positive tests		Number of correctly identified positive tests	
N	%	N	%
217	87.5 %	210	96.8 %

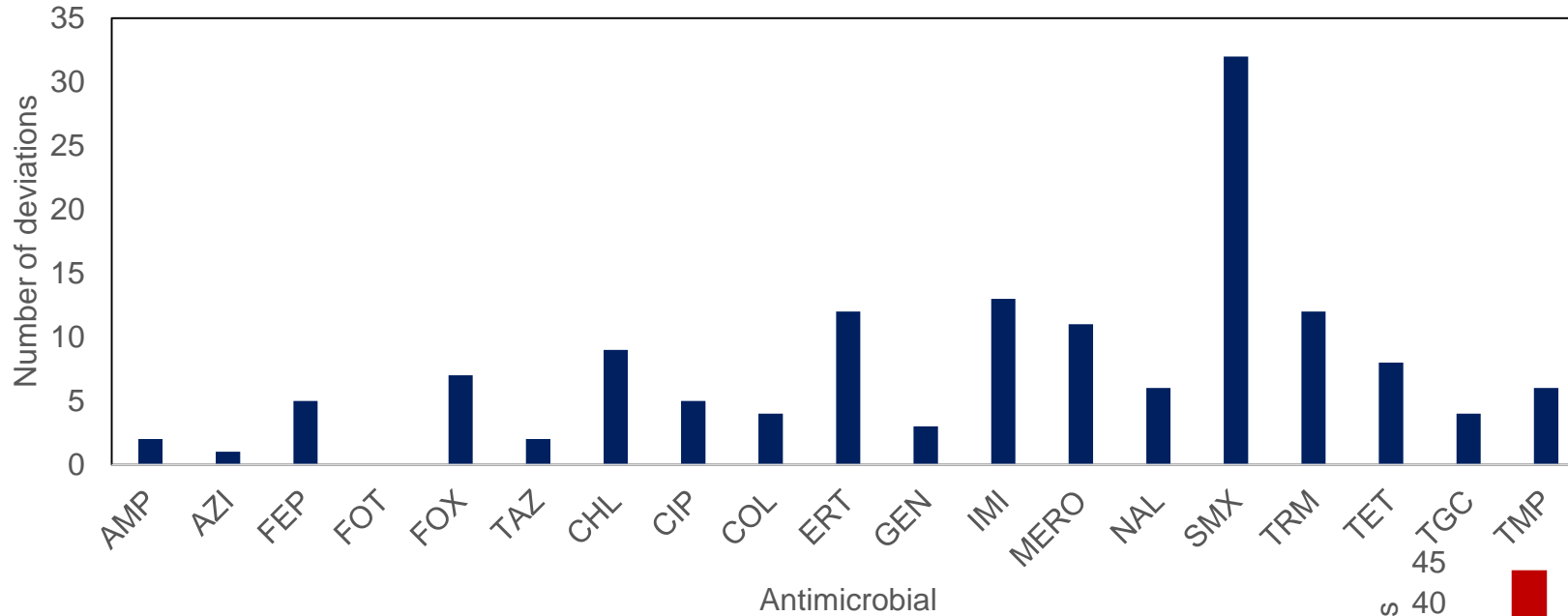
Overall 94 % correct results – 7 qualitative deviations

Deviations in AST results per lab – tentative results

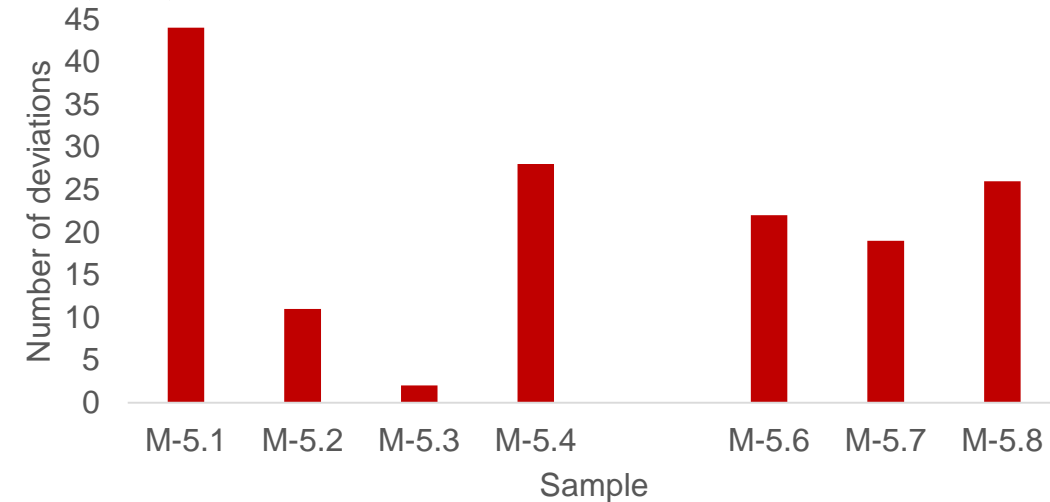
- Overall 97.1 % of AST results are correct
- Tentative result – not disregarding 1-MIC step variation



Deviations in AST results per antimicrobial and sample –tentative results



-Issue with SMX (Sample M-5.1)
 -Carbapenem variation



ESBL/Carba/AmpC-producing test strains phenotypic conclusion

		M 5.1	M 5.2	M 5.3	M 5.4	M 5.6	M 5.7	M 5.8
ESBL-, pAmpC- and carbapenemase-producing strain – expected results		ESBL+ AmpC	ESBL	ESBL	Carba	ESBL (+AmpC)	AmpC	Carba
Obtained results	Presumptive ESBL-producer	1/31	30/31	31/31		10/31		1/31
	Presumptive AmpC-producer	7/31	1/31			1/31	28/29	
	Presumptive ESBL+AmpC	22/31				19/31	1/29	
	Presumptive carbapenemase				24/26	1/31		30/31
	Other phenotype				2/26			

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EURL-AR Training Course 2020

- Online training course
- Week 43 (19 -23 October)
- Practical use of the knowledge obtained and WGS tools demonstrated in the past TC's
- Simulated exercise (tentative)
 - MIC reading (photos) and selection of relevant stains
 - QC analysis of sequences
 - Characterisation of AMR genes and plasmids
 - Cluster analysis
- Obtain data online - submit result by survey
- Online introduction, Q & A sessions and final feedback

Thank you for attending!

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**Please fill in the online evaluation
-link sent by email**