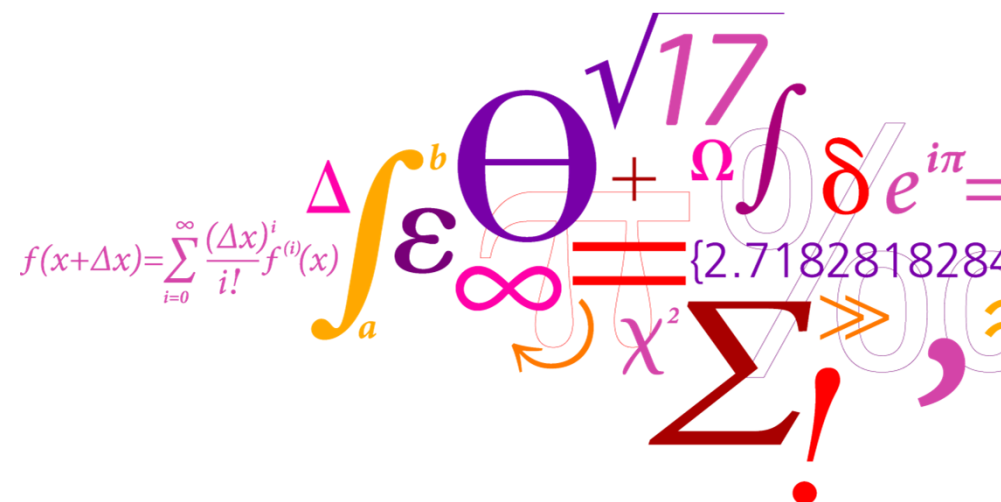




EQAS ESBL/AmpC 2015

Lina M. Cavaco



Background for this EQAS

- EURL-AR protocols released in 2014 regarding the mandatory selective isolation in the monitoring of ESBL /AmpC according to regulation EC 652/2013
- Need for knowledge on ESBL AmpC epidemiology
- Lack of laboratory experience on ESBL AmpC selective isolation from ceacal samples/ meat

ESBL AmpC EQAS 2015- Objectives

- Assess the performance of laboratories on the use of selective isolation procedures for detection of ESBL/ AmpC from meat samples and ceacal samples in laboratories involved in the monitoring determined by EC regulation 652/2013
- Assess the MIC testing and confirmation of ESBL AmpC status of the obtained isolates

Description of the EQAS

- Selection of strains with known resistance mechanism
 - Choice of up to eight samples for EQAS
 - Samples consisting of either ceacal samples or meat samples which might contain *E. coli* strains producing AmpC or ESBL
 - Sample preparation is was validated
 - Sample transportation is was validated

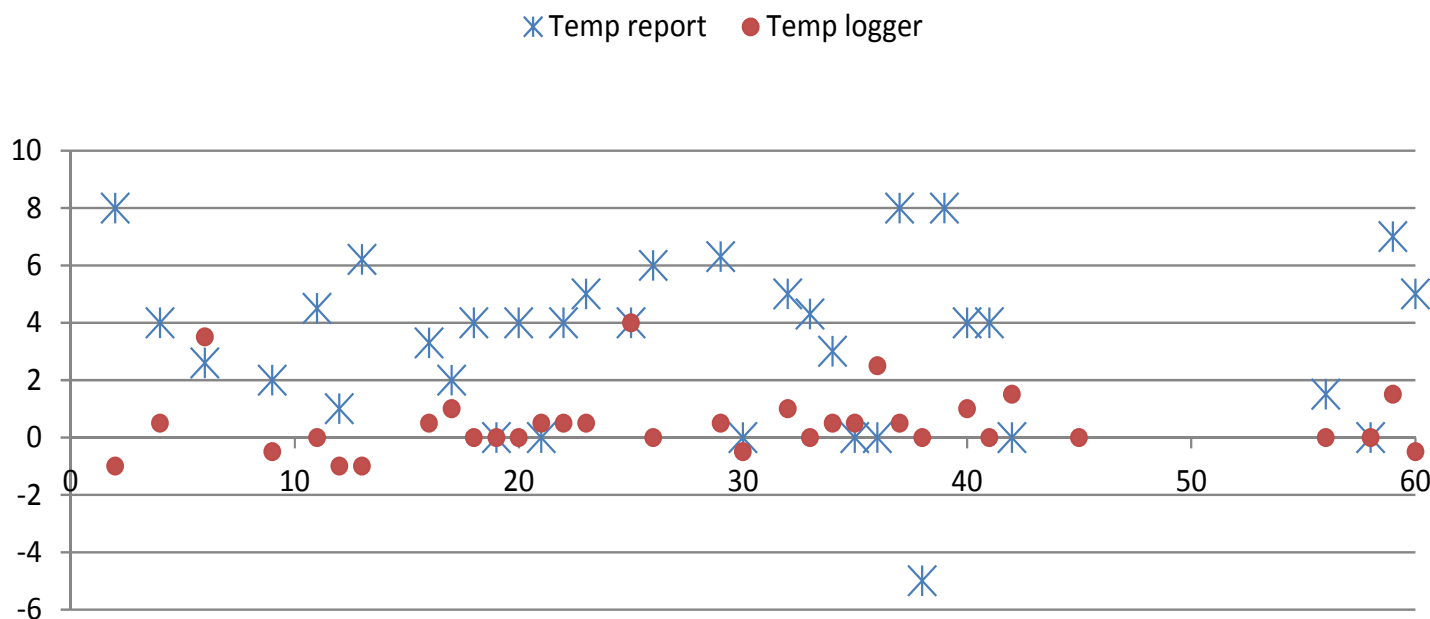
Description of the ESBL AmpC EQAS 2015

- Sent in November:
 - 5 meat samples: 2 spiked with ESBL (M-1.1 and M-1.4) in different amounts, one with an AmpC strain (M-1.2) and another with ATCC E. Coli (M-1.5) , remaining sample (M-1.3) left blank
 - 3 caecal samples: one spiked with ESBL strain (M-1.7) and one naturally positive with AmpC phenotype (m-1.8) and the remaining (M1.6) left blank

Shipping of parcels

- Shipping of parcels 2nd November with temperature controlling devices sent along in the parcels and were returned to us for reading/ re-use, temperature measurement registered

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Participation

E. coli

31 countries

34 sets of *EQAS matrix* results included as
in three countries samples divided by type

2 sets excluded from reporting due to
shipment

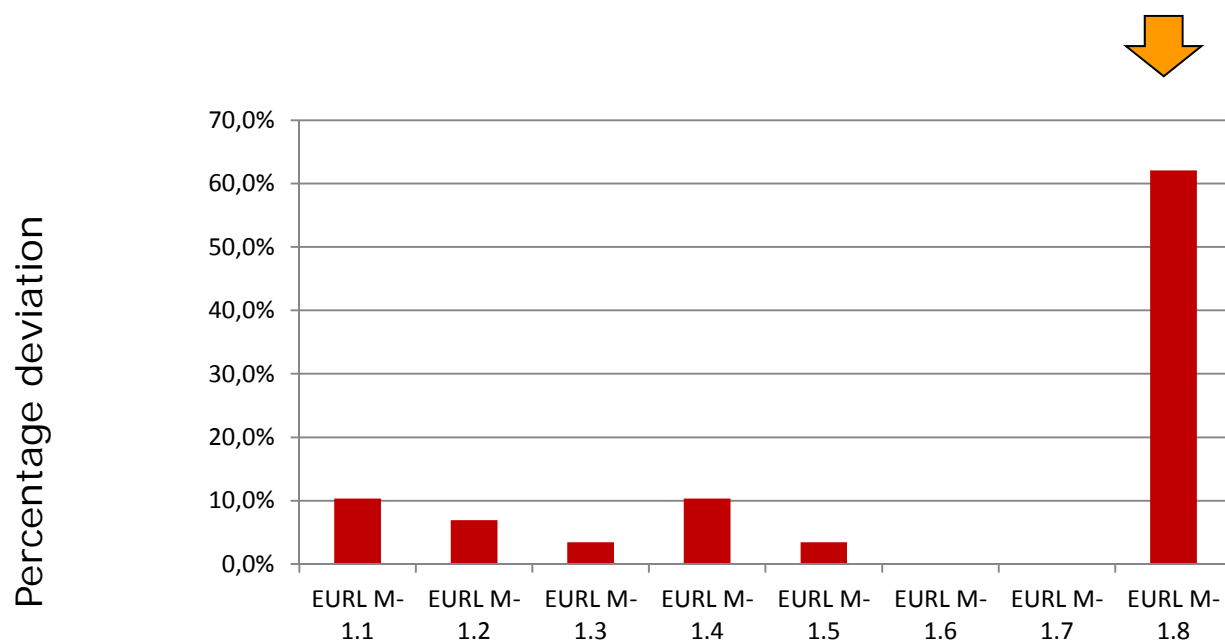


Overall Qualitative results

Isolation of ESBL /AMPC from samples		Correctly classified samples	
Number of performed tests		Number of correct tests N(%)	
N	%	N	%
232	100	204	87.9 ←
Number of expected negative tests		Number of correctly identified negative tests	
N	%	N	%
87	37.5	85	97.7 ←
Number of expected positive tests		Number of correctly identified positive tests	
N	%	N	%
145	62.5	119	82.1 ←

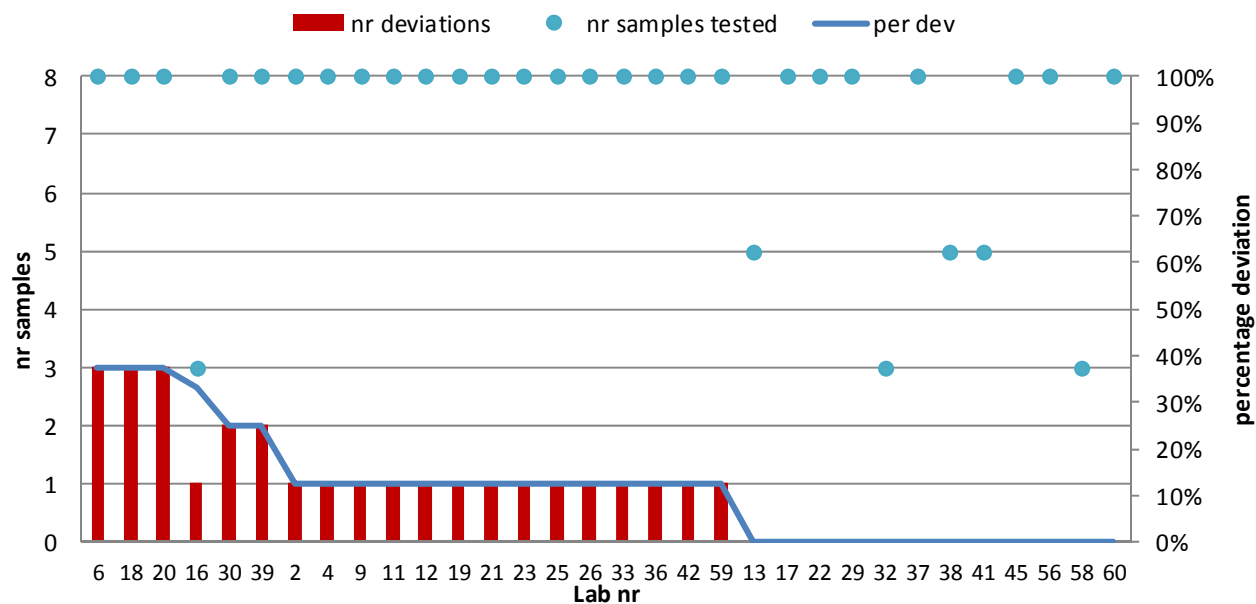
Overall 87.9% correct results but there is room for improvement in identification of positive samples

Per sample



Issues with stability of sample M-1.8 (18 dev= 62%)

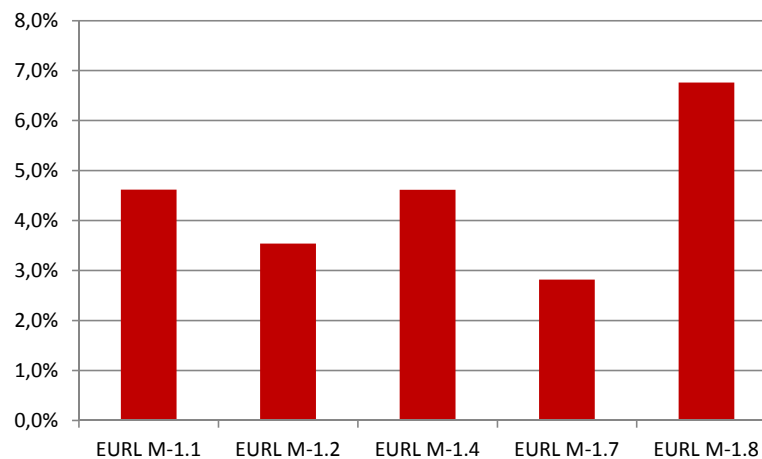
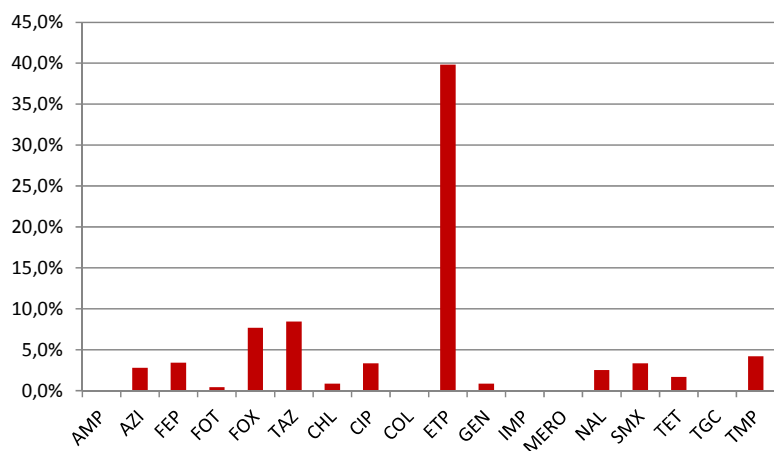
E. Coli matrix results – pr. lab



12 labs had all results right, 15 had one deviation (mostly M-1.8), two had two deviations and 3 others had three deviations each



Deviation percentage regarding AST results per antimicrobial /sample



Data per lab not analysed as it is dependent in further factors than AST alone

ESBL/ampC-producing test strains phenotypic conclusion

Percentage reporting correct ESBL-results	M 1.1	M 1.2	M 1.4	M 1.7	M-1.8	
ESBL-genes harboured in the test strain	CTX-M.1	CMY-2	CTX-M.1	CTX-M.9	AmpC mut	
ESBL-, pAmpC- and carbapenemase-producing strain – expected results	ESBL or ESBL+AmpC (Fox R)	AmpC or ESBL+AmpC (FEP R)	ESBL or ESBL+AmpC (Fox R)	ESBL	AmpC	
Obtained results	Presumptive ESBL-producer	6/26		6/26	30/30	1/12
	Presumptive pAmpC-producer		11/28			9/12
	Presumptive ESBL+pAmpC	18/26	15/28	18/26		
	Presumptive carbapenemase-producer	2/26	1/28	2/26		
	unusual phenotype		1/28			
	Not ESBL-, pAmpC- or carbapenemase-producing					2/12

Most deviations (5 in total) due to ertapenem used to decide if carbapenemase presumptive



Summary

- 31 countries participated- 32 sets data analysed and two excluded due to late shipment (one of these will be offered re-test)
- Temperature tracking and shipment with low temperatures worked out as expected
- Overall 87.9% results correct and good specificity, however sensitivity needs improvements as only 82.1% positive samples were identified correctly
- Issues with stability of sample M-1.8
- Few issues with ertapenem
- Mostly good results in ESBL AmpC categorization, but some issues with ertapenem R interpretation as carbapenemase, cefepime, and mixed phenotypes

