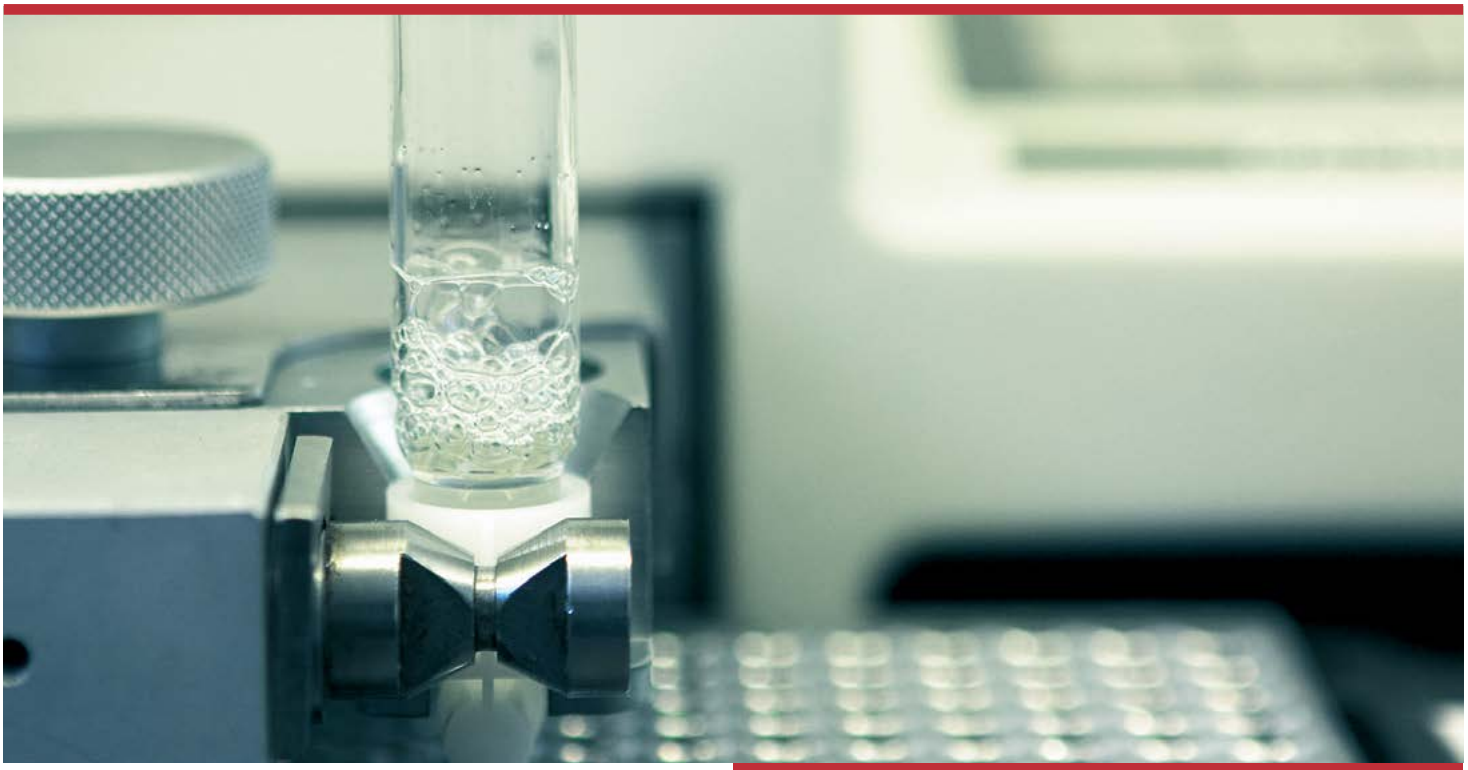
The 17th EURL-AR Proficiency Test *Salmonella, Campylobacter* and genotypic characterisation 2014



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1. Introduction

This report describes and summarises results from the seventeenth proficiency test trial conducted by the National Food Institute (DTU Food) as the EU Reference Laboratory for Antimicrobial Resistance (EURL-AR). This proficiency test focuses on antimicrobial susceptibility testing (AST) of *Salmonella* and *Campylobacter* and is the eigth External Quality Assurance System (EQAS) conducted for these microorganisms (the first was EQAS 2006). In addition, the proficiency test for the sixth time includes an optional element consisting of genotypic characterization by PCR/sequencing of antimicrobial resistance genes. This optional component included characterization of genes related to production of AmpC, ESBL- and carbapenemases in the *Salmonella* test strains.

This EQAS aims to: i) monitor the quality of AST results produced by National Reference Laboratories (NRL-AR), ii) identify laboratories which may need assistance to improve their performance in AST, and iii) determine possible topics for further research or collaboration.

In reading this report, the following important considerations should be taken into account:

1) Expected results were generated by performing Minimum Inhibitory Concentration (MIC) determinations for all test strains in two different occasions at the Technical University of Denmark, National Food Institute (DTU Food). These results were then verified by the United States Food and Drug Administration (FDA), Centre for Veterinary Medicine. Finally, a fourth MIC determination was performed at DTU Food after preparation of the agar stab culture for shipment to participants to confirm that the vials contained the correct strains with the expected MIC values.

2) Evaluation is based on interpretations of AST values determined by the participants. This is in agreement with the method used by MS to report AST data to the European Food Safety Authority (EFSA), and complies with the main objective of this EQAS, i.e. “to assess and improve the comparability of surveillance and antimicrobial susceptibility data reported to EFSA by the different NRLs”, as stated in the protocol.

3) The EURL-AR network agreed on setting the accepted deviation level for laboratory performance on AST to 5%. For the optional genotypic characterisation, no specific acceptance level has been set.

Evaluation of a result as “deviating from the expected interpretation” should be carefully analyzed in a self-evaluation procedure performed by the participant and considering the introduction of corrective actions in the laboratory, if necessary. Note, that since methods used for MIC determination have limitations, it is not considered a mistake to obtain a one-fold dilution difference in the MIC of a specific antimicrobial when testing the same strains. If, however, the expected MIC is close to the breakpoint value for categorizing the strain as susceptible or resistant, a one-fold dilution difference - which is acceptable - may result in two different interpretations, i.e. the same strain can be categorized as susceptible and resistant. This result will be evaluated as correct in one case and incorrect in the other if the evaluation is based on interpretation of MIC values. This report is based on evaluation of AST interpretations, therefore some participants may find their results classified as incorrect even though the actual MIC they reported is only a one-fold dilution different from the expected MIC. In these cases, the participants should be confident about the good quality of their performance of AST by MIC. In the organization of the EQAS, we try to avoid these situations by choosing test strains with MIC values distant from the breakpoints for resistance, which is not always feasible for all strains and all antimicrobials. Therefore, the

EURL-AR network unanimously established in 2008 that if there are less than 75% correct results for a specific strain/antimicrobial combination, the reasons for this situation must be further examined and, on selected occasions explained in details case by case, these results may subsequently be subtracted from the evaluation report.

This report is approved in its final version by a technical advisory group composed by competent representatives from all NRL-ARs. This group meets annually at the EURL-AR workshop.

All conclusions presented in this report are publically available. Participating laboratories are identified by codes and each code is known only by the corresponding laboratory. The full list of laboratory codes is confidential information known only by relevant representatives of the EURL-AR and the EU Commission.

The EURL-AR is accredited by DANAK as provider of proficiency testing (accreditation no. 516); working with zoonotic pathogens and indicator organisms as bacterial isolates (identification, serotyping and antimicrobial susceptibility testing).

2. Materials and Methods

2.1 Participants in EQAS 2014

A pre-notification (App. 1) to announce the EURL-AR EQAS on AST of *Salmonella* and *Campylobacter* was distributed on the 30th June 2014 by e-mail to the 43 NRLs in the EURL-AR-network including all EU countries and Iceland, Norway, Serbia, Switzerland and Turkey. One laboratory from Spain did not participate as they had neither *Salmonella* nor *Campylobacter* AST as their field of responsibility. One NRL from France did not participate as they perform AST by disk diffusion and for this EQAS, results obtained by MICs, only, are accepted. Therefore results from one laboratory was excluded from the evaluation, since they were not obtained by dilution methods in the full range of antimicrobial concentrations specified in Decision 2013/652/EU. The NRL from Serbia did not participate in this year's iteration. In addition to the AST of *Salmonella* and *Campylobacter*, an optional genotypic characterization by PCR/sequencing of antimicrobial resistance genes of the AmpC-, ESBL- and carbapenemase-producing *Salmonella* test strains was offered.

Appendix 2 shows that 35 of the 40 participating NRLs were appointed by the individual Member States' Competent Authority. Eight additional laboratories were included; one from each of the following countries: Denmark, Iceland, the Netherlands, Norway, Serbia, Spain, Switzerland, and Turkey. These were invited to take part in the EQAS 2014 on the basis of their participation in previous EQAS iterations and/or affiliation to the EU network. These laboratories were charged a fee for their participation in the EQAS, whereas the NRLs from EU Member States participated free of charge.

Figure 1 illustrates that of the 32 participating countries, 31 tested both *Salmonella* and *Campylobacter*. One country uploaded *Salmonella* results, only, for evaluation (Turkey). Eleven laboratories participated in the optional genotypic characterisation of the ESC-producing *Salmonella* test strains (not illustrated in Figure 1; see Appendix 2).

The results from the NRLs designated by the MS are presented and evaluated in this report in addition to national reference laboratories in affiliated non-MS; i.e. results from 32 countries consisting of 35 laboratories submitting *Salmonella* results and 32 laboratories submitting *Campylobacter* results. Results from

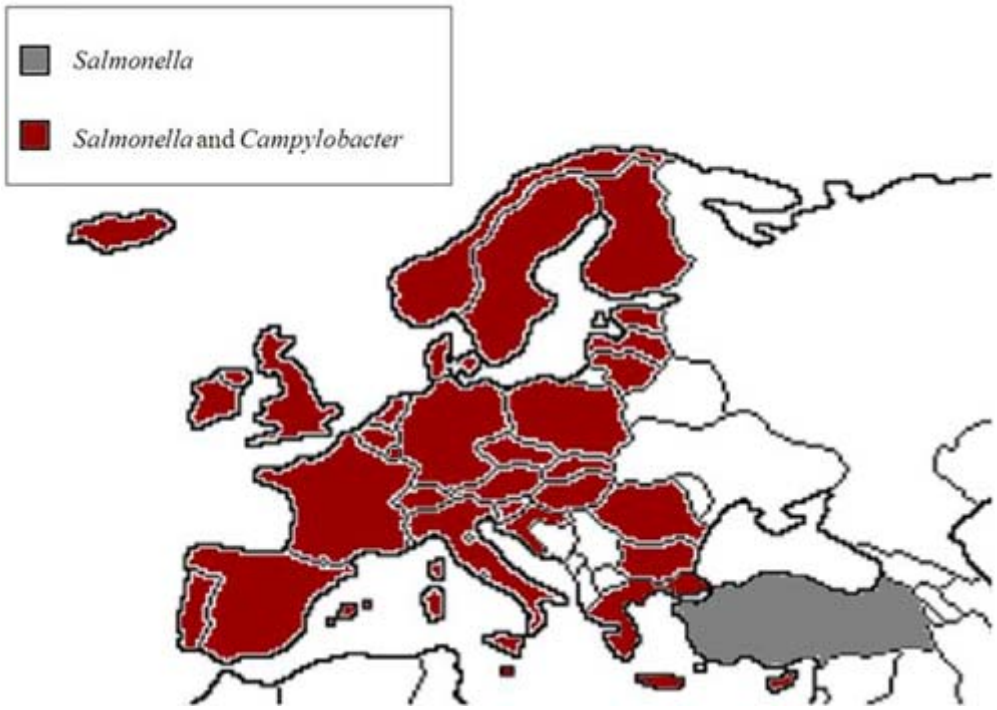

Figure 1: Participating countries that performed antimicrobial susceptibility testing of *Salmonella* or both *Salmonella* and *Campylobacter.*

the three laboratories not designated by the MS but enrolled on equal terms as these are not further presented or evaluated in this report.

2.2 Strains

Eight *Salmonella* strains and eight *Campylobacter* strains were selected for this trial among isolates from the strain collection at DTU Food on the basis of antimicrobial resistance profiles and MIC values. For quality assurance purposes, one strain per bacterial species has been included in all EQAS iterations performed to date, representing an internal control.

Prior to distribution of the strains, AST was performed on the *Salmonella* and *Campylobacter* strains at DTU Food and verified by the US Food and Drug Administration (FDA). When MIC-values were not in agreement but varied +/- one MIC-step, the value obtained by DTU Food was selected as the reference value. The obtained MIC values served as reference for the test strains (App. 3a and 3b). Results from the following antimicrobials were not verified by FDA: cefepime, cefotaxime, cefotaxime/clavulanic acid, ceftazidime, ceftazidime/clavulanic acid, colistin, ertapenem, imipenem, meropenem, temocillin, tigecycline and trimethoprim for *Salmonella* and furthermore, streptomycin for *Campylobacter*.

Reference strains *Escherichia coli* CCM 3954 (ATCC 25922) and *Campylobacter jejuni* CCM 6214 (ATCC 33560) were provided to new participating laboratories with instructions to store and maintain them for quality assurance purposes and future EQAS trials.

2.3 Antimicrobials

The antimicrobials tested in this EQAS are listed in the protocol (App. 4b).

The antimicrobials tested correspond to the panel of antimicrobials listed in Decision 2013/652/EU.

Guidelines for performing AST were set

according to the Clinical and Laboratory Standards Institute (CLSI) document; M7-A9 (2012) “Methods for Dilution Antimicrobial Susceptibility Tests for Bacteria That Grow Aerobically; Approved Standard - Ninth Edition”; M100-S24 (2014) “Performance Standards for Antimicrobial Susceptibility Testing” (Twenty-Fourth Informational Supplement) and document VET01-A4 (2013) “Performance Standards for Antimicrobial Disk and Dilution Susceptibility Tests for Bacterial Isolated From Animals” (Approved Standard – Fourth Edition).

MIC results were interpreted by using the interpretative criteria listed in Decision 2013/652/EU. Where values were not available, the list of interpretative criteria was supplemented with EUCAST epidemiological cut-off values (www.eucast.org) or CLSI-interpretative criteria as described and indicated in the protocol (App. 4). No interpretative criteria were available to determine the interpretation of MIC-values from testing of azithromycin, cefepime and temocillin. Results of ESC detection tests were interpreted according to the most recent EFSA recommendations (EFSA Journal 2012; 10(6):2742).

The selection of antimicrobials used in the trial for *Salmonella* were: ampicillin (AMP), azithromycin (AZI), cefepime (FEP), cefotaxime (FOT), cefotaxime/clavulanic acid (FOT/Cl), cefoxitin (FOX), ceftazidime (TAZ), ceftazidime/clavulanic acid (TAZ/Cl), chloramphenicol (CHL), ciprofloxacin (CIP), colistin (COL), ertapenem (ERT), gentamicin (GEN), imipenem (IMI), meropenem (MER), nalidixic acid (NAL), sulfonamides (sulfamethoxazole) (SMX), tetracycline (TET), tigecycline (TGC), temocillin (TRM) and trimethoprim (TMP).

Minimum Inhibitory Concentration (MIC) determination of the *Salmonella* test strains was performed using the Sensititre system from Trek Diagnostic Systems Ltd, UK. For ESC confirmatory test, the analysis included MIC determination by microbroth dilution.

For *Campylobacter* the following antimicrobials were included: ciprofloxacin (CIP), erythromycin (ERY), gentamicin (GEN), nalidixic acid (NAL), streptomycin (STR), and tetracycline (TET). MIC determination was performed using the Sensititre systems from Trek Diagnostic Systems Ltd, UK, according to guidelines from the CLSI document M45-A2 (2010) “Methods for Antimicrobial Dilution and Disk Susceptibility Testing of Infrequently Isolated or Fastidious Bacteria” (Approved Guideline – Second Edition) and VET01-S2 (2013) “Performance Standards for Antimicrobial Disk and Dilution Susceptibility Tests for Bacterial Isolated From Animals” (Second Informational Supplement). Participants of the *Campylobacter* EQAS were additionally requested to identify the species of the *Campylobacter* spp. as either *C. jejuni* or *C. coli*.

2.4 Distribution

On the 14th October 2014, bacterial strains in agar stab cultures (*Salmonella* spp.) or charcoal swabs in transport media (Stuarts) (*Campylobacter* spp.) together with a welcome letter (App. 4a) were dispatched in double pack containers (class UN 6.2) to the participating laboratories according to the International Air Transport Association (IATA) regulations as UN3373, biological substances category B.

2.5 Procedure

Protocols and all relevant information were uploaded on the EURL-AR website (http://www.eurl-ar.eu), thereby EQAS participants could access necessary information at any time.

Participants were instructed to subculture charcoal swabs immediately, store the agar stabs 4ºC (dark) and the freeze-dried strains cool and dark until performance of AST. Information related to the handling of the test strains and reference strains (App. 4b, c, d, e)

was made available. Participants receiving an ATCC reference strain were requested to save and maintain this strain for future proficiency tests.

The participants were instructed to apply the interpretative criteria listed in the protocol (App. 4). Instructions for interpretation of AST results allowed for categorization of results as resistant or susceptible. Categorisations as 'intermediate' were not accepted.

The EURL-AR is aware that there are two different types of interpretative criteria of results, clinical breakpoints and epidemiological cut-off values. The terms 'susceptible', 'intermediate' and 'resistant' should be reserved for classifications made in relation to the therapeutic application of antimicrobial agents. When reporting data using epidemiological cut-off values, bacteria should be reported as 'wild-type' or 'non-wild-type' (Schwarz et al., 2010). Due to the different methods of AST used by the participants and also to simplify the interpretation of results, throughout this report, we will still maintain the terms susceptible and resistant, even in cases where we are referring to wild-type and non-wild-type strains.

As regards the method for performing the antimicrobial susceptibility testing, the protocol referred to Decision 2013/652/EU and instructed participants to perform a dilution method, i.e. microbroth dilution or agar dilution. Results obtained by methods not complying with the description in Decision 2013/652/EU were disregarded in the present analysis.

A mandatory part of the proficiency test was to detect ESC-producing strains and interpret results according to the most recent EFSA recommendations (EFSA Journal 2012; 10(6):2742) as described in the protocol.

Results from QC reference strains would consist of MIC values for the reference strains *E. coli* (ATCC 25922) and *C. jejuni* (ATCC 33560). The results were evaluated towards the quality control ranges according to the relevant guidelines; i.e. the CLSI documents VET01-S2 (2013) or M100-S24 (2014) (App. 5).

For the optional genotypic characterisation of the ESC-producing *Salmonella* test strains, participating laboratories were requested to report the genes conferring resistance to extended-spectrum beta lactam antimicrobials. The organizers, however, decided to include none-ESC TEM-genes resulting in $bla_{\text{TEM-1}}$ registered as an expected gene, also. The genes listed in the table in the protocol (App. 4b) were included in the test. Identification of additional genes not listed in the protocol was not evaluated by the database. The results were evaluated based on the actual genes and variants identified.

The participating laboratories were encouraged to use their own laboratory's method(s) for the genotypic characterisation. The expected results for this component of the EQAS were obtained by whole-genome-sequencing and subsequent analysis using the ResFinder 2.1 platform available at http://cge.cbs.dtu.dk/services/ResFinder/. The positive identification of genes was not verified elsewhere.

All participating laboratories were invited to enter the obtained results into an electronic record sheet at the EURL-AR web-based database through a secured individual login and password. The record sheet contained space for reporting the results obtained for the QC reference strains. Alternatively, it was offered the possibility to fill-in a record sheet (provided with the protocol) and to send it to the EURL-AR by fax, mail or email.

In addition, participants were encouraged to complete an evaluation form available at the EURL-AR database with the aim to improve future EQAS trials.

The database was finally closed and evaluations were made available to participants

on the 17th February 2015. After this date, the participants were invited to login to retrieve an individual, database-generated report which contained an evaluation of the submitted results including possible deviations from the expected interpretations. Deviations in the interpretation as resistant or susceptible were categorised as 'incorrect', as were also deviations concerning confirmation of an isolate as extended spectrum beta-lactamase- (ESBL-), ampC- or carbapenemase-producer.

3. Results

The participants were asked to report results, i.e. MIC values and the categorisation as resistant or susceptible. Only the categorisation was evaluated, whereas the MIC values were used as supplementary information.

3.1 Data omitted from the report

As mentioned in the introduction, the EURL-AR network established that data should be examined and possibly omitted from the general analysis if there are less than 75% correct results based on strain/antimicrobial combination (see Appendix 8 for an overview of correct/incorrect results). In the present EQAS this occurred in two cases which have been examined and consequently omitted from the analysis; 1) S9.8/colistin (expected interpretation was 'susceptible', however, 36% (12 laboratories) found the strain resistant to colistin. All except one presented MIC values only one step from the expected; 2) C9.6/tetracycline (expected interpretation was 'resistant', however, 67% of participants found the strain 'susceptible' to tetracycline. In this case, there was no obvious reason why there were so few results in concordance with the expected. Both these combinations were subsequently omitted from further analysis.

Additional combinations that presented a low level of concordance with the expected were S-9.5/meropenem (66%) and S-9.7/tigecycline (71%). These data could indicate possible difficulties with the testing, and will therefore be included in the analysis presented in this report.

3.2 Methods

The agar dilution method and MIC determination were evaluated together as they are both quantitative methods giving results corresponding to the MIC of the bacterial strain tested.

In the *Salmonella* trial, 34 laboratories performed microbroth dilution and one performed agar dilution). For the *Campylobacter* trial, 31 laboratories performed microbroth dilution and one performed agar dilution).

Two panels of antimicrobials were included in the testing of the *Salmonella* strains; the test strains found resistant to cefotaxime, ceftazidime or meropenem on the first panel were additionally tested on the second panel according to the protocol indications aiming at concluding on the strain's presumptive ESBL, AmpC or carbapenemase phenotype.

3.3 Deviations, overall

The list of deviations is shown in Appendix 8a and 8b. Figure 2 shows the total percentage of deviations from the expected results of AST performed by participating laboratories. The internal control strains mainly followed the trend in deviation level of the different EQAS trials (Figure 2). The deviation level in 2014 is acceptable for both the *Salmonella* and the *Campylobacter* trials. For both microorganisms, however, it appears that there has been a slight increase in the level of deviations, to 2.4% for *Salmonella* and 4% for *Campylobacter*. For *Campylobacter*, this increase can be explained

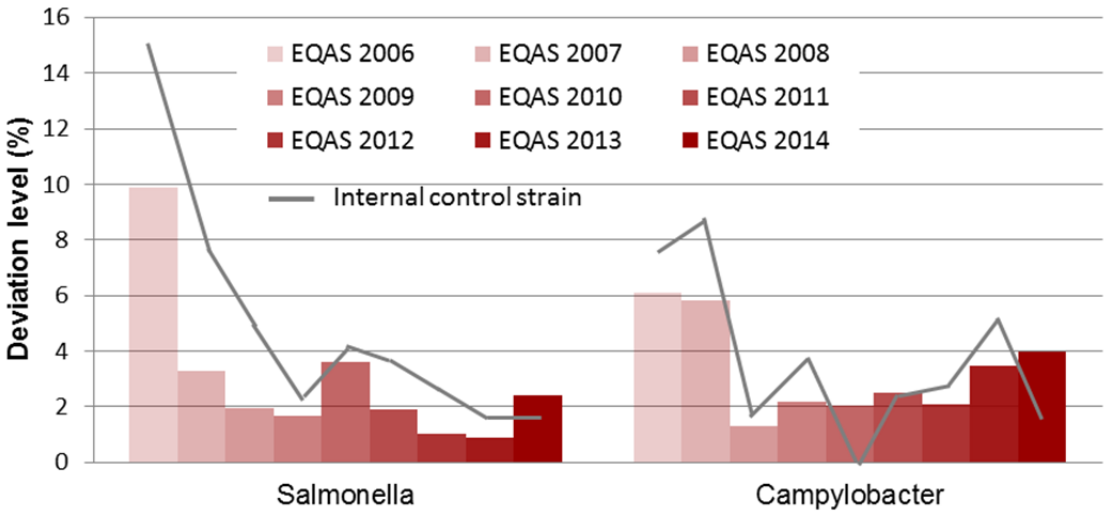

Figure 2: A comparison between the EURL-AR EQAS's since 2006, showing the total percentage of deviations for antimicrobial susceptibility testing performed by participating laboratories.

by two laboratories' high deviation levels (at 34.0% and 22.9%).

3.3.1 *Salmonella* trial

For the *Salmonella* strains, 97.6% of the AST's were interpreted correctly. The number of AST's performed and the percentage of correct results for the individual strains in the EQAS, are listed in Table 1. Variations of obtained correct results ranged from 94.8-99.8% for *Salmonella*. Table 2 illustrates the percentage of correct AST per antimicrobial by bacterial species. The level of correct AST was at 88.9% and 90.6% for imipenem and meropenem, but otherwise above 96.7% for the *Salmonella* test strains.

ESC-producing *Salmonella* test strains

Confirmation of beta-lactamase production is a mandatory component of this EQAS.

According to the protocol, which was based on the EFSA recommendations, the confirmatory test for ESC-production requires use of both cefotaxime (FOT) and ceftazidime (TAZ) alone and in combination with a β-lactamase inhibitor for either antimicrobial agent tested in combination with clavulanic acid vs. its MIC when tested alone (three dilution steps difference; MIC FOT:CTX/Cl or TAZ:TAZ/Cl ratio ≥8) (CLSI M100 Table 2A; Enterobacteriaceae). Participants were instructed to test strains presenting resistance to cefotaxime (FOT), ceftazidime (TAZ or meropenem (MERO) on the second panel of antimicrobials.

The classification of the phenotypic results was based on the most recent EFSA recommendations (EFSA 2012), indicating:

- Presumptive ESBL-phenotype: strains with positive synergy test, susceptible to cefoxitin and resistant to cefepime
- Presumptive ESBL+pAmpC-phenotype: strains with positive or negative synergy test, resistant to cefoxitin and resistant to cefepime
- Presumptive pAmpC phenotype: strains with negative synergy test resistant to cefoxitin and susceptible to cefepime
- Presumptive carbapenemase phenotype: strain resistant to meropenem
- Unusual phenotype: any other combinations

In this EQAS, all laboratories uploaded results for the strains harbouring resistance to the cephalosporins tested.

The strain S-9.3 was a pAmpC-producer, S-9.4 was an ESBL-producer whereas S-9.5 and S-9.6 were carbapenemase producers. Note that when categorizing the presumptive phenotypes, the interpretation of the cefepime result had to be disregarded, as no interpretative criteria were available.

In total the categorization as ESBL-, pAmpC- or carbapenemase-producer was incorrect in 21 cases, with two of the incorrect results submitted for S9.7 which was not resistant to cephalosporins or carbapenems. One laboratory (#39) presented four deviations in relation to the ESC-production of the test strains. Six other laboratories each presented two incorrect results (#23, #26, #29, #41, #42, and #58).

Three laboratories (#32, #41 and #42) categorized strain S-9.3 (presumptive pAmpC-phenotype based on negative synergy test with clavulanate and resistance to cefoxitin) as presumptive ESBL + pAmpC phenotype. One of the laboratories had interpreted the MIC for cefepime at 0.25 mg/L as 'resistant' but for the other two laboratories, no results on the second panel could indicate the background for this categorization.

Two laboratories (#23 and #39) found strain S-9.4 (presumptive ESBL-phenotype based on positive synergy test with clavulanate and susceptibility to cefoxitin) to be an 'unusual phenotype and one laboratory (#29) indicated that it was not ESBL, AmpC- or carbapenemase-producing. The submitted results from the second panel from these three laboratories were all evaluated as 'correct' and therefore could not indicate why this categorization had been selected.

For the strains S-9.5 and S-9.6 (presumptive carbapanemase phenotypes based on resistance to meropenem), seven laboratories (#23, #26, #29, #36, #39, #57, #58) and six (#26, #33, #37, #39, #42, #58), respectively, had selected and incorrect category. S-9.5 was incorrectly categorized as 'unusual phenotype' and 'presumptive pAmpC', whereas S-9.6 was incorrectly categorized as 'unusual phenotype' and 'no ESBL, AmpC- or carbapenemase'. Laboratory #29 and #58 found S-9.5 and S-9.6, respectively, resistant to meropenem, but categorized the strain as 'unusual phenotype'. Laboratory #39 did not report results for meropenem for the first panel, and discovered no meropenem resistance for either of the two strains in the second panel. One laboratory (#26) had detected meropenem in the first but not the second panel and one (#37) had not detected meropenem resistance in the first panel and therefore did not proceed with tested of the second panel. For neither of the remaining of the laboratories with incorrect categorizations for S-9.5 and S-9.6, none had detected meropenem-resistance for the first or the second panel. The obtained MIC-results for S-9.5 and S-9.6 were at <0.03 or 0.12 for the first panel, and at 0.12 or <=1 for the second panel.

3.3.2 *Campylobacter* trial

For the *Campylobacter* strains, 96.0% of AST's were correctly tested. Table 1 presents that the variation in the obtained correct results ranged from 92.4-98.7% and Table 2 illustrates that the percentage of correct AST per antimicrobial was above 94.4% for the *Campylobacter* test strains with tetracycline exhibiting the lowest level.

The participants were requested to identify the *Campylobacter* species. All 32 laboratories delivered in total 256 results of which seven identifications were incorrect. Three laboratories presented two deviations each (#19, #36, and #40).

3.4 Deviations by laboratory

Figure 3 and 4 illustrate the percentage of deviations for each participating laboratory. The laboratories are ranked according to their performance determined by the percentage of

Table 1. The number of AST performed and the percentage of correct results for each strain of *Salmonella* and *Campylobacter*.

EQAS 2014 – *Salmonella*			EQAS 2014 – *Campylobacter*		
Test strain	AST in total	% correct	Test strain	AST in total	% correct
S-9.1	448	98.9	C-9.1 (*C. jejuni*)	191	98.4
S-9.2	448	98.0	C-9.2 (*C. coli*)	184	92.4
S-9.3	659	99.2	C-9.3 (*C. coli*)	185	96.2
S-9.4	652	98.2	C-9.4 (*C. jejuni*)	179	98.3
S-9.5	655	94.8	C-9.5 (*C. jejuni*)	185	94.1
S-9.6	637	95.4	C-9.6 (*C. coli*)	159	98.7
S-9.7	446	98.0	C-9.7 (*C. jejuni*)	179	93.3
S-9.8	415	99.8	C-9.8 (*C. coli*)	191	96.9

Table 2: Percentage of correct antimicrobial susceptibility tests per antimicrobial by microorganism.

Antimicrobial	*Salmonella*	*Campylobacter*
Ampicillin	100	-
Cefotaxime	99.0	-
Cefoxitin	97.8	
Ceftazidime	98.3	-
Chloramphenicol	99.6	-
Ciprofloxacin	98.6	96.0
Colistin	98.0	-
Ertapenem	97.0	-
Erythromycin	-	95.6
Gentamicin	99.6	98.4
Imipenem	88.9	-
Meropenem	90.6	-
Nalidixic acid	97.1	95.6
Streptomycin	-	95.9
Sulphonamides	98.9	-
Tetracycline	100	94.4
Tigecycline	96.7	-
Trimethoprim	98.9	-

deviating results in the antimicrobial susceptibility tests.

3.4.1 *Salmonella* trial

Thirty-three of the 35 participating laboratories obtained a result within the acceptance limit at 5% deviations for the *Salmonella* strains. The maximum percentage of deviations was 9.4%. The performance of two (6%) laboratories resulted in a deviation level above the level of performance expected by the EURL-AR (#57 and #58), however, none of the laboratories are regarded as outliers.

3.4.2 *Campylobacter* trial

In the *Campylobacter* trial, most laboratories performed very well. Applying the 5% acceptance threshold, 24 of 32 participating laboratories performed acceptably, with 17 laboratories having no deviations (Figure 4). Eight laboratories present a deviation level above the 5% acceptance level (#19, #29, #34, #36, #39, #40, #42, and #58). Of these, the two with deviation levels at 22.9% and 34.0% were regarded as outliers (#29, and #40).

3.5 Deviations by reference strains

In the following section, deviations are defined as results of antimicrobial susceptibility tests on the reference strain that are outside the quality control (QC) acceptance intervals (App. 5).

Values from the participants' testing of the QC strains are listed in Appendix 6a and 6b, and in Table 4-5. For both the *Salmonella* and *Campylobacter* trial, all laboratories uploaded data from QC-testing on the relevant reference strain.

Appendix 6a indicates that of the 26 laboratories submitting AST-results for the reference strain *E. coli* ATCC 25922, nine

Table 3: Overview of ESBL-, pAmpC- and carbapenemase-producing *Salmonella* test strains and proportion of laboratories that obtained the expected result; number and percentages of laboratories which correctly detected and confirmed the ESBL-, pAmpC- and carbapenemase-producing *Salmonella* strains. Fields shaded in grey with numbers in *italics* indicate an unexpected result.

		Strain S-9.3	Strain S-9.4	Strain S-9.5	Strain S-9.6
ESC-genes harboured in the test strain		***bla*$_{CMY-2}$**	***bla*$_{CTX-M-9}$** ***bla*$_{TEM-1}$**	***bla*$_{VIM-2}$** ***bla*$_{TEM-1}$**	***bla*$_{OXA-48}$**
ESBL-, pAmpC- and carbapenemase-producing strain – expected results		pAmpC	ESBL	carbapenemase	carbapenemase
Obtained results	Confirmed ESBL-producer	-	32/35 (91%)	-	-
	Confirmed ESBL + pAmpC-producer	*3/35 (9%)*	-	-	-
	Confirmed pAmpC-producer	32/35 (91%)	-	*4/35 (11%)*	-
	Confirmed carbapenemase-producer	-	-	28/35 (80%)	29/35 (83%)
	Confirmed unusual phenotype	-	*2/35 (6%)*	*3/35 (9%)*	*4/35 (11%)*
	Not ESBL-, pAmpC- or carbapenemase-producing	-	*1/35 (3%)*	-	*2/35 (6%)*

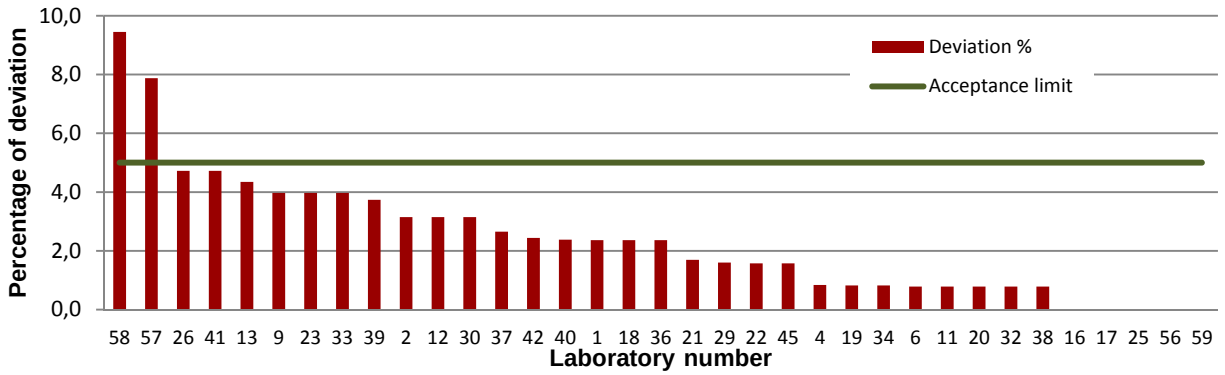

Figure 3: Individual participants' deviations in percent of their total number of *Salmonella* AST's.

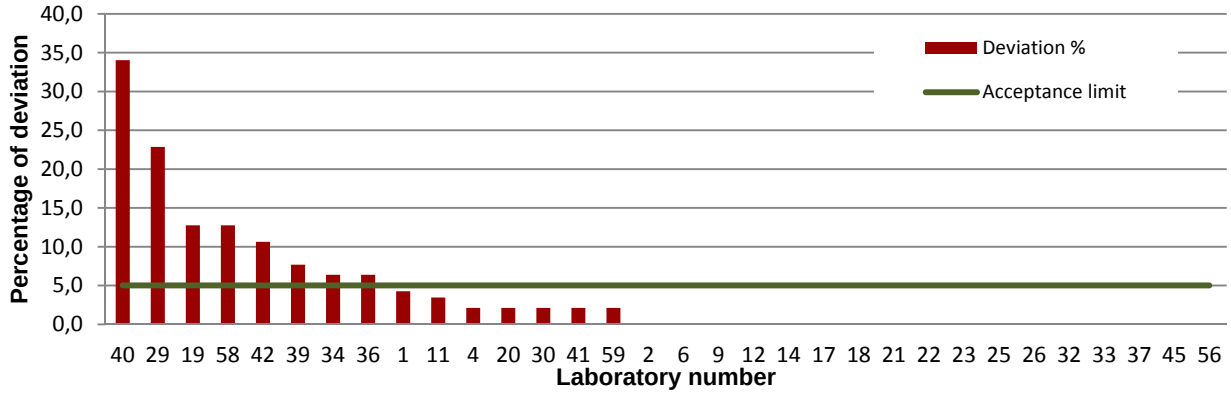

Figure 4: Individual participants' deviations in percent of their total number of *Campylobacter* AST's.

Table 4 Obtained values for AST of *E. coli* ATCC 25922. AMP; ampicillin, FEP; cefepime FOT; cefotaxime, FOX; cefoxitin, TAZ; ceftazidime, CHL; chloramphenicol, CIP; ciprofloxacin, COL; colistin, ERT: ertapenem, GEN; gentamicin, IMI; imipenem, MER; meropenem, NAL; nalidixic acid, SMX; sulphonamides, TET; tetracycline, TGC; tigecycline, TMP; trimethoprim.

MIC determination *E. coli* ATCC 25922			
Antimicrobial	Proportion outside QC range	Obtained values in MIC steps (min/max)	
		Below lower QC limit	Above upper QC limit
Panel 1, AMP	1/35 (3%)	-	3 steps
Panel 1, FOT	2/34 (6%)	-	6 steps
Panel 1, TAZ	1/34 (3%)	-	3 steps
Panel 1, CHL	0/35 (0%)	-	-
Panel 1, CIP	1/35 (3%)	-	2 steps
Panel 1, COL	0/35 (0%)	-	-
Panel 1, GEN	1/35 (3%)	2 steps	-
Panel 1, MER	0/34 (0%)	-	-
Panel 1, NAL	0/35 (0%)	-	-
Panel 1, SMX	2/24 (8%)	-	1 step
Panel 1, TET	0/35 (0%)	-	-
Panel 1, TGC	0/32 (0%)	-	-
Panel 1, TMP	4/35 (11%)	1 step	1 step
Panel 2, FEP	1/27 (4%)	-	4 steps
Panel 2, FOT	1/24 (4%)	-	3 steps
Panel 2, FOX	2/26 (8%)	1 step	3 steps
Panel 2, TAZ	1/26 (4%)	-	3 steps
Panel 2, ERT	1/27 (4%)	-	1 step
Panel 2, IMI	0/28 (0%)	-	-
Panel 2, MER	0/28 (0%)	-	-

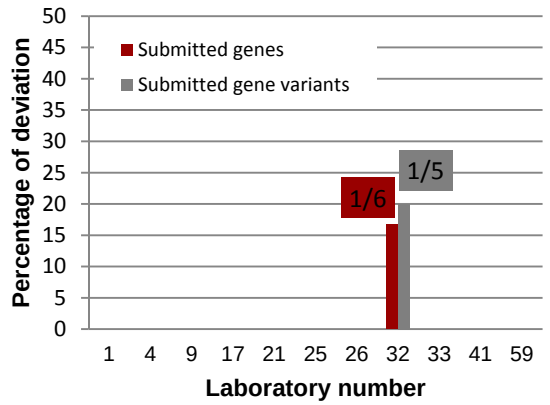

Figure 5: Individual participants' deviations in percent of their total number of results from the genotypic characterization.

Table 5 Obtained values for AST of *C. jejuni* ATCC 33560. CIP; ciprofloxacin, ERY; erythromycin, GEN; gentamicin, NAL; nalidixic acid, TET; tetracycline.

MIC determination *C. jejuni* ATCC 33560			
Antimicrobial	Proportion outside QC range	Obtained values in MIC steps (min/max)	
		Below lower QC limit	Above upper QC limit
CIP	2/32 (6%)	-	1 step
ERY	0/32 (0%)	-	-
GEN	2/29 (7%)	2 steps	-
NAL	0/31 (0%)	-	-
TET	4/31 (13%)	-	2 steps

laboratories produced in all 18 values outside the QC-limit. Of these, eight could be attributed to one laboratory obtaining MIC-values several two-fold dilutions above the QC-range (#57). Table 4 illustrates the obtained results which are shown in full in Appendix 6a.

Table 5 presents the proportion of laboratories with results for the *C. jejuni* reference strain ATCC 33560 below or above the QC interval. eight deviations were seen, all from different laboratories.

3.6 Genotypic characterisation

For the optional genotypic characterisation of the ESC-producing *Salmonella* test strains, eleven laboratories participated. In Appendix 9, information is collected on detected genes, genes which were tested but not detected, primers used, and references for the method used. Two laboratories performed whole genome sequencing of the ESC-producing *Salmonella*, the remaining nine laboratories indicated the use of various types of conventional PCR to identify the relevant genes.

Table 6 indicate the obtained results, both on gene and variant level. Moreover, Figure 5 indicates that the discordant results were submitted by one laboratory (#32). This laboratory should evaluate the procedure to assess how the relevant test could be improved in the future.

Table 6: Results from the participation of eleven laboratories in the optional genotypic characterisation component of the EQAS

Test strain	Expected gene	Proportion of correct results (gene level)	Proportion of correct results (variant level)	Additional genes/variants identified
S-9.3	CMY-2	11/11 (100%)	10/10 (100%)	
S-9.4	CTX-M-9	11/11 (100%)	8/9 (89%)	CTX M-14
	TEM-1	8/8 (100%)	5/5 (100%)	
S-9.5	VIM-2	10/10 (100%)	7/7 (100%)	
	TEM-1	5/5 (100%)	3/3 (100%)	
S-9.6	OXA-48	10/10 (100%)	10/10 (100%)	VIM*

*Participant informed that this gene was not detected, but was incorrectly introduced to the database.

4. Discussion

It is important to consider that the number of EQAS participants differs from year to year, which implies that comparisons among different EQAS iterations should be interpreted with caution.

As also specified in the EU regulation 2013/652/EU, all participants in the present EQAS performed AST by dilution methods, primarily as microbroth determination.

4.1 Salmonella trial

Overall, the percentage of correct antimicrobial susceptibility test results of *Salmonella* was 97.6%. The majority (n=33) of participants obtained satisfactory results according to the level of acceptance (<5% deviation).

As indicated in Figure 2, the overall quality of the results in the 2014-EQAS would appear to have decreased slightly, whereas the measure when comparing results obtained from testing the internal control strain indicates a steady and very good quality of results.

This proficiency test is the first possibility of testing the strains with the panels designed to follow the requirements of Decision 2013/652/EU. For the testing of *Salmonella* test strains, imipenem and meropenem both presented low levels of concordance with the expected (88.9% and 90.6%, respectively) which also affects the deviation level in the context of categorization of pAmpC-, ESBL-, and carbapenemase phenotypes.

As indicated by Figure 3, deviation levels higher than 5% were exhibited by two laboratories (#57 and #58). Laboratory #57 in particular obtained deviating results related to S-9.5 which was also incorrectly categorized as a presumptive pAmpC instead of a presumptive carbapanemase phenotype. For laboratory #58, the 12 deviations also had deviating results in relation to S-9.5 for meropenem and imipenem, but the remaining deviations were due to detection of a high MIC-level and a categorization as resistant where the expected result was susceptible. In fact, this also was the case when looking at the results obtained by laboratory #58 in the 2013-iteration. Both laboratories presenting deviation levels above 5% have been contacted by the EURL-AR to discuss and work towards improving the quality of results. None of these laboratories were defined as outliers.

For the *E. coli* reference strain, the obtained results were in general in agreement with the CLSI recommendations. Disregarding the laboratory that obtained eight of the 18 values

outside of the QC-ranges, trimethoprim and sulfamethoxazole appeared to be the antimicrobials causing problems with some of the values above and some below the QC-range.

For the two laboratories #42, and #57 which had a deviation level above the acceptance limit in EQAS 2013 with values of 5.3% and 7.4%, respectively, one has this year increased their performance (#42) to a deviation level at 2.4%, and the other (#57) present has a deviation level at 9.4% in the 2014-iteration.

ESC-producing *Salmonella* test strains

The detection of ESC-producing microorganisms remain to be important and is a mandatory part of this EQAS.

Of the four *Salmonella* test strains relevant for this component of the EQAS (S-9.3, S-9.4, S-9.5, and S-9.6), one was a pAmpC-phenotype, one was an ESBL-phenotype and two were carbapenemase phenotypes. The testing and interpretation of results in particular caused difficulties for the two carbapenemase producing strains where meropenem resistance would be the reason to classify this strain as a carbapenemase-producer. The expected meropenem MIC was at 1 mg/L and 0.5 mg/L for S-9.5 and S-9.6, respectively. These were both more than one dilution step above the cutoff-value (at 0.125 mg/L), however, still only 80% and 83% of the participating laboratories could detect the carbapenemase production in these strains. Three laboratories indicated the MIC result for meropenem to be <=1 mg/L when testing the second panel, indicating that some laboratories do not test the range required by Decision 2013/652/EU (0.03-16 mg/L for meropenem). With a cutoff value at 0.125 mg/L, a range of concentration with the lowest at 1 mg/L gives difficulties in detecting resistance and therefore also in detecting carbapenemase production. These results present examples of issues which the NRLs face when performing laboratory testing of ESC-producing strains and will be brought up for discussion in the network to discuss which tools to apply to obtain better analysis and interpretation.

Of the 35 laboratories which tested *Salmonella*, one (#39) submitted results which were incorrect for four test strains in relation to ESC-production. This laboratory has been contacted by the EURL-AR to identify possible causes of this unsatisfactory performance and to improve the quality of results.

Laboratory #57 which had one deviation for the categorization as ESBL-, pAmpC- or carbapenemase-producers (S-9.5) obtained a high number of incorrect AST-results in the *Salmonella* strains and also in the *E. coli* QC-reference strain, indicating that there could issues related to the handling of the strains or other procedures in the laboratory that would need a review.

For the test strains S-9.3 and S-9.4 which were pAmpC-phenotype and ESBL-phenotype, the six results not in concordance with the expected appeared to relate to the interpretation of the obtained MIC-values, as there could not be detected any discordance when comparing the obtained and expected MIC-values. The six results were reported by six different laboratories.

4.2 Campylobacter trial

For the *Campylobacter* component of this year's EQAS, 32 laboratories submitted results leading to an overall percentage of correct AST results at 96.0%. The performance varied from no deviations up to 34.0% deviations, with 24 laboratories performing satisfactorily according to the established acceptance range.

For both microorganisms, it appears that there has been a slight increase in the level of deviations, to 2.4% for *Salmonella* and 4% for *Campylobacter*.

Eight laboratories (#19, #29, #34, #36, #39, #40, #42, and #58) obtained deviation levels

above 5%, two of these were defined as outliers (#29 and #40) with deviation levels at 22.9% and 34.0%. For none of these laboratories, the values obtained for the QC-strain indicate methodical issues to be the reason for the obtained deviations. Two reported that they suspect a switch of strains in the laboratory to have been the cause of the deviation. The two outliers have been requested to investigate and report the cause of the high number of deviations. The EURL-AR awaits responses in this regard.

Laboratory #19 obtained three deviations when testing C-9.7 and three when testing C-9.8 which indicates the testing of two other strains, possibly a switch or contaminants. Laboratory #29 presents eight deviations of which seven have a higher MIC than expected and therefore are categorized as resistant. Four of the deviations are related to the same test strain (C-9.2). Laboratory #34 suspected a cut and paste-error, whereas #36 suspected a switch of strains, but due to a heavy work load a re-testing has not yet been performed. Laboratory #39 and #42 both reported an expected MIC value which was incorrectly interpreted. Laboratory #40 presented 16 deviating results of which four, five and three related to strains C-9.2, C-9.5 and C-9.8. Laboratory #58 presented six deviations, all relating to the same strain (C-9.5), and all obtaining interpretations as resistant instead of susceptible, which could indicate a switch of strains. All eight laboratories presenting deviation levels above 5% have been contacted by the EURL-AR to identify possible causes of this unsatisfactory performance and to improve the quality of results.

All participating laboratories uploaded data from tests performed on the *C. jejuni* reference strain and the proportion of results within the QC intervals was 94.8%. Six of the eight values outside the QC intervals were just one step below or above the QC-limits, the remaining two were two dilution steps above or below the QC-limits. The laboratories obtaining these values should monitor these over time to ensure that their tests render a reliable result for the particular antimicrobial.

Laboratories #37, #6, and #22 which were regarded as outliers in EQAS 2013 with deviation levels at 12.5%, 14.6% and 19.0%, respectively, all increased their performance extensively in the 2014-iteration and obtained deviation levels at 0%, 0% and 0%, respectively. Laboratory #29 which in 2013 also was considered as an outlier with a deviation level at 12.5%, was again in 2014 considered as an outlier due to a deviation level at 22.9%.

4.3 Genotypic characterisation

The focus on genotypic characterization of microorganisms is increasing in the EU and worldwide. In EU, communication has been ongoing to improve laboratory detection and confirmation of ESBL- and pAmpC-producing *Enterobacteriaceae.*

Furthermore, the agenda now is focusing at the implementation of detection of carbapenemase resistant organisms, with the recent EFSA Scientific Opinion (EFSA BIOHAZ Panel, 2013) describing the importance of determining the identity of the genes responsible for the carbapenemase production by molecular methods.

The optional genotypic characterisation offered as a supplementary part of this EQAS should therefore be seen as an important possibility for the NRL-AR's to introduce this method in the laboratory and thereby be at the forefront when the method proposals are adopted. This year, eleven laboratories participated in this optional EQAS component.

5. Conclusions

The goal of the EURL-AR EQAS is to have all participating NRLs performing antimicrobial susceptibility testing of *Salmonella* and *Campylobacter* with a deviation level below 5%. This seems within reach for *Salmonella* as well as for *Campylobacter*.

The performance of the NRL's appear to be slightly lower for *Salmonella* AST's in this EQAS (97.6%) when compared to the results from the previous EQAS 2011, 2012, and 2013 (98.1%, 99.0%, and 99.3%). Regarding *Campylobacter* AST's, the level of deviation appears to have risen and this year it reached a level of 4.0% compared to 1.9%, 2.1%, and 3.5% in 2011, 2012, and 2013. Two laboratories have contributed substantially to this increase in the general deviation level in the *Campylobacter* AST as they were regarded as outliers (#29, and #40) and presented high deviation levels (22.9% and 34.0%).

Eleven NRLs participated in the EQAS component consisting of genotypic testing of ESBL-, AmpC- and carbapenemase-producing *Enterobacteriaceae*. Improvement is needed to correctly identify the phenotype of *Salmonella* spp. producing beta-lactamases of the ESBL-, AmpC, and carbapenemase-type as this is a priority area within the EURL-AR activities. We strongly encourage participants having problems in identifying these strains to perform a re-test of the test strains as a training exercise and to contact the EURL-AR in case any discussion is needed.

Finally, the EURL-AR is open to suggestions to improve future EQAS trials and invites the entire network to contribute with ideas for training courses and specific focus areas to expand the network's knowledge in antimicrobial resistance.

6. References

EFSA BIOHAZ Panel (EFSA Panel on Biological Hazards), 2013. Scientific Opinion on Carbapenem resistance in food animal ecosystems. EFSA Journal 2013;11(12):3501, 70 pp. doi:10.2903/j.efsa.2013.3501

EFSA, Technical specifications on the harmonised monitoring and reporting of antimicrobial resistance in *Salmonella*, *Campylobacter* and indicator *Escherichia coli* and *Enterococcus* spp. bacteria transmitted through food. EFSA Journal 2012;10(6):2742 [64 pp.].

European Commission, 2013/652/EU: Commission Implementing Decision of 12 November 2013 on the monitoring and reporting of antimicrobial resistance in zoonotic and commensal bacteria

Schwarz S, Silley P, Simjee S, Woodford N, van DE, Johnson AP & Gaastra W. (2010) Editorial: assessing the antimicrobial susceptibility of bacteria obtained from animals. J Antimicrob Chemother 65: 601-604

DTU Food
National Food Institute

European Union Reference Laboratory Antimicrobial Resistance

M00-06-001/01.12.2011

EQAS 2014

FOR *SALMONELLA*, *CAMPYLOBACTER* AND OPTIONAL GENOTYPIC CHARACTERISATION

The EURL-AR announces the launch of another EQAS, thus providing the opportunity for proficiency testing which is considered an essential tool for the generation of reliable laboratory results of consistently good quality.

This EQAS consists of antimicrobial susceptibility testing of eight *Salmonella* isolates and eight *Campylobacter* isolates. For the optional genotypic characterisation, the ESBL-genes in the relevant *Salmonella* strains should be detected. Additionally, quality control (QC) strains *E. coli* ATCC 25922 (CCM 3954) and *C. jejuni* ATCC 33560 (CCM 6214) will be distributed to new participants.

This EQAS is specifically for NRL's on antimicrobial resistance. Therefore, laboratories designated to be NRL-AR do not need to sign up to participate but are automatically regarded as participants. You may contact the EQAS-Coordinator if you wish to inform of changes. Participation is free of charge for all above-mentioned designated laboratories.

TO AVOID DELAY IN SHIPPING THE ISOLATES TO YOUR LABORATORY
The content of the parcel is "UN3373, Biological Substance Category B": Eight *Salmonella* strains, eight *Campylobacter* and, for new participants, also the QC strains mentioned above. Please provide the EQAS coordinator with documents or other information that can simplify customs procedures (e.g. specific text that should be written on the pro-forma invoice). To avoid delays, we kindly ask you to send this information already at this stage.

TIMELINE FOR RESULTS TO BE RETURNED TO THE NATIONAL FOOD INSTITUTE
Shipment of isolates and protocol: The isolates will be shipped in October 2014. The protocol for this proficiency test will be available for download from the website (www.eurl-ar.eu).

Submission of results: Results must be submitted to the National Food Institute **no later than December 5th 2014** via the password-protected website.
Upon reaching the deadline, each participating laboratory is kindly asked to enter the password-protected website once again to download an automatically generated evaluation report.
EQAS report: A report summarising and comparing results from all participants will be issued. In the report, laboratories will be presented coded, which ensures full anonymity. The EURL-AR and the EU Commission, only, will have access to un-coded results. The report will be publicly available.

Next EQAS: The next EURL-AR EQAS that we will have is on antimicrobial susceptibility testing of *E. coli*, staphylococci and enterococci which will be carried out in June 2015.

Please contact me if you have comments or questions regarding the EQAS.

Sincerely,

Susanne Karlsmose (suska@food.dtu.dk)
EQAS-Coordinator

Participant list

Salmonella	*Campylobacter*	Genotypic characterisation	Institute	Country
X	X	-	Austrian Agency for Health and Food Safety	Austria
X	X	X	Institute of Public Health	Belgium
X	X	-	National Diagnostic and Research Veterinary Institute	Bulgaria
X	X	-	Croatian Veterinary Institut	Croatia
X	X	-	Veterinary Services	Cyprus
X	X	X	State Veterinary Institute Praha	Czech Republic
X	X	X	National Food Institute	Denmark
X	X	-	Danish Veterinary and Food Administration, DVFA	Denmark
X	X	-	Estonian Veterinary and Food Laboratory	Estonia
X	X	-	Finnish Food Safety Authority EVIRA	Finland
X	-	-	Agence nationale de sécurité sanitaire ANSES - Fougères LERMVD	France
X	-	-	Agence nationale de sécurité sanitaire ANSES - LERQAP	France
-	-	-	Agence nationale de sécurité sanitaire ANSES - Lyon	France
-	X	-	Agence nationale de sécurité sanitaire ANSES - Ploufragan - LERAP	France
X	X	X	Federal Institute for Risk Assessment	Germany
X	X	-	Veterinary Laboratory of Chalkis	Greece
X	X	-	Central Agricultural Office Veterinary Diagnostic Directorate	Hungary
X	X	-	University of Iceland	Iceland
X	X	-	Central Veterinary Research Laboratory	Ireland
X	X	X	Istituto Zooprofilattico Sperimentale delle Regioni Lazio e Toscana	Italy
X	X	-	Institute of Food Safety, Animal Health and Enviroment "BIOR"	Latvia
X	X	-	National Food and Veterinary Risk Assessment Institute	Lithuania
X	X	X	Laboratoire national de Santé	Luxembourg
X	X	-	Public Health Laboratory	Malta
X	X	X	Central Veterinary Institute of Wageningen UR	Netherlands
X	X	-	Food and Consumer Product Safety Authority (VWA)	Netherlands
X	X	-	Veterinærinstituttet	Norway
X	X	X	National Veterinary Research Institute	Poland
X	X	-	Laboratorio National de Investigacáo Veterinaria	Portugal
X	X	-	Institute for Diagnosis and Animal Health	Romania
X	X	X	Institute for Hygiene and Veterinary Public Health	Romania
-	-	-	Institute of Veterinary Medicine of Serbia	Serbia
X	X	-	State Veterinary and Food Institute (SVFI)	Slovakia
X	X	-	National Veterinary Institute	Slovenia
X	-	-	Centro nacional de Alimentacion. Agencia Espanola de Seguridad Alimentaria y Nutricion	Spain
X	X	X	Laboratorio Central de Sanidad, Animal de Algete	Spain
-	-	-	Laboratorio Central de Sanidad, Animal de Santa Fe	Spain
X	X	-	VISAVET Health Surveillance Center, Complutense University	Spain
X	X	X	National Veterinary Institute, SVA	Sweden
X	X	-	Vetsuisse Faculty Bern, Institute of Veterinary Bacteriology	Switzerland
X	-	-	National Food Reference Laboratory	Turkey
-	-	-	Public Health England - Colindale	United Kingdom
X	X	-	The Veterinary Laboratory Agency	United Kingdom

Designated NRL-AR by the compentent authority of the member state
Non-NRL-AR enrolled by the EURL-AR
Not a Member State of the EU

Reference values (MIC-value and interpretation) - *Salmonella*

	Ampicillin AMP		Azithromycin AZI		Cefepime FEP		Cefotaxime FOT		Cefotaxime/clav F/C		F:F/C ratio	Cefoxitin FOX		Ceftazidime TAZ		Ceftazidime/clav T/C		T:T/C ratio	Chloramphenicol CHL		Ciprofloxacin CIP		Colistin COL		Ertapenem ETP	
EURL S-9.1	= 1	SUSC	= 8	-			<= 0.25	SUSC						<= 0.5	SUSC				<= 8	SUSC	= 0.03	SUSC	= 8	RESIST		
EURL S-9.2	> 64	RESIST	= 8	-			<= 0.25	SUSC						<= 0.5	SUSC				<= 8	SUSC	= 0.5	RESIST	<= 1	SUSC		
EURL S-9.3	> 64	RESIST	= 8	-	= 0.25	-	= 16	RESIST	= 8/4	-	<8	= 32	RESIST	= 16	RESIST	= 8/4	-	<8	= 128	RESIST	= 0.03	SUSC	<= 1	SUSC	<= 0.015	SUSC
EURL S-9.4	> 64	RESIST	= 8	-	= 2	-	= 16	RESIST	= 0.12/4	-	>=8	= 2	SUSC	= 1	SUSC	= 0.25/4	-	<8	<= 8	SUSC	= 0.5	RESIST	<= 1	SUSC	<= 0.015	SUSC
EURL S-9.5	> 64	RESIST	= 8	-	= 2	-	> 64	RESIST	> 64/4	-	<8	> 64	RESIST	= 64	RESIST	= 64/4	-	<8	<= 8	SUSC	> 8	RESIST	<= 1	SUSC	= 0.5	RESIST
EURL S-9.6	> 64	RESIST	= 32	-	= 0.12	-	= 0.5	SUSC	= 0.25/4	-	<8	= 8	SUSC	= 0.5	SUSC	= 0.25/4	-	<8	<= 8	SUSC	= 8	RESIST	<= 1	SUSC	= 0.25	RESIST
EURL S-9.7	> 64	RESIST	= 16	-			<= 0.25	SUSC						<= 0.5	SUSC				<= 8	SUSC	= 0.06	SUSC	<= 1	SUSC		
EURL S-9.8	<= 1	SUSC	= 8	-			<= 0.25	SUSC						<= 0.5	SUSC				<= 8	SUSC	<= 0.015	SUSC	= 2	SUSC		

	Gentamicin GEN		Imipenem IMI		Meropenem MER		Nalidixic acid NAL		Sulfamethoxazole SMX		Temocillin TRM		Tetracycline TETRA		Tigecycline TGC		Trimethoprim TMP		ESBL-category	Relevant genes
EURL S-9.1	<= 0.5	SUSC			= 0.06	SUSC	<= 4	SUSC	= 32	SUSC			<= 2	SUSC	<= 0.25	SUSC	<= 0.25	SUSC	No ESBL, AmpC- or carbapenemase	N/A
EURL S-9.2	> 32	RESIST			= 0.06	SUSC	= 32	RESIST	= 128	SUSC			<= 2	SUSC	<= 0.25	SUSC	<= 0.25	SUSC	No ESBL, AmpC- or carbapenemase	N/A
EURL S-9.3	<= 0.5	SUSC	= 0.25	SUSC	<= 0.03	SUSC	<= 4	SUSC	> 1024	RESIST	= 8	-	> 64	RESIST	= 0.5	SUSC	<= 0.25	SUSC	Presumptive pAmpC-phenotype	CMY-2
EURL S-9.4	<= 0.5	SUSC	= 0.25	SUSC	<= 0.03	SUSC	> 128	RESIST	= 64	SUSC	<= 4	-	= 32	RESIST	<= 0.25	SUSC	<= 0.25	SUSC	Presumptive ESBL-phenotype	TEM-1; CTXM-9
EURL S-9.5	= 32	RESIST	= 4	RESIST	= 1	RESIST	> 128	RESIST	> 1024	RESIST	> 128	-	= 64	RESIST	= 0.5	SUSC	<= 0.25	SUSC	Presumptive carbapenemase phenotype	TEM-1; VIM-2
EURL S-9.6	<= 0.5	SUSC	= 1	SUSC	= 0.5	RESIST	> 128	RESIST	= 16	SUSC	> 128	-	<= 2	SUSC	= 0.5	SUSC	<= 0.25	SUSC	Presumptive carbapenemase phenotype	OXA-48
EURL S-9.7	<= 0.5	SUSC			<= 0.03	SUSC	<= 4	SUSC	> 1024	RESIST			> 64	RESIST	= 2	RESIST	> 32	RESIST	No ESBL, AmpC- or carbapenemase	N/A
EURL S-9.8	= 1	SUSC			<= 0.03	SUSC	<= 4	SUSC	= 16	SUSC			<= 2	SUSC	<= 0.25	SUSC	<= 0.25	SUSC	No ESBL, AmpC- or carbapenemase	N/A

Resistant

Reference values (MIC-value and interpretation) - *Campylobacter*

Species	Code	Ciprofloxacin CIP		Erythromycin ERY		Gentamicin GEN		Nalidixic acid NAL		Streptomycin STR		Tetracycline TET	
C. jejuni	EURL C-9.1	= 8	RESIST	<= 1	SUSC	= 0.25	SUSC	> 64	RESIST	= 0.5	SUSC	> 64	RESIST
C. coli	EURL C-9.2	= 0.25	SUSC	> 128	RESIST	= 0.5	SUSC	= 8	SUSC	= 1	SUSC	= 2	SUSC
C. coli	EURL C-9.3	> 16	RESIST	= 4	SUSC	= 0.25	SUSC	> 64	RESIST	> 16	RESIST	> 64	RESIST
C. jejuni	EURL C-9.4	> 16	RESIST	> 128	RESIST	> 16	RESIST	> 64	RESIST	> 16	RESIST	> 64	RESIST
C. jejuni	EURL C-9.5	<= 0.12	SUSC	<= 1	SUSC	= 0.25	SUSC	= 4	SUSC	= 1	SUSC	<= 0.5	SUSC
C. coli	EURL C-9.6	= 4	RESIST	> 128	RESIST	= 1	SUSC	= 64	RESIST	> 16	RESIST	= 4	RESIST
C. jejuni	EURL C-9.7	= 16	RESIST	<= 1	SUSC	= 0.25	SUSC	= 2	SUSC	= 0.5	SUSC	<= 0.5	SUSC
C. coli	EURL C-9.8	<= 0.12	SUSC	> 128	RESIST	= 1	SUSC	= 8	SUSC	> 16	RESIST	= 1	SUSC

Resistant

M00-06-001/01.12.2011

EURL-AR External Quality Assurance System 2014

- *Salmonella, Campylobacter* and optional genotypic characterisation

Id: «Lab_no_»
«Name»
«Institute__»
«Country»

Kgs. Lyngby, October 2014

Dear «Name»,

Please find enclosed the bacterial strains for the EURL-AR EQAS 2014. Upon arrival to your laboratory, the strains should be stored dark and at 4°C for stabs, and dark and cool for freeze-dried strains. Charcoal swabs must be subcultured straight away.

On the EURL-AR-website (www.eurl-ar.eu) the following documents relevant for the EURL-AR EQAS are available:

- Protocol for *Salmonella* and *Campylobacter* including test forms
- Instructions for Opening and Reviving Lyophilised Cultures
- Subculture and Maintenance of Quality Control Strains

We ask you to examine the eight *Salmonella* and the eight *Campylobacter* strains that we sent to you by performing antimicrobial susceptibility testing. The ESBL-producing *Salmonella* strains should be characterised genotypically (optional) according to the description in the protocol. In the protocol you can find detailed description of the procedures to follow. Additionally, you can find a description of the procedure to enter your results into the interactive web database. For accessing the database, you need this username and password.

Your username: «Username»

Your password: «Password»

Please keep this document
Your username and password will not appear in other documents

Results should be submitted to the database no later than December 5th 2014.

Please acknowledge receipt of this parcel immediately upon arrival (to suska@food.dtu.dk).
Do not hesitate to contact us for further information.

Yours sincerely,

Susanne Karlsmose
EQAS-Coordinator

EU Reference Laboratory for Antimicrobial Resistance
External Quality Assurance System (EQAS) 2014

DTU Food
National Food Institute

PROTOCOL

For antimicrobial susceptibility testing of *Salmonella*, *Campylobacter* and optional genotypic characterisation of AmpC-, ESBL- and carbapenemase-producing test strains

1 INTRODUCTION

The organisation and implementation of an External Quality Assurance System (EQAS) on antimicrobial susceptibility testing (AST) of *Salmonella* and *Campylobacter* is among the tasks of the EU Reference Laboratory for Antimicrobial Resistance (EURL-AR). The Salm/Camp EQAS 2014 will include AST of eight *Salmonella* and *Campylobacter* strains and AST of reference strains *E. coli* ATCC 25922 (CCM 3954) and *C. jejuni* ATCC 33560 (CCM 6214).

The above-mentioned reference strains are included in the parcel only for new participants of the EQAS who did not receive them previously. The reference strains are original CERTIFIED cultures provided free of charge, and should be used for future internal quality control for antimicrobial susceptibility testing in your laboratory. The reference strains will not be included in the years to come. Therefore, please take proper care of these strains. Handle and maintain them as suggested in the manual 'Subculture and Maintenance of QC Strains' available on the EURL-AR website (see www.eurl-ar.eu).

Various aspects of the proficiency test scheme may from time to time be subcontracted. When subcontracting occurs it is placed with a competent subcontractor and the National Food Institute is responsible to the scheme participants for the subcontractor's work.

Technical University of Denmark

2 OBJECTIVES

This EQAS aims to support laboratories to assess and, if necessary, to improve the quality of results obtained by AST of pathogens of food- and animal-origin, with special regard to *Salmonella* and *Campylobacter*. Further objectives are to evaluate and improve the comparability of surveillance data on antimicrobial susceptibility of *Salmonella* and *Campylobacter* reported to EFSA by different laboratories.

3 OUTLINE OF THE EQAS 2014

3.1 Shipping, receipt and storage of strains

In October 2014, the National Reference Laboratories for Antimicrobial Resistance (NRL-AR) will receive a parcel containing eight *Salmonella* and *Campylobacter* strains from the National Food Institute. This parcel will also contain reference strains, but only for participants who did not receive them previously. All strains belong to UN3373, Biological substance, category B. Extended spectrum beta-lactamase (ESBL)-producing strains as well as carbapenamase producing strains are included in the selected material and are part of the optional EQAS-item, consisting of characterization of genes conferring ESBL- or carbapenemase production.

The reference strains are shipped lyophilised, the *Campylobacter* test strains are shipped as a charcoal swabs and the *Salmonella* test strains are stab cultures. On arrival, the stab cultures and the charcoal swabs must be subcultured, and all cultures should be adequately stored until testing. A suggested procedure for reconstitution of the lyophilised reference strains is presented below.

3.2 Suggested procedure for reconstitution of the lyophilised reference strains

Please refer to the document 'Instructions for opening and reviving lyophilised cultures' on the EURL-AR-website (see www.eurl-ar.eu).

3.3 Antimicrobial susceptibility testing

The strains should be tested for susceptibility to the antimicrobials listed in Tables 1, 2 and 3, using the method implemented in your laboratory for performing monitoring for EFSA and applying the interpretative criteria listed below.

Participants should perform minimum inhibitory concentration (MIC) determination using the methods stated in the EC regulation EC 652/2013. For interpretation of results, use the cut-off values listed in Tables 1, 2 and 3 (except where indicated) represent the current epidemiological cut-off values developed by EUCAST (www.eucast.org), and allow categorisation of bacterial isolates into two categories; resistant or susceptible. A categorisation as intermediate is not accepted**.**

As the current regulation and recommendations focus on MIC testing only, disk diffusion results cannot be submitted.

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3.3.1 *Salmonella*

The interpretative criteria that should be applied for categorizing the *Salmonella* test strain as resistant or susceptible are those listed in Tables 1 and 2.

Table 1: Antimicrobials recommended for AST of *Salmonella* spp. and interpretative criteria according to table 1 in EC regulation 652/2013

Antimicrobial	MIC (µg/mL) (R>)
Ampicillin (AMP)	8
Azithromycin (AZI)	Not available*
Cefotaxime (FOT)	0.5
Ceftazidime (TAZ)	2
Chloramphenicol (CHL)	16
Ciprofloxacin (CIP)	0.06
Colistin (COL)	2
Gentamicin (GEN)	2
Meropenem (MERO)	0.125
Nalidixic acid (NAL)	16
Sulfonamides (SMX)	256**
Tetracycline (TET)	8
Tigecycline (TGC)	1***
Trimethoprim (TMP)	2

* Participants are requested to upload the MIC value obtained without selecting an interpretation.
** CLSI M100 Table 2A
*** Data from EUCAST is available for *S.* Enteritidis, *S.* Typhimurium, *S.* Typhi and *S.* Paratyphi.

Table 2: Antimicrobials recommended for additional AST of *Salmonella* spp. resistant to cefotaxime, ceftazidime or meropenem and interpretative criteria according to table 4 in EC regulation 652/2013

Antimicrobial	MIC (µg/mL) (R>)
Cefepime, FEP	Not available*
Cefotaxime, FOT	0.5
Cefotaxime + clavulanic acid (F/C)	Not applicable
Cefoxitin, FOX	8
Ceftazidime, TAZ	2
Ceftazidime+ clavulanic acid (T/C)	Not applicable
Ertapenem, ETP	0.06
Imipenem, IMI	1
Meropenem, MERO	0.125
Temocillin, TRM	Not available*

* Participants are requested to upload the MIC value obtained without selecting an interpretation

Plasmid-mediated quinolone resistance

When performing antimicrobial susceptibility testing of the *Salmonella* test strains, the interpretative criteria listed in Table 1 should be able to detect plasmid mediated quinolone resistant test strains.

Extended-beta-lactam- and carbapenem resistance

Confirmatory tests for AmpC-, ESBL- and carbapenemase production are **mandatory** on all strains resistant to cefotaxime (CTX), ceftazidime (TAZ) or meropenem and should be performed by testing the second panel of antimicrobials (Table 2 in this document corresponding to Table 4 in EC regulation 652/2013).

Confirmatory tests for AmpC-, ESBL- and carbapenemase production require the use of both cefotaxime (FOT) and ceftazidime (TAZ) alone and in combination with a β-lactamase inhibitor (clavulanic acid). Synergy is defined either as a ≥ 3 twofold concentration decrease in an MIC for either antimicrobial agent tested in combination with clavulanic acid vs. its MIC when tested alone (MIC FOT : FOT/CL or TAZ : TAZ/CL ratio ≥ 8) (CLSI M100 Table 2A; Enterobacteriaceae). The presence of synergy indicates ESBL production. Resistance to cefepime gives further indication of ESBL production, but is not essential. Confirmatory test for carbapenemase production requires the testing of meropenem (MERO).

Detection of AmpC-type beta-lactamases can be performed by testing the bacterium for susceptibility to cefoxitin (FOX). Resistance to FOX could indicate the presence of an AmpC-type beta-lactamase that may be verified by PCR and sequencing.

The classification of the phenotypic results should be based on the most recent EFSA recommendations (EFSA 2012[1]) indicating the strains as:

- Presumptive ESBL: strains with positive synergy test, susceptible to cefoxitin and resistant to cefepime
- Presumptive ESBL+pAmpC: strains with positive or negative synergy test, resistant to cefoxitin and resistant to cefepime
- Presumptive pAmpC phenotype: strains with negative synergy test
- Presumptive carbapenemase phenotype: strain resistant to meropenem
- Unusual phenotype: any other combinations

[1] European Food Safety Authority; Technical specifications on the harmonised monitoring and reporting of antimicrobial resistance in *Salmonella*, *Campylobacter* and indicator *Escherichia coli* and *Enterococcus* spp. bacteria transmitted through food. EFSA Journal 2012; 10(6):2742. [64 pp.] doi:10.2903/j.efsa.2012.2742. Available online: www.efsa.europa.eu/efsajournal

We recommend, however, that strains showing synergy with clavulanic acid for at least one of the third generation cephalosporins (cefotaxime or ceftazidime) should be considered ESBL-producing, independently of the cefepime result.

3.3.2 *Campylobacter*

For AST of *Campylobacter*, MIC methods should be applied, i.e. broth or agar dilution methods using incubation at 36-37ºC for 48 hours or 42ºC for 24 hours.

Table 3: Antimicrobials recommended for AST of *Campylobacter jejuni* and *C. coli* and interpretative criteria according to table 1 in EC regulation 652/2013

Antimicrobial	*C. jejuni*	*C. coli*
	MIC (µg/mL) (R>)	MIC (µg/mL) (R>)
Ciprofloxacin (CIP)	0.5	0.5
Erythromycin (ERY)	4	8
Gentamicin (GEN)	2	2
Nalidixic acid (NAL)	16	16
Streptomycin (STR)	4	4
Tetracycline (TET)	1	2

Identification of *Campylobacter* species

Species identification of the *Campylobacter* test strains must be performed by the NRLs using in-house methods or adopting the protocol available on the EURL-AR website under: http://eurl-ar.eu/233-protocols.htm.

3.4 Optional genotypic characterisation

For the optional genotypic characterisation of the AmpC-, ESBL- or carbepenemase producing *Salmonella* test strains, the requested results are the genes conferring AmpC-, ESBL- or carbepenemase -production harboured in the test strains. The genes included in the test are the following: ACC, ACT, CMY, CTX, DHA, FOX, GES, IMP, KPC, MOX, NDM, OXA, PER, SHV, TEM, VEB, and VIM. The database lists the relevant variants of the genes.

When uploading the results in the database, the identified genes will be evaluated against the expected results. The results will be evaluated on the detected gene (ACC-, ACT-, CMY-, etc.) as well as the variant identified.

The method used for the genotypic characterisation should be your laboratory's routine method. The expected results listed in the database are those obtained by the EURL-AR.

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4 REPORTING OF RESULTS AND EVALUATION

Test forms are available for recording your results before you enter them into the interactive web database.

We recommend reading carefully the description reported in paragraph 5 before entering your results in the web database. **Results must be submitted no later than December 5th, 2014.** After the deadline when all participants have uploaded results, you will be able to login to the database once again, and to view and print an automatically generated report evaluating your results. Results in agreement with the expected interpretation are categorised as 'correct', while results deviating from the expected interpretation are categorised as 'incorrect'.

If you experience difficulties in entering your results, please contact us directly.

All results will be summarized in a report which will be publicly available. The data in the report will be presented with laboratory codes. A laboratory code is known to the individual laboratory, whereas the complete list of laboratories and their codes is confidential and known only to the EURL-AR and the EU Commission. All conclusions will be public.

If you have questions, please do not hesitate to contact the EQAS Coordinator:

Susanne Karlsmose

National Food Institute

Technical University of Denmark

Kemitorvet, Building 204, DK-2800 Lyngby

Denmark

Tel: +45 3588 6601

Fax: +45 3588 6341

E-mail: suska@food.dtu.dk

5 HOW TO ENTER RESULTS IN THE INTERACTIVE DATABASE

Please read carefully this paragraph before entering the web page.

Remember that you need by your side the completed test forms.

Enter the EURL-AR EQAS 2014 start web page (http://eurl-ar.food.dtu.dk), write your username and password (lower-case) and press enter. Your username and password are indicated in the letter following your strains. Do not hesitate to contact us if you experience problems with the login.

You can browse back and forth by using the Home or back keys, but please remember to save your inputs before.

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Click on either "*Salmonella* test results" or "*Campylobacter* test results" for input of test results.

Click on "Start of Data Entry - Methods"

In the next page, you navigate among fields with the Tab-key and the mouse.

Complete the fields related to the method used for antimicrobial susceptibility testing and the brand of MIC trays, etc.

When submitting *Campylobacter* results, fill in the incubation conditions applied for susceptibility testing of *Campylobacter* – 36°C/48h or 42°C/24h.

Click on "save and go to next page"

In the data entry pages, you enter the species (for *Campylobacter* only), the obtained MIC-value and the interpretation (R, resistant or S, susceptible) for each *Salmonella* and *Campylobacter* strain.

For *Salmonella*, remember to also report the results for the ESBL detection tests.

If you did not test for susceptibility to a given antimicrobial, please leave the field empty.

Click on "save and go to next page"

When uploading data on the reference strains, please enter MIC values in µg/ml. Remember to use the operator keys to show symbols like "equal to", etc.

Click on "save".

Review the input pages by browsing through them and make corrections if necessary. Remember to save a page if you make corrections. If you press home a page without saving changes, you will see an error screen. In this case, click on "save" to save your results, browse back to the page and then continue.

Please complete the evaluation form.

Before approving your input, please be sure that you have filled in all the relevant fields as YOU CAN ONLY APPROVE ONCE! The approval blocks your data entry in the interactive database.

If you have performed the optional genotypic characterisation:

Click on "Gene test" and follow the description in the database for upload of the results of the optional genotypic characterization. Approve your input. Be sure that you have filled in all the results before approval. The approval blocks your data entry in the interactive database, but allows you to see the submitted results.

Salmonella, Campylobacter and genetic characterisation

TEST FORMS

Name:
Name of laboratory:
Name of institute:
City:
Country:
E-mail:
Fax:

Comments:

TEST FORM

Does your laboratory have an accreditation for performing *Salmonella* AST? ☐ Yes ☐ No

Which method did you use for antimicrobial susceptibility testing of *Salmonella* in this EQAS:

☐ Broth microdilution
☐ Agar dilution

Brand of microbroth plates/agar**:**
Incubation conditions: °C/ h

How many *Salmonella* isolates does your laboratory annually isolate:

How many *Salmonella* isolates does your laboratory annually test for antimicrobial susceptibility by a MIC method:

Comments or additional information:

TEST FORM

Does your laboratory have an accreditation for *Campylobacter* AST? ☐ Yes ☐ No

Incubation conditions: ☐ 36-37ºC / 48h ☐ 42ºC / 24h

Method used for antimicrobial susceptibility testing of *Campylobacter* in this EQAS::
☐ Broth microdilution
☐ Agardilution

Brand of microbroth plates/agar:

Additional comments:

How many *Campylobacter* isolates does your laboratory annually isolate:
How many *Campylobacter* isolates does your laboratory annually susceptibility test:

TEST FORM

Strain	Antimicrobial	Results and interpretation		
		≤ >	MIC-value (µg/ml)	S / R
Salmonella EURL S. 9.X	Ampicillin, AMP			
	Azithromycin, AZI			
	Cefotaxime, FOT			
	Ceftazidime, TAZ			
	Chloramphenicol, CHL			
	Ciprofloxacin CIP			
	Colistin, COL			
	Gentamicin, GEN			
	Meropenem, MERO			
	Nalidixic acid, NAL			
	Sulfamethoxazole, SMX			
	Tetracycline, TET			
	Tigecycline, TGC			
	Trimethoprim, TMP			

All strains resistant to cefotaxime (FOT), ceftazidime (TAZ) or meropenem (MERO) must be included for testing in the second panel as part of confirmatory tests for ESBL-, AmpC or carbapenemase production. See further description in the protocol section '3.3.1 *Salmonella*'.

Strain	Antimicrobial	Results and interpretation		
		≤ >	MIC-value (µg/ml)	S / R
Salmonella EURL S. 9.X	Cefepime, FEP			
	Cefotaxime, FOT			
	Cefotaxime + clavulanic acid (F/C)			
	Cefoxitin, FOX			
	Ceftazidime, TAZ			
	Ceftazidime+ clavulanic acid (T/C)			
	Ertapenem, ETP			
	Imipenem, IMI			
	Meropenem, MERO			
	Temocillin, TRM			

☐ Presumptive ESBL ☐ Presumptive pAmpC ☐ Unusual phenotype
☐ Presumptive ESBL+ pAmpC ☐ Presumptive carbapenemase ☐ No ESBL, AmpC- or carbapenemase

Comments (include optional genotype or other results):

TEST FORM

Antimicrobial susceptibility testing of reference strain *E. coli* ATCC 25922

	Antimicrobial	MIC-value (µg/ml)
1st panel	Ampicillin, AMP	
	Azithromycin, AZT	
	Cefotaxime, FOT	
	Ceftazidime, TAZ	
	Chloramphenicol, CHL	
	Ciprofloxacin, CIP	
	Colistin, COL	
	Gentamicin, GEN	
	Meropenem, MERO	
	Nalidixic acid, NAL	
	Sulfisoxazole, FIS*	
	Tetracycline, TET	
	Tigecycline, TGC	
	Trimethoprim, TMP	
2nd panel	Cefepime, FEP	
	Cefotaxime, FOT	
	Cefotaxime + clavulanic acid (F/C)	
	Cefoxitin, FOX	
	Ceftazidime, TAZ	
	Ceftazidime+ clavulanic acid (T/C)	
	Ertapenem, ETP	
	Imipenem, IMI	
	Meropenem, MERO	
	Temocillin, TRM	

*The antimicrobial which is mentioned in the CLSI M100 performance standard as representative for the sulfonamides concerning acceptable limits for quality control strains (CLSI M100, Table 3)

TEST FORM

Strain	Antimicrobial	Interpretation	
		MIC-value (µg/ml)	S / R
Campylobacter EURL C. 9.1 ☐ *C. jejuni* ☐ *C. coli*	Ciprofloxacin		
	Erythromycin		
	Gentamicin		
	Nalidixic Acid		
	Streptomycin		
	Tetracycline		
Campylobacter EURL C. 9.2 ☐ *C. jejuni* ☐ *C. coli*	Ciprofloxacin		
	Erythromycin		
	Gentamicin		
	Nalidixic Acid		
	Streptomycin		
	Tetracycline		
Campylobacter EURL C. 9.3 ☐ *C. jejuni* ☐ *C. coli*	Ciprofloxacin		
	Erythromycin		
	Gentamicin		
	Nalidixic Acid		
	Streptomycin		
	Tetracycline		
Campylobacter EURL C. 9.4 ☐ *C. jejuni* ☐ *C. coli*	Ciprofloxacin		
	Erythromycin		
	Gentamicin		
	Nalidixic Acid		
	Streptomycin		
	Tetracycline		

TEST FORM

Susceptibility testing of *Campylobacter jejuni* reference strain ATCC 33560

Strain	Antimicrobial	MIC-value (µg/ml)	
		36 °C/48 hours	42 °C/24 hours
C. jejuni ATCC 33560	Ciprofloxacin		
	Erythromycin		
	Nalidixic Acid		
	Tetracycline		

For Agar dilution:

Susceptibility testing of *Campylobacter jejuni* reference strain ATCC 33560

Strain	Antimicrobial	MIC-value (µg/ml)
C. jejuni ATCC 33560	Ciprofloxacin	
	Doxycycline	
	Erythromycin	
	Gentamicin	
	Meropenem	
	Nalidixic Acid	
	Tetracycline	

TEST FORM – genotypic characterisation

Genotypic characterisation of the test strains

Strain code:	Method used: If PCR-methods, additional information should be given below
Gene: ☐ Found ☐ Tested, not found	☐ Published method , reference:
	☐ In-house method
	Primer used 5'→3':
	Primer used 3'→5':
Gene: ☐ Found ☐ Tested, not found	☐ Published method , reference:
	☐ In-house method
	Primer used 5'→3':
	Primer used 3'→5':
Gene: ☐ Found ☐ Tested, not found	☐ Published method , reference:
	☐ In-house method
	Primer used 5'→3':
	Primer used 3'→5':
Gene: ☐ Found ☐ Tested, not found	☐ Published method , reference:
	☐ In-house method
	Primer used 5'→3':
	Primer used 3'→5':
Gene: ☐ Found ☐ Tested, not found	☐ Published method , reference:
	☐ In-house method
	Primer used 5'→3':
	Primer used 3'→5':

Comments:

INSTRUCTIONS FOR OPENING AND REVIVING LYOPHILISED CULTURES

Manual from Czech Collection of Microorganisms (CCM)
Masaryk University
Tvrdého 14
602 00 BRNO
Czech Republic

Lyophilised cultures are supplied in vacuum-sealed ampoules. Care should be taken in opening the ampoule. All instructions given below should be followed closely to ensure the safety of the person who opens the ampoule and to prevent contamination of the culture.

a. Check the number of the culture on the label inside the ampoule
b. Make a file cut on the ampoule near the middle of the plug
c. Disinfect the ampoule with alcohol-dampened gauze or alcohol-dampened cotton wool from just below the plug to the pointed end
d. Apply a red-hot glass rod to the file cut to crack the glass and allow air to enter slowly into the ampoule
e. Remove the pointed end of the ampoule into disinfectant
f. Add about 0.3 ml appropriate broth to the dried suspension using a sterile Pasteur pipette and mix carefully to avoid creating aerosols. Transfer the contents to one or more suitable solid and /or liquid media
g. Incubate the inoculated medium at appropriate conditions for several days
h. Autoclave or disinfect effectively the used Pasteur pipette, the plug and all the remains of the original ampoule before discarding

Please note that:

- Cultures should be grown on media and under conditions as recommended in the CCM catalogue
- Cultures may need at least one subculturing before they can be optimally used in experiments
- Unopened ampoules should be kept in a dark and cool place!

SUBCULTURE AND MAINTENANCE OF QUALITY CONTROL STRAINS

1.1 Purpose

Improper storage and repeated subculturing of bacteria can produce alterations in antimicrobial susceptibility test results. The Clinical and Laboratory Standards Institute (CLSI, formerly NCCLS) has published a guideline for Quality Control (QC) stock culture maintenance to ensure consistent antimicrobial susceptibility test results.

1.2 References

M100-S21, January 2011 (Performance Standards for Antimicrobial Susceptibility Testing)

M7-A8, January 2009 (Methods for Dilution Antimicrobial Susceptibility Test for Bacteria That Grow Aerobically; Approved Standard)

1.3 Definition of Terms

Reference Culture: A reference culture is a microorganism preparation that is acquired from a culture type collection.

Reference Stock Culture: A reference stock culture is a microorganism preparation that is derived from a reference culture. Guidelines and standards outline how reference stock cultures must be processed and stored.

Working Stock Cultures: A working stock culture is growth derived from a reference stock culture. Guidelines and standards outline how working stock cultures must be processed and how often they can be subcultured.

Subcultures (Passages): A subculture is simply the transfer of established microorganism growth on media to fresh media. The subsequent growth on the fresh media constitutes a subculture or passage. Growing a reference culture or reference stock culture from its preserved status (frozen or lyophilized) is not a subculture. The preserved microorganism is not in a stage of established growth until it is thawed or hydrated and grown for the first time

1.4 Important Considerations

- Do not use disc diffusion strains for MIC determination.
- Obtain QC strains from a reliable source such as ATCC
- CLSI requires that QC be performed either on the same day or weekly (only after 30 day QC validation)
- Any changes in materials or procedure must be validated with QC before implemented
- For example: Agar and broth methods may give different QC ranges for drugs such as glycopeptides, aminoglycosides and macrolides

- Periodically perform colony counts to check the inoculum preparation procedure
- Ideally, test values should be in the middle of the acceptable range
- Graphing QC data points over time can help identify changes in data helpful for troubleshooting problems

1.5 Storage of Reference Strains

Preparation of stock cultures

- Use a suitable stabilizer such as 50% fetal calf serum in broth, 10-15% glycerol in tryptic soy broth, defibrinated sheep blood or skim milk to prepare multiple aliquots.
- Store at -20°C, -70°C or liquid nitrogen. (Alternatively, freeze dry.)
- Before using rejuvenated strains for QC, subculture to check for purity and viability.

Working cultures

- Set up on agar slants with appropriate medium, store at 4-8°C and subculture weekly.
- Replace the working strain with a stock culture at least monthly.
- If a change in the organisms inherent susceptibility occurs, obtain a fresh stock culture or a new strain from a reference culture collection e.g. ATCC.

1.6 Frequency of Testing

Weekly vs. daily testing

Weekly testing is possible if the lab can demonstrate satisfactory performance with daily testing as follows:

- Documentation showing reference strain results from 30 consecutive test days were within the acceptable range.
- For each antimicrobial/organism combination, no more than 3 out of 30 MIC values may be outside the acceptable range.

When the above are fulfilled, each quality control strain may be tested once a week and whenever any reagent component is changed.

Corrective Actions

If an MIC is outside the range in weekly testing, corrective action is required as follows:

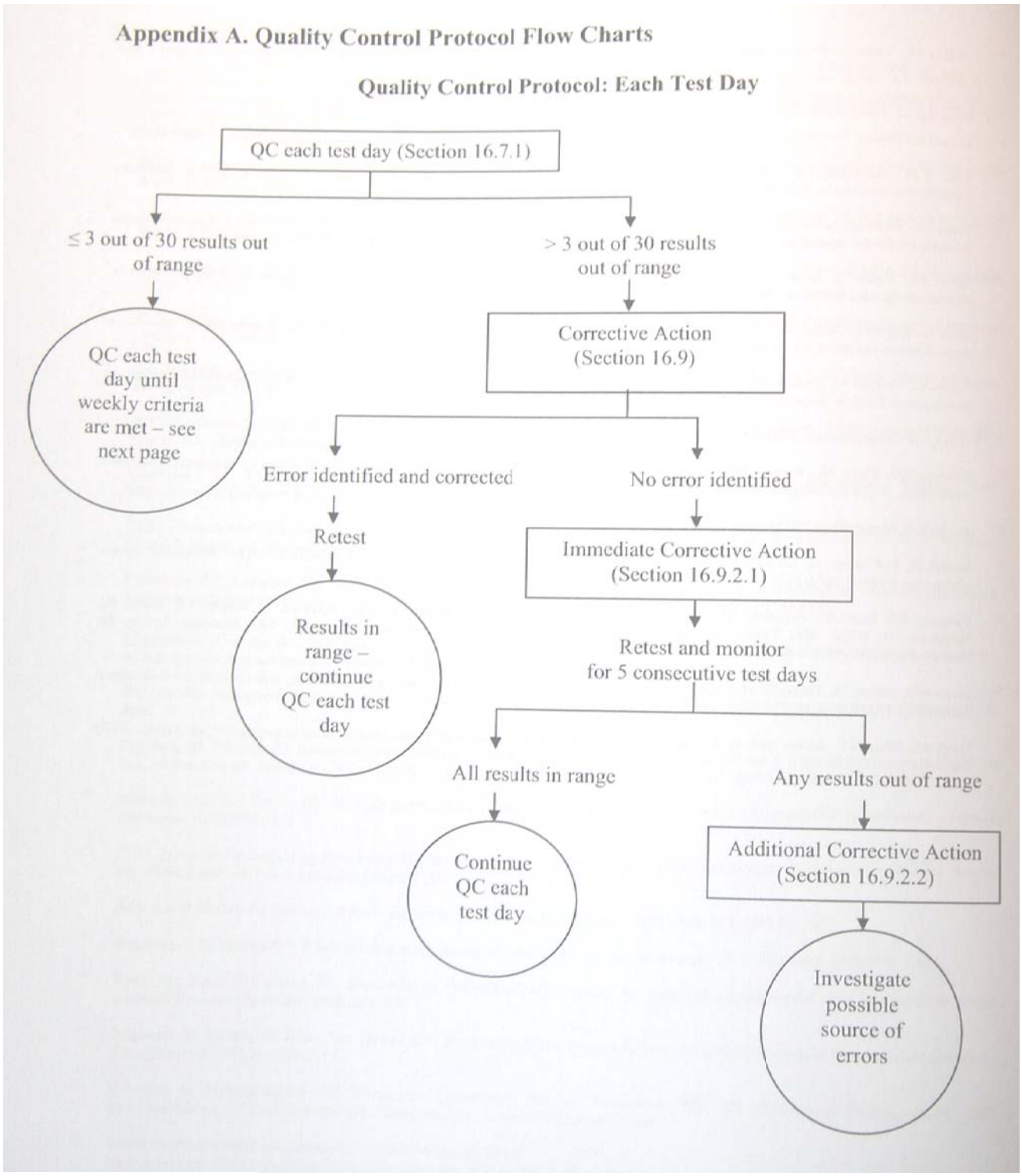
- Repeat the test if there is an obvious error e.g. wrong strain or incubation conditions used
- If there is no obvious error, return to daily control testing

The problem is considered resolved only after the reference strain is tested for 5 consecutive days and each drug/organism result is within specification on each day.

If the problem cannot be resolved, continue daily testing until the errors are identified.

Repeat the 30 days validation before resuming weekly testing.

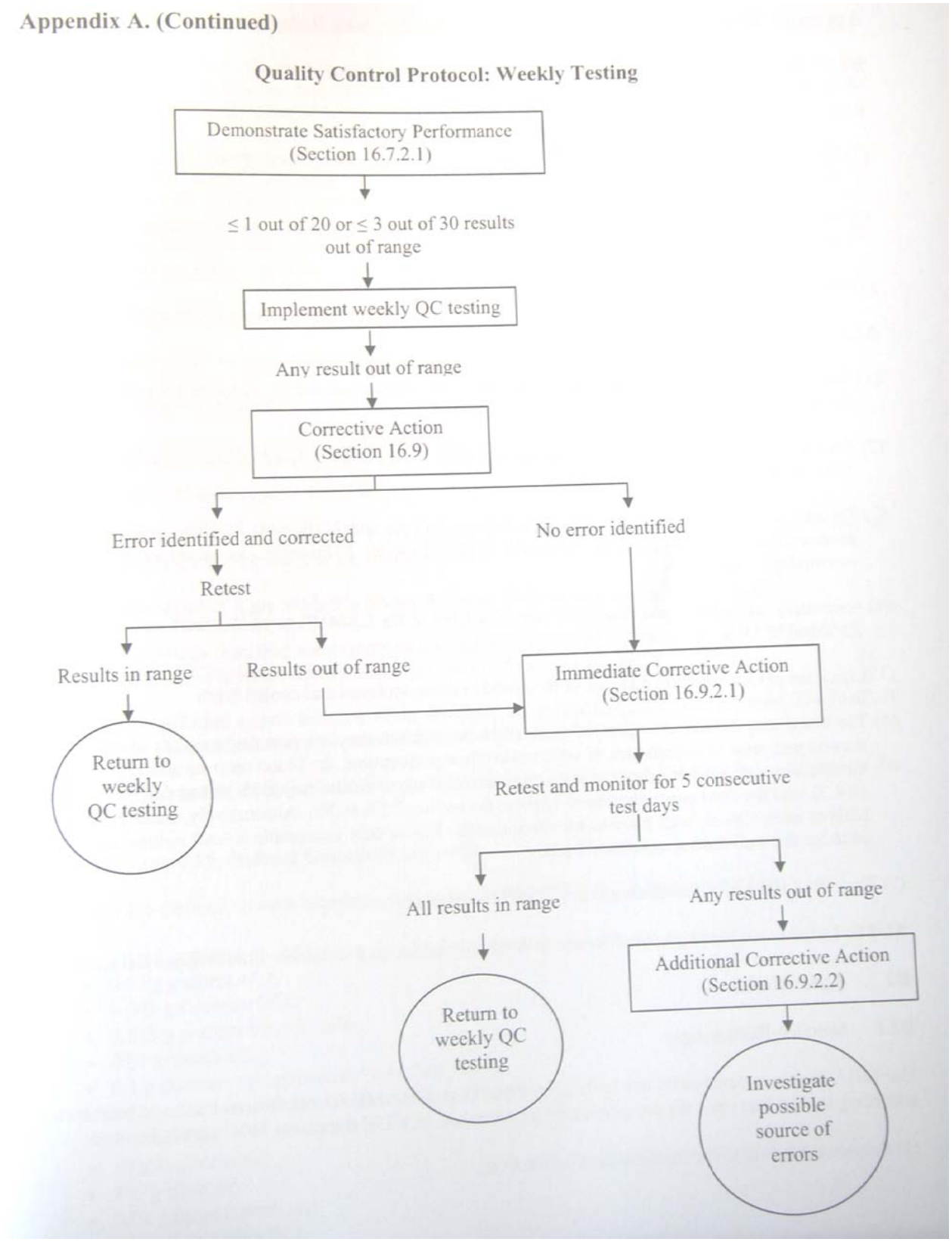
DAILY MIC QC CHART



Reference: CLSI M7-A8, page 44

WEEKLY MIC QC CHART

Appendix A. (Continued)



Reference: CLSI M7-A8, page 45

Quality Control ranges for ATCC reference strains

E. coli ATCC 25922	
Antimicrobial	**MIC**
Ampicillin, AMP	2-8
Azithromycin, AZT	none
Cefepime, FEP	0.015-0.12
Cefotaxime, FOT	0.03-0.12
Cefotaxime + clavulanic acid, F/C	none
Cefoxitin, FOX	2-8
Ceftazidime, CAZ	0.06-0.5
Ceftazidime + clavulanic acid, T/C	none
Chloramphenicol, CHL	2-8
Ciprofloxacin, CIP	0.004-0.016
Colistin, COL	0.25-2
Ertapenem, ETP	0.004-0.016
Gentamicin, GEN	0.25-1
Imipenem, IMI	0.06-0.25
Meropenem, MERO	0.008-0.06
Nalidixic acid, NAL	1-4
Sulfisoxazole, FIS	8-32
Temocillin, TRM	none
Tetracycline, TET	0.5-2
Tigecycline, TGC	0.03-0.25
Trimethoprim, TMP	0.5-2

MIC ranges (µg/mL) are according to CLSI M100 S24 (range for ciprofloxacin and ertapenem extended to include 0.016).

Campylobacter jejuni ATCC 33560				
Antimicrobial	**Microbroth (36-37°C/48h)**	**Microbroth (42°C/24h)**	**Agar dilution (36-37°C/48h)**	**Agar dilution (42°C/24h)**
Ciprofloxacin, CIP	0.06-0.25	0.03-0.12	0.12-1	0.06-0.5
Erythromycin, ERY	0.5-2	0.25-2	1-8	1-4
Gentamicin, GEN	0.5-2	0.25-2	0.5-2	0.5-4
Nalidixic acid, NAL	4-16	4-16	None	None
Tetracycline, TET	0.25-2	0.25-1	None	None

MIC ranges (µg/mL) are according to CLSI (VET01-S2)

Test results from the reference strain *E. coli* ATCC 25922

Lab no.	Panel	Antimicrobial	Operator	Value	Low limit	High limit	Mark	Method
1	Panel 1	Ampicillin	=	4	2	8	1	MIC
1	Panel 1	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
1	Panel 1	Ceftazidime	<=	0.5	0.06	0.5	1	MIC
1	Panel 1	Chloramphenicol	<=	8	2	8	1	MIC
1	Panel 1	Ciprofloxacin	<=	0.015	0.004	0.016	1	MIC
1	Panel 1	Colistin	<=	1	0.25	2	1	MIC
1	Panel 1	Gentamicin	<=	0.5	0.25	1	1	MIC
1	Panel 1	Meropenem	<=	0.03	0.008	0.06	1	MIC
1	Panel 1	Nalidixic acid	<=	4	1	4	1	MIC
1	Panel 1	Tetracycline	<=	2	0.5	2	1	MIC
1	Panel 1	Tigecycline	<=	0.25	0.03	0.25	1	MIC
1	Panel 1	Trimethoprim	=	0.5	0.5	2	1	MIC
1	Panel 2	Cefepime	<=	0.06	0.015	0.125	1	MIC
1	Panel 2	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
1	Panel 2	Cefoxitin	=	2	2	8	1	MIC
1	Panel 2	Ceftazidime	<=	0.25	0.06	0.5	1	MIC
1	Panel 2	Ertapenem	<=	0.015	0.004	0.016	1	MIC
1	Panel 2	Imipenem	=	0.25	0.06	0.25	1	MIC
1	Panel 2	Meropenem	<=	0.03	0.008	0.06	1	MIC
2	Panel 1	Ampicillin	=	4	2	8	1	MIC
2	Panel 1	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
2	Panel 1	Ceftazidime	<=	0.5	0.06	0.5	1	MIC
2	Panel 1	Chloramphenicol	<=	8	2	8	1	MIC
2	Panel 1	Ciprofloxacin	=	0.06	0.004	0.016	**0**	MIC
2	Panel 1	Colistin	<=	1	0.25	2	1	MIC
2	Panel 1	Gentamicin	<=	0.5	0.25	1	1	MIC
2	Panel 1	Meropenem	<=	0.03	0.008	0.06	1	MIC
2	Panel 1	Nalidixic acid	<=	4	1	4	1	MIC
2	Panel 1	Sulfisoxazole	=	32	8	32	1	MIC
2	Panel 1	Tetracycline	<=	2	0.5	2	1	MIC
2	Panel 1	Tigecycline	<=	0.25	0.03	0.25	1	MIC
2	Panel 1	Trimethoprim	=	5	0.5	2	**0**	MIC
2	Panel 2	Cefepime	<=	0.06	0.015	0.125	1	MIC
2	Panel 2	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
2	Panel 2	Cefoxitin	=	2	2	8	1	MIC
2	Panel 2	Ceftazidime	<=	0.25	0.06	0.5	1	MIC
2	Panel 2	Ertapenem	<=	0.015	0.004	0.016	1	MIC
2	Panel 2	Imipenem	<=	0.12	0.06	0.25	1	MIC
2	Panel 2	Meropenem	<=	0.03	0.008	0.06	1	MIC
4	Panel 1	Ampicillin	=	8	2	8	1	MIC
4	Panel 1	Cefotaxime	=	0.25	0.03	0.125	**0**	MIC
4	Panel 1	Ceftazidime	=	0.5	0.06	0.5	1	MIC
4	Panel 1	Chloramphenicol	=	8	2	8	1	MIC
4	Panel 1	Ciprofloxacin	=	0.015	0.004	0.016	1	MIC
4	Panel 1	Colistin	=	1	0.25	2	1	MIC
4	Panel 1	Gentamicin	=	0.5	0.25	1	1	MIC
4	Panel 1	Meropenem	=	0.03	0.008	0.06	1	MIC
4	Panel 1	Nalidixic acid	=	4	1	4	1	MIC
4	Panel 1	Sulfisoxazole	=	16	8	32	1	MIC
4	Panel 1	Tetracycline	=	2	0.5	2	1	MIC
4	Panel 1	Tigecycline	=	0.25	0.03	0.25	1	MIC
4	Panel 1	Trimethoprim	=	0.5	0.5	2	1	MIC
6	Panel 1	Ampicillin	=	4	2	8	1	MIC
6	Panel 1	Cefotaxime	<	0.25	0.03	0.125	1	MIC
6	Panel 1	Ceftazidime	<	0.5	0.06	0.5	1	MIC
6	Panel 1	Chloramphenicol	<	8	2	8	1	MIC
6	Panel 1	Ciprofloxacin	<	0.015	0.004	0.016	1	MIC
6	Panel 1	Colistin	<	1	0.25	2	1	MIC
6	Panel 1	Gentamicin	<	0.5	0.25	1	1	MIC
6	Panel 1	Meropenem	<	0.03	0.008	0.06	1	MIC
6	Panel 1	Nalidixic acid	<	4	1	4	1	MIC
6	Panel 1	Tetracycline	<	2	0.5	2	1	MIC
6	Panel 1	Tigecycline	<	0.25	0.03	0.25	1	MIC

Lab no.	Panel	Antimicrobial	Operator	Value	Low limit	High limit	Mark	Method
6	Panel 1	Trimethoprim	=	0.5	0.5	2	1	MIC
6	Panel 2	Cefepime	<	0.06	0.015	0.125	1	MIC
6	Panel 2	Cefotaxime	<	0.25	0.03	0.125	1	MIC
6	Panel 2	Cefoxitin	=	2	2	8	1	MIC
6	Panel 2	Ceftazidime	<	0.25	0.06	0.5	1	MIC
6	Panel 2	Ertapenem	<	0.015	0.004	0.016	1	MIC
6	Panel 2	Imipenem	=	0.25	0.06	0.25	1	MIC
6	Panel 2	Meropenem	<	0.03	0.008	0.06	1	MIC
9	Panel 1	Ampicillin	=	4	2	8	1	MIC
9	Panel 1	Ceftazidime	<=	5	0.06	0.5	1	MIC
9	Panel 1	Chloramphenicol	<=	8	2	8	1	MIC
9	Panel 1	Ciprofloxacin	<=	0.015	0.004	0.016	1	MIC
9	Panel 1	Colistin	<=	1	0.25	2	1	MIC
9	Panel 1	Gentamicin	<=	0.5	0.25	1	1	MIC
9	Panel 1	Meropenem	<=	0.03	0.008	0.06	1	MIC
9	Panel 1	Nalidixic acid	<=	4	1	4	1	MIC
9	Panel 1	Sulfisoxazole	=	16	8	32	1	MIC
9	Panel 1	Tetracycline	<=	2	0.5	2	1	MIC
9	Panel 1	Tigecycline	<=	0.25	0.03	0.25	1	MIC
9	Panel 1	Trimethoprim	=	1	0.5	2	1	MIC
9	Panel 2	Cefepime	<=	0.06	0.015	0.125	1	MIC
9	Panel 2	Cefoxitin	=	4	2	8	1	MIC
9	Panel 2	Ceftazidime	<=	0.25	0.06	0.5	1	MIC
9	Panel 2	Ertapenem	<=	0.015	0.004	0.016	1	MIC
9	Panel 2	Imipenem	<=	0.12	0.06	0.25	1	MIC
9	Panel 2	Meropenem	<=	0.03	0.008	0.06	1	MIC
11	Panel 1	Ampicillin	=	4	2	8	1	MIC
11	Panel 1	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
11	Panel 1	Ceftazidime	<=	0.25	0.06	0.5	1	MIC
11	Panel 1	Chloramphenicol	<=	8	2	8	1	MIC
11	Panel 1	Ciprofloxacin	<=	0.015	0.004	0.016	1	MIC
11	Panel 1	Colistin	<=	1	0.25	2	1	MIC
11	Panel 1	Gentamicin	<=	0.05	0.25	1	**0**	MIC
11	Panel 1	Meropenem	<=	0.03	0.008	0.06	1	MIC
11	Panel 1	Nalidixic acid	<=	4	1	4	1	MIC
11	Panel 1	Sulfisoxazole	=	32	8	32	1	MIC
11	Panel 1	Tetracycline	<=	2	0.5	2	1	MIC
11	Panel 1	Tigecycline	<=	0.25	0.03	0.25	1	MIC
11	Panel 1	Trimethoprim	=	0.5	0.5	2	1	MIC
11	Panel 2	Cefepime	<=	0.06	0.015	0.125	1	MIC
11	Panel 2	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
11	Panel 2	Cefoxitin	=	2	2	8	1	MIC
11	Panel 2	Ceftazidime	<=	0.25	0.06	0.5	1	MIC
11	Panel 2	Ertapenem	<=	0.015	0.004	0.016	1	MIC
11	Panel 2	Imipenem	<=	0.12	0.06	0.25	1	MIC
11	Panel 2	Meropenem	<=	0.03	0.008	0.06	1	MIC
12	Panel 1	Ampicillin	=	4	2	8	1	MIC
12	Panel 1	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
12	Panel 1	Ceftazidime	<=	0.5	0.06	0.5	1	MIC
12	Panel 1	Chloramphenicol	<=	8	2	8	1	MIC
12	Panel 1	Ciprofloxacin	<=	0.015	0.004	0.016	1	MIC
12	Panel 1	Colistin	<=	1	0.25	2	1	MIC
12	Panel 1	Gentamicin	<=	0.5	0.25	1	1	MIC
12	Panel 1	Meropenem	<=	0.03	0.008	0.06	1	MIC
12	Panel 1	Nalidixic acid	<=	4	1	4	1	MIC
12	Panel 1	Tetracycline	<=	2	0.5	2	1	MIC
12	Panel 1	Tigecycline	<=	0.25	0.03	0.25	1	MIC
12	Panel 1	Trimethoprim	=	1	0.5	2	1	MIC
12	Panel 2	Cefepime	<=	0.06	0.015	0.125	1	MIC
12	Panel 2	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
12	Panel 2	Cefoxitin	=	4	2	8	1	MIC
12	Panel 2	Ceftazidime	<=	0.25	0.06	0.5	1	MIC
12	Panel 2	Ertapenem	<=	0.015	0.004	0.016	1	MIC
12	Panel 2	Imipenem	=	0.25	0.06	0.25	1	MIC
12	Panel 2	Meropenem	<=	0.03	0.008	0.06	1	MIC

Lab no.	Panel	Antimicrobial	Operator	Value	Low limit	High limit	Mark	Method
13	Panel 1	Ampicillin	=	4	2	8	1	MIC
13	Panel 1	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
13	Panel 1	Ceftazidime	<=	0.5	0.06	0.5	1	MIC
13	Panel 1	Chloramphenicol	<=	8	2	8	1	MIC
13	Panel 1	Ciprofloxacin	<=	0.015	0.004	0.016	1	MIC
13	Panel 1	Colistin	<=	1	0.25	2	1	MIC
13	Panel 1	Gentamicin	<=	0.5	0.25	1	1	MIC
13	Panel 1	Meropenem	<=	0.03	0.008	0.06	1	MIC
13	Panel 1	Nalidixic acid	<=	4	1	4	1	MIC
13	Panel 1	Sulfisoxazole	=	32	8	32	1	MIC
13	Panel 1	Tetracycline	<=	2	0.5	2	1	MIC
13	Panel 1	Tigecycline	<=	0.25	0.03	0.25	1	MIC
13	Panel 1	Trimethoprim	=	0.5	0.5	2	1	MIC
13	Panel 2	Cefepime	<=	0.06	0.015	0.125	1	MIC
13	Panel 2	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
13	Panel 2	Cefoxitin	=	2	2	8	1	MIC
13	Panel 2	Ceftazidime	<=	0.25	0.06	0.5	1	MIC
13	Panel 2	Ertapenem	<=	0.015	0.004	0.016	1	MIC
13	Panel 2	Imipenem	<=	0.12	0.06	0.25	1	MIC
13	Panel 2	Meropenem	<=	0.03	0.008	0.06	1	MIC
16	Panel 1	Ampicillin	=	4	2	8	1	MIC
16	Panel 1	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
16	Panel 1	Ceftazidime	<=	0.5	0.06	0.5	1	MIC
16	Panel 1	Chloramphenicol	<=	8	2	8	1	MIC
16	Panel 1	Ciprofloxacin	<=	0.015	0.004	0.016	1	MIC
16	Panel 1	Colistin	<=	1	0.25	2	1	MIC
16	Panel 1	Gentamicin	=	1	0.25	1	1	MIC
16	Panel 1	Meropenem	<=	0.03	0.008	0.06	1	MIC
16	Panel 1	Nalidixic acid	<=	4	1	4	1	MIC
16	Panel 1	Tetracycline	<=	2	0.5	2	1	MIC
16	Panel 1	Tigecycline	<=	0.25	0.03	0.25	1	MIC
16	Panel 1	Trimethoprim	=	1	0.5	2	1	MIC
16	Panel 2	Cefepime	<=	0.06	0.015	0.125	1	MIC
16	Panel 2	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
16	Panel 2	Cefoxitin	=	4	2	8	1	MIC
16	Panel 2	Ceftazidime	<=	0.25	0.06	0.5	1	MIC
16	Panel 2	Ertapenem	<=	0.015	0.004	0.016	1	MIC
16	Panel 2	Imipenem	<=	0.12	0.06	0.25	1	MIC
16	Panel 2	Meropenem	<=	0.03	0.008	0.06	1	MIC
17	Panel 1	Ampicillin	=	4	2	8	1	MIC
17	Panel 1	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
17	Panel 1	Ceftazidime	<=	0.5	0.06	0.5	1	MIC
17	Panel 1	Chloramphenicol	<=	8	2	8	1	MIC
17	Panel 1	Ciprofloxacin	<=	0.015	0.004	0.016	1	MIC
17	Panel 1	Colistin	<=	1	0.25	2	1	MIC
17	Panel 1	Gentamicin	<=	0.5	0.25	1	1	MIC
17	Panel 1	Meropenem	<=	0.03	0.008	0.06	1	MIC
17	Panel 1	Nalidixic acid	<=	4	1	4	1	MIC
17	Panel 1	Sulfisoxazole	=	32	8	32	1	MIC
17	Panel 1	Tetracycline	<=	2	0.5	2	1	MIC
17	Panel 1	Tigecycline	<=	0.25	0.03	0.25	1	MIC
17	Panel 1	Trimethoprim	=	1	0.5	2	1	MIC
17	Panel 2	Cefepime	<=	0.06	0.015	0.125	1	MIC
17	Panel 2	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
17	Panel 2	Cefoxitin	=	4	2	8	1	MIC
17	Panel 2	Ceftazidime	<=	0.25	0.06	0.5	1	MIC
17	Panel 2	Ertapenem	<=	0.015	0.004	0.016	1	MIC
17	Panel 2	Imipenem	<=	0.125	0.06	0.25	1	MIC
17	Panel 2	Meropenem	<=	0.03	0.008	0.06	1	MIC
18	Panel 1	Ampicillin	=	4	2	8	1	MIC
18	Panel 1	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
18	Panel 1	Ceftazidime	<=	0.5	0.06	0.5	1	MIC
18	Panel 1	Chloramphenicol	<=	8	2	8	1	MIC
18	Panel 1	Ciprofloxacin	<=	0.015	0.004	0.016	1	MIC
18	Panel 1	Colistin	<=	1	0.25	2	1	MIC

Lab no.	Panel	Antimicrobial	Operator	Value	Low limit	High limit	Mark	Method
18	Panel 1	Gentamicin	<=	0.5	0.25	1	1	MIC
18	Panel 1	Meropenem	<=	0.03	0.008	0.06	1	MIC
18	Panel 1	Nalidixic acid	<=	4	1	4	1	MIC
18	Panel 1	Sulfisoxazole	=	32	8	32	1	MIC
18	Panel 1	Tetracycline	<=	2	0.5	2	1	MIC
18	Panel 1	Tigecycline	<=	0.25	0.03	0.25	1	MIC
18	Panel 1	Trimethoprim	=	5	0.5	2	**0**	MIC
19	Panel 1	Ampicillin	=	4	2	8	1	MIC
19	Panel 1	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
19	Panel 1	Ceftazidime	<=	0.5	0.06	0.5	1	MIC
19	Panel 1	Chloramphenicol	<=	8	2	8	1	MIC
19	Panel 1	Ciprofloxacin	<=	0.015	0.004	0.016	1	MIC
19	Panel 1	Colistin	<=	1	0.25	2	1	MIC
19	Panel 1	Gentamicin	<=	0.5	0.25	1	1	MIC
19	Panel 1	Meropenem	<=	0.03	0.008	0.06	1	MIC
19	Panel 1	Nalidixic acid	<=	4	1	4	1	MIC
19	Panel 1	Sulfisoxazole	=	32	8	32	1	MIC
19	Panel 1	Tetracycline	<=	2	0.5	2	1	MIC
19	Panel 1	Tigecycline	<=	0.25	0.03	0.25	1	MIC
19	Panel 1	Trimethoprim	=	1	0.5	2	1	MIC
20	Panel 1	Ampicillin	=	8	2	8	1	MIC
20	Panel 1	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
20	Panel 1	Ceftazidime	<=	0.5	0.06	0.5	1	MIC
20	Panel 1	Chloramphenicol	<=	8	2	8	1	MIC
20	Panel 1	Ciprofloxacin	<=	0.015	0.004	0.016	1	MIC
20	Panel 1	Colistin	<=	1	0.25	2	1	MIC
20	Panel 1	Gentamicin	<=	0.5	0.25	1	1	MIC
20	Panel 1	Meropenem	<=	0.03	0.008	0.06	1	MIC
20	Panel 1	Nalidixic acid	<=	4	1	4	1	MIC
20	Panel 1	Sulfisoxazole	=	16	8	32	1	MIC
20	Panel 1	Tetracycline	<=	2	0.5	2	1	MIC
20	Panel 1	Tigecycline	<=	0.25	0.03	0.25	1	MIC
20	Panel 1	Trimethoprim	=	0.5	0.5	2	1	MIC
20	Panel 2	Cefepime	<=	0.06	0.015	0.125	1	MIC
20	Panel 2	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
20	Panel 2	Cefoxitin	=	4	2	8	1	MIC
20	Panel 2	Ceftazidime	<=	0.25	0.06	0.5	1	MIC
20	Panel 2	Ertapenem	<=	0.015	0.004	0.016	1	MIC
20	Panel 2	Imipenem	<=	0.12	0.06	0.25	1	MIC
20	Panel 2	Meropenem	<=	0.03	0.008	0.06	1	MIC
21	Panel 1	Ampicillin	=	2	2	8	1	MIC
21	Panel 1	Cefotaxime	<	0.25	0.03	0.125	1	MIC
21	Panel 1	Ceftazidime	<=	0.5	0.06	0.5	1	MIC
21	Panel 1	Chloramphenicol	<=	8	2	8	1	MIC
21	Panel 1	Ciprofloxacin	<=	0.015	0.004	0.016	1	MIC
21	Panel 1	Colistin	=	1	0.25	2	1	MIC
21	Panel 1	Gentamicin	=	0.5	0.25	1	1	MIC
21	Panel 1	Meropenem	=	0.03	0.008	0.06	1	MIC
21	Panel 1	Nalidixic acid	<=	4	1	4	1	MIC
21	Panel 1	Sulfisoxazole	=	16	8	32	1	MIC
21	Panel 1	Tetracycline	<=	2	0.5	2	1	MIC
21	Panel 1	Tigecycline	=	0.25	0.03	0.25	1	MIC
21	Panel 1	Trimethoprim	=	0.5	0.5	2	1	MIC
21	Panel 2	Cefepime	=	0.12	0.015	0.125	1	MIC
21	Panel 2	Cefotaxime	<	0.25	0.03	0.125	1	MIC
21	Panel 2	Cefoxitin	=	2	2	8	1	MIC
21	Panel 2	Ceftazidime	=	0.25	0.06	0.5	1	MIC
21	Panel 2	Ertapenem	<=	0.015	0.004	0.016	1	MIC
21	Panel 2	Imipenem	=	0.12	0.06	0.25	1	MIC
21	Panel 2	Meropenem	=	0.03	0.008	0.06	1	MIC
22	Panel 1	Ampicillin	=	4	2	8	1	MIC
22	Panel 1	Cefotaxime	<	0.25	0.03	0.125	1	MIC
22	Panel 1	Ceftazidime	<	0.5	0.06	0.5	1	MIC
22	Panel 1	Chloramphenicol	<	8	2	8	1	MIC
22	Panel 1	Ciprofloxacin	<	0.015	0.004	0.016	1	MIC

Lab no.	Panel	Antimicrobial	Operator	Value	Low limit	High limit	Mark	Method
22	Panel 1	Colistin	<	1	0.25	2	1	MIC
22	Panel 1	Gentamicin	=	1	0.25	1	1	MIC
22	Panel 1	Meropenem	<	0.03	0.008	0.06	1	MIC
22	Panel 1	Nalidixic acid	<	4	1	4	1	MIC
22	Panel 1	Tetracycline	<	2	0.5	2	1	MIC
22	Panel 1	Tigecycline	<	0.25	0.03	0.25	1	MIC
22	Panel 1	Trimethoprim	=	0.5	0.5	2	1	MIC
22	Panel 2	Cefoxitin	=	4	2	8	1	MIC
22	Panel 2	Ceftazidime	<	0.5	0.06	0.5	1	MIC
22	Panel 2	Ertapenem	<	0.015	0.004	0.016	1	MIC
22	Panel 2	Imipenem	<	0.12	0.06	0.25	1	MIC
22	Panel 2	Meropenem	<	0.03	0.008	0.06	1	MIC
23	Panel 1	Ampicillin	=	4	2	8	1	MIC
23	Panel 1	Cefotaxime	<	0.25	0.03	0.125	1	MIC
23	Panel 1	Chloramphenicol	<	8	2	8	1	MIC
23	Panel 1	Ciprofloxacin	<	0.015	0.004	0.016	1	MIC
23	Panel 1	Colistin	<	1	0.25	2	1	MIC
23	Panel 1	Gentamicin	=	1	0.25	1	1	MIC
23	Panel 1	Meropenem	<	0.03	0.008	0.06	1	MIC
23	Panel 1	Nalidixic acid	<	4	1	4	1	MIC
23	Panel 1	Sulfisoxazole	=	16	8	32	1	MIC
23	Panel 1	Tetracycline	<	2	0.5	2	1	MIC
23	Panel 1	Trimethoprim	=	0.5	0.5	2	1	MIC
23	Panel 2	Cefepime	<	0.06	0.015	0.125	1	MIC
23	Panel 2	Imipenem	<	0.12	0.06	0.25	1	MIC
23	Panel 2	Meropenem	<	0.03	0.008	0.06	1	MIC
25	Panel 1	Ampicillin	=	4	2	8	1	MIC
25	Panel 1	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
25	Panel 1	Ceftazidime	<=	0.5	0.06	0.5	1	MIC
25	Panel 1	Chloramphenicol	<=	8	2	8	1	MIC
25	Panel 1	Ciprofloxacin	<=	0.015	0.004	0.016	1	MIC
25	Panel 1	Colistin	<=	1	0.25	2	1	MIC
25	Panel 1	Gentamicin	=	1	0.25	1	1	MIC
25	Panel 1	Meropenem	<=	0.03	0.008	0.06	1	MIC
25	Panel 1	Nalidixic acid	<=	4	1	4	1	MIC
25	Panel 1	Sulfisoxazole	<=	8	8	32	1	MIC
25	Panel 1	Tetracycline	<=	2	0.5	2	1	MIC
25	Panel 1	Tigecycline	<=	0.25	0.03	0.25	1	MIC
25	Panel 1	Trimethoprim	=	0.5	0.5	2	1	MIC
26	Panel 1	Ampicillin	=	2	2	8	1	MIC
26	Panel 1	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
26	Panel 1	Ceftazidime	<=	0.5	0.06	0.5	1	MIC
26	Panel 1	Chloramphenicol	<=	8	2	8	1	MIC
26	Panel 1	Ciprofloxacin	<=	0.015	0.004	0.016	1	MIC
26	Panel 1	Colistin	<=	1	0.25	2	1	MIC
26	Panel 1	Gentamicin	<=	0.5	0.25	1	1	MIC
26	Panel 1	Meropenem	<=	0.03	0.008	0.06	1	MIC
26	Panel 1	Nalidixic acid	<=	4	1	4	1	MIC
26	Panel 1	Tetracycline	<=	2	0.5	2	1	MIC
26	Panel 1	Tigecycline	<=	0.25	0.03	0.25	1	MIC
26	Panel 1	Trimethoprim	=	0.5	0.5	2	1	MIC
29	Panel 1	Ampicillin	=	4	2	8	1	MIC
29	Panel 1	Cefotaxime	=	0.12	0.03	0.125	1	MIC
29	Panel 1	Ceftazidime	=	0.5	0.06	0.5	1	MIC
29	Panel 1	Chloramphenicol	<	8	2	8	1	MIC
29	Panel 1	Ciprofloxacin	<	0.015	0.004	0.016	1	MIC
29	Panel 1	Colistin	=	1	0.25	2	1	MIC
29	Panel 1	Gentamicin	=	0.5	0.25	1	1	MIC
29	Panel 1	Meropenem	<	0.03	0.008	0.06	1	MIC
29	Panel 1	Nalidixic acid	<	4	1	4	1	MIC
29	Panel 1	Tetracycline	=	2	0.5	2	1	MIC
29	Panel 1	Trimethoprim	=	0.5	0.5	2	1	MIC
29	Panel 2	Cefepime	=	0.06	0.015	0.125	1	MIC
29	Panel 2	Ertapenem	<	0.015	0.004	0.016	1	MIC
29	Panel 2	Imipenem	=	0.25	0.06	0.25	1	MIC

Lab no.	Panel	Antimicrobial	Operator	Value	Low limit	High limit	Mark	Method
29	Panel 2	Meropenem	=	0.03	0.008	0.06	1	MIC
30	Panel 1	Ampicillin	=	4	2	8	1	MIC
30	Panel 1	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
30	Panel 1	Ceftazidime	<=	0.5	0.06	0.5	1	MIC
30	Panel 1	Chloramphenicol	<=	8	2	8	1	MIC
30	Panel 1	Ciprofloxacin	<=	0.015	0.004	0.016	1	MIC
30	Panel 1	Colistin	<=	1	0.25	2	1	MIC
30	Panel 1	Gentamicin	<=	0.5	0.25	1	1	MIC
30	Panel 1	Meropenem	<=	0.03	0.008	0.06	1	MIC
30	Panel 1	Nalidixic acid	<=	4	1	4	1	MIC
30	Panel 1	Sulfisoxazole	=	16	8	32	1	MIC
30	Panel 1	Tetracycline	<=	2	0.5	2	1	MIC
30	Panel 1	Tigecycline	<=	0.25	0.03	0.25	1	MIC
30	Panel 1	Trimethoprim	=	0.5	0.5	2	1	MIC
30	Panel 2	Cefepime	<=	0.06	0.015	0.125	1	MIC
30	Panel 2	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
30	Panel 2	Cefoxitin	=	4	2	8	1	MIC
30	Panel 2	Ceftazidime	<=	0.25	0.06	0.5	1	MIC
30	Panel 2	Ertapenem	<=	0.015	0.004	0.016	1	MIC
30	Panel 2	Imipenem	<=	0.12	0.06	0.25	1	MIC
30	Panel 2	Meropenem	<=	0.03	0.008	0.06	1	MIC
32	Panel 1	Ampicillin	=	4	2	8	1	MIC
32	Panel 1	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
32	Panel 1	Ceftazidime	<=	0.5	0.06	0.5	1	MIC
32	Panel 1	Chloramphenicol	<=	8	2	8	1	MIC
32	Panel 1	Ciprofloxacin	<=	0.015	0.004	0.016	1	MIC
32	Panel 1	Colistin	=	2	0.25	2	1	MIC
32	Panel 1	Gentamicin	=	1	0.25	1	1	MIC
32	Panel 1	Meropenem	<=	0.03	0.008	0.06	1	MIC
32	Panel 1	Nalidixic acid	<=	4	1	4	1	MIC
32	Panel 1	Sulfisoxazole	=	32	8	32	1	MIC
32	Panel 1	Tetracycline	<=	2	0.5	2	1	MIC
32	Panel 1	Tigecycline	<=	0.25	0.03	0.25	1	MIC
32	Panel 1	Trimethoprim	=	1	0.5	2	1	MIC
32	Panel 2	Cefepime	<=	0.06	0.015	0.125	1	MIC
32	Panel 2	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
32	Panel 2	Cefoxitin	=	2	2	8	1	MIC
32	Panel 2	Ceftazidime	=	0.5	0.06	0.5	1	MIC
32	Panel 2	Ertapenem	<=	0.015	0.004	0.016	1	MIC
32	Panel 2	Imipenem	=	0.25	0.06	0.25	1	MIC
32	Panel 2	Meropenem	<=	0.03	0.008	0.06	1	MIC
33	Panel 1	Ampicillin	=	4	2	8	1	MIC
33	Panel 1	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
33	Panel 1	Ceftazidime	<=	0.5	0.06	0.5	1	MIC
33	Panel 1	Chloramphenicol	<=	8	2	8	1	MIC
33	Panel 1	Ciprofloxacin	<=	0.015	0.004	0.016	1	MIC
33	Panel 1	Colistin	<=	1	0.25	2	1	MIC
33	Panel 1	Gentamicin	<=	0.5	0.25	1	1	MIC
33	Panel 1	Meropenem	<=	0.03	0.008	0.06	1	MIC
33	Panel 1	Nalidixic acid	<=	4	1	4	1	MIC
33	Panel 1	Sulfisoxazole	=	32	8	32	1	MIC
33	Panel 1	Tetracycline	<=	2	0.5	2	1	MIC
33	Panel 1	Tigecycline	<=	0.25	0.03	0.25	1	MIC
33	Panel 1	Trimethoprim	=	1	0.5	2	1	MIC
33	Panel 2	Cefepime	<=	0.06	0.015	0.125	1	MIC
33	Panel 2	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
33	Panel 2	Cefoxitin	=	2	2	8	1	MIC
33	Panel 2	Ceftazidime	<=	0.25	0.06	0.5	1	MIC
33	Panel 2	Ertapenem	<=	0.015	0.004	0.016	1	MIC
33	Panel 2	Imipenem	<=	0.12	0.06	0.25	1	MIC
33	Panel 2	Meropenem	<=	0.03	0.008	0.06	1	MIC
34	Panel 1	Ampicillin	=	4	2	8	1	MIC
34	Panel 1	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
34	Panel 1	Ceftazidime	<=	0.5	0.06	0.5	1	MIC
34	Panel 1	Chloramphenicol	<=	8	2	8	1	MIC

Lab no.	Panel	Antimicrobial	Operator	Value	Low limit	High limit	Mark	Method
34	Panel 1	Ciprofloxacin	<=	0.015	0.004	0.016	1	MIC
34	Panel 1	Colistin	<=	1	0.25	2	1	MIC
34	Panel 1	Gentamicin	<=	0.5	0.25	1	1	MIC
34	Panel 1	Meropenem	<=	0.03	0.008	0.06	1	MIC
34	Panel 1	Nalidixic acid	<=	4	1	4	1	MIC
34	Panel 1	Sulfisoxazole	=	16	8	32	1	MIC
34	Panel 1	Tetracycline	<=	2	0.5	2	1	MIC
34	Panel 1	Tigecycline	<=	0.25	0.03	0.25	1	MIC
34	Panel 1	Trimethoprim	=	0.5	0.5	2	1	MIC
34	Panel 2	Cefepime	<=	0.06	0.015	0.125	1	MIC
34	Panel 2	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
34	Panel 2	Cefoxitin	=	4	2	8	1	MIC
34	Panel 2	Ceftazidime	<=	0.25	0.06	0.5	1	MIC
34	Panel 2	Ertapenem	<=	0.015	0.004	0.016	1	MIC
34	Panel 2	Imipenem	<=	0.12	0.06	0.25	1	MIC
34	Panel 2	Meropenem	<=	0.03	0.008	0.06	1	MIC
36	Panel 1	Ampicillin	=	4	2	8	1	MIC
36	Panel 1	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
36	Panel 1	Ceftazidime	<=	0.5	0.06	0.5	1	MIC
36	Panel 1	Chloramphenicol	<=	8	2	8	1	MIC
36	Panel 1	Ciprofloxacin	<=	0.015	0.004	0.016	1	MIC
36	Panel 1	Colistin	<=	1	0.25	2	1	MIC
36	Panel 1	Gentamicin	<=	0.5	0.25	1	1	MIC
36	Panel 1	Meropenem	<=	0.03	0.008	0.06	1	MIC
36	Panel 1	Nalidixic acid	<=	4	1	4	1	MIC
36	Panel 1	Sulfisoxazole	<=	8	8	32	1	MIC
36	Panel 1	Tetracycline	<=	2	0.5	2	1	MIC
36	Panel 1	Tigecycline	<=	0.25	0.03	0.25	1	MIC
36	Panel 1	Trimethoprim	<=	0.25	0.5	2	**0**	MIC
36	Panel 2	Cefepime	<=	0.06	0.015	0.125	1	MIC
36	Panel 2	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
36	Panel 2	Cefoxitin	=	4	2	8	1	MIC
36	Panel 2	Ceftazidime	<=	0.25	0.06	0.5	1	MIC
36	Panel 2	Ertapenem	<=	0.015	0.004	0.016	1	MIC
36	Panel 2	Imipenem	<=	0.12	0.06	0.25	1	MIC
36	Panel 2	Meropenem	<=	0.03	0.008	0.06	1	MIC
37	Panel 1	Ampicillin	=	4	2	8	1	AGA
37	Panel 1	Cefotaxime	<=	0.25	0.03	0.125	1	AGA
37	Panel 1	Ceftazidime	<=	0.5	0.06	0.5	1	AGA
37	Panel 1	Chloramphenicol	<=	8	2	8	1	AGA
37	Panel 1	Ciprofloxacin	<=	0.015	0.004	0.016	1	AGA
37	Panel 1	Colistin	<=	1	0.25	2	1	AGA
37	Panel 1	Gentamicin	<=	0.5	0.25	1	1	AGA
37	Panel 1	Meropenem	<=	0.03	0.008	0.06	1	AGA
37	Panel 1	Nalidixic acid	<=	4	1	4	1	AGA
37	Panel 1	Tetracycline	<=	2	0.5	2	1	AGA
37	Panel 1	Tigecycline	<=	0.25	0.03	0.25	1	AGA
37	Panel 1	Trimethoprim	=	0.5	0.5	2	1	AGA
37	Panel 2	Cefepime	=	0.125	0.015	0.125	1	AGA
37	Panel 2	Cefotaxime	<=	0.25	0.03	0.125	1	AGA
37	Panel 2	Cefoxitin	=	4	2	8	1	AGA
37	Panel 2	Ceftazidime	<=	0.25	0.06	0.5	1	AGA
37	Panel 2	Ertapenem	<=	0.015	0.004	0.016	1	AGA
37	Panel 2	Imipenem	<=	0.125	0.06	0.25	1	AGA
37	Panel 2	Meropenem	<=	0.03	0.008	0.06	1	AGA
38	Panel 1	Ampicillin	=	4	2	8	1	MIC
38	Panel 1	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
38	Panel 1	Ceftazidime	<=	0.5	0.06	0.5	1	MIC
38	Panel 1	Chloramphenicol	<=	8	2	8	1	MIC
38	Panel 1	Ciprofloxacin	<=	0.015	0.004	0.016	1	MIC
38	Panel 1	Colistin	=	1	0.25	2	1	MIC
38	Panel 1	Gentamicin	<=	0.5	0.25	1	1	MIC
38	Panel 1	Meropenem	<=	0.03	0.008	0.06	1	MIC
38	Panel 1	Nalidixic acid	<=	4	1	4	1	MIC
38	Panel 1	Sulfisoxazole	=	64	8	32	**0**	MIC

Lab no.	Panel	Antimicrobial	Operator	Value	Low limit	High limit	Mark	Method
38	Panel 1	Tetracycline	<=	2	0.5	2	1	MIC
38	Panel 1	Tigecycline	<=	0.25	0.03	0.25	1	MIC
38	Panel 1	Trimethoprim	<=	0.25	0.5	2	**0**	MIC
38	Panel 2	Cefepime	<=	0.06	0.015	0.125	1	MIC
38	Panel 2	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
38	Panel 2	Cefoxitin	=	2	2	8	1	MIC
38	Panel 2	Ceftazidime	<=	0.25	0.06	0.5	1	MIC
38	Panel 2	Ertapenem	<=	0.015	0.004	0.016	1	MIC
38	Panel 2	Imipenem	=	0.25	0.06	0.25	1	MIC
38	Panel 2	Meropenem	<=	0.03	0.008	0.06	1	MIC
39	Panel 1	Ampicillin	=	4	2	8	1	MIC
39	Panel 1	Cefotaxime	=	0.06	0.03	0.125	1	MIC
39	Panel 1	Ceftazidime	=	0.5	0.06	0.5	1	MIC
39	Panel 1	Chloramphenicol	=	4	2	8	1	MIC
39	Panel 1	Ciprofloxacin	=	0.016	0.004	0.016	1	MIC
39	Panel 1	Colistin	<=	0.5	0.25	2	1	MIC
39	Panel 1	Gentamicin	=	0.5	0.25	1	1	MIC
39	Panel 1	Nalidixic acid	=	2	1	4	1	MIC
39	Panel 1	Tetracycline	<=	1	0.5	2	1	MIC
39	Panel 1	Trimethoprim	=	1	0.5	2	1	MIC
40	Panel 1	Ampicillin	=	4	2	8	1	MIC
40	Panel 1	Cefotaxime	=	0.12	0.03	0.125	1	MIC
40	Panel 1	Ceftazidime	=	0.5	0.06	0.5	1	MIC
40	Panel 1	Chloramphenicol	=	8	2	8	1	MIC
40	Panel 1	Ciprofloxacin	=	0.015	0.004	0.016	1	MIC
40	Panel 1	Colistin	=	1	0.25	2	1	MIC
40	Panel 1	Gentamicin	=	0.5	0.25	1	1	MIC
40	Panel 1	Meropenem	=	0.03	0.008	0.06	1	MIC
40	Panel 1	Nalidixic acid	=	4	1	4	1	MIC
40	Panel 1	Sulfisoxazole	=	16	8	32	1	MIC
40	Panel 1	Tetracycline	=	2	0.5	2	1	MIC
40	Panel 1	Tigecycline	=	0.25	0.03	0.25	1	MIC
40	Panel 1	Trimethoprim	=	0.5	0.5	2	1	MIC
40	Panel 2	Cefepime	=	0.12	0.015	0.125	1	MIC
40	Panel 2	Cefotaxime	=	0.12	0.03	0.125	1	MIC
40	Panel 2	Cefoxitin	=	4	2	8	1	MIC
40	Panel 2	Ceftazidime	=	0.5	0.06	0.5	1	MIC
40	Panel 2	Ertapenem	=	0.015	0.004	0.016	1	MIC
40	Panel 2	Imipenem	=	0.25	0.06	0.25	1	MIC
40	Panel 2	Meropenem	=	0.06	0.008	0.06	1	MIC
41	Panel 1	Ampicillin	=	2	2	8	1	MIC
41	Panel 1	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
41	Panel 1	Ceftazidime	<=	0.5	0.06	0.5	1	MIC
41	Panel 1	Chloramphenicol	<=	8	2	8	1	MIC
41	Panel 1	Ciprofloxacin	<=	0.015	0.004	0.016	1	MIC
41	Panel 1	Colistin	<=	1	0.25	2	1	MIC
41	Panel 1	Gentamicin	<=	0.5	0.25	1	1	MIC
41	Panel 1	Meropenem	<=	0.03	0.008	0.06	1	MIC
41	Panel 1	Nalidixic acid	<=	4	1	4	1	MIC
41	Panel 1	Tetracycline	<=	2	0.5	2	1	MIC
41	Panel 1	Tigecycline	<=	0.25	0.03	0.25	1	MIC
41	Panel 1	Trimethoprim	=	0.5	0.5	2	1	MIC
41	Panel 2	Cefepime	<=	0.06	0.015	0.125	1	MIC
41	Panel 2	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
41	Panel 2	Cefoxitin	=	1	2	8	**0**	MIC
41	Panel 2	Ceftazidime	=	0.5	0.06	0.5	1	MIC
41	Panel 2	Ertapenem	<=	0.015	0.004	0.016	1	MIC
41	Panel 2	Imipenem	=	0.25	0.06	0.25	1	MIC
41	Panel 2	Meropenem	<=	0.03	0.008	0.06	1	MIC
42	Panel 1	Ampicillin	=	4	2	8	1	MIC
42	Panel 1	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
42	Panel 1	Ceftazidime	<=	0.5	0.06	0.5	1	MIC
42	Panel 1	Chloramphenicol	<=	8	2	8	1	MIC
42	Panel 1	Ciprofloxacin	<=	0.015	0.004	0.016	1	MIC
42	Panel 1	Colistin	<=	1	0.25	2	1	MIC

Lab no.	Panel	Antimicrobial	Operator	Value	Low limit	High limit	Mark	Method
42	Panel 1	Gentamicin	<=	0.5	0.25	1	1	MIC
42	Panel 1	Meropenem	<=	0.03	0.008	0.06	1	MIC
42	Panel 1	Nalidixic acid	<=	4	1	4	1	MIC
42	Panel 1	Sulfisoxazole	=	32	8	32	1	MIC
42	Panel 1	Tetracycline	<=	2	0.5	2	1	MIC
42	Panel 1	Tigecycline	<=	0.25	0.03	0.25	1	MIC
42	Panel 1	Trimethoprim	=	0.5	0.5	2	1	MIC
45	Panel 1	Ampicillin	=	4	2	8	1	MIC
45	Panel 1	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
45	Panel 1	Ceftazidime	<=	0.5	0.06	0.5	1	MIC
45	Panel 1	Chloramphenicol	<=	8	2	8	1	MIC
45	Panel 1	Ciprofloxacin	<=	0.015	0.004	0.016	1	MIC
45	Panel 1	Colistin	<=	1	0.25	2	1	MIC
45	Panel 1	Gentamicin	<=	0.5	0.25	1	1	MIC
45	Panel 1	Meropenem	<=	0.03	0.008	0.06	1	MIC
45	Panel 1	Nalidixic acid	<=	4	1	4	1	MIC
45	Panel 1	Sulfisoxazole	=	64	8	32	**0**	MIC
45	Panel 1	Tetracycline	<=	2	0.5	2	1	MIC
45	Panel 1	Tigecycline	<=	0.25	0.03	0.25	1	MIC
45	Panel 1	Trimethoprim	=	0.5	0.5	2	1	MIC
45	Panel 2	Cefepime	<=	0.06	0.015	0.125	1	MIC
45	Panel 2	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
45	Panel 2	Cefoxitin	=	4	2	8	1	MIC
45	Panel 2	Ceftazidime	<=	0.25	0.06	0.5	1	MIC
45	Panel 2	Ertapenem	<=	0.015	0.004	0.016	1	MIC
45	Panel 2	Imipenem	=	0.25	0.06	0.25	1	MIC
45	Panel 2	Meropenem	<=	0.03	0.008	0.06	1	MIC
56	Panel 1	Ampicillin	=	4	2	8	1	MIC
56	Panel 1	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
56	Panel 1	Ceftazidime	<=	0.5	0.06	0.5	1	MIC
56	Panel 1	Chloramphenicol	<=	8	2	8	1	MIC
56	Panel 1	Ciprofloxacin	<=	0.015	0.004	0.016	1	MIC
56	Panel 1	Colistin	<=	1	0.25	2	1	MIC
56	Panel 1	Gentamicin	<=	0.5	0.25	1	1	MIC
56	Panel 1	Meropenem	<=	0.03	0.008	0.06	1	MIC
56	Panel 1	Nalidixic acid	<=	4	1	4	1	MIC
56	Panel 1	Sulfisoxazole	=	16	8	32	1	MIC
56	Panel 1	Tetracycline	<=	2	0.5	2	1	MIC
56	Panel 1	Tigecycline	<=	0.25	0.03	0.25	1	MIC
56	Panel 1	Trimethoprim	=	0.5	0.5	2	1	MIC
56	Panel 2	Cefepime	<=	0.06	0.015	0.125	1	MIC
56	Panel 2	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
56	Panel 2	Cefoxitin	=	4	2	8	1	MIC
56	Panel 2	Ceftazidime	<=	0.25	0.06	0.5	1	MIC
56	Panel 2	Ertapenem	<=	0.015	0.004	0.016	1	MIC
56	Panel 2	Imipenem	<=	0.12	0.06	0.25	1	MIC
56	Panel 2	Meropenem	<=	0.03	0.008	0.06	1	MIC
57	Panel 1	Ampicillin	>	64	2	8	**0**	MIC
57	Panel 1	Cefotaxime	=	8	0.03	0.125	**0**	MIC
57	Panel 1	Ceftazidime	=	4	0.06	0.5	**0**	MIC
57	Panel 1	Chloramphenicol	<=	8	2	8	1	MIC
57	Panel 1	Ciprofloxacin	<=	0.015	0.004	0.016	1	MIC
57	Panel 1	Colistin	<=	1	0.25	2	1	MIC
57	Panel 1	Gentamicin	=	1	0.25	1	1	MIC
57	Panel 1	Meropenem	<=	0.03	0.008	0.06	1	MIC
57	Panel 1	Nalidixic acid	<=	4	1	4	1	MIC
57	Panel 1	Sulfisoxazole	=	32	8	32	1	MIC
57	Panel 1	Tetracycline	<=	32	0.5	2	1	MIC
57	Panel 1	Tigecycline	<=	0.25	0.03	0.25	1	MIC
57	Panel 1	Trimethoprim	=	1	0.5	2	1	MIC
57	Panel 2	Cefepime	=	4	0.015	0.125	**0**	MIC
57	Panel 2	Cefotaxime	=	2	0.03	0.125	**0**	MIC
57	Panel 2	Cefoxitin	>	64	2	8	**0**	MIC
57	Panel 2	Ceftazidime	=	4	0.06	0.5	**0**	MIC
57	Panel 2	Ertapenem	=	0.03	0.004	0.016	**0**	MIC

Lab no.	Panel	Antimicrobial	Operator	Value	Low limit	High limit	Mark	Method
57	Panel 2	Imipenem	<=	0.5	0.06	0.25	1	MIC
57	Panel 2	Meropenem	<=	0.03	0.008	0.06	1	MIC
58	Panel 1	Ampicillin	=	4	2	8	1	MIC
58	Panel 1	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
58	Panel 1	Ceftazidime	<=	0.5	0.06	0.5	1	MIC
58	Panel 1	Chloramphenicol	<=	8	2	8	1	MIC
58	Panel 1	Ciprofloxacin	<=	0.015	0.004	0.016	1	MIC
58	Panel 1	Colistin	<=	1	0.25	2	1	MIC
58	Panel 1	Gentamicin	<=	0.5	0.25	1	1	MIC
58	Panel 1	Meropenem	<=	0.03	0.008	0.06	1	MIC
58	Panel 1	Nalidixic acid	<=	4	1	4	1	MIC
58	Panel 1	Tetracycline	<=	2	0.5	2	1	MIC
58	Panel 1	Tigecycline	<=	0.25	0.03	0.25	1	MIC
58	Panel 1	Trimethoprim	=	0.5	0.5	2	1	MIC
58	Panel 2	Cefepime	<=	0.06	0.015	0.125	1	MIC
58	Panel 2	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
58	Panel 2	Cefoxitin	=	2	2	8	1	MIC
58	Panel 2	Ceftazidime	<=	0.25	0.06	0.5	1	MIC
58	Panel 2	Ertapenem	<=	0.015	0.004	0.016	1	MIC
58	Panel 2	Imipenem	=	0.25	0.06	0.25	1	MIC
58	Panel 2	Meropenem	<=	0.03	0.008	0.06	1	MIC
59	Panel 1	Ampicillin	=	8	2	8	1	MIC
59	Panel 1	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
59	Panel 1	Ceftazidime	<=	0.5	0.06	0.5	1	MIC
59	Panel 1	Chloramphenicol	<=	8	2	8	1	MIC
59	Panel 1	Ciprofloxacin	<=	0.015	0.004	0.016	1	MIC
59	Panel 1	Colistin	<=	1	0.25	2	1	MIC
59	Panel 1	Gentamicin	<=	0.5	0.25	1	1	MIC
59	Panel 1	Meropenem	<=	0.03	0.008	0.06	1	MIC
59	Panel 1	Nalidixic acid	<=	4	1	4	1	MIC
59	Panel 1	Sulfisoxazole	=	16	8	32	1	MIC
59	Panel 1	Tetracycline	<=	2	0.5	2	1	MIC
59	Panel 1	Tigecycline	<=	0.25	0.03	0.25	1	MIC
59	Panel 1	Trimethoprim	=	1	0.5	2	1	MIC
59	Panel 2	Cefepime	<=	0.06	0.015	0.125	1	MIC
59	Panel 2	Cefotaxime	<=	0.25	0.03	0.125	1	MIC
59	Panel 2	Cefoxitin	=	2	2	8	1	MIC
59	Panel 2	Ceftazidime	<=	0.25	0.06	0.5	1	MIC
59	Panel 2	Ertapenem	<=	0.015	0.004	0.016	1	MIC
59	Panel 2	Imipenem	<=	0.12	0.06	0.25	1	MIC
59	Panel 2	Meropenem	<=	0.03	0.008	0.06	1	MIC

MIC: Microbroth dilution
AGA: Agar dilution

Test results from the reference strain *C. jejuni* ATCC 33560

Lab no.	Antimicrobial	Operator	Value	Low limit	High limit	Mark	Method	36-37ºC/48h	42ºC/24h
1	Ciprofloxacin	=	0.25	0.06	0.25	1	MIC	X	
1	Erythromycin	=	2	0.5	2	1	MIC	X	
1	Gentamicin	=	0.5	0.5	2	1	MIC	X	
1	Nalidixic acid	=	8	4	16	1	MIC	X	
1	Tetracycline	=	4	0.25	2	**0**	MIC	X	
2	Ciprofloxacin	=	0.12	0.06	0.25	1	MIC	X	
2	Erythromycin	=	1	0.5	2	1	MIC	X	
2	Gentamicin	<=	0.12	0.5	2	**0**	MIC	X	
2	Nalidixic acid	=	4	4	16	1	MIC	X	
2	Tetracycline	=	1	0.25	2	1	MIC	X	
4	Ciprofloxacin	=	0.12	0.06	0.25	1	MIC	X	
4	Erythromycin	=	1	0.5	2	1	MIC	X	
4	Nalidixic acid	=	4	4	16	1	MIC	X	
4	Tetracycline	=	0.5	0.25	2	1	MIC	X	
6	Ciprofloxacin	<=	0.12	0.03	0.125	1	MIC		X
6	Erythromycin	<=	1	0.25	2	1	MIC		X
6	Gentamicin	=	1	0.25	2	1	MIC		X
6	Nalidixic acid	=	8	4	16	1	MIC		X
6	Tetracycline	<=	0.5	0.25	1	1	MIC		X
9	Ciprofloxacin	<=	0.12	0.06	0.25	1	MIC	X	
9	Erythromycin	=	1	0.5	2	1	MIC	X	
9	Gentamicin	=	1	0.5	2	1	MIC	X	
9	Nalidixic acid	=	8	4	16	1	MIC	X	
9	Tetracycline	<=	0.5	0.25	2	1	MIC	X	
11	Ciprofloxacin	=	0.12	0.06	0.25	1	MIC	X	
11	Erythromycin	<=	0.5	0.5	2	1	MIC	X	
11	Gentamicin	=	1	0.5	2	1	MIC	X	
11	Nalidixic acid	=	8	4	16	1	MIC	X	
11	Tetracycline	=	0.25	0.25	2	1	MIC	X	
12	Ciprofloxacin	=	0.25	0.06	0.25	1	MIC	X	
12	Erythromycin	<=	1	0.5	2	1	MIC	X	
12	Gentamicin	=	1	0.5	2	1	MIC	X	
12	Nalidixic acid	=	8	4	16	1	MIC	X	
12	Tetracycline	=	1	0.25	2	1	MIC	X	
14	Ciprofloxacin	<=	0.125	0.03	0.125	1	MIC		X
14	Erythromycin	<=	1	0.25	2	1	MIC		X
14	Gentamicin	=	0.5	0.25	2	1	MIC		X
14	Nalidixic acid	=	4	4	16	1	MIC		X
14	Tetracycline	<=	0.5	0.25	1	1	MIC		X
17	Ciprofloxacin	=	0.25	0.06	0.25	1	MIC	X	
17	Erythromycin	<=	1	0.5	2	1	MIC	X	
17	Gentamicin	=	1	0.5	2	1	MIC	X	
17	Nalidixic acid	=	8	4	16	1	MIC	X	
17	Tetracycline	=	1	0.25	2	1	MIC	X	
18	Ciprofloxacin	<=	0.12	0.03	0.125	1	MIC		X
18	Erythromycin	<=	1	0.25	2	1	MIC		X
18	Gentamicin	=	1	0.25	2	1	MIC		X
18	Nalidixic acid	=	4	4	16	1	MIC		X
18	Tetracycline	=	1	0.25	1	1	MIC		X

Lab no.	Antimicrobial	Operator	Value	Low limit	High limit	Mark	Method	36-37ºC/48h	42ºC/24h
19	Ciprofloxacin	=	0.12	0.03	0.125	1	MIC		X
19	Erythromycin	=	1	0.25	2	1	MIC		X
19	Gentamicin	=	2	0.25	2	1	MIC		X
19	Nalidixic acid	=	8	4	16	1	MIC		X
19	Tetracycline	=	2	0.25	1	**0**	MIC		X
20	Ciprofloxacin	<=	0.12	0.03	0.125	1	MIC		X
20	Erythromycin	<=	1	0.25	2	1	MIC		X
20	Gentamicin	=	1	0.25	2	1	MIC		X
20	Nalidixic acid	=	4	4	16	1	MIC		X
20	Tetracycline	=	4	0.25	1	**0**	MIC		X
21	Ciprofloxacin	=	0.12	0.03	0.125	1	MIC		X
21	Erythromycin	<	1	0.25	2	1	MIC		X
21	Gentamicin	=	0.25	0.25	2	1	MIC		X
21	Nalidixic acid	=	4	4	16	1	MIC		X
21	Tetracycline	=	0.5	0.25	1	1	MIC		X
22	Ciprofloxacin	<	0.06	0.03	0.125	1	MIC		X
22	Erythromycin	<	1	0.25	2	1	MIC		X
22	Nalidixic acid	=	4	4	16	1	MIC		X
22	Tetracycline	=	1	0.25	1	1	MIC		X
23	Ciprofloxacin	=	0.12	0.03	0.125	1	MIC		X
23	Erythromycin	<	0.5	0.25	2	1	MIC		X
23	Gentamicin	=	1	0.25	2	1	MIC		X
23	Nalidixic acid	=	4	4	16	1	MIC		X
23	Tetracycline	=	0.5	0.25	1	1	MIC		X
25	Ciprofloxacin	=	0.25	0.06	0.25	1	MIC	X	
25	Erythromycin	=	2	0.5	2	1	MIC	X	
25	Gentamicin	=	0.25	0.5	2	**0**	MIC	X	
25	Nalidixic acid	=	8	4	16	1	MIC	X	
25	Tetracycline	=	2	0.25	2	1	MIC	X	
26	Ciprofloxacin	<=	0.12	0.06	0.25	1	MIC	X	
26	Erythromycin	<=	1	0.5	2	1	MIC	X	
26	Gentamicin	=	0.5	0.5	2	1	MIC	X	
26	Nalidixic acid	=	8	4	16	1	MIC	X	
26	Tetracycline	=	1	0.25	2	1	MIC	X	
29	Ciprofloxacin	=	0.25	0.06	0.25	1	MIC	X	
29	Erythromycin	<	1	0.5	2	1	MIC	X	
29	Gentamicin	=	1	0.5	2	1	MIC	X	
29	Nalidixic acid	=	16	4	16	1	MIC	X	
29	Tetracycline	=	2	0.25	2	1	MIC	X	
30	Ciprofloxacin	=	0.5	0.06	0.25	**0**	MIC	X	
30	Erythromycin	<=	1	0.5	2	1	MIC	X	
30	Nalidixic acid	=	4	4	16	1	MIC	X	
30	Tetracycline	<=	0.5	0.25	2	1	MIC	X	
32	Ciprofloxacin	<=	0.12	0.06	0.25	1	MIC	X	
32	Erythromycin	<=	1	0.5	2	1	MIC	X	
32	Gentamicin	=	1	0.5	2	1	MIC	X	
32	Nalidixic acid	=	8	4	16	1	MIC	X	
32	Tetracycline	=	1	0.25	2	1	MIC	X	
33	Ciprofloxacin	=	0.25	0.06	0.25	1	MIC	X	
33	Erythromycin	=	2	0.5	2	1	MIC	X	
33	Gentamicin	=	0.5	0.5	2	1	MIC	X	
33	Nalidixic acid	=	8	4	16	1	MIC	X	
33	Tetracycline	=	1	0.25	2	1	MIC	X	

Lab no.	Antimicrobial	Operator	Value	Low limit	High limit	Mark	Method	36-37ºC/48h	42ºC/24h
34	Ciprofloxacin	<=	0.12	0.06	0.25	1	MIC	X	
34	Erythromycin	<=	1	0.5	2	1	MIC	X	
34	Gentamicin	=	0.5	0.5	2	1	MIC	X	
34	Nalidixic acid	=	4	4	16	1	MIC	X	
34	Tetracycline	=	1	0.25	2	1	MIC	X	
36	Ciprofloxacin	=	0.5	0.06	0.25	**0**	MIC	X	
36	Erythromycin	<=	0.5	0.5	2	1	MIC	X	
36	Gentamicin	=	1	0.5	2	1	MIC	X	
36	Nalidixic acid	=	16	4	16	1	MIC	X	
36	Tetracycline	=	2	0.25	2	1	MIC	X	
37	Ciprofloxacin	=	0.25	0.12	1	1	AGA	X	
37	Erythromycin	<=	1	1	8	1	AGA	X	
37	Gentamicin	=	1	0.5	2	1	AGA	X	
39	Ciprofloxacin	=	0.12	0.03	0.125	1	MIC		X
39	Erythromycin	=	0.5	0.25	2	1	MIC		X
39	Gentamicin	=	0.5	0.25	2	1	MIC		X
39	Nalidixic acid	<=	4	4	16	1	MIC		X
39	Tetracycline	=	1	0.25	1	1	MIC		X
40	Ciprofloxacin	=	0.12	0.03	0.125	1	MIC		X
40	Erythromycin	=	1	0.25	2	1	MIC		X
40	Gentamicin	=	0.25	0.25	2	1	MIC		X
40	Nalidixic acid	=	8	4	16	1	MIC		X
40	Tetracycline	=	1	0.25	1	1	MIC		X
41	Ciprofloxacin	<=	0.12	0.03	0.125	1	MIC		X
41	Erythromycin	<=	1	0.25	2	1	MIC		X
41	Gentamicin	=	0.25	0.25	2	1	MIC		X
41	Nalidixic acid	=	4	4	16	1	MIC		X
41	Tetracycline	<=	0.5	0.25	1	1	MIC		X
42	Ciprofloxacin	=	0.25	0.06	0.25	1	MIC	X	
42	Erythromycin	=	2	0.5	2	1	MIC	X	
42	Gentamicin	=	0.5	0.5	2	1	MIC	X	
42	Nalidixic acid	=	16	4	16	1	MIC	X	
42	Tetracycline	=	2	0.25	2	1	MIC	X	
45	Ciprofloxacin	<=	0.12	0.06	0.25	1	MIC	X	
45	Erythromycin	<=	1	0.5	2	1	MIC	X	
45	Gentamicin	=	1	0.5	2	1	MIC	X	
45	Nalidixic acid	=	8	4	16	1	MIC	X	
45	Tetracycline	=	2	0.25	2	1	MIC	X	
56	Ciprofloxacin	=	0.12	0.03	0.125	1	MIC		X
56	Erythromycin	<=	0.5	0.25	2	1	MIC		X
56	Gentamicin	=	1	0.25	2	1	MIC		X
56	Nalidixic acid	=	8	4	16	1	MIC		X
56	Tetracycline	=	0.5	0.25	1	1	MIC		X
58	Ciprofloxacin	<=	0.12	0.03	0.125	1	MIC		X
58	Erythromycin	=	2	0.25	2	1	MIC		X
58	Gentamicin	=	1	0.25	2	1	MIC		X
58	Nalidixic acid	=	4	4	16	1	MIC		X
58	Tetracycline	=	1	0.25	1	1	MIC		X
59	Ciprofloxacin	<=	0.12	0.03	0.125	1	MIC		X
59	Erythromycin	<=	1	0.25	2	1	MIC		X
59	Gentamicin	=	0.5	0.25	2	1	MIC		X
59	Nalidixic acid	=	8	4	16	1	MIC		X
59	Tetracycline	=	2	0.25	1	**0**	MIC		X

MIC: microbroth dilution
AGA: agar dilution

Salmonella - expected and obtained interpretation

Antimicrobial	Strain	Panel	Expected	% R	% S	No. correct	No. incorrect
Ampicillin AMP	EURL S-9.1	Panel 1	S	0	100	35	0
	EURL S-9.2	Panel 1	R	100	0	35	0
	EURL S-9.3	Panel 1	R	100	0	35	0
	EURL S-9.4	Panel 1	R	100	0	35	0
	EURL S-9.5	Panel 1	R	100	0	35	0
	EURL S-9.6	Panel 1	R	100	0	35	0
	EURL S-9.7	Panel 1	R	100	0	35	0
	EURL S-9.8	Panel 1	S	0	100	35	0
Cefotaxime FOT	EURL S-9.1	Panel 1	S	0	100	35	0
	EURL S-9.2	Panel 1	S	0	100	35	0
	EURL S-9.3	Panel 1	R	100	0	35	0
	EURL S-9.3	Panel 2	R	100	0	35	0
	EURL S-9.4	Panel 1	R	100	0	35	0
	EURL S-9.4	Panel 2	R	97	3	33	1
	EURL S-9.5	Panel 1	R	100	0	35	0
	EURL S-9.5	Panel 2	R	100	0	35	0
	EURL S-9.6	Panel 1	S	6	94	33	2
	EURL S-9.6	Panel 2	S	3	97	31	1
	EURL S-9.7	Panel 1	S	0	100	35	0
	EURL S-9.8	Panel 1	S	0	100	35	0
Cefoxitin FOX	EURL S-9.3	Panel 2	R	100	0	35	0
	EURL S-9.4	Panel 2	S	0	100	34	0
	EURL S-9.5	Panel 2	R	100	0	35	0
	EURL S-9.6	Panel 2	S	9	91	29	3
Ceftazidime TAZ	EURL S-9.1	Panel 1	S	0	100	35	0
	EURL S-9.2	Panel 1	S	0	100	35	0
	EURL S-9.3	Panel 1	R	100	0	35	0
	EURL S-9.3	Panel 2	R	100	0	35	0
	EURL S-9.4	Panel 1	S	6	94	33	2
	EURL S-9.4	Panel 2	S	9	91	31	3
	EURL S-9.5	Panel 1	R	100	0	35	0
	EURL S-9.5	Panel 2	R	100	0	35	0
	EURL S-9.6	Panel 1	S	0	100	35	0
	EURL S-9.6	Panel 2	S	3	97	31	1
	EURL S-9.7	Panel 1	S	3	97	34	1
	EURL S-9.8	Panel 1	S	0	100	35	0
Chloramphenicol CHL	EURL S-9.1	Panel 1	S	0	100	35	0
	EURL S-9.2	Panel 1	S	0	100	35	0
	EURL S-9.3	Panel 1	R	100	0	35	0
	EURL S-9.4	Panel 1	S	3	97	34	1
	EURL S-9.5	Panel 1	S	0	100	35	0
	EURL S-9.6	Panel 1	S	0	100	35	0
	EURL S-9.7	Panel 1	S	0	100	35	0
	EURL S-9.8	Panel 1	S	0	100	35	0
Ciprofloxacin CIP	EURL S-9.1	Panel 1	S	3	97	34	1
	EURL S-9.2	Panel 1	R	100	0	35	0
	EURL S-9.3	Panel 1	S	3	97	34	1
	EURL S-9.4	Panel 1	R	100	0	35	0
	EURL S-9.5	Panel 1	R	97	3	34	1
	EURL S-9.6	Panel 1	R	100	0	35	0
	EURL S-9.7	Panel 1	S	0	100	35	0
	EURL S-9.8	Panel 1	S	3	97	34	1
Colistin COL	EURL S-9.1	Panel 1	R	88	12	30	4
	EURL S-9.2	Panel 1	S	3	97	34	1
	EURL S-9.3	Panel 1	S	0	100	35	0
	EURL S-9.4	Panel 1	S	0	100	35	0
	EURL S-9.5	Panel 1	S	0	100	35	0

Antimicrobial	Strain	Panel	Expected	% R	% S	No. correct	No. incorrect
	EURL S-9.6	Panel 1	S	0	100	35	0
	EURL S-9.7	Panel 1	S	0	100	35	0
	*EURL S-9.8**	*Panel 1*	*S*	*38*	*63*	*20*	*12*
Ertapenem ETP	EURL S-9.3	Panel 2	S	0	100	34	0
	EURL S-9.4	Panel 2	S	3	97	32	1
	EURL S-9.5	Panel 2	R	94	6	32	2
	EURL S-9.6	Panel 2	R	97	3	30	1
Gentamicin GEN	EURL S-9.1	Panel 1	S	0	100	35	0
	EURL S-9.2	Panel 1	R	100	0	35	0
	EURL S-9.3	Panel 1	S	3	97	34	1
	EURL S-9.4	Panel 1	S	0	100	35	0
	EURL S-9.5	Panel 1	R	100	0	35	0
	EURL S-9.6	Panel 1	S	0	100	35	0
	EURL S-9.7	Panel 1	S	0	100	35	0
	EURL S-9.8	Panel 1	S	0	100	35	0
Imipenem IMI	EURL S-9.3	Panel 2	S	0	100	35	0
	EURL S-9.4	Panel 2	S	3	97	33	1
	EURL S-9.5	Panel 2	R	77	23	27	8
	EURL S-9.6	Panel 2	S	19	81	25	6
Meropenem MER	EURL S-9.1	Panel 1	S	0	100	34	0
	EURL S-9.2	Panel 1	S	0	100	34	0
	EURL S-9.3	Panel 1	S	0	100	34	0
	EURL S-9.3	Panel 2	S	0	100	35	0
	EURL S-9.4	Panel 1	S	0	100	34	0
	EURL S-9.4	Panel 2	S	3	97	33	1
	EURL S-9.5	Panel 1	R	64	36	21	12
	EURL S-9.5	Panel 2	R	68	32	23	11
	EURL S-9.6	Panel 1	R	82	18	28	6
	EURL S-9.6	Panel 2	R	74	26	23	8
	EURL S-9.7	Panel 1	S	0	100	34	0
	EURL S-9.8	Panel 1	S	0	100	34	0
Nalidixic acid NAL	EURL S-9.1	Panel 1	S	0	100	35	0
	EURL S-9.2	Panel 1	R	79	21	27	7
	EURL S-9.3	Panel 1	S	0	100	35	0
	EURL S-9.4	Panel 1	R	97	3	34	1
	EURL S-9.5	Panel 1	R	100	0	35	0
	EURL S-9.6	Panel 1	R	100	0	35	0
	EURL S-9.7	Panel 1	S	0	100	35	0
	EURL S-9.8	Panel 1	S	0	100	35	0
Sulfamethoxazole SMX	EURL S-9.1	Panel 1	S	0	100	34	0
	EURL S-9.2	Panel 1	S	3	97	33	1
	EURL S-9.3	Panel 1	R	97	3	33	1
	EURL S-9.4	Panel 1	S	3	97	33	1
	EURL S-9.5	Panel 1	R	100	0	34	0
	EURL S-9.6	Panel 1	S	0	100	34	0
	EURL S-9.7	Panel 1	R	100	0	34	0
	EURL S-9.8	Panel 1	S	0	100	34	0
Tetracycline TET	EURL S-9.1	Panel 1	S	0	100	35	0
	EURL S-9.2	Panel 1	S	0	100	35	0
	EURL S-9.3	Panel 1	R	100	0	35	0
	EURL S-9.4	Panel 1	R	100	0	35	0
	EURL S-9.5	Panel 1	R	100	0	35	0
	EURL S-9.6	Panel 1	S	0	100	35	0
	EURL S-9.7	Panel 1	R	100	0	35	0
	EURL S-9.8	Panel 1	S	0	100	35	0

Antimicrobial	Strain	Panel	Expected	% R	% S	No. correct	No. incorrect
Tigecycline TGC	EURL S-9.1	Panel 1	S	0	100	31	0
	EURL S-9.2	Panel 1	S	0	100	31	0
	EURL S-9.3	Panel 1	S	0	100	32	0
	EURL S-9.4	Panel 1	S	0	100	31	0
	EURL S-9.5	Panel 1	S	0	100	30	0
	EURL S-9.6	Panel 1	S	0	100	30	0
	EURL S-9.7	Panel 1	R	71	29	20	8
	EURL S-9.8	Panel 1	S	0	100	33	0
Trimethoprim TMP	EURL S-9.1	Panel 1	S	0	100	35	0
	EURL S-9.2	Panel 1	S	0	100	35	0
	EURL S-9.3	Panel 1	S	6	94	33	2
	EURL S-9.4	Panel 1	S	0	100	35	0
	EURL S-9.5	Panel 1	S	0	100	35	0
	EURL S-9.6	Panel 1	S	3	97	34	1
	EURL S-9.7	Panel 1	R	100	0	35	0
	EURL S-9.8	Panel 1	S	0	100	34	0

*Strain/antimicrobial-combination excluded from the evaluation

Campylobacter - expected and obtained interpretation

Antimicrobial	Strain	Expected	% R	% S	No. correct	No. incorrect
Ciprofloxacin, CIP	EURL C-9.1	R	97	3	31	1
	EURL C-9.2	S	6	94	29	2
	EURL C-9.3	R	97	3	30	1
	EURL C-9.4	R	100	0	30	0
	EURL C-9.5	S	6	94	29	2
	EURL C-9.6	R	100	0	32	0
	EURL C-9.7	R	93	7	28	2
	EURL C-9.8	S	6	94	30	2
Erythromycin, ERY	EURL C-9.1	S	3	97	31	1
	EURL C-9.2	R	100	0	31	0
	EURL C-9.3	S	13	87	27	4
	EURL C-9.4	R	100	0	30	0
	EURL C-9.5	S	6	94	29	2
	EURL C-9.6	R	100	0	32	0
	EURL C-9.7	S	10	90	27	3
	EURL C-9.8	R	97	3	31	1
Gentamicin, GEN	EURL C-9.1	S	0	100	32	0
	EURL C-9.2	S	0	100	31	0
	EURL C-9.3	S	0	100	31	0
	EURL C-9.4	R	93	7	28	2
	EURL C-9.5	S	3	97	30	1
	EURL C-9.6	S	3	97	31	1
	EURL C-9.7	S	0	100	30	0
	EURL C-9.8	S	0	100	32	0
Nalidixic acid, NAL	EURL C-9.1	R	100	0	32	0
	EURL C-9.2	S	6	94	29	2
	EURL C-9.3	R	97	3	30	1
	EURL C-9.4	R	97	3	29	1
	EURL C-9.5	S	6	94	29	2
	EURL C-9.6	R	97	3	31	1
	EURL C-9.7	S	10	90	27	3
	EURL C-9.8	S	3	97	31	1
Streptomycin, STR	EURL C-9.1	S	3	97	30	1
	EURL C-9.2	S	10	90	27	3
	EURL C-9.3	R	100	0	30	0
	EURL C-9.4	R	100	0	29	0
	EURL C-9.5	S	7	93	28	2
	EURL C-9.6	R	100	0	31	0
	EURL C-9.7	S	10	90	26	3
	EURL C-9.8	R	97	3	30	1
Tetracycline, TET	EURL C-9.1	R	100	0	32	0
	EURL C-9.2	S	23	77	23	7
	EURL C-9.3	R	97	3	30	1
	EURL C-9.4	R	100	0	30	0
	EURL C-9.5	S	6	94	29	2
	*EURL C-9.6**	*R*	*68*	*32*	*21*	*10*
	EURL C-9.7	S	3	97	29	1
	EURL C-9.8	S	3	97	31	1

*Strain/antimicrobial-combination excluded from the evaluation

Deviations - *Salmonella*

Lab no.	Strain	Panel	Antimicrobial	Obtained interpretation	Obtained value	Expected interpretation	Expected MIC / ESBL conclusion
1	EURL S-9.6	Panel 1	Cefotaxime FOT	R	1	S	= 0.5
1	EURL S-9.6	Panel 2	Cefoxitin FOX	R	16	S	8
1	EURL S-9.6	Panel 2	Imipenem IMI	R	2	S	1
2	EURL S-9.5	Panel 1	Meropenem MER	S	0.12	R	1
2	EURL S-9.5	Panel 2	Meropenem MER	S	0.12	R	1
2	EURL S-9.6	Panel 1	Meropenem MER	S	0.12	R	= 0.5
2	EURL S-9.6	Panel 2	Meropenem MER	S	0.12	R	= 0.5
4	EURL S-9.6	Panel 2	Meropenem MER	S	0.12	R	= 0.5
6	EURL S-9.6	Panel 2	Imipenem IMI	R	2	S	1
9	EURL S-9.7	Panel 1	Tigecycline TGC	S	1	R	2
11	EURL S-9.2	Panel 1	Nalidixic acid NAL	S	16	R	32
12	EURL S-9.5	Panel 1	Meropenem MER	S	0.12	R	1
12	EURL S-9.6	Panel 1	Meropenem MER	S	0.12	R	= 0.5
12	EURL S-9.6	Panel 2	Meropenem MER	S	0.12	R	= 0.5
12	EURL S-9.7	Panel 1	Tigecycline TGC	S	1	R	2
13	EURL S-9.2	Panel 1	Nalidixic acid NAL	S	16	R	32
13	EURL S-9.3	Panel 1	Trimethoprim TMP	R	>32	S	<= 0.25
13	EURL S-9.5	Panel 1	Meropenem MER	S	0.12	R	1
13	EURL S-9.5	Panel 2	Imipenem IMI	S	1	R	4
13	EURL S-9.5	Panel 2	Meropenem MER	S	0.12	R	1
19	EURL S-9.5	Panel 1	Meropenem MER	S	0.12	R	1
20	EURL S-9.5	Panel 1	Ciprofloxacin CIP	S	>8	R	> 8
21	EURL S-9.2	Panel 1	Nalidixic acid NAL	S	16	R	32
21	EURL S-9.5	Panel 2	Imipenem IMI	S	1	R	4
22	EURL S-9.6	Panel 1	Trimethoprim TMP	R	4	S	<= 0.25
22	EURL S-9.6	Panel 2	Cefoxitin FOX	R	16	S	8
23	EURL S-9.1	Panel 1	Colistin COL	S	2	R	8
23	EURL S-9.4		ESBL test conclusion	Unusual phenotype		Presumptive ESBL	
23	EURL S-9.5	Panel 1	Meropenem MER	S	<0.03	R	1
23	EURL S-9.5	Panel 2	Imipenem IMI	S	1	R	4
23	EURL S-9.5	Panel 2	Meropenem MER	S	0.12	R	1
23	EURL S-9.5		ESBL test conclusion	Presumptive pAmpC		Presumptive carbapenemase	
23	EURL S-9.7	Panel 1	Tigecycline TGC	S	1	R	2
26	EURL S-9.2	Panel 1	Nalidixic acid NAL	S	16	R	32
26	EURL S-9.5	Panel 1	Meropenem MER	S	0.12	R	1
26	EURL S-9.5	Panel 2	Imipenem IMI	S	1	R	4
26	EURL S-9.5	Panel 2	Meropenem MER	S	0.12	R	1
26	EURL S-9.5		ESBL test conclusion	Unusual phenotype		Presumptive carbapenemase	
26	EURL S-9.6	Panel 2	Meropenem MER	S	0.12	R	= 0.5
26	EURL S-9.6		ESBL test conclusion	Unusual phenotype		Presumptive carbapenemase	
26	EURL S-9.7	Panel 1	Tigecycline TGC	S	1	R	2
29	EURL S-9.1	Panel 1	Colistin COL	S	2	R	8
29	EURL S-9.4		ESBL test conclusion	No ESBL, AmpC- or carba		Presumptive ESBL	
29	EURL S-9.5		ESBL test conclusion	Unusual phenotype		Presumptive carbapenemase	
30	EURL S-9.5	Panel 1	Meropenem MER	S	0.125	R	1
30	EURL S-9.5	Panel 2	Imipenem IMI	S	1	R	4
30	EURL S-9.5	Panel 2	Meropenem MER	S	0.12	R	1
30	EURL S-9.7	Panel 1	Tigecycline TGC	S	1	R	2
32	EURL S-9.3		ESBL test conclusion	Presumptive ESBL + pAmpC		Presumptive pAmpC	
32	EURL S-9.6	Panel 2	Meropenem MER	S	<=0.12	R	= 0.5
33	EURL S-9.2	Panel 1	Nalidixic acid NAL	S	16	R	32
33	EURL S-9.5	Panel 1	Meropenem MER	S	0.12	R	1
33	EURL S-9.6	Panel 1	Meropenem MER	S	0.12	R	= 0.5
33	EURL S-9.6	Panel 2	Meropenem MER	S	0.12	R	= 0.5
33	EURL S-9.6		ESBL test conclusion	Unusual phenotype		Presumptive carbapenemase	
33	EURL S-9.7	Panel 1	Tigecycline TGC	S	1	R	2
34	EURL S-9.4	Panel 1	Nalidixic acid NAL	S	<=4	R	> 128
36	EURL S-9.5	Panel 1	Meropenem MER	S	0.12	R	1
36	EURL S-9.5	Panel 2	Meropenem MER	S	0.12	R	1
36	EURL S-9.5		ESBL test conclusion	Unusual phenotype		Presumptive carbapenemase	
36	EURL S-9.7	Panel 1	Tigecycline TGC	S	1	R	2
37	EURL S-9.5	Panel 1	Meropenem MER	S	0.06	R	1
37	EURL S-9.5	Panel 2	Meropenem MER	S	0.125	R	1
37	EURL S-9.6	Panel 1	Meropenem MER	S	0.125	R	= 0.5

Lab no.	Strain	Panel	Antimicrobial	Obtained interpretation	Obtained value	Expected interpretation	Expected MIC / ESBL conclusion
37	EURL S-9.6		ESBL test conclusion	No ESBL, AmpC- or carba		Presumptive carbapenemase	
38	EURL S-9.6	Panel 2	Imipenem IMI	R	2	S	1
39	EURL S-9.1	Panel 1	Colistin COL	S	2	R	8
39	EURL S-9.2	Panel 1	Nalidixic acid NAL	S	16	R	32
39	EURL S-9.4		ESBL test conclusion	Unusual phenotype		Presumptive ESBL	
39	EURL S-9.5	Panel 2	Meropenem MER	S	<=1	R	1
39	EURL S-9.5		ESBL test conclusion	Presumptive pAmpC		Presumptive carbapenemase	
39	EURL S-9.6	Panel 2	Meropenem MER	S	<=1	R	= 0.5
39	EURL S-9.6		ESBL test conclusion	No ESBL, AmpC- or carba		Presumptive carbapenemase	
39	EURL S-9.7		ESBL test conclusion	Presumptive pAmpC		No ESBL, AmpC- or carba	
40	EURL S-9.1	Panel 1	Colistin COL	S	2	R	8
40	EURL S-9.3	Panel 1	Sulfamethoxazole SMX	S	128	R	> 1024
40	EURL S-9.6	Panel 2	Cefoxitin FOX	R	16	S	8
41	EURL S-9.3		ESBL test conclusion	Presumptive ESBL + pAmpC		Presumptive pAmpC	
41	EURL S-9.4	Panel 1	Ceftazidime TAZ	R	1	S	1
41	EURL S-9.4	Panel 2	Ceftazidime TAZ	R	1	S	1
41	EURL S-9.6	Panel 1	Cefotaxime FOT	R	0.5	S	= 0.5
41	EURL S-9.6	Panel 2	Cefotaxime FOT	R	0.5	S	= 0.5
41	EURL S-9.6	Panel 2	Imipenem IMI	R	2	S	1
41	EURL S-9.7	Panel 1	Ceftazidime TAZ	R	1	S	<= 0.5
41	EURL S-9.7		ESBL test conclusion	Unusual phenotype		No ESBL, AmpC- or carba	
42	EURL S-9.2	Panel 1	Nalidixic acid NAL	S	16	R	32
42	EURL S-9.3		ESBL test conclusion	Presumptive ESBL + pAmpC		Presumptive pAmpC	
42	EURL S-9.6	Panel 1	Meropenem MER	S	0.12	R	= 0.5
42	EURL S-9.6	Panel 2	Meropenem MER	S	0.12	R	= 0.5
42	EURL S-9.6		ESBL test conclusion	Unusual phenotype		Presumptive carbapenemase	
45	EURL S-9.6	Panel 2	Imipenem IMI	R	2	S	1
45	EURL S-9.7	Panel 1	Tigecycline TGC	S	1	R	2
57	EURL S-9.2	Panel 1	Sulfamethoxazole SMX	R	128	S	128
57	EURL S-9.3	Panel 1	Trimethoprim TMP	R	32	S	<= 0.25
57	EURL S-9.4	Panel 2	Cefotaxime FOT	S	8	R	16
57	EURL S-9.4	Panel 2	Ceftazidime TAZ	R	0.5	S	1
57	EURL S-9.5	Panel 1	Meropenem MER	S	0.12	R	1
57	EURL S-9.5	Panel 2	Ertapenem ETP	S	0.06	R	= 0.5
57	EURL S-9.5	Panel 2	Imipenem IMI	S	1	R	4
57	EURL S-9.5	Panel 2	Meropenem MER	S	<=1	R	1
57	EURL S-9.5		ESBL test conclusion	Presumptive pAmpC		Presumptive carbapenemase	
57	EURL S-9.6	Panel 1	Meropenem MER	S	<=0.25	R	= 0.5
57	EURL S-9.6	Panel 2	Ertapenem ETP	S	<=0.25	R	= .25
58	EURL S-9.1	Panel 1	Ciprofloxacin CIP	R	0.12	S	= 0.03
58	EURL S-9.2	Panel 1	Colistin COL	R	4	S	<= 1
58	EURL S-9.3	Panel 1	Ciprofloxacin CIP	R	0.25	S	= 0.03
58	EURL S-9.3	Panel 1	Gentamicin GEN	R	>32	S	<= 0.5
58	EURL S-9.4	Panel 1	Ceftazidime TAZ	R	8	S	1
58	EURL S-9.4	Panel 1	Chloramphenicol CHL	R	128	S	<= 8
58	EURL S-9.4	Panel 1	Sulfamethoxazole SMX	R	>1024	S	64
58	EURL S-9.4	Panel 2	Ceftazidime TAZ	R	8	S	1
58	EURL S-9.5	Panel 1	Meropenem MER	S	0.12	R	1
58	EURL S-9.5	Panel 2	Imipenem IMI	S	1	R	4
58	EURL S-9.5	Panel 2	Meropenem MER	S	0.12	R	1
58	EURL S-9.5		ESBL test conclusion	Presumptive pAmpC		Presumptive carbapenemase	
58	EURL S-9.6		ESBL test conclusion	Unusual phenotype		Presumptive carbapenemase	
58	EURL S-9.8	Panel 1	Ciprofloxacin CIP	R	0.12	S	<= 0.015

Deviations - *Campylobacter*

Lab no.	Strain	Antimicrobial	Obtained interpretation	Obtained value	Expected interpretation	Expected MIC
1	EURL C-9.2	Tetracycline TET	R	4	S	2
1	EURL C-9.7	Nalidixic acid NAL	R	>64	S	2
4	EURL C-9.3	Erythromycin ERY	R	16	S	4
11	EURL C-9.6	Nalidixic acid NAL	S	8	R	64
19	EURL C-9.7	Erythromycin ERY	R	>32	S	<= 1
19	EURL C-9.7	Nalidixic acid NAL	R	>64	S	2
19	EURL C-9.7	Streptomycin STR	R	>16	S	= 0.5
19	EURL C-9.8	Ciprofloxacin CIP	R	>4	S	<= 0.1
19	EURL C-9.8	Erythromycin ERY	S	<=0.5	R	> 128
19	EURL C-9.8	Streptomycin STR	S	4	R	> 16
20	EURL C-9.2	Streptomycin STR	R	8	S	1
29	EURL C-9.1	Erythromycin ERY	R	32	S	<= 1
29	EURL C-9.1	Streptomycin STR	R	>16	S	= 0.5
29	EURL C-9.2	Ciprofloxacin CIP	R	2	S	= 0.3
29	EURL C-9.2	Nalidixic acid NAL	R	32	S	8
29	EURL C-9.2	Streptomycin STR	R	>16	S	1
29	EURL C-9.2	Tetracycline TET	R	4	S	2
29	EURL C-9.3	Erythromycin ERY	R	32	S	4
29	EURL C-9.4	Gentamicin GEN	S	0.5	R	> 16
30	EURL C-9.2	Tetracycline TET	R	4	S	2
34	EURL C-9.2	Tetracycline TET	R	4	S	2
34	EURL C-9.3	Tetracycline TET	S	2	R	> 64
34	EURL C-9.7	Tetracycline TET	R	>64	S	<= 0.5
36	EURL C-9.7	Ciprofloxacin CIP	S	0.12	R	16
36	EURL C-9.7	Erythromycin ERY	R	>64	S	<= 1
36	EURL C-9.7	Streptomycin STR	R	>64	S	= 0.5
39	EURL C-9.1	Ciprofloxacin CIP	S	4	R	8
39	EURL C-9.3	Nalidixic acid NAL	S	16	R	> 64
39	EURL C-9.4	Nalidixic acid NAL	S	16	R	> 64
40	EURL C-9.2	Ciprofloxacin CIP	R	1	S	= 0.3
40	EURL C-9.2	Nalidixic acid NAL	R	64	S	8
40	EURL C-9.2	Streptomycin STR	R	8	S	1
40	EURL C-9.2	Tetracycline TET	R	64	S	2
40	EURL C-9.3	Ciprofloxacin CIP	S	0.5	R	> 16
40	EURL C-9.3	Erythromycin ERY	R	32	S	4
40	EURL C-9.4	Gentamicin GEN	S	0.25	R	> 16
40	EURL C-9.5	Ciprofloxacin CIP	R	64	S	<= 0.1
40	EURL C-9.5	Erythromycin ERY	R	64	S	<= 1
40	EURL C-9.5	Nalidixic acid NAL	R	64	S	4
40	EURL C-9.5	Streptomycin STR	R	16	S	1
40	EURL C-9.5	Tetracycline TET	R	64	S	<= 0.5
40	EURL C-9.7	Nalidixic acid NAL	R	32	S	2
40	EURL C-9.8	Ciprofloxacin CIP	R	4	S	<= 0.1
40	EURL C-9.8	Nalidixic acid NAL	R	64	S	8
40	EURL C-9.8	Tetracycline TET	R	64	S	1
41	EURL C-9.2	Tetracycline TET	R	4	S	2
42	EURL C-9.2	Tetracycline TET	R	4	S	2
42	EURL C-9.6	Gentamicin GEN	R	1	S	1
42	EURL C-9.7	Ciprofloxacin CIP	S	<=0.06	R	16
42	EURL C-9.7	Erythromycin ERY	R	>32	S	<= 1
42	EURL C-9.7	Streptomycin STR	R	>16	S	= 0.5
58	EURL C-9.5	Ciprofloxacin CIP	R	8	S	<= 0.1
58	EURL C-9.5	Erythromycin ERY	R	>128	S	<= 1
58	EURL C-9.5	Gentamicin GEN	R	>16	S	= 0.3
58	EURL C-9.5	Nalidixic acid NAL	R	32	S	4
58	EURL C-9.5	Streptomycin STR	R	>16	S	1
58	EURL C-9.5	Tetracycline TET	R	32	S	<= 0.5
59	EURL C-9.3	Erythromycin ERY	R	>128	S	4

Genotypic characterization (optional); obtained results

Labno	Strain	Genetype	Gene number	Not detected	Method	Reference	Primer 5 3	Primer 3 5
1	EURL-S9.3	CMY	-2		Whole genome sequenced	Zankari, E. et al, 2012	-	-
1	EURL-S9.4	CTX	M-9		Whole genome sequenced	Zankari, E. et al, 2012	-	-
1	EURL-S9.5	VIM	-2		Whole genome sequenced	Zankari, E. et al, 2012	-	-
1	EURL-S9.6	OXA	-48		Whole genome sequenced	Zankari, E. et al, 2012	-	-
4	EURL-S9.3	CMY	-2		PCR (in-house)	Hasman et al. 2005	-	-
4	EURL-S9.4	OXA	-	X	PCR (in-house)	Hasman et al. 2005	-	-
4	EURL-S9.4	SHV	-	X	PCR (in-house)	Arlet et al. 1997	-	-
4	EURL-S9.4	CTX	M-9		PCR (in-house)	Pagani et al. 2003	-	-
4	EURL-S9.4	TEM	-1		PCR (in-house)	Olesen et al 2004	-	-
4	EURL-S9.5	CTX	-	X	PCR (published)	Pagani et al. 2003	-	-
4	EURL-S9.5	IMP	-	X	PCR (published)	Poirel et al. 2011	-	-
4	EURL-S9.5	KPC	-	X	PCR (published)	Poirel et al. 2011	-	-
4	EURL-S9.5	NDM	-	X	PCR (published)	Poirel et al. 2011	-	-
4	EURL-S9.5	OXA	-	X	PCR (published)	Hasman et al. 2005	-	-
4	EURL-S9.5	OXA	-	X	PCR (published)	Poirel et al. 2011	-	-
4	EURL-S9.5	SHV	-	X	PCR (published)	Arlet et al. 1997	-	-
4	EURL-S9.5	TEM	-1		PCR (published)	Olesen et al 2004	-	-
4	EURL-S9.5	VIM	-2		PCR (published)	Poirel et al. 2011	-	-
4	EURL-S9.6	IMP	-	X	PCR (published)	Poirel et al. 2011	-	-
4	EURL-S9.6	KPC	-	X	PCR (published)	Poirel et al. 2011	-	-
4	EURL-S9.6	NDM	-	X	PCR (published)	Poirel et al. 2011	-	-
4	EURL-S9.6	VIM	-	X	PCR (published)	Poirel et al. 2011	-	-
4	EURL-S9.6	OXA	-48		PCR (published)	Poirel et al. 2011	-	-
9	EURL-S9.3	CMY	-2		PCR (published)	JAC 2010;65;490-495;	-	-
9	EURL-S9.4	CTX	M-9		PCR (published)	JAC 2010;65;490-495;	-	-
9	EURL-S9.4	TEM	-1		PCR (published)	JAC 2010;65;490-495;	-	-
9	EURL-S9.5	TEM	-1		PCR (published)	JAC 2010;65;490-495;	-	-
9	EURL-S9.5	VIM	-2		PCR (published)	JAC 2010;65;490-495;	-	-
9	EURL-S9.6	OXA	-48		PCR (published)	JAC 2010;65;490-495;	-	-
17	EURL-S9.3	ACC	-	X	PCR (published)	Pérez-Pérez et al. JCM 2002	-	-
17	EURL-S9.3	CTX	-	X	PCR (published)	Batchelor et al. AAC 2005	-	-
17	EURL-S9.3	DHA	-	X	PCR (published)	Pérez-Pérez et al. JCM 2002	-	-
17	EURL-S9.3	FOX	-	X	PCR (published)	Pérez-Pérez et al. JCM 2002	-	-
17	EURL-S9.3	MOX	-	X	PCR (published)	Pérez-Pérez et al. JCM 2002	-	-
17	EURL-S9.3	SHV	-	X	PCR (published)	Weill et al. JCM 2004	-	-
17	EURL-S9.3	TEM	-	X	PCR (published)	Guerra et al. AAC 2001	-	-
17	EURL-S9.3	CMY	-2		PCR (published)	Zhao et al. AAC 2001	-	-
17	EURL-S9.4	ACC	-	X	PCR (published)	-	-	-
17	EURL-S9.4	DHA	-	X	PCR (published)	-	-	-
17	EURL-S9.4	FOX	-	X	PCR (published)	-	-	-
17	EURL-S9.4	MOX	-	X	PCR (published)	-	-	-
17	EURL-S9.4	SHV	-	X	PCR (published)	-	-	-
17	EURL-S9.4	TEM	-	X	PCR (published)	-	-	-
17	EURL-S9.4	CTX	M-9		PCR (published)	Paauw et al. EID 2006	-	-

Labno	Strain	Genetype	Gene number	Not detected	Method	Reference	Primer 5 3	Primer 3 5
17	EURL-S9.5	ACC	-	X	PCR (published)	-	-	-
17	EURL-S9.5	CTX	-	X	PCR (published)	-	-	-
17	EURL-S9.5	DHA	-	X	PCR (published)	-	-	-
17	EURL-S9.5	FOX	-	X	PCR (published)	-	-	-
17	EURL-S9.5	IMP	-	X	PCR (published)	Dallene et al. JAC 2010	-	-
17	EURL-S9.5	KPC	-	X	PCR (published)	Dallene et al. JAC 2010	-	-
17	EURL-S9.5	MOX	-	X	PCR (published)	-	-	-
17	EURL-S9.5	NDM	-	X	PCR (published)	Poirel et al. DMID 2011	-	-
17	EURL-S9.5	OXA	-48	X	PCR (published)	Dallene et al. JAC 2010	-	-
17	EURL-S9.5	SHV	-	X	PCR (published)	-	-	-
17	EURL-S9.5	TEM	-	X	PCR (published)	-	-	-
17	EURL-S9.5	VIM	-2		PCR (in-house)	see comments	-	-
17	EURL-S9.6	ACC	-	X	PCR (published)	-	-	-
17	EURL-S9.6	CTX	-	X	PCR (published)	-	-	-
17	EURL-S9.6	DHA	-	X	PCR (published)	-	-	-
17	EURL-S9.6	FOX	-	X	PCR (published)	-	-	-
17	EURL-S9.6	IMP	-	X	PCR (published)	-	-	-
17	EURL-S9.6	KPC	-	X	PCR (published)	-	-	-
17	EURL-S9.6	MOX	-	X	PCR (published)	-	-	-
17	EURL-S9.6	NDM	-	X	PCR (published)	-	-	-
17	EURL-S9.6	PER	-	X	PCR (published)	-	-	-
17	EURL-S9.6	SHV	-	X	PCR (published)	-	-	-
17	EURL-S9.6	TEM	-	X	PCR (published)	-	-	-
17	EURL-S9.6	VIM	-	X	PCR (published)	-	-	-
17	EURL-S9.6	OXA	-48		PCR (published)	Aubert JB 2006	-	-
21	EURL-S9.3	CMY	-2		PCR (published)	Pérez-Pérez & Hanson, 2002	-	-
21	EURL-S9.4	CTX	-		PCR (published)	Woodford et al., 2006	-	-
21	EURL-S9.5	VIM	-		PCR (published)	Poirel et al., 2011	-	-
21	EURL-S9.6	OXA	-48		PCR (published)	Poirel et al., 2011	-	-
25	EURL-S9.3	CMY	-2		PCR (published)	Dierikx, Vet Mic, 2010	-	-
25	EURL-S9.4	CTX	M-9		PCR (published)	Paauw A, EID, 2006	-	-
25	EURL-S9.4	TEM	-1		PCR (published)	Dierikx, Vet Mic, 2010	-	-
25	EURL-S9.5	TEM	-1		PCR (published)	Dierikx, Vet MIc, 2010	-	-
25	EURL-S9.5	VIM	-2		PCR (published)	Ellington, JAC, 2007	-	-
25	EURL-S9.6	OXA	-48		PCR (published)	Poirel, AAC., 2004	-	-
26	EURL-S9.3	CMY	-2		PCR (published)	JAC 2005, 56, 115	GCACTTAGCCACCTATACGGCAG	GCTTTTCAAGAATGCGCCAGG
26	EURL-S9.4	SHV	-	X	PCR (published)	JCM, 2010, 48, 460	CAAAACGCCGGGTTATTC	TTAGCGTTGCCAGTGCT
26	EURL-S9.4	CTX	-		PCR (published)	JCM, 2003, 41, 460	ATGTGCAGYACCAGTAARGTKATGGC	TGGGTRAARTARGTSACCAGAAYCAGCGG
26	EURL-S9.4	TEM	-		PCR (published)	JCM, 2010, 48, 460	TGAGTATTCAACATTTCCGTGT	TTACCAATGCTTAATCAGTGA
26	EURL-S9.5	CMY	-2	X	PCR (published)	JAC, 2005, 56, 115	GCACTTAGCCACCTATACGGCAG	GCTTTTCAAGAATGCGCCAGG
32	EURL-S9.3	ACC	-	X	PCR (published)	Hasman et al. 2005	-	-
32	EURL-S9.3	ACT	-	X	PCR (published)	Voets et al. 2011	-	-
32	EURL-S9.3	CTX	-	X	PCR (published)	PediaInfectDisJ28:814-818.2009	-	-
32	EURL-S9.3	DHA	-	X	PCR (published)	Gonzalez-Sanz et al.2009	-	-
32	EURL-S9.3	FOX	-	X	PCR (published)	ANTIMAGENTCHEMOTHe2006.618–624	-	-
32	EURL-S9.3	IMP	-	X	PCR (published)	L. Poirel et al 2011	-	-
32	EURL-S9.3	KPC	-	X	PCR (published)	Dallanne et al 2010	-	-
32	EURL-S9.3	MOX	-	X	PCR (published)	Voets et al. 2011	-	-
32	EURL-S9.3	NDM	-	X	PCR (published)	L. Poirel et al 2011	-	-

Labno	Strain	Genetype	Gene number	Not detected	Method	Reference	Primer 5 3	Primer 3 5
32	EURL-S9.3	OXA	-48	X	PCR (published)	Voets et al 2011	-	-
32	EURL-S9.3	OXA	-30	X	PCR (published)	JAntimChemoth2009641181–1186;	-	-
32	EURL-S9.3	OXA	-10	X	PCR (published)	Voets et al. 2011	-	-
32	EURL-S9.3	SHV	-	X	PCR (published)	FEMSMicrobiLett.1997152:163-7	-	-
32	EURL-S9.3	TEM	-	X	PCR (published)	AntimicrAgentsChemoth2009	-	-
32	EURL-S9.3	VEB	-	X	PCR (published)	Dallanne et al 2010	-	-
32	EURL-S9.3	VIM	-	X	PCR (published)	Dallanne et al 2010	-	-
32	EURL-S9.3	CMY	-2		PCR (published)	JAntimChemother200656:115-121.	-	-
32	EURL-S9.4	ACC	-	X	PCR (published)	-	-	-
32	EURL-S9.4	ACT	-	X	PCR (published)	-	-	-
32	EURL-S9.4	CMY	-	X	PCR (published)	-	-	-
32	EURL-S9.4	DHA	-	X	PCR (published)	-	-	-
32	EURL-S9.4	FOX	-	X	PCR (published)	-	-	-
32	EURL-S9.4	IMP	-	X	PCR (published)	-	-	-
32	EURL-S9.4	KPC	-	X	PCR (published)	-	-	-
32	EURL-S9.4	MOX	-	X	PCR (published)	-	-	-
32	EURL-S9.4	NDM	-	X	PCR (published)	-	-	-
32	EURL-S9.4	OXA	-48	X	PCR (published)	-	-	-
32	EURL-S9.4	OXA	-30	X	PCR (published)	-	-	-
32	EURL-S9.4	OXA	-10	X	PCR (published)	-	-	-
32	EURL-S9.4	SHV	-	X	PCR (published)	-	-	-
32	EURL-S9.4	VEB	-	X	PCR (published)	-	-	-
32	EURL-S9.4	VIM	-	X	PCR (published)	-	-	-
32	EURL-S9.4	CTX	M-14		PCR (published)	-	-	-
32	EURL-S9.4	TEM	-1		PCR (published)	-	-	-
32	EURL-S9.5	ACC	-	X	PCR (published)	-	-	-
32	EURL-S9.5	ACT	-	X	PCR (published)	-	-	-
32	EURL-S9.5	CMY	-	X	PCR (published)	-	-	-
32	EURL-S9.5	CTX	-	X	PCR (published)	-	-	-
32	EURL-S9.5	DHA	-	X	PCR (published)	-	-	-
32	EURL-S9.5	FOX	-	X	PCR (published)	-	-	-
32	EURL-S9.5	IMP	-	X	PCR (published)	-	-	-
32	EURL-S9.5	KPC	-	X	PCR (published)	-	-	-
32	EURL-S9.5	MOX	-	X	PCR (published)	-	-	-
32	EURL-S9.5	NDM	-	X	PCR (published)	-	-	-
32	EURL-S9.5	OXA	-48	X	PCR (published)	-	-	-
32	EURL-S9.5	OXA	-30	X	PCR (published)	-	-	-
32	EURL-S9.5	OXA	-10	X	PCR (published)	-	-	-
32	EURL-S9.5	SHV	-	X	PCR (published)	-	-	-
32	EURL-S9.5	TEM	-	X	PCR (published)	-	-	-
32	EURL-S9.5	VEB	-	X	PCR (published)	-	-	-
32	EURL-S9.5	VIM	-2		PCR (published)	-	-	-
32	EURL-S9.6	ACC	-	X	PCR (published)	-	-	-
32	EURL-S9.6	ACT	-	X	PCR (published)	-	-	-
32	EURL-S9.6	CMY	-	X	PCR (published)	-	-	-
32	EURL-S9.6	CTX	-	X	PCR (published)	-	-	-
32	EURL-S9.6	DHA	-	X	PCR (published)	-	-	-
32	EURL-S9.6	FOX	-	X	PCR (published)	-	-	-
32	EURL-S9.6	IMP	-	X	PCR (published)	-	-	-

Labno	Strain	Genetype	Gene number	Not detected	Method	Reference	Primer 5 3	Primer 3 5
32	EURL-S9.6	KPC	-	X	PCR (published)	-	-	-
32	EURL-S9.6	MOX	-	X	PCR (published)	-	-	-
32	EURL-S9.6	NDM	-	X	PCR (published)	-	-	-
32	EURL-S9.6	OXA	-30	X	PCR (published)	-	-	-
32	EURL-S9.6	OXA	-10	X	PCR (published)	-	-	-
32	EURL-S9.6	SHV	-	X	PCR (published)	-	-	-
32	EURL-S9.6	TEM	-	X	PCR (published)	-	-	-
32	EURL-S9.6	VEB	-	X	PCR (published)	-	-	-
32	EURL-S9.6	OXA	-48		PCR (published)	-	-	-
32	EURL-S9.6	VIM	-		PCR (published)	-	-	-
33	EURL-S9.3	ACC	-	X	PCR (published)	Perez-Perez et al (2002)	ACCAGCCTCAGCAGCCGGTTA	TTCGCCGCAATCATCCCTAGC
33	EURL-S9.3	ACT	-	X	PCR (published)	Perez-Perez et al (2002)	TCGGTAAAGCCGATGTTGCGG	CTTCCACTGCGGCTGCCAGTT
33	EURL-S9.3	DHA	-	X	PCR (published)	Perez-Perez et al (2002)	AACTTTCACAGGTGTGCTGGGT	CCGTACGCATACTGGCTTTGC
33	EURL-S9.3	FOX	-	X	PCR (published)	Perez-Perez et al (2002)	AACATGGGGTATCAGGGAGATG	CAAAGCGCGTAACCGGATTGG
33	EURL-S9.3	MOX	-	X	PCR (published)	Perez-Perez et al (2002)	GCTGCTCAAGGAGCACAGGAT	CACATTGACATAGGTGTGGTGC
33	EURL-S9.3	CMY	-		PCR (published)	Perez-Perez et al (2002)	TGGCCAGAACTGACAGGCAAA	TTTCTCCTGAACGTGGCTGGC
33	EURL-S9.4	CTX	-	X	PCR (published)	Woodford,Fagan, et al. (2006)	AAAAATCACTGCGYCAGTTC	AGCTTATTCATCGCCACGTT
33	EURL-S9.4	CTX	-	X	PCR (published)	Woodford,Fagan, et al. (2006)	CGACGCTACCCCTGCT	CCAGCGTCAGATTTTTCAGG
33	EURL-S9.4	CTX	-	X	PCR (published)	Woodford,Fagan, et al. (2006)	TCGCGTTAAGCGGATGATGATGC	AACCCACGATGTGGGTAGC
33	EURL-S9.4	CTX	-	X	PCR (published)	Woodford,Fagan, et al. (2006)	GCACGATGACATTCGGG	AACCCACGATGTGGGTAGC
33	EURL-S9.4	OXA	-	X	PCR (published)	Fang,Ataker, et al. (2008)	ACACAATACATATCAACTTCGC	AGTGTGTTTAGAATGGTGATC
33	EURL-S9.4	SHV	-	X	PCR (published)	Fang,Ataker, et al. (2008)	CTTTATCGGCCCTCACTCAA	AGGTGCTCATCATGGGAAAG
33	EURL-S9.4	CTX	M-9		PCR (published)	Woodford,Fagan, et al. (2006)	CCAAGAGARTGCAACGGATG	ATTGGAAAGCGTTCATCACC
33	EURL-S9.4	TEM	-		PCR (published)	Fang,Ataker, et al. (2008)	CGCCGCATACACTATTCTCAGAATGA	ACGCTCACCGGCTCCAGATTTAT
33	EURL-S9.5	ACC	-	X	PCR (published)	Perez-Perez et al,2002	AAC AGC CTC AGC AGC CGG TTA	TTC GCC GCA ATC ATC CCT AGC
33	EURL-S9.5	ACT	-	X	PCR (published)	Perez-Perez et al,2002	TCG GTA AAG CCG ATG TTG CGG	CTT CCA CTG CGG CTG CCA GTT
33	EURL-S9.5	CMY	-	X	PCR (published)	Perez-Perez et al,2002	TGG CCA GAA CTG ACA GGC AAA	TTT CTC CTG AAC GTG GCT GGC
33	EURL-S9.5	CTX	-	X	PCR (published)	Woodford et al,2006	AAA AAT CAC TGC GYC AGT TC	AGC TTA TTC ATC GCC ACG TT
33	EURL-S9.5	CTX	-	X	PCR (published)	Woodford et al,2006	CGA CGC TAC CCC TGC T	CCA GCG TCA GAT TTT TCA GG
33	EURL-S9.5	CTX	-	X	PCR (published)	Woodford et al,2006	CAA AGA GAR TGC AAC GGA TG	ATT GGA AAG CGT TCA TCA CC
33	EURL-S9.5	CTX	-	X	PCR (published)	Woodford et al,2006	GCA CGA TGA CAT TCG GG	AAC CCA CGA TGT GGG TAG C
33	EURL-S9.5	CTX	-	X	PCR (published)	Woodford et al,2006	TCG CGT TAA GCG GAT GAT GC	AAC CCA CGA TGT GGG TAG C
33	EURL-S9.5	DHA	-	X	PCR (published)	Perez-Perez et al,2002	AAC TTT CAC AGG TGT GCT GGG T	CCG TAC GCA TAC TGG CTT TGC
33	EURL-S9.5	FOX	-	X	PCR (published)	Perez-Perez et al,2002	AAC ATG GGG TAT CAG GGA GAT G	CTT CCA CTG CGG CTG CCA GTT
33	EURL-S9.5	IMP	-	X	PCR (published)	Poirel et al,2011	GGAATAGAGTGGCTTAAYTCTC	GGTTTAAYAAAACAACCACC
33	EURL-S9.5	KPC	-	X	PCR (published)	Poirel et al,2011	CGTCTAGTTCTGCTGTCTTG	CTTGTCATCCTTGTTAGGCG
33	EURL-S9.5	MOX	-	X	PCR (published)	Perez-Perez et al,2002	GCT GCT CAA GGA GCA CAG GAT	CAC ATT GAC ATA GGT GTG GTG C
33	EURL-S9.5	NDM	-	X	PCR (published)	Poirel et al,2011	GGTTTGGCGATCTGGTTTTC	CGGAATGGCTCATCACGATC
33	EURL-S9.5	OXA	-	X	PCR (published)	Poirel et al,2011	GCGTGGTTAAGGATGAACAC	CATCAAGTTCAACCCAACCG
33	EURL-S9.5	OXA	-	X	PCR (published)	Fang et al,2008	ACACAATACATATCAACTTCGC	AGTGTGTTTAGAATGGTGATC
33	EURL-S9.5	SHV	-	X	PCR (published)	Fang et al,2008	CTTTATCGGCCCTCACTCAA	AGGTGCTCATCATGGGAAAG
33	EURL-S9.5	TEM	-		PCR (published)	Fang et al,2008	CGCCGCATACACTATTCTCAGAATGA	ACGCTCACCGGCTCCAGATTTAT
33	EURL-S9.5	VIM	-		PCR (published)	Poirel et al,2011	GATGGTGTTTGGTCGCATA	CGAATGCGCAGCACCAG
33	EURL-S9.6	ACC	-	X	PCR (published)	Perez-Perez et al 2002	AAC AGC CTC AGC AGC CGG TTA	TTC GCC GCA ATC ATC CCT AGC
33	EURL-S9.6	ACT	-	X	PCR (published)	Perez-Perez et al 2002	TCG GTA AAG CCG ATG TTG CGG	CTT CCA CTG CGG CTG CCA GTT
33	EURL-S9.6	CMY	-	X	PCR (published)	Perez-Perez et al 2002	TGG CCA GAA CTG ACA GGC AAA	TTT CTC CTG AAC GTG GCT GGC
33	EURL-S9.6	CTX	-	X	PCR (published)	Woodford er al,2006	AAA AAT CAC TGC GYC AGT TC	AGC TTA TTC ATC GCC ACG TT
33	EURL-S9.6	CTX	-	X	PCR (published)	Woodford er al,2006	CGA CGC TAC CCC TGC T	CCA GCG TCA GAT TTT TCA GG
33	EURL-S9.6	CTX	-	X	PCR (published)	Woodford er al,2006	CAA AGA GAR TGC AAC GGA TG	ATT GGA AAG CGT TCA TCA CC

Labno	Strain	Genetype	Gene number	Not detected	Method	Reference	Primer 5 3	Primer 3 5
33	EURL-S9.6	CTX	-	X	PCR (published)	Woodford er al,2006	TCG CGT TAA GCG GAT GAT GC	AAC CCA CGA TGT GGG TAG C
33	EURL-S9.6	CTX	-	X	PCR (published)	Woodford er al,2006	GCA CGA TGA CAT TCG GG	AAC CCA CGA TGT GGG TAG C
33	EURL-S9.6	DHA	-	X	PCR (published)	Perez-Perez et al 2002	AAC TTT CAC AGG TGT GCT GGG T	CCG TAC GCA TAC TGG CTT TGC
33	EURL-S9.6	FOX	-	X	PCR (published)	Perez-Perez et al 2002	AAC ATG GGG TAT CAG GGA GAT G	CAA AGC GCG TAA CCG GAT TGG
33	EURL-S9.6	IMP	-	X	PCR (published)	Poirel et al,2011	GGAATAGAGTGGCTTAAYTCTC	GGTTTAAYAAAACAACCACC
33	EURL-S9.6	KPC	-	X	PCR (published)	Poirel et al,2011	CGTCTAGTTCTGCTGTCTTG	CTTGTCATCCTTGTTAGGCG
33	EURL-S9.6	MOX	-	X	PCR (published)	Perez-Perez et al 2002	GCT GCT CAA GGA GCA CAG GAT	CAC ATT GAC ATA GGT GTG GTG C
33	EURL-S9.6	NDM	-	X	PCR (published)	Poirel et al,2011	GGTTTGGCGATCTGGTTTTC	CGGAATGGCTCATCACGATC
33	EURL-S9.6	OXA	-	X	PCR (published)	Fang et al,2008	ACACAATACATATCAACTTCGC	AGTGTGTTTAGAATGGTGATC
33	EURL-S9.6	SHV	-	X	PCR (published)	Fang et al,2008	CTTTATCGGCCCTCACTCAA	AGGTGCTCATCATGGGAAAG
33	EURL-S9.6	TEM	-	X	PCR (published)	Fang et al,2008	GCCGCATACACTATTCTCAGAATGA	ACGCTCACCGGCTCCAGATTTAT
33	EURL-S9.6	VIM	-	X	PCR (published)	Poirel et al,2011	GATGGTGTTTGGTCGCATA	CGAATGCGCAGCACCAG
33	EURL-S9.6	OXA	48		PCR (published)	Poirel et al,2011	GCGTGGTTAAGGATGAACAC	CATCAAGTTCAACCCAACCG
41	EURL-S9.3	ACC	-1	X	PCR (published)	-	5'-AGCCTCAGCAGCCGGTTAC -3'	5'-GAAGCCGTTAGTTGATCCGG -3
41	EURL-S9.3	CMY	-	X	PCR (published)	-	5'-ATGCAACAACGACAATCC-3	5'-TTGGCCAGCATGACGATG-3
41	EURL-S9.3	CTX	-	X	PCR (published)	-	5'-ATGTGCAGYACCAGTAARGTKATGGC-3	5'-TGGGTRAARTARGTSACCAGAAYSAGCGG-3'
41	EURL-S9.3	CTX	M-1	X	PCR (published)	-	5'-CCATGGTTAAAAAATCACTGCG-3	5'-TGGGTRAARTARGTSACCAGAAYSAGCGG-3
41	EURL-S9.3	CTX	M-2	X	PCR (published)	-	5'-ATGATGACTCAGAGCATTCG-3'	5'-GAAACCGTGGGTTACGATTT-3'
41	EURL-S9.3	CTX	M-9	X	PCR (published)	-	5'-GTGACAAAGAGAGTGCAACGG-3'	5'-ATGATTCTCGCCGCTGAAGCC-3'
41	EURL-S9.3	IMP	-	X	PCR (published)	-	5'-GGAATAGAGTGGCTTAAYTCTC-3'	5'-GGTTTAAYAAAACAACCACC-3'
41	EURL-S9.3	KPC	-	X	PCR (published)	-	5'-CGTCTAGTTCTGCTGTCTTG-3'	5'-CTTGTCATCCTTGTTAGGCG-3'
41	EURL-S9.3	NDM	-	X	PCR (published)	-	5'-GGTTTGGCGATCTGGTTTTC-3'	5'-CGGAATGGCTCATCACGATC-3
41	EURL-S9.3	OXA	-48	X	PCR (published)	-	5'-GCGTGGTTAAGGATGAACAC-3'	5'-CATCAAGTTCAACCCAACCG-3
41	EURL-S9.3	TEM	-	X	PCR (published)	-	5'-GCGGAACCCCTATTTG-3	5'-ACC AAT GCT TAA TCA GTG AG-3
41	EURL-S9.3	VIM	-	X	PCR (published)	-	5'-GATGGTGTTTGGTCGCATA-3'	5'-CGAATGCGCAGCACCAG-3
41	EURL-S9.3	CMY	-2		PCR (published)	-	5'-ATGATGAAAAAATCGTTATGCTGC-3	5'-GCTTTTCAAGAATGCGCCAGG-3
41	EURL-S9.4	ACC	-1	X	PCR (published)	-	-	-
41	EURL-S9.4	CMY	-2	X	PCR (published)	-	-	-
41	EURL-S9.4	CMY	-	X	PCR (published)	-	-	-
41	EURL-S9.4	CTX	M-1	X	PCR (published)	-	-	-
41	EURL-S9.4	CTX	M-2	X	PCR (published)	-	-	-
41	EURL-S9.4	IMP	-	X	PCR (published)	-	-	-
41	EURL-S9.4	KPC	-	X	PCR (published)	-	-	-
41	EURL-S9.4	NDM	-	X	PCR (published)	-	-	-
41	EURL-S9.4	OXA	-48	X	PCR (published)	-	-	-
41	EURL-S9.4	VIM	-	X	PCR (published)	-	-	-
41	EURL-S9.4	CTX	-		PCR (published)	-	-	-
41	EURL-S9.4	CTX	M-9		PCR (published)	-	-	-
41	EURL-S9.4	TEM	-		PCR (published)	-	-	-
41	EURL-S9.5	ACC	-1	X	PCR (published)	-	-	-
41	EURL-S9.5	CMY	-2	X	PCR (published)	-	-	-
41	EURL-S9.5	CMY	-	X	PCR (published)	-	-	-
41	EURL-S9.5	CTX	-	X	PCR (published)	-	-	-
41	EURL-S9.5	CTX	M-1	X	PCR (published)	-	-	-
41	EURL-S9.5	CTX	M-2	X	PCR (published)	-	-	-
41	EURL-S9.5	CTX	M-9	X	PCR (published)	-	-	-
41	EURL-S9.5	IMP	-	X	PCR (published)	-	-	-
41	EURL-S9.5	KPC	-	X	PCR (published)	-	-	-
41	EURL-S9.5	NDM	-	X	PCR (published)	-	-	-

Labno	Strain	Genetype	Gene number	Not detected	Method	Reference	Primer 5 3	Primer 3 5
41	EURL-S9.5	OXA	-48	X	PCR (published)	-	-	-
41	EURL-S9.5	TEM	-		PCR (published)	-	-	-
41	EURL-S9.5	VIM	-		PCR (published)	-	-	-
41	EURL-S9.6	ACC	-1	X	PCR (published)	-	-	-
41	EURL-S9.6	CMY	-2	X	PCR (published)	-	-	-
41	EURL-S9.6	CMY	-	X	PCR (published)	-	-	-
41	EURL-S9.6	CTX	-	X	PCR (published)	-	-	-
41	EURL-S9.6	CTX	M-1	X	PCR (published)	-	-	-
41	EURL-S9.6	CTX	M-2	X	PCR (published)	-	-	-
41	EURL-S9.6	CTX	M-9	X	PCR (published)	-	-	-
41	EURL-S9.6	IMP	-	X	PCR (published)	-	-	-
41	EURL-S9.6	KPC	-	X	PCR (published)	-	-	-
41	EURL-S9.6	NDM	-	X	PCR (published)	-	-	-
41	EURL-S9.6	TEM	-	X	PCR (published)	-	-	-
41	EURL-S9.6	VIM	-	X	PCR (published)	-	-	-
41	EURL-S9.6	OXA	-48		PCR (published)	-	-	-
41	EURL-S9.7	ACC	-1	X	PCR (published)	-	-	-
41	EURL-S9.7	CMY	-2	X	PCR (published)	-	-	-
41	EURL-S9.7	CMY	-	X	PCR (published)	-	-	-
41	EURL-S9.7	CTX	-	X	PCR (published)	-	-	-
41	EURL-S9.7	CTX	M-1	X	PCR (published)	-	-	-
41	EURL-S9.7	CTX	M-2	X	PCR (published)	-	-	-
41	EURL-S9.7	CTX	M-9	X	PCR (published)	-	-	-
41	EURL-S9.7	IMP	-	X	PCR (published)	-	-	-
41	EURL-S9.7	KPC	-	X	PCR (published)	-	-	-
41	EURL-S9.7	NDM	-	X	PCR (published)	-	-	-
41	EURL-S9.7	OXA	-48	X	PCR (published)	-	-	-
41	EURL-S9.7	VIM	-	X	PCR (published)	-	-	-
41	EURL-S9.7	TEM	-		PCR (published)	-	-	-
59	EURL-S9.3	CMY	-2		Whole genome sequenced	-	-	-
59	EURL-S9.4	CTX	M-9		Whole genome sequenced	-	-	-
59	EURL-S9.4	TEM	-1B		Whole genome sequenced	-	-	-
59	EURL-S9.5	VIM	-2		Whole genome sequenced	-	-	-
59	EURL-S9.6	OXA	-48		Whole genome sequenced	-	-	-

Legend:

Fields shaded grey indicate that the gene was expected

Genes in bold and white font, were detected but not expected

Genotypic characterization (optional); comments by participants

Labno	Strain	Comment
1	S-9.4	Also contains blaTEM1-b, which is not a cephalosporinase or a carbapenemase
1	S-9.5	Also contains blaTEM1-b, which is not a cephalosporinase or a carbapenemase
17	S-9.3	The strain was positive for CIT in the Perez-Perez multiplex. A 1000 bp PCR fragment obtained with the Zhao primers was then sequenced.
17	S-9.4	All other primers references can be found by strain 9.3. We tested for all CTX-M groups (CTX-M-1g, CTX-M-2g, CTX-M-9g CTX-M-8g). CTX-9g was positive and sequenced with the primers cited above. All other primers references can be found by strain 9.3.
17	S-9.5	The strain was positive for VIM genes in a PCR multiplex (Dallene et al. JAC 2010), and a 400 bp fragment obtained with unpublished primers provided by Y. Pfeifer were sequenced resulting VIM-2. The sequencing of a longer sequence with other primers failed. All other primers references can be found by strain 9.3.
17	S-9.6	The strain was positive for oxa-48 with the Dallene et al. JAC 2010 multiplex, and then a 744 bp PCR fragment obtained wth primers provided by Y Pfeiffer (Aubert et el. J Bacteriol. 2006)was sequenced. All other primers references can be found by strain 9.3.
21	S-9.4	blaCTX-M group4
32	S-9.3	SPM Gene tested for/not detected (L. Poirel et al 2011)
32	S-9.4	SPM Gene tested for/not detected (L. Poirel et al 2011)
32	S-9.5	SPM Gene tested for/not detected (L. Poirel et al 2011)
32	S-9.6	SPM Gene tested for/not detected (L. Poirel et al 2011)
33	S-9.3	As CMY belongs to the CIT Group we would prefere to have that choice as we use a Muliplex PCR. Why is not the CIT Group listed?
41	S-9.3	The genes SPM and BIC were tested, but they did not detected
41	S-9.4	The genes SPM and BIC were tested, but they did not detected
41	S-9.5	The genes SPM and BIC were tested, but they did not detected
41	S-9.6	The genes SPM and BIC were tested, but they did not detected
41	S-9.7	The genes SPM and BIC were tested, but they did not detected

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