THE 8th EURL-AR PROFICIENCY TEST ON SELECTIVE ISOLATION OF *ESCHERICHIA COLI* WITH PRESUMPTIVE ESBL OR AMPC PHENOTYPES FROM MEAT OR CAECAL SAMPLES

Matrix EQAS 2022

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Description of the ESBL/AmpC Matrix EQAS

- 5 chicken meat and 3 chicken caecal samples inoculated with *E. coli*
- Samples sent out 7 November 2022

Table 1: Characteristics of the strains used to spike the meat and caecal samples.

| Strain ID	Phenotype	Gene(s)	Source
M-8.1	ESBL AmpC	CMY-2, SHV-12	meat
M-8.2	ESBL	CTM-X-14	meat
M-8.3	Carbapenemase	OXA-48, CTX-M-27	meat
M-8.4	AmpC	CMY-2	meat
M-8.5	None (*E. coli* ATCC 29522)	No gene (Susceptible)	meat
M-8.6	Blank	-	caecal
M-8.7	Carbapenem	VIM-1	caecal
M-8.8	AmpC	CMY-2	caecal

Participants

- 33 participating laboratories
  - Some laboratories (Labs #032, #038, #041, #058) handle only meat <u>or</u> caecal samples

- One dataset per country included in evaluation
  - 35 sample sets sent, and data included from 31 countries

Challenges in Matrix EQAS 2022 – background bacteria

- **M-8.1 (ESBL+AmpC)**

- One laboratory isolated a carbapenem resistant strain and reported it as "carbapenem with AmpC and ESBL" phenotype (MERO = 0.12 mg/L and 0.25 mg/L, ERT = 1 and IMI = 0.5)

- One laboratory reported "Other phenotype" due to ERT = 0.06 mg/L which has been interpreted as R as per the EURL guidelines.

Due to the background microflora observed at EURL-AR: *Aeromonas veronii*, other strains could have been isolated or contaminating the sample in these two labs.
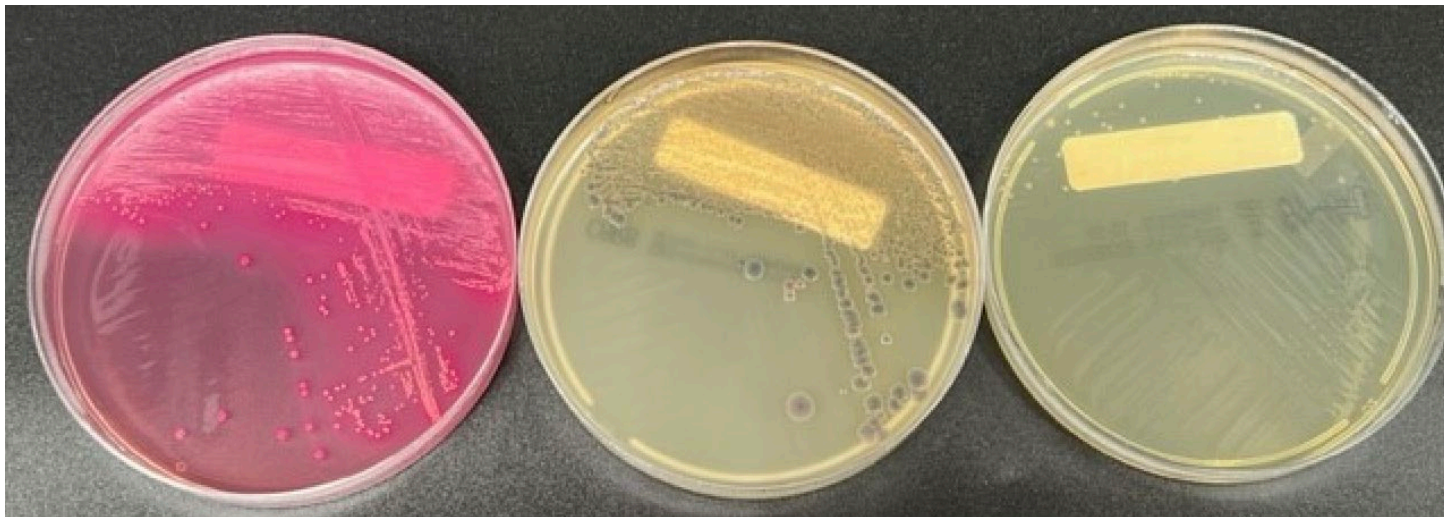
Challenges in Matrix EQAS 2022

- **M-8.2 (meat)**
  - ESBL (CTM-X-14)
  - Two labs (#039 and #019) interpreted the result as carbapenem and ESBL+AmpC-producing, respectively.

- **M-8.4 (meat)**
  - AmpC phenotype (CMY-2); Other phenotype accepted due to ERT resistance
  - Still 16% deviation due to isolation of carbapenem resistant isolates

- **M-8.8 (caecal)**
  - AmpC phenotype (CMY-2)
  - a lot of background microflora in the EURL-AR lab (*Escherichia fergusonii*), however only one laboratory (#017) reported "Other phenotype".

Deviations in ESBL/AmpC and carbapenemase phenotype identification

| Strain ID	Expected phenotype	Gene(s)	Deviations, %	Additional phenotype approved	Deviations (%) after changing phenotype
M-8.1	ESBL AmpC	CMY-2, SHV-12	6.5	None	-
M-8.2	ESBL	CTM-X-14	6.5	None	-
M-8.3	Carbapenemase	OXA-48, CTX-M-27	0.0	None	-
M-8.4	AmpC	CMY-2	25.8	Other phenotype*	16.1
M-8.7	Carbapenemase	VIM-1	6.5	None	-
M-8.8	AmpC	CMY-2	3.2	None	-

*Due to ERT resistance. It is possible to be resistant to ERT due to CMY-2.

The overall performance of ESBL/AmpC isolation and identification, 2022
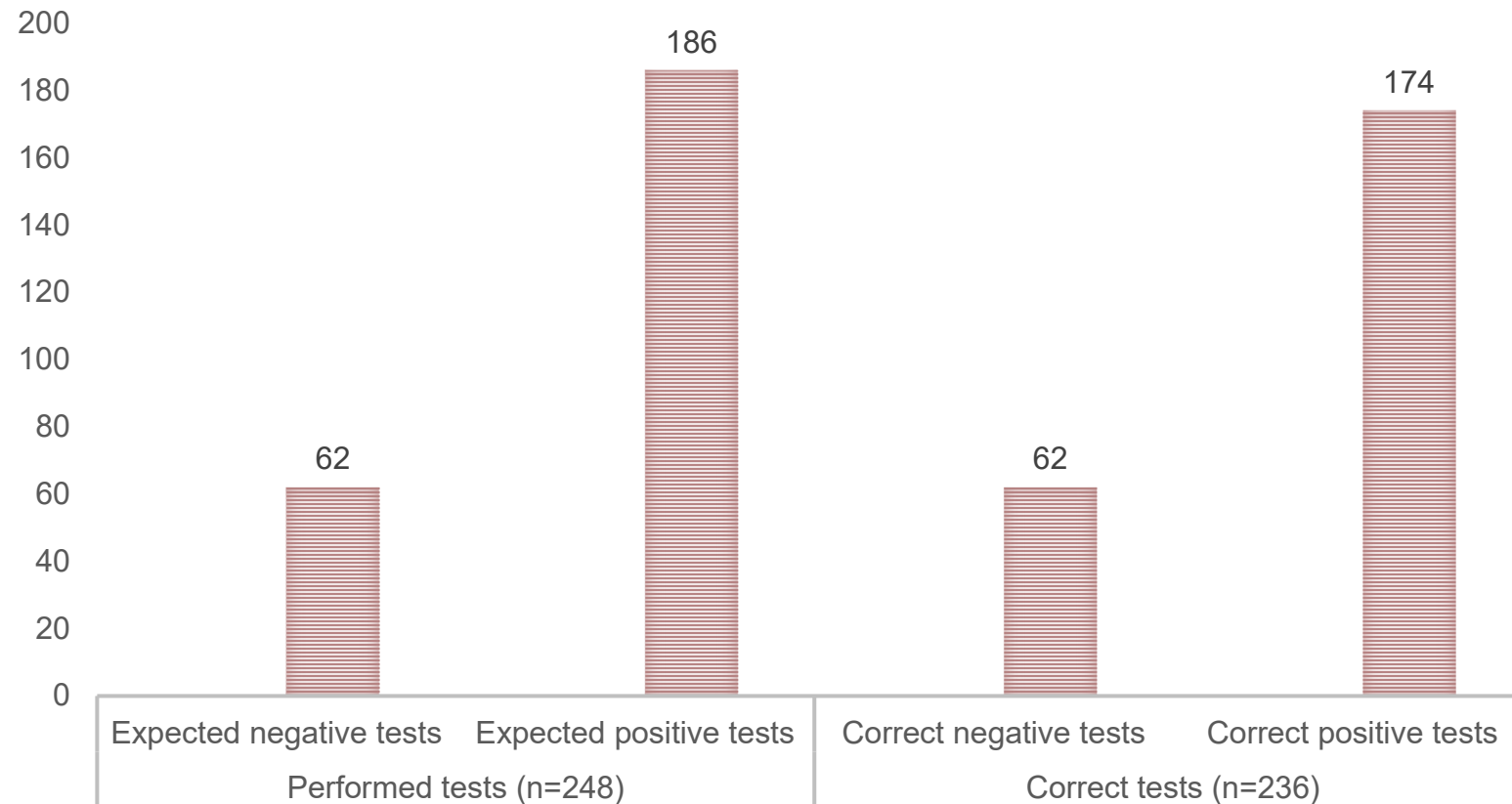
➢ Overall, 94% correct results and 12 qualitative deviations.

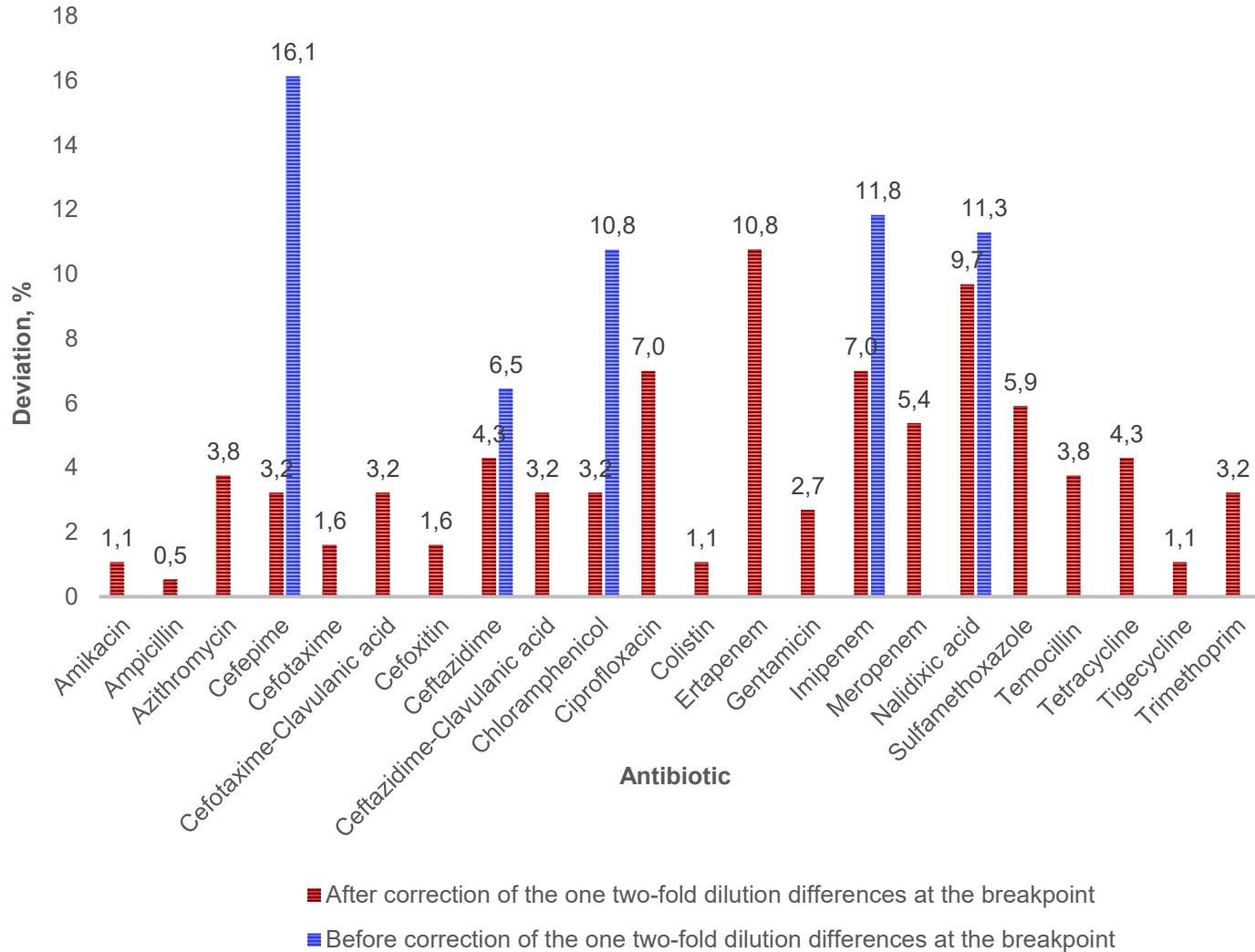# Deviations in AST results per lab
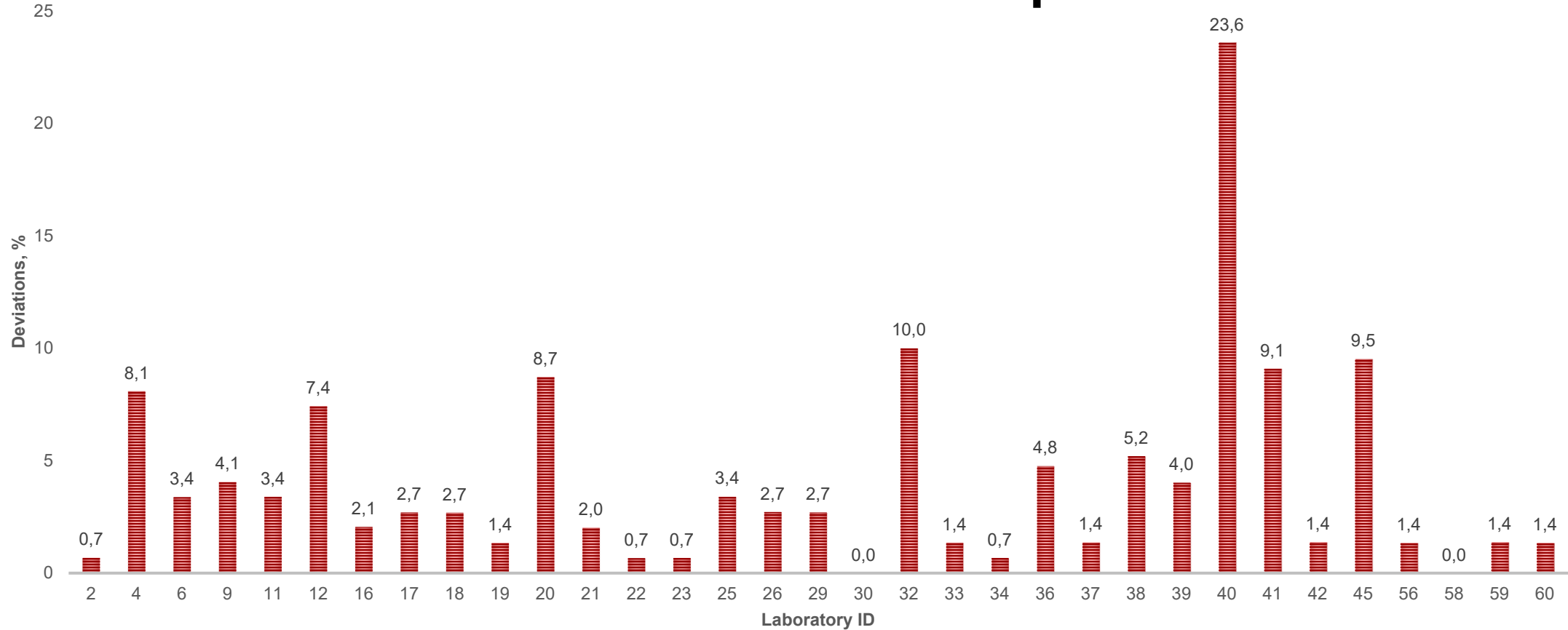
Observations:

M-8.1: Lab #036 reported a very rare amikacin resistance in *E.coli*, which might be an indicator that something else than *E. coli* was isolated.

Lab #040 did not report for sample M-8.2.

Deviations in AST results per antimicrobial

After "blanking" the one two-fold diliution differences (blue), deviations per antimicrobial (red) are based on:

- Wrong interpretation
- Errors: more than one two-fold dilution difference, which could be due to acquisition or loss of plasmids (especially regarding TET, SUL, NAL, CIP)

Deviations in beta-lactam classification per sample
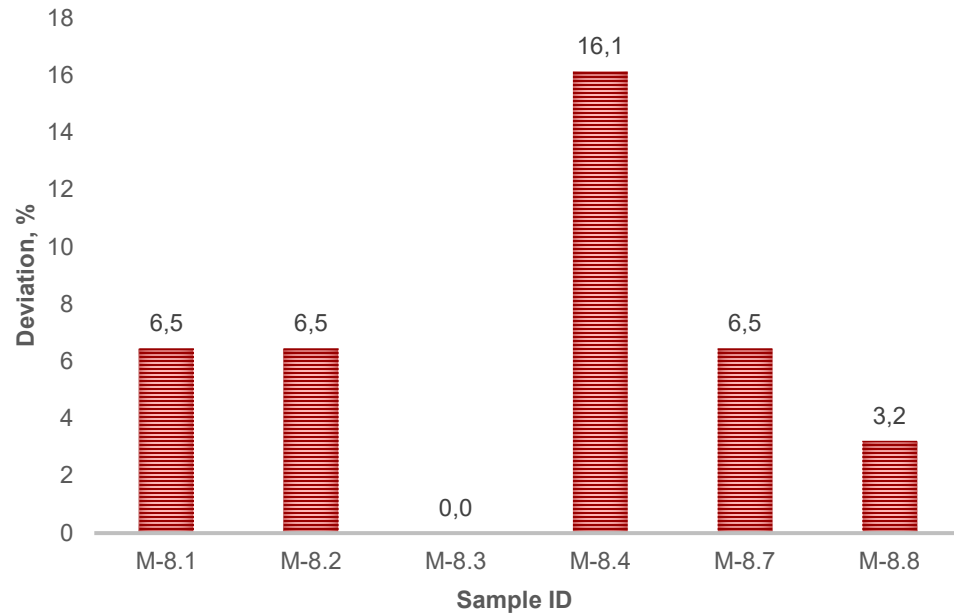
Errors:

M-8.1	Lab #004 – Carbapenemase phenotype Lab #017 – Other phenotype due to ERT resistance
M-8.2	Lab #039 – Carbapenemase phenotype Lab #019 - ESBL + AmpC
M-8.3	-
M-8.4	Labs #020, #012, #041, #039 – carbapenem phenotype Lab #060 – reported ESBL growth but nothing on carba plates
M-8.7	Lab #039 – isolated an ESBL phenotype, but reported that the sample dies not grow on carba plated. Lab #040 – Other phenotype
M-8.8	Lab #017 – Other phenotype

Conclusions of *E. coli* Matrix EQAS 2022

- **Overall interpretation of the phenotypes**
  - 12 qualitative deviations => background microflora
  - "Other phenotype" allowed (elevated ERT MIC)

- **Overall good AST results**
  - 94% of AST results correct

- **Many one two-fold dilution differences**
  - MIC close to the breakpoints