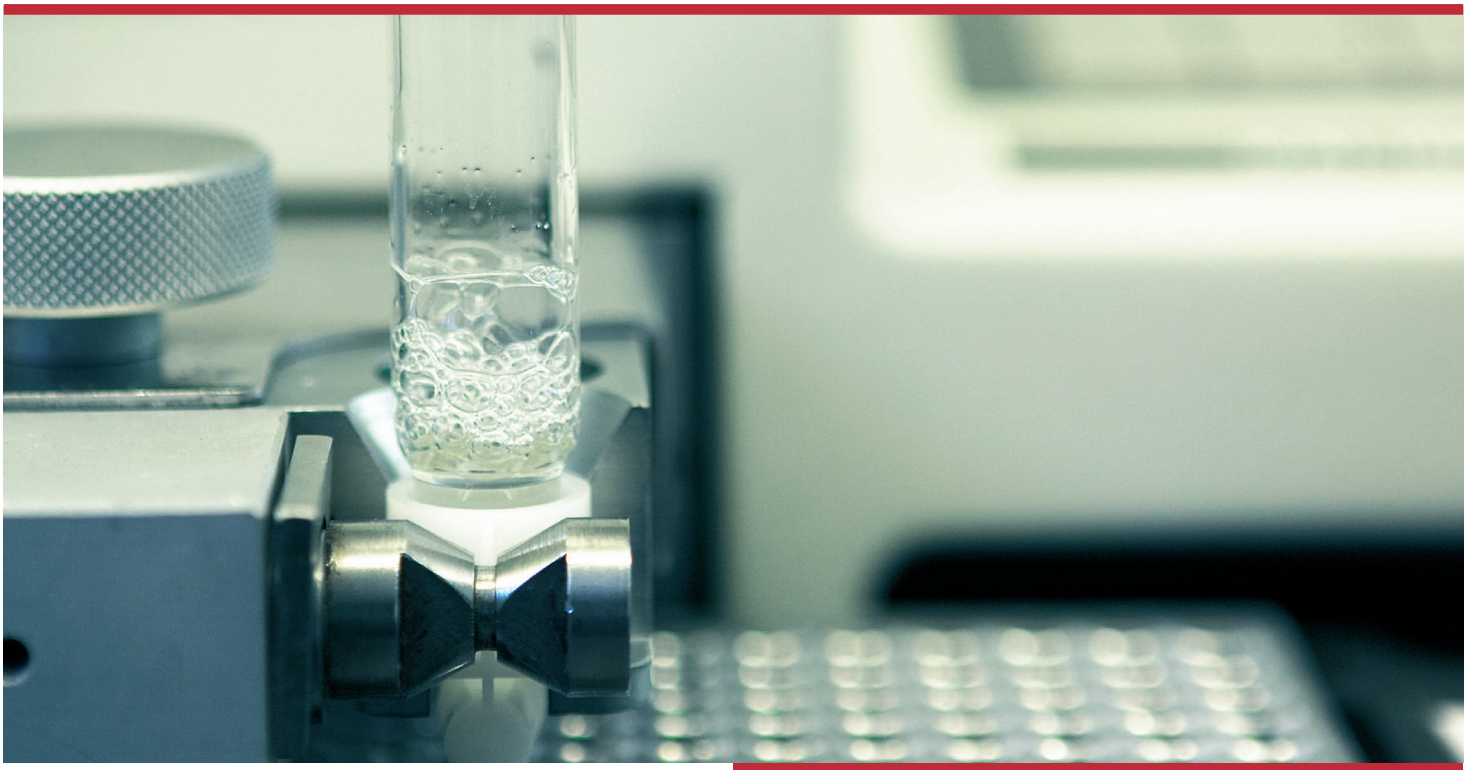
The 15th EURL-AR Proficiency Test *Salmonella, Campylobacter* and genotypic characterisation 2013



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The 15th EURL-AR Proficiency Test *Salmonella, Campylobacter* and genotypic characterisation 2013

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1. Introduction

This report describes and summarises results from the fifteenth 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 fifth 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 extended spectrum cephalosporinases (ESC) in the ESC-producing *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 elaboration.

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 evaluates 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 2013

A pre-notification (App. 1) to announce the EURL-AR EQAS on AST of *Salmonella* and *Campylobacter* was distributed on the 25th June 2013 by e-mail to the 41 NRLs in the EURL-AR-network including all EU countries (except Luxembourg where no NRL-AR was designated) and including Iceland, Norway, Serbia, Switzerland and Turkey. One laboratory did not participate as they had neither *Salmonella* nor *Campylobacter* AST as their field of responsibility. Serbia, Turkey and one NRL 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 ESC-producing *Salmonella* test strains was offered.

Appendix 2 shows that 33 of the 37 participating NRLs were appointed by the individual Member States' Competent Authority. Two NRLs were enrolled in the network on equal terms as the designated NRLs, based on their participation in an EU funded concerned action (FAIR5-QLK2-2002-01146), the ARBAO II project (Antibiotic Resistance in Bacteria of Animal Origin). These two laboratories, together with those in Norway and Switzerland, 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 30 participating countries, 28 tested both *Salmonella* and *Campylobacter*. Two countries, for different reasons, uploaded *Salmonella* results, only, for evaluation (Greece and Malta), and one country uploaded results both for *Salmonella* and *Campylobacter*, however, for *Campylobacter* they delivered species identification, only. Eight 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 30 countries consisting of 34 laboratories submitting *Salmonella* results and 30 laboratories submitting *Campylobacter* results. Results from the two laboratories not designated by the MS but enrolled on equal terms as these are not

further presented or evaluated in this report.

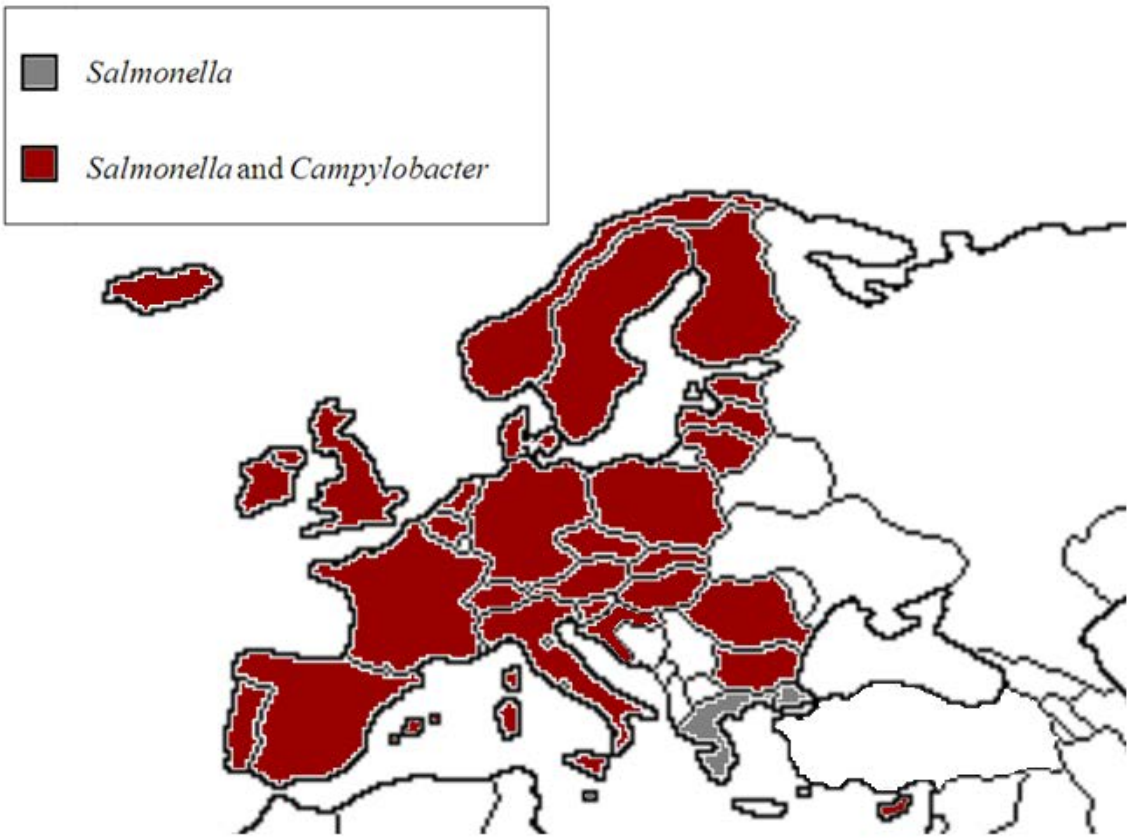

Figure 1: Participating countries that performed antimicrobial susceptibility testing of *Salmonella* or both *Salmonella* and *Campylobacter.*

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, and trimethoprim for *Salmonella* and furthermore, chloramphenicol and 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 were changed in relation to previous trials and were - to the extent possible - adjusted towards the panel of antimicrobials listed in the new the EU regulation (Decision 2013/652/EU). Antimicrobials listed in the new regulation for which MIC-panels for AST and interpretative criteria for interpretation of the result were available, were included for the proficiency test.

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-S23 (2013) "Performance Standards for Antimicrobial Susceptibility Testing" (Twenty-Third 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 EUCAST epidemiological cut-off values (www.eucast.org) as described and listed in the protocol (App. 4). Where EUCAST interpretative criteria were not available, CLSI-interpretative criteria were listed as the alternative. 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), cefepime (FEP), cefotaxime (CTX), cefotaxime/clavulanic acid (CTX/CI), cefoxitin (FOX), ceftazidime (CAZ), ceftazidime/clavulanic acid (CAZ/CI), chloramphenicol (CHL), ciprofloxacin (CIP), colistin (COL), ertapenem (ERT), gentamicin (GEN), imipenem (IMI), meropenem (MER), nalidixic acid (NAL), sulfonamides (sulfamethoxazole) (SMX), tetracycline (TET) 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 (panel code ESB1F), and in addition, for the antimicrobials cefotaxime/clavulanic acid, cefoxitin, ceftazidime/clavulanic acid, tests were performed using E-test from AB-Biodisk, Sweden.

For *Campylobacter* the following antimicrobials were included: chloramphenicol (CHL), 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). This year, 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 14th October 2013, 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). 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.

The aim is that only MIC methods are used when performing AST for monitoring conducted by the Commission, and thereby also when performing the EURL-AR EQAS's. Consequently, it was decided in May 2007 by the participants at the EURL-AR workshop that the NRLs should work towards harmonising to MIC methods for these AST analyses. Additionally, it was agreed that all NRLs should work towards covering the antimicrobial panel and epidemiological cut-off values recommended by the EURL-AR. For this EQAS, the participants were instructed to use as many as possible of the antimicrobials listed, using the method carried out when performing monitoring for EFSA.

It should be noted that for AST of *Campylobacter* the EURL-AR does not recommend the use of either disk diffusion or E-test for AST of *Campylobacter*. I.e. only results obtained by broth or agar dilution methods are accepted for this EQAS, as also agreed at the EURL-AR workshop 2009.

A mandatory part of the proficiency test was to detect ESC-producing strains and interpret results according to recommendations by EUCAST 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) or, for *E. coli* (ATCC 25922), the inhibition zone diameters in millimetres. The results were evaluated towards the quality control ranges according to the relevant guidelines; i.e. the CLSI documents VET01-S2 (2013) or M100-S23 (2013) (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 and OXA-genes resulting in $bla_{\text{TEM-1}}$ and $bla_{\text{OXA-30}}$ registered as expected genes, 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 1.4 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 11th December 2013. 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.

Upon review of the submitted data, the EQAS organizers came to realise that it was necessary to make changes in the EQAS-database as regards the expected results of two strains, i.e. S-8.4 and S-8.5. Detailed information was sent to the participants on February 5th 2014 with description of background for the changes and encouragement to login to the database again to retrieve updated evaluation reports.

3. Results

The participants were asked to report results, including MIC values or inhibition zone diameters obtained by DD together with the categorisation as resistant or susceptible. Only the categorisation was evaluated, whereas the MIC values and disk diffusion inhibition zones 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 one case: for the combination of the test strain S-8.4/meropenem with a level of disagreement with the expected results at 62% based on 13 results of which 5 were assigned with the expected interpretation as resistant. The testing and interpretation in relation to this strain/antimicrobial combination was complex and ultimately, it was decided to leave out the database evaluation as correct/incorrect of both the categorization in relation to meropenem resistant and the classification as ESBL/AmpC/carbapenemase-producer, and consequently leave this data out from further evaluation in this report

This conclusion was based on the following; 1) EUCAST cut off for meropenem is R>0.125; 2) in the currently available MIC-panels, the

EUCAST cutoff for meropenem is not covered (lowest meropenem dilution is 1 mg/L); 3) interpretative criteria for disk diffusion results corresponding to the EUCAST cut off value are not available; 4) to obtain an MIC-value that could be interpreted according to the interpretative criteria listed in the protocol, the EQAS participants had to perform AST by E-test or agar dilution; 5) at the EURL-AR, the expected value was obtained by performing AST by E-test; 6) participants submitted results based on either microbroth dilution, DD and E-test (for each method results reported by one third of NRLs); and 7) some participants submitted an MIC-value but no interpretation or an interpretation but no MIC-value.

Follow-up at the EURL-AR on the strain S-8.4 regarding the MIC for meropenem included additional E-tests on a number agar sticks that had been stored since the production for the EQAS. These results indicated that the expected value should be adjusted and lowered to 0.125. Based on these results together with the results submitted by the participants, it was decided to adjust the expected value for meropenem to an MIC of 0.125 with an interpretation as 'susceptible'.

Classifying the phenotypic results according to the EFSA recommendations (EFSA Journal 2012; 10(6):2742), the updated conclusion is 'presumptive pAmpC phenotype'. This classification is not correct, and the EURL-AR has decided not to follow the EFSA recommendations in this particular case, since the strain expresses phenotypical resistance to e.g. ertapenem and imipenem and harbours the VIM-2-gene.

3.2 Methods

In the data analysis, results were grouped according to the methods used by the participants. 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, 30 laboratories used MIC determination (28 used microbroth and two agar dilution), and four laboratories used disk diffusion. For the *Campylobacter* trial, all 30 included laboratories reported the use of MIC determination (microbroth or agar dilution).

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 strain mainly followed the trend in deviation level of the different EQAS trials (Figure 2). The deviation level in 2013 is acceptable for both the *Salmonella* and the *Campylobacter* trials. For the *Campylobacter* AST, however, it appears that there has been an increase in the level of deviations, to 3.5% in 2013 compared to 2.1% in 2012. Four laboratories' high deviation levels (between 12.5% and 19.0%) caused this increase.

3.3.1 *Salmonella* trial

For the *Salmonella* strains, 99.3% of the AST's were interpreted correctly. Figure 3 shows the total percentage of deviations from the expected results of AST performed by MIC-methods as opposed to disk diffusion. The deviation percentage is significantly higher ($p<0.05$) when AST is performed by disk diffusion compared to a MIC-method.

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 97.9-99.5% for *Salmonella*. Table 2 illustrates the percentage of correct AST per antimicrobial by bacterial species. The level of correct AST was above 97.7% for the *Salmonella* test strains. Sulfonamides exhibited the lowest deviation level.

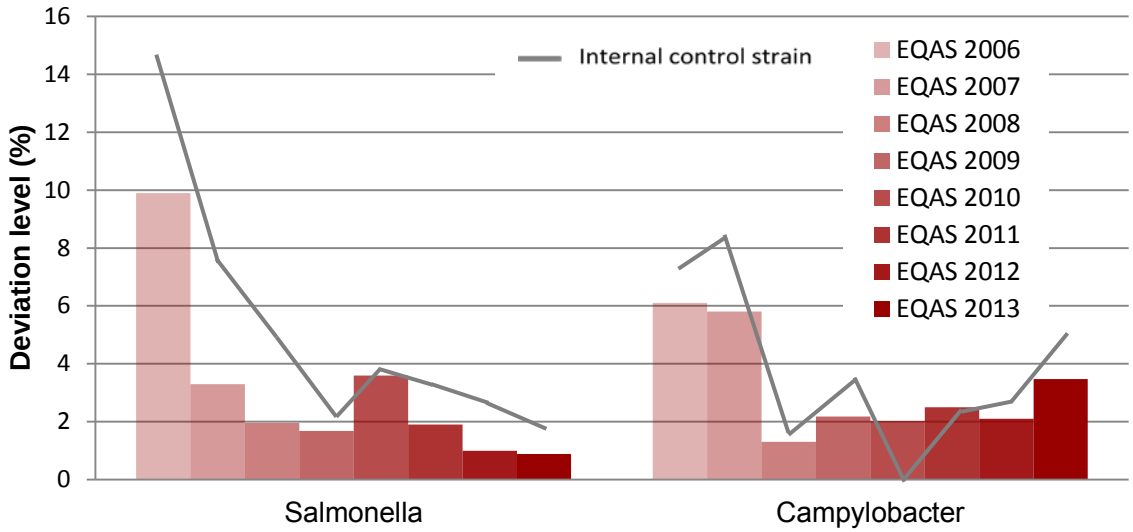

Figure 2: A comparison between the EURL-AR EQAS's since 2006, showing the total percentage of deviations for antimicrobial susceptibility testing performed by participating laboratories.

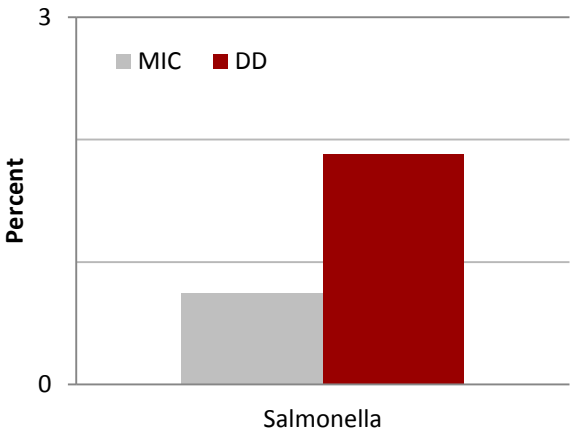

Figure 3: The total percentage of deviations for AST's performed using MIC-methods as opposed to disk diffusion.

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 (CTX) and ceftazidime (CAZ) 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 CTX:CTX/CI or CAZ:CAZ/CI ratio ≥8) or ii) a ≥5 mm increase in a zone diameter for either antimicrobial agent tested in combination with clavulanic acid vs. its zone when tested alone (CLSI M100 Table 2A; Enterobacteriaceae). The presence of synergy indicates ESBL-production. Resistance to cefepime gives further indication of ESBL production.

Confirmatory test for carbapenemase production requires the testing of meropenem (MER).

Detection of AmpC-type beta-lactamase producing bacteria can be performed by testing the isolates for susceptibility to cefoxitin (FOX). Resistance to FOX could indicate the presence of an AmpC-type beta-lactamase, which may be verified by PCR and sequencing.

The classification of the phenotypic results should be 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
- 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-8.4 was a carbapenemase producer, however, results for this will not be further evaluated in this report (see description above (section 3.1)), S-8.5, S-8.6 and S-8.7 were ESC producers. For the strain S-8.5, both interpretations as unusual phenotype and ESBL phenotype were considered correct. The categorization as 'unusual' was based on the phenotypic testing, whereas the categorization as ESBL-producer required additional genotypic testing. Phenotypic and genotypic tests indicated that this particular strain expresses synergy when testing CTX and CTX/CI as well as CAZ and CAZ/CI, it is susceptible to cefoxitin. In addition, the strain does not express resistance to cefepime (in the absence of EUCAST epidemiological cut-off values, CLSI interpretative criteria were applied) but harbours a CTX-M9-gene.

Deviations from expected results in relation to the strains S-8.5, S-8.6 and S-8.7 were as follows:

In total the categorization as ESBL-, pAmpC- or carbapenemase-producer was incorrect in 12 cases, with five of the incorrect results submitted for strains which were not resistant to cephalosporins or carbapenems. Six of the 12 incorrect results related to one laboratory (#58), whereas the other six related to six different laboratories. Of these, four had detected cefepime resistance for strain S-8.7 (#6, #18, #30 and #56) and therefore categorized this as unusual phenotype, one (#22) had registered S-8.3 as unusual phenotype, the registered data for this strain, however, did not indicate this. Finally, laboratory #41 had observed imipenem resistance for strain S-8.6 and based on this categorized the strain to have an unusual phenotype. For laboratory #58 the high number of incorrect results in this context appears to be related to the handling of the strains or other procedures in the laboratory.

3.3.2 *Campylobacter* trial

For the *Campylobacter* strains, 96.5% of AST's were correctly tested. Table 1 presents that the variation in the obtained correct results ranged from 93.9-98.9% and Table 2 illustrates that the percentage of correct AST per antimicrobial was above 93.2% for the *Campylobacter* test strains with nalidixic acid exhibiting the lowest level.

For the first time, the participants were requested to identify the *Campylobacter* species. The exercise went very well with 30 laboratories delivering in total 240 results with only three identifications incorrect. One participant did not upload data for *Campylobacter* identity (Lab #23). The registered deviations were obtained by two participants who failed to identify one strain (#40) and two strains (#36), respectively.

3.4 Deviations by laboratory

Figure 4 and 5 illustrate the percentage of deviations for each participating laboratory. The laboratories are ranked according to their performance determined by the percentage of deviating results in the antimicrobial susceptibility tests.

3.4.1 *Salmonella* trial

Thirty-two of the laboratories obtained a result within the acceptance limit at 5% deviations for the *Salmonella* strains. The maximum

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

EQAS 2013 – *Salmonella*			EQAS 2013 – *Campylobacter*		
Test strain	AST in total	% correct	Test strain	AST in total	% correct
S-8.1	382	99.0	C-8.1 (*C. coli*)	179	93.9
S-8.2	381	99.5	C-8.2 (*C. coli*)	180	97.8
S-8.3	383	99.5	C-8.3 (*C. jejuni*)	174	94.8
S-8.4	369	99.7	C-8.4 (*C. jejuni*)	161	96.9
S-8.5	382	98.2	C-8.5 (*C. jejuni*)	180	97.8
S-8.6	383	99.7	C-8.6 (*C. coli*)	180	96.1
S-8.7	384	99.5	C-8.7 (*C. coli*)	180	96.1
S-8.8	382	97.9	C-8.8 (*C. coli*)	180	98.9

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

Antimicrobial	*Salmonella*	*Campylobacter*
Ampicillin	99.6	-
Cefotaxime	99.6	-
Ceftazidime	98.9	-
Chloramphenicol	99.3	-
Ciprofloxacin	98.2	96.6
Colistin	98.3	-
Erythromycin	-	97.5
Gentamicin	99.6	99.6
Meropenem	100	-
Nalidixic acid	99.3	93.2
Streptomycin	-	96.6
Sulphonamides	97.7	-
Tetracycline	99.6	95.7
Trimethoprim	99.6	-

percentage of deviations was 7.4%. The performance of two (6%) laboratories resulted in a deviation level above the level of performance expected by the EURL-AR (#42 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 30 participating laboratories performed acceptably, with 13 laboratories having no deviations (Figure 5). Six laboratories present a deviation level above the 5% acceptance level (#6, #12, #22, #29, #37 and #44) and of these, the four with deviation levels at 12.5%, 12.5%, 14.6% and 19.0% were regarded as outliers (#29, #37, #6, and #22).

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 laboratories performing disk diffusion to test the *E. coli* reference strain (ATCC 25922), all but three of the obtained results were within the QC-range. Results from #15 for colistin and for #45 for ampicillin and gentamicin were slightly below or above the QC-range.

From the 26 laboratories submitting AST-results for the reference strain *E. coli* ATCC 25922 tested by MIC determination, eight laboratories produced in all 9 values outside the QC-limit. Table 4 illustrates the obtained results which are shown in full in Appendix 6a.

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-8.4	Strain S-8.5	Strain S-8.6	Strain S-8.7
ESC-genes harboured in the test strain		***bla*$_{VIM-2}$** ***bla*$_{TEM-1}$**	***bla*$_{CTX-M-9}$** ***bla*$_{TEM-1}$**	***bla*$_{CTX-M-3}$** ***bla*$_{OXA-30}$**	***bla*$_{TEM-52}$**
ESBL-, pAmpC- and carbapenemase-producing strain – expected results		Carbapenemase	ESBL unusual	ESBL	ESBL
Obtained results	Confirmed ESBL-producer	NA	22/34 (65%)	33/34 (97%)	29/34 (85%)
	Confirmed pAmpC-producer	NA	-	-	-
	Confirmed carbapenemase-producer	NA	-	-	-
	Confirmed unusual phenotype	NA	11/34 (32%)	*1/34 (3%)*	*4/34 (12%)*
	Not ESBL-, pAmpC- or carbapenemase-producing	NA	*1/34 (3%)*	-	*1/34 (3%)*

NA: Not applicable; see explanation above in section 3.1

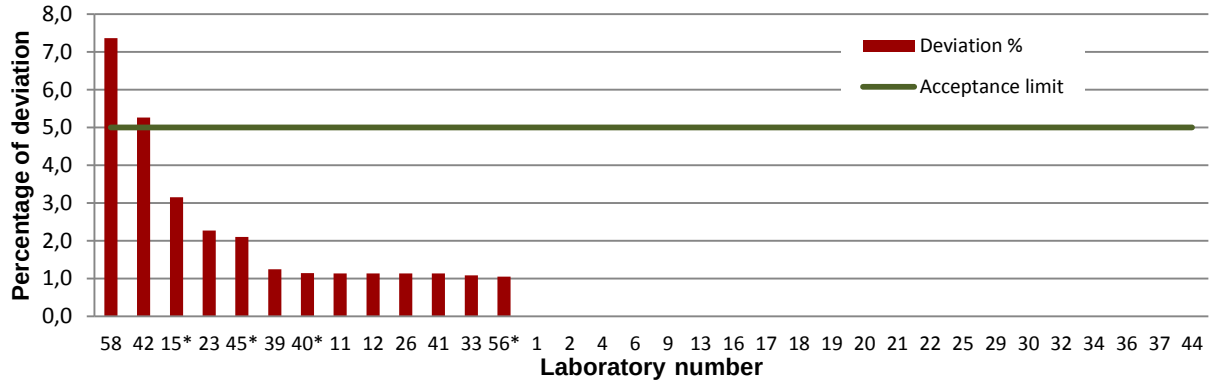

Figure 4: Individual participants' deviations in percent of their total number of *Salmonella* AST's. An asterisk indicates that the laboratory performed AST using disk diffusion

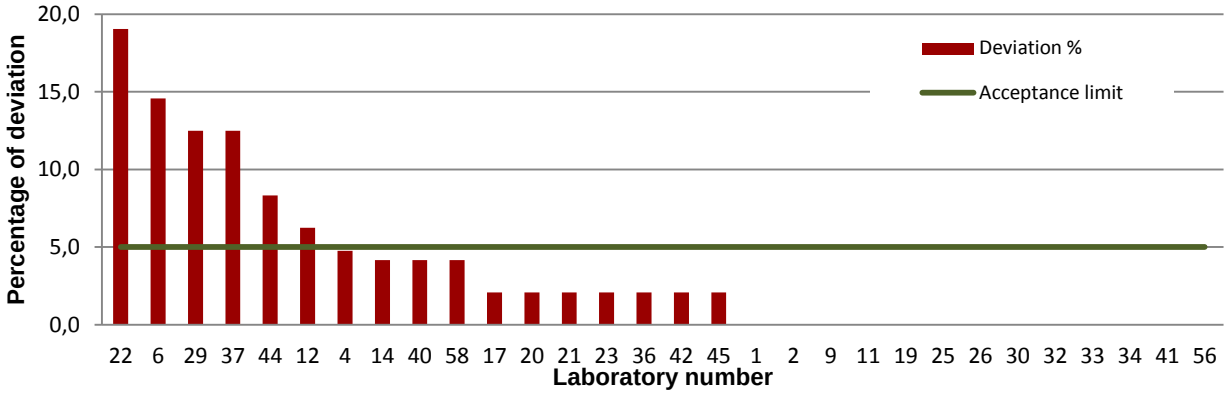

Figure 5: Individual participants' deviations in percent of their total number of *Campylobacter* AST's.

Table 5 presents the proportion of laboratories with results for the *C. jejuni* reference strain ATCC 33560 below or above the QC interval. Nine deviations were seen, three presented by one laboratory (#21) and the remaining by six laboratory with one each.

3.6 Genotypic characterisation

For the optional genotypic characterisation of the ESC-producing *Salmonella* test strains, eight 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. One laboratory performed whole genome sequencing of the ESC-producing *Salmonella*, the remaining seven 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 6 indicates that the discordant results were submitted by three laboratories. Additional genes/variants not correlating with the expected were also found indicating false positive results. The laboratories which obtained these results should evaluate the procedure to assess how the relevant test could be improved in the future.

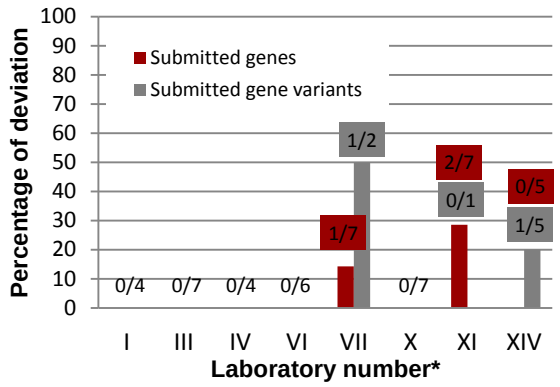

Figure 6: Individual participants' deviations in percent of their total number of results from the genotypic characterization.
*Note, laboratory numbers are different from those assigned in the susceptibility testing component.

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

MIC determination *E. coli* ATCC 25922			
Anti-microbial	Proportion outside QC range	Obtained values in MIC steps (min/max)	
		Below lower QC limit	Above upper QC limit
AMP	0/31 (0%)	-	-
FEB	0/5 (0%)	-	-
CTX	0/31 (0%)	-	-
FOX	0/7 (0%)	-	-
CAZ	0/30 (0%)	-	-
CHL	0/31 (0%)	-	-
CIP	3/31 (10%)	-	1 step
COL	0/27 (0%)	-	-
ERT	2/4 (50%)	-	5 steps
GEN	0/31 (0%)	-	-
IMI	1/5 (20%)	-	1 step
MER	0/7 (0%)	-	-
NAL	1/31 (3%)	1 step	-
SMX	2/21 (10%)	-	2 steps
TET	0/31 (0%)	-	-
TMP	0/31 (0%)	-	-

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

MIC determination *C. jejuni* ATCC 33560			
Anti-microbial	Proportion outside QC range	Obtained values in MIC steps (min/max)	
		Below lower QC limit	Above upper QC limit
CIP	3/30 (10%)	-	1 step
ERY	0/30 (0%)	-	-
GEN	5/30 (17%)	1 step	-
NAL	1/28 (4%)	1 step	-
TET	0/28 (0%)	-	-

Table 6: Results from the participation of eight 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-8.4	VIM-2	4/4 (100%)	3/3 (100%)	CTX
	TEM-1	6/6 (100%)	5/5 (100%)	SHV
S-8.5	CTXM-9	8/8 (100%)	7/7 (100%)	
	TEM-1	6/6 (100%)	4/4 (100%)	
S-8.6	CTXM-3	8/8 (100%)	5/7 (71%)	CTXM-1
	OXA-30	6/6 (100%)	4/4 (100%)	CTXM-15
S-8.7	TEM-52	8/8 (100%)	6/6 (100%)	CTX

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.

The EURL-AR has emphasized the need for harmonization of AST methodology among NRLs, and has recommended MIC determination on several occasions. In this EQAS trial, the number of participants performing MIC determination is comparable to the high numbers observed last year. Moreover, the EU regulation specifying the AST method to be performed from the 2014 monitoring, refers to MIC testing alone.

4.1 *Salmonella* trial

Overall, the percentage of correct antimicrobial susceptibility test results of *Salmonella* was 99.3%. The majority (n=32) 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 2013-EQAS would appear to be at the same level or increasing compared to the performance in the former iterations.

In previous years, the testing of ciprofloxacin towards strains exhibiting reduced susceptibility to this antimicrobial and the correct interpretation of these results has caused problems to laboratories performing disk diffusion. This year, one laboratory obtained a deviation on this account when submitting a zone diameter of 19 mm for ciprofloxacin and an interpretation as susceptible (S-8.1). The protocol (App. 4b) refers to the CLSI interpretative criteria for ciprofloxacin which allow laboratories performing DD for AST to detect plasmid-mediated quinolone resistance.

As indicated by Figure 4, deviation levels higher than 5% were exhibited by two laboratories (#42 and #58). For laboratory #42, all deviations were related to S-8.8 where resistance to five antimicrobials was expected, and none of these were detected. This could be caused by a technical error causing mix-up of strains in the laboratory or it could be due to the loss of a plasmid in the test strain. For laboratory #58, the seven deviations all are caused by detection of a high MIC-level and a categorization as resistant where the expected result was susceptible. In two of the cases, sulfonamides caused a high MIC which could be due to the bacteriostatic property of this drug (the MIC should be read at 80% inhibition) that might have caused an incorrect determination of the MIC. 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. Four laboratories performed AST on *Salmonella* by the use of disk diffusion and uploaded data for the testing of the reference strain with a total of three (7%) values out of range. For the laboratories performing AST on *Salmonella* by an MIC-method, two laboratories observed problems when testing ertapenem, one indicated a value five steps above the QC-range. Also, two laboratories indicated the reading of a value for sulphonamides which was above the QC-limit. This reading of sulphonamides is known to cause problems and these laboratories are encouraged to look into whether this could be the reason for the high MIC-value for the QC-strain.

Laboratories #42, #44, #56, and #57 which had a deviation level above the acceptance limit in EQAS 2012 with values of 5.6%, 6.9%, 6.9%, and 6.9%, respectively, have increased their performance and in the 2013-iteration present a deviation level at 5.3%, 0% and 1.1% for #42, #44 and #56. Laboratory #57 did not participate in this year's iteration of the *Salmonella* EQAS.

ESC-producing *Salmonella* test strains

ESC-producing microorganisms continue to be emerging worldwide. A mandatory part of this EQAS is to be able to detect them as this ability should be of a high priority for the NRLs.

Of the four *Salmonella* test strains relevant for this component of the EQAS (S-8.4, S-8.5, S-8.6 and S-8.7), one was a carbapenemase-producer and three were ESBL-producing strains. The testing and interpretation of results caused difficulties especially for two strains; 1) For S-8.4, the test for meropenem resistance would be the reason to classify this strain as a carbapenemase-producer. The meropenem range in the MIC-panels used by most NRLs for the EQAS-test strains is too high to indicate resistance for this strain and disk diffusion interpretative criteria corresponding to the EUCAST MIC-cut off value are not available. The EURL-AR followed up on the strain regarding the MIC for meropenem by performing E-tests on a number agar sticks that had been stored since the production for the EQAS. These results indicated a lower expected value than the one presented in the database. The expected MIC value was therefore adjusted to 0.125 mg/L with an interpretation as 'susceptible'. For these reasons, the evaluation of both the testing of meropenem and the classification as carbapenemase-producer was not further evaluated in this report. 2) For S-8.5, the classification in relation to ESBL-production referred to the EFSA technical specifications (EFSA, 2012) and thereby was intended to be based on the phenotypic analysis, only, which would result in a classification as 'unusual phenotype'. Upon deadline, it was clear that many laboratories had performed further testing and based their submitted results as 'ESBL-producing' on these. Obtained results from these two strains 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 work towards better tools for analysis and interpretation.

Of the 34 laboratories which tested *Salmonella*, one (#58) submitted results which were incorrect for six of the eight test strains. This laboratory has been contacted by the EURL-AR to identify possible causes of this unsatisfactory performance and to improve the quality of results.

When disregarding the results of laboratory #58, 94% of the ESC-classifications were in accordance with the expected in relation to the three relevant ESBL-producing strains (S-8.5, S-8.6, and S-8.7) from the 33 participating

In the present report, results from the *Salmonella* and *Campylobacter* EQAS 2013 are assessed in relation to the database evalution and referring to the interpretation as susceptible or resistant as the reference value.

At the annual workshops, the network has discussed whether this could be improved by instead assessing the obtained MIC-value. The suggestion is that the reference value is set at the expected MIC-value +/- one dilution step.

At the upcoming workshop in April 2014, the results presented in this report will be presented based on analysis according to this suggestion. After that it will be decided how to proceed to obtain the best evaluation of the proficiency of the NRLs in relation to AST-results obtained by microbroth dilution.

laboratories. The six results not in concordance with the expected and relevant for discussion were caused by various problems with confirmatory testing causing an incorrect answer. These deviations were submitted by six different laboratories and thus do not indicate methodical issues at particular laboratories.

4.2 *Campylobacter* trial

For the *Campylobacter* component of this year's EQAS, 30 laboratories submitted results leading to an overall percentage of correct AST results at 96.5%. The performance varied from no deviations up to 19.0% deviations, with 24 laboratories performing satisfactorily according to the established acceptance ranges.

Six laboratories (#6, #12, #22, #29, #37 and #44) obtained deviation levels above 5%, four of these were defined as outliers (#29, #37, #6, and #22) with deviation levels at 12.5%, 12.5%, 14.6% and 19.0%. For none of these laboratories, the values obtained for the QC-strain indicate methodical issues to be the reason for the obtained deviations. Of the four outliers, one (#6) indicated issues with reviving one *Campylobacter* strain (C-8.3) and the results indicate that upon subculture of the revived strain, a contamination was subcultured and tested. This laboratory in addition incorrectly interpreted two MIC-values concluding resistance where susceptible was the correct interpretation. Laboratory #22 obtained three deviations when testing C-8.3 and five incorrect interpretations when testing C-8.7 which indicates the testing of two other strains, possibly contaminants. Laboratory #29 presents six deviations (12.5%) which do not exhibit an obvious pattern. This laboratory should follow up on these results by performing trouble and thereby detecting the cause of the deviating results. Finally, one laboratory (#37) indicated the use of a non-standardized method of the EQAS-strains due to financial constraints. This laboratory has confirmed that re-testing of some of the strains applying the standardized method rendered the expected results. All six 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 93.8%. The nine values outside the QC intervals were all just one step below or above 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 #36, #40, and #44 which were regarded as outliers in EQAS 2012 with deviation levels at 10.3%, 12.8%, and 15.4%, respectively, all increased their performance in the 2013-iteration and obtained deviation levels at 2.1%, 4.2% and 8.3%, respectively.

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.*

Especially, the agenda now is focused at 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, eight laboratories participated in this optional EQAS item.

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 at the same level for *Salmonella* AST's in this EQAS (99.3%) when compared to the results from the EQAS 2009, 2010, 2011 and 2012 (98.4%, 97.8%, 98.1%, and 99.0%). Regarding *Campylobacter* AST's, the level of deviation appears to have risen and this year reach a level of 3.5% in 2013 compared to 2.2%, 2.0%, 1.9%, and 2.1% in 2009, 2010, 2011, and 2012. Four laboratories were regarded as outliers for the *Campylobacter* AST (#29, #37, #6, and #22) due to their higher deviation levels (12.5%, 12.5%, 14.6% and 19.0%).

Eight 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 carbepenemase-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

PRENOTIFICATION:

European Union Reference Laboratory Antimicrobial Resistance

M00-06-001/01.12.2011

EQAS 2013

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. Participation is free of charge for all designated NRL-AR's.

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 proforma 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 2013. 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 6th 2013** 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 2014.

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	-	Institute of Public Health	Belgium
X	X	-	Nacional 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	-	Estonian Veterinary and Food Laboratory	Estonia
X	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
X	-	-	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	-	-	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*	-	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	-	National Veterinary Research Institute	Poland
X	X	-	Laboratorio National de Investigacáo Veterinaria	Portugal
X	X	-	Institute for Diagnosis and Animal Health	Romania
X	X	-	Institute for Hygiene and Veterinary Public Health	Romania
X	X	-	State Veterinary and Food Institute (SVFI)	Slovakia
X	X	-	National Veterinary Institute	Slovenia
X	X	X	Laboratorio Central de Sanidad, Animal de Algete	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	X	-	Public Health England - Colindale	United Kingdom
X	X	-	The Veterinary Laboratory Agency	United Kingdom

*ID of *Campylobacter* species performed. AST not performed

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		Cefepime FEP		Cefotaxime CTX		ESBL-confirmation CTX:CTX/Cl		Cefoxitin FOX		Ceftazidime CAZ		ESBL-confirmation CAZ:CAZ/Cl		Chloramphenicol CHL		Ciprofloxacin CIP	
EURL S-8.1	<= 1	SUSC			<= 0.12	SUSC					= 0.5	SUSC			= 8	SUSC	= 0.25	RESIST
EURL S-8.2	= 2	SUSC			<= 0.12	SUSC					= 0.25	SUSC			= 8	SUSC	= 0.03	SUSC
EURL S-8.3	> 32	RESIST			<= 0.12	SUSC					= 0.5	SUSC			= 8	SUSC	> 4	RESIST
EURL S-8.4	> 32	RESIST	<= 1	SUSC	> 4	RESIST	ratio <8	No synergy	> 64	RESIST	= 32	RESIST	ratio <8	No synergy	= 4	SUSC	> 4	RESIST
EURL S-8.5	> 32	RESIST	= 2	SUSC	> 4	RESIST	ratio >8	Synergy (E-test: Phantom zone)	<= 4	SUSC	= 1	SUSC	ratio <8	No synergy	= 8	SUSC	= 0.5	RESIST
EURL S-8.6	> 32	RESIST	> 16	RESIST	> 4	RESIST	ratio >8	Synergy	<= 4	SUSC	= 16	RESIST	ratio =8	Synergy	> 64	RESIST	= 1	RESIST
EURL S-8.7	> 32	RESIST	> 16	RESIST	> 4	RESIST	ratio >8	Synergy (E-test: deformation)	<= 4	SUSC	= 64	RESIST	ratio >8	Synergy	= 8	SUSC	= 0.03	SUSC
EURL S-8.8	> 32	RESIST			<= 0.12	SUSC					= 0.25	SUSC			> 64	RESIST	= 0.03	SUSC

	Colistin COL		Ertapenem ERT		Gentamicin GEN		Imipenem IMI		Meropenem MER		Nalidixic acid NAL		Sulfamethoxazole SMX		Tetracycline TETRA		Trimethoprim TMP		Relevant genes
EURL S-8.1	<= 1	SUSC			<= 0.5	SUSC			<= 0.03	SUSC	= 8	SUSC	<= 64	SUSC	<= 2	SUSC	<= 1	SUSC	
EURL S-8.2	<= 1	SUSC			= 0.5	SUSC			<= 0.03	SUSC	<= 4	SUSC	<= 64	SUSC	<= 2	SUSC	<= 1	SUSC	
EURL S-8.3	<= 1	SUSC			= 16	RESIST			<= 0.03	SUSC	> 64	RESIST	> 1024	RESIST	> 32	RESIST	<= 1	SUSC	
EURL S-8.4	<= 1	SUSC	= 0.25	RESIST	= 16	RESIST	= 2	RESIST	= 0.125	SUSC	> 64	RESIST	> 1024	RESIST	> 32	RESIST	<= 1	SUSC	TEM-1; VIM-2
EURL S-8.5	<= 1	SUSC	= 0.016	SUSC	<= 0.5	SUSC	<= 0.5	SUSC	<= 0.03	SUSC	> 64	RESIST	<= 64	SUSC	> 32	RESIST	<= 1	SUSC	TEM-1, CTXM-9
EURL S-8.6	<= 1	SUSC	= 0.06	SUSC	> 16	RESIST	<= 0.5	SUSC	= 0.06	SUSC	> 64	RESIST	> 1024	RESIST	> 32	RESIST	> 32	RESIST	CTX M-3; OXA-30
EURL S-8.7	<= 1	SUSC	= 0.03	SUSC	<= 0.5	SUSC	<= 0.5	SUSC	= 0.06	SUSC	<= 4	SUSC	<= 64	SUSC	<= 2	SUSC	<= 1	SUSC	TEM-52
EURL S-8.8	<= 1	SUSC			<= 0.5	SUSC			<= 0.03	SUSC	<= 4	SUSC	> 1024	RESIST	> 32	RESIST	> 32	RESIST	

Resistant

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

Species	Code	Ciprofloxacin CIP		Erythromycin ERY		Gentamicin GEN		Nalidixic acid NAL		Streptomycin STR		Tetracycline TET	
C. coli	EURL C-8.1	> 4	RESIST	> 32	RESIST	= 0.5	SUSC	> 64	RESIST	> 16	RESIST	= 8	RESIST
C. coli	EURL C-8.2	= 0.12	SUSC	> 32	RESIST	= 0.5	SUSC	= 8	SUSC	= 2	SUSC	= 1	SUSC
C. jejuni	EURL C-8.3	> 4	RESIST	= 2	SUSC	= 0.25	SUSC	> 64	RESIST	<= 1	SUSC	> 16	RESIST
C. jejuni	EURL C-8.4	= 0.5	SUSC	= 1	SUSC	= 0.25	SUSC	= 64	RESIST	<= 1	SUSC	> 16	RESIST
C. jejuni	EURL C-8.5	> 4	RESIST	= 2	SUSC	= 0.5	SUSC	> 64	RESIST	= 2	SUSC	= 0.25	SUSC
C. coli	EURL C-8.6	= 0.25	SUSC	= 4	SUSC	= 0.5	SUSC	= 16	SUSC	> 16	RESIST	> 16	RESIST
C. coli	EURL C-8.7	= 0.06	SUSC	= 1	SUSC	= 0.25	SUSC	= 4	SUSC	<= 1	SUSC	= 0.5	SUSC
C. coli	EURL C-8.8	> 4	RESIST	= 0.5	SUSC	= 0.25	SUSC	= 64	RESIST	> 16	RESIST	> 16	RESIST

Resistant

DTU Food
National Food Institute

M00-06-001/01.12.2011

EURL-AR External Quality Assurance System 2013

- *Salmonella, Campylobacter* and optional genotypic characterisation

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

Kgs. Lyngby, October 2013

Dear «Name»,

Please find enclosed the bacterial strains for the EURL-AR EQAS 2013. 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 6th 2013.

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) 2013

DTU Food
National Food Institute

PROTOCOL

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

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1 INTRODUCTION

One of the tasks as the EU Reference Laboratory for Antimicrobial Resistance (EURL-AR) is to organise and conduct an External Quality Assurance System (EQAS) on antimicrobial susceptibility testing (AST) of *Salmonella* and *Campylobacter*. The *Salmonella* and *Campylobacter* EQAS 2013 will include susceptibility testing of eight *Salmonella* and eight *Campylobacter* strains together with susceptibility testing of the reference strains *E. coli* ATCC 25922 (CCM 3954) and *C. jejuni* ATCC 33560 (CCM 6214). As part of the AST of the *Campylobacter*, species identification of the test strains must be performed. Additionally, optional characterization of genes conferring ESBL-production in the *Salmonella* test strains is offered.

For new participants of the EQAS who have not already received the mentioned reference strains, these are included in the parcel. The reference strains will not be included in the years to come. The reference strains are original certified cultures and are free of charge. Please take proper care of the strains. Handle and maintain them as suggested in the manual ‘Subculture and Maintenance of QC Strains’. Please use them for future internal quality control for susceptibility testing in your laboratory.

For this EQAS, members of the Food- and Waterborne Diseases and Zoonoses Programme (FWD) based at ECDC are also participating, however, for these participants the EQAS has been slightly adjusted. Description of this can be found in this protocol, i.e. that for antimicrobial susceptibility testing (AST) of *Campylobacter*, results obtained by disk diffusion or E-test are also accepted.

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.

2 OBJECTIVES

The main objective of this EQAS is to support laboratories to assess and if necessary improve the quality of susceptibility testing of pathogens originating from food and animal sources, especially *Salmonella* and *Campylobacter*. Furthermore, to assess and improve the comparability of surveillance and antimicrobial susceptibility data reported to EFSA by different laboratories on *Salmonella* and *Campylobacter* and to harmonise the interpretative criteria used within the EU.

3 OUTLINE OF THE EQAS 2013

3.1 Shipping, receipt and storage of strains

In October 2013, the EU appointed National Reference Laboratories will receive a parcel from the National Food Institute containing eight *Salmonella* and eight *Campylobacter* strains. QC reference strains will be included for participants who have not previously received these. Some of the *Salmonella* test strains are ESBL- or carbapenemase producing and are included as test strains in 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 see the document 'Instructions for opening and reviving lyophilised cultures' on the EURL-AR-website (see www.eurl-ar.eu).

3.3 Susceptibility testing

The strains should be susceptibility tested towards as many as possible of the antimicrobials listed in Tables 1 and 2, by the method used in the laboratory when performing monitoring for EFSA.

Laboratories from the FWD-network should use their routine method for testing the bacterial strains.

The expected interpretation is based on MIC-values according to the interpretative criteria listed in Tables 1 and 2. Please note that if applying a method for susceptibility testing that does not render an MIC-value for interpretation by the given cut-off values, the interpretation may not correspond to the expected result, even if the analysis is correctly performed. This consideration should be included in the self-evaluation performed subsequent to the disclosure of the expected results.

With regard to MIC range and/or disk content we ask you to fill in these pieces of information in the database. Also, if you do ***not*** use the cut-off values listed in the protocol for interpretation of the susceptibility results, please fill in or update this information in the database.

Interpretation of obtained MIC-values or disk diffusion zone diameters: Interpretations in concordance with the expected will be categorized as 'correct', whereas interpretations that deviate from the expected will be categorized as 'incorrect'. Note: A categorization as intermediary is not accepted.

For the interpretation of obtained MIC-values, the cut off values listed in Tables 1 and 2 should be applied. The epidemiological cut-off values allow two categories of characterisation – resistant or sensitive. The cut off values used in the interpretation of the MIC results are developed by EUCAST (www.eucast.org).

For the interpretation of obtained disk diffusion zone diameters, the interpretative criteria should correspond to those listed in Tables 1 and 2, categorising the results into the terms resistant and susceptible.

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.

EU Reference Laboratory for Antimicrobial Resistance
External Quality Assurance System (EQAS) 2013

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Table 1: Interpretative criteria for the AST results for *Salmonella* spp.

Antimicrobial	MIC (µg/mL) (R>)	DD (zone mm) (R<)
Ampicillin (AMP)	8	14
Cefotaxime (CTX)	0.5	20
Ceftazidime (CAZ)	2	NA*
Chloramphenicol (CHL)	16	13**
Ciprofloxacin (CIP)	0.06	31**
Colistin (COL)	2	NA*
Gentamicin (GEN)	2	NA*
Meropenem (MER)	0.125	NA*
Nalidixic acid (NAL)	16	16
Sulfonamides (SMX)	256***	17**
Tetracycline (TET)	8	12**
Trimethoprim (TMP)	2	NA*

* Not available from EUCAST
** the DD zone diameter corresponding to the MIC-value (reference: CLSI M100-S23 Table 2A); note: for some of these, results which according to the CLSI document would be interpreted as 'intermediary', should be categorized as resistant in this proficiency test
*** CLSI M100 Table 2A

Plasmid-mediated quinolone resistance

When performing antimicrobial susceptibility testing of the *Salmonella* test strains, the interpretative criteria listed in Table 1 for results obtained by MIC-determination detect plasmid mediated quinolone resistant test strains. When interpreting a disk diffusion result, reference should be made to the CLSI interpretative criteria as indicated in Table 1.

Extended-beta-lactam- and carbapenem resistance

Confirmatory tests for ESBL- or carbapenemase production are **mandatory** on all strains resistant to cefotaxime (CTX), ceftazidime (CAZ) or meropenem (MER).

Confirmatory tests for ESBL production require the use of both cefotaxime (CTX) and ceftazidime (CAZ) alone and in combination with a β-lactamase inhibitor (clavulanic acid). Synergy is defined either as i) a ≥ 3 twofold concentration decrease in an MIC for either antimicrobial agent tested in combination with clavulanic acid vs. its MIC when tested alone (three dilution steps difference; CTX : CTX/CL or CAZ : CAZ/CL ratio ≥ 8) or ii) a ≥ 5 mm increase in a zone diameter for either antimicrobial agent tested in combination with clavulanic acid vs. its zone when tested alone (CLSI M100 Table 2A; Enterobacteriaceae). The presence of synergy indicates ESBL production. Resistance to cefepime gives further indication of ESBL production. Confirmatory test for carbapenemase production requires the testing of meropenem (MER).

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]) and indicated 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

MIC values and relative interpretation of cefotaxime, ceftazidime and meropenem used for detection of beta-lactamase- and carbapenemase producing strains in this EQAS should be reported as found.

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. Laboratories in the EURL-AR network must use one of these methods. For the laboratories of the FWD-network, results of AST of *Campylobacter* may be obtained by disk diffusion or in-house E-test-method.

Table 2: Interpretative criteria for the AST results for *Campylobacter jejuni* and *C. coli*

Antimicrobial	*C. jejuni*		*C. coli*	
	MIC (µg/mL) (R>)	DD (zone mm) (R<)	MIC (µg/mL) (R>)	DD (zone mm) (R<)
Ciprofloxacin (CIP)	0.5	26	0.5	26
Erythromycin (ERY)	4	22	8	24
Gentamicin (GEN)	2	NA*	2	NA*
Nalidixic acid (NAL)	16	NA*	16	NA*
Streptomycin (STR)	4	NA*	4	NA*
Tetracycline (TET)	1	30	2	30

* Not available from EUCAST

[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

Identification of *Campylobacter* species

Species identification of the *Campylobacter* test strains must be performed. For this purpose, the protocol available on the EURL-AR website (http://eurl-ar.eu/233-protocols.htm) or in-house methods may be adopted.

3.4 Optional genotypic characterisation

For the optional genotypic characterisation of the ESBL-producing *Salmonella* test strains, the requested results are the genes conferring ESBL-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.

4 REPORTING OF RESULTS AND EVALUATION

Test forms are available for recording your results before you enter them into the interactive web database. We kindly ask you to report in the database the tested MIC range and/or antimicrobial disk content. **If you did not use the cut-off values recommended in the protocol for interpretation of AST results, please report the interpretative criteria applied.**

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 6th, 2013.** After the deadline, the database will be closed and you will be able 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 do not have access to the Internet, or if you experience difficulties in entering your results, try a few days later or, alternatively, return the completed test forms by e-mail, fax or mail to the National Food Institute, Denmark.

All results will be summarised in reports available to all participants. The data will be collected in an overall summary report in which anonymous laboratory results will be analyzed. This summary

report will focus on comparing the results from the EURL-AR network, and public health laboratories (FWD-laboratories) to assess the level of harmonization need.

In addition, separate reports for the EURL-AR network (by DTU) and for public health laboratories (by ECDC) will be prepared.

The data in the report will be presented with laboratory codes. A laboratory code is only known to the individual laboratory, while the complete list of laboratories and their respective codes is confidential and only known to the EURL-AR (all participants), the ECDC (FWD-laboratories) and the EU Commission (NRL-ARs). All conclusions and all three reports will be publicly available.

If you have any 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 this passage before entering the web page. Before you go ahead, you need your test form by your side together with your breakpoint values.

You are able to browse back and forth by using the forward and back keys or click on the EURL logo.

You enter the EURL-AR EQAS 2013 web page (http://thor.dfvf.dk/crl) then write your username and password in low cases and press enter. Your username and password is the same as in the previous EQAS's arranged by the National Food Institute. If you have problems with the login please contact us.

Click on either "*Salmonella* test results" or "*Campylobacter* test results" depending on your results. The below description is aimed at *Salmonella* entry but is the same for *Campylobacter* entry.

Click on "Start of Data Entry - Methods and Breakpoints for Salm."

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

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Fill in what kind of method you have used for the susceptibility testing of *Salmonella* and the brand of discs, tablets, MIC trays etc.

Fill in the relevant information, either disk content or MIC range. If you use disk diffusion, please upload the breakpoints used.

You will find one more box to fill in on this page when testing *Campylobacter*: Fill in the actual incubation condition used 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 for each *Salmonella* and *Campylobacter* strain, you enter the species (for *Campylobacter* only), the obtained value and the interpretation as R or S.

For *Salmonella*, you also type in results for the ESBL tests.

If you have not used an antimicrobial, please leave the field empty.

Click on "save and go to next page"

When uploading data on the reference strains please enter the zonediameters in mm or MIC values in µg/ml. Remember to use the operator keys to show e.g. equal to, etc. If you do not use CLSI guidelines for AST on the reference strains, please add a comment on the method used.

Click on "save and go to next page"

This page is a menu, from where you can review the input pages, approve your input and finally see and print the submitted results:

Browse through the pages and make corrections if necessary. Remember to save a page if you make any corrections. If you save a page without changes, you will see an error screen, and you just have to click on "back" to get back to the page and "go to next page" to continue.

Please fill in the evaluation form.

Approve your input. Be sure that you have filled in all the results before approval, as YOU CAN ONLY APPROVE ONCE! The approval blocks your data entry in the interactive database, but allows you to see the evaluated results.

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 *Salmonella* AST? ☐ Yes ☐ No

Does your laboratory have an accreditation for other laboratory methods/tests? ☐ Yes ☐ No

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

- ☐ Broth Microdilution
- ☐ Agar dilution
- ☐ E-test (strips)
- ☐ Disk diffusion (paper disks)
- ☐ Rosco Neo Sensitabs (tablets)

Brand of microdilution plate, strips or disks:

Method used for detection of ESBL-producing strains, see pictures of the methods on http://www.eurl-ar.eu/201-resources.htm

- ☐ E-test
- ☐ Double disk
- ☐ Combination disk
- ☐ MIC determination (microbroth)
- ☐ Selective media please specify:
- ☐ Other, please specify

Comments or additional information:

TEST FORM

Breakpoints used (zonediameters) and general info regarding disk content and test-range used for MIC:

- Please fill in the disk content or the test-range used for MIC, respectively.
- Please, *only* fill in breakpoints if you did not use a MIC method, that is, *only* if you used other breakpoints/cut-off values than the ones listed in the protocol for interpretation of AST results for *Salmonella*. Otherwise leave breakpoint fields empty.

Antimicrobial	General info The relevant information in the two columns below should be filled in		Zonediameter (mm) Please, *only* fill in breakpoint information if you did not use the cut-off values listed in the protocol		
	Disk content (µg)	Test-range for MIC (µg/mL)	Resistant (mm)	Intermediate (mm)	Sensitive (mm)
Ampicillin, AMP			≤		≥
Cefotaxime, CTX			≤		≥
Ceftazidime, CAZ			≤		≥
Chloramphenicol, CHL			≤		≥
Ciprofloxacin, CIP			≤		≥
Colistin, COL			≤		≥
Gentamicin, GEN			≤		≥
Meropenem, MER			≤		≥
Nalidixic acid, NAL			≤		≥
Sulfamethoxazole, SMX			≤		≥
Tetracycline, TET			≤		≥
Trimethoprim, TMP			≤		≥

TEST FORM

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

Does your laboratory have an accreditation for other laboratory methods/tests? ☐ Yes ☐ No

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

Method used for antimicrobial susceptibility testing of *Campylobacter* in this EQAS::

- ☐ Microbroth
- ☐ Agardilution
- ☐ Disk diffusion
- ☐ In-house (E-test)

Brand of broth/agar:

Additional comments:

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

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

If using disk diffusion test or an in-house method (E-test),
- Please fill in the disk content or the test-range used for E-test, respectively.
- Please fill in interpretative criteria if you used other breakpoints/cut-off values than the ones listed in the protocol for interpretation of AST results for *Campylobacter*. Otherwise leave breakpoint fields empty.

Antimicrobial	General info The relevant information in the two columns below should be filled in		Zonediameter (mm) Please, *only* fill in breakpoint information if you did not use the cut-off values listed in the protocol		
	Disk content (µg)	Test-range for MIC (µg/mL)	Resistant (mm)	Intermediate (mm)	Sensitive (mm)
Ciprofloxacin			≤		≥
Erythromycin			≤		≥
Gentamicin			≤		≥
Nalidixic Acid			≤		≥
Streptomycin			≤		≥
Tetracycline			≤		≥

TEST FORM

Strain	Antimicrobial	Interpretation		
		≤ >	Zonediam (mm) or MIC-value (µg/ml)	S / R
Salmonella EURL S. 8.X	Ampicillin, AMP			
	Cefotaxime, CTX			
	Ceftazidime, CAZ			
	Chloramphenicol, CHL			
	Ciprofloxacin, CIP			
	Colistin, COL			
	Gentamicin, GEN			
	Meropenem, MER			
	Nalidixic acid, NAL			
	Sulfonamides, SMX			
	Tetracycline, TET			
	Trimethoprim, TMP			

All strains resistant to cefotaxime (CTX), ceftazidime (CAZ) or meropenem (MER) should be included for confirmatory tests for ESBL or carbapenemase production. See further description of confirmatory tests in the protocol section '3.3.1 *Salmonella*'.

	MIC, value or ratio		**Disks, zone diameter or increase**
CTX/CL : CTX MIC ratio	☐ MIC ratio ≥ 8 (synergy) ☐ MIC ratio < 8 ☐ Phantom zone (synergy) ☐ Deformation (synergy) ☐ Not determinable	Incr. in zone diam	☐ Incr. ≥ 5 mm (synergy) ☐ Incr.< 5 mm
CAZ/CL : CAZ MIC ratio	☐ MIC ratio ≥ 8 (synergy) ☐ MIC ratio < 8 ☐ Phantom zone (synergy) ☐ Deformation (synergy) ☐ Not determinable	Incr. in zone diam	☐ Incr. ≥ 5 mm (synergy) ☐ Incr.< 5 mm
Cefoxitin, FOX MIC value	☐ MIC value > 8 ☐ MIC value ≤ 8	Zone diameter	☐ D < 18 mm ☐ D ≥ 18 mm
Cefepime, FEP MIC value	☐ MIC value > 8 ☐ MIC value ≤ 8	Zone diameter	☐ D < 18 mm ☐ D ≥ 18 mm
Imipenem, IMI MIC value	☐ MIC value > 1 ☐ MIC value ≤ 1	Zone diameter	☐ D < 23 mm ☐ D ≥ 23 mm
Ertapenem, ERP MIC value	☐ MIC value > 0.06 ☐ MIC value ≤ 0.06	Zone diameter	☐ D < 22mm ☐ D ≥ 22 mm
☐ Presumptive ESBL	☐ Presumptive pAmpC	☐ Unusual phenotype	
☐ Presumptive ESBL+ pAmpC	☐ Presumptive carbapenemase	☐ Not ESBL-producing	

Comments (include genotype or other results):

TEST FORM

Susceptibility testing of *E. coli* reference strain ATCC 25922

Strain	Antimicrobial	Zonediameter (mm) or MIC-value (µg/ml)
E. coli ATCC 25922	Ampicillin, AMP	
	Cefepime, FEP	
	Cefotaxime, CTX	
	Cefoxitin, FOX	
	Ceftazidime, CAZ	
	Chloramphenicol, CHL	
	Ciprofloxacin, CIP	
	Colistin, COL	
	Ertapenem, ERP	
	Gentamicin, GEN	
	Imipenem, IMI	
	Meropenem, MER	
	Nalidixic acid, NAL	
	Sulfisoxazole, FIS*	
	Tetracycline, TET	
	Trimethoprim, TMP	

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

TEST FORM

Strain	Antimicrobial	Interpretation	
		MIC-value (µg/ml)	S / R
Campylobacter EURL C. 8.1 ☐ *C. jejuni* ☐ *C. coli*	Ciprofloxacin		
	Erythromycin		
	Gentamicin		
	Nalidixic Acid		
	Streptomycin		
	Tetracycline		
Campylobacter EURL C. 8.2 ☐ *C. jejuni* ☐ *C. coli*	Ciprofloxacin		
	Erythromycin		
	Gentamicin		
	Nalidixic Acid		
	Streptomycin		
	Tetracycline		
Campylobacter EURL C. 8.3 ☐ *C. jejuni* ☐ *C. coli*	Ciprofloxacin		
	Erythromycin		
	Gentamicin		
	Nalidixic Acid		
	Streptomycin		
	Tetracycline		
Campylobacter EURL C. 8.4 ☐ *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		
	Gentamicin		
	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:

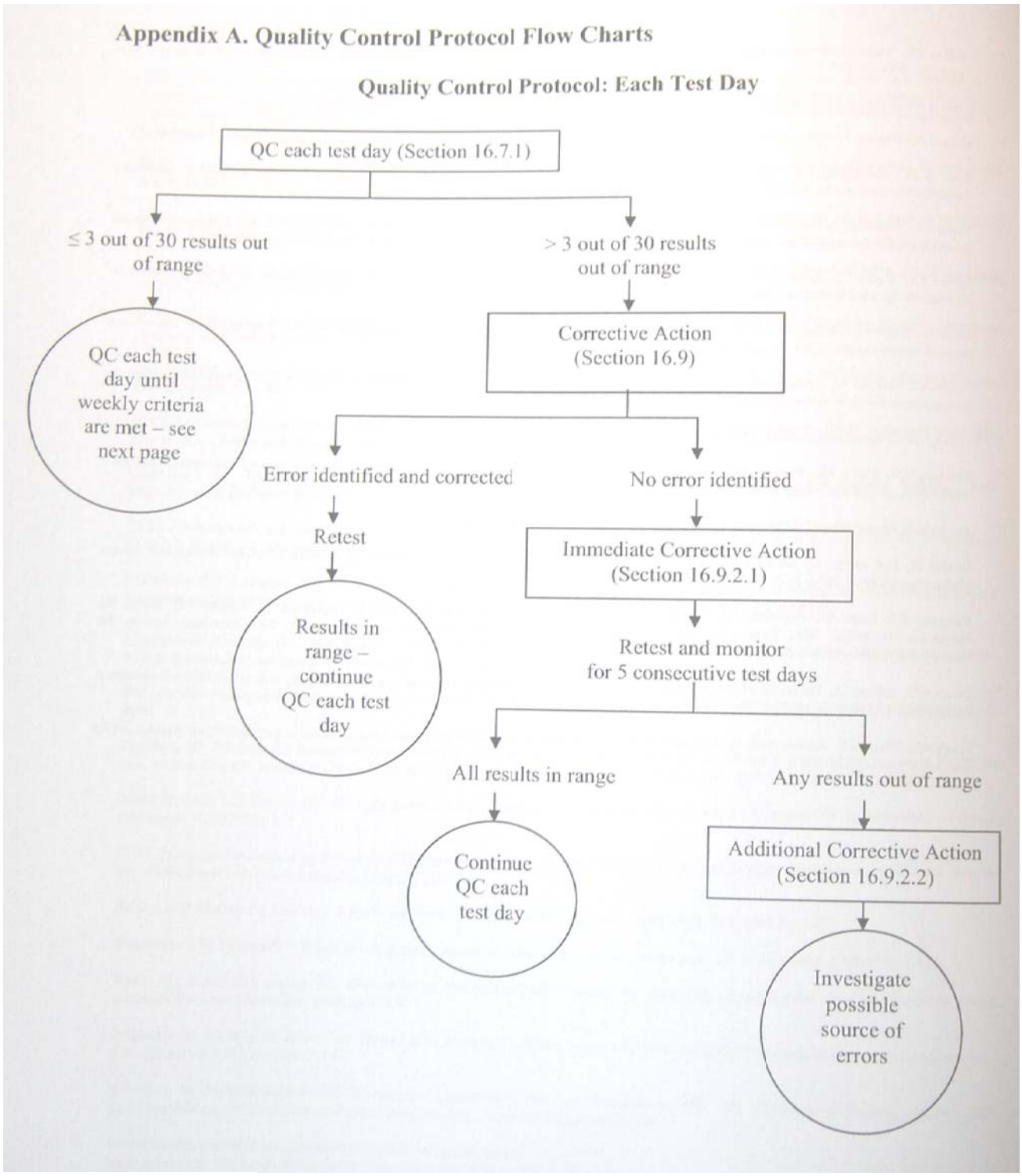
- Repeat the test if there is an obvious error e.g. wrong strain or incubation conditions used
- If there is no obvious error, return to daily control testing

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.

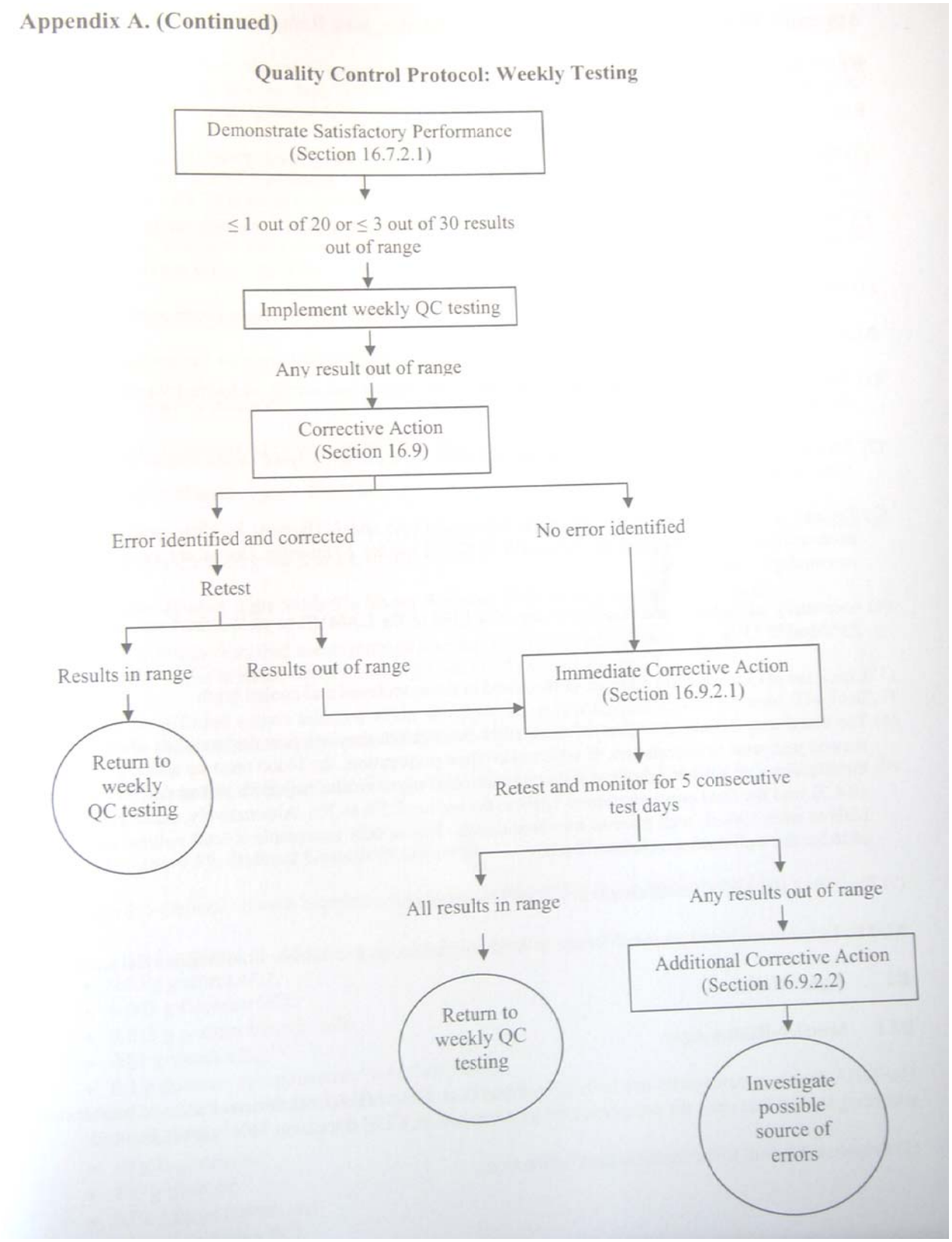
DAILY MIC QC CHART



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**	**DD (disc content)**
Ampicillin, AMP	2-8	16-22 (10µg)
Cefepime, FEP	0.015-0.12	31-37 (30µg)
Cefotaxime, CTX	0.03-0.12	29-35 (30µg)
Ceftazidime, CAZ	0.06-0.5	25-32 (30µg)
Chloramphenicol, CHL	2-8	21-27 (30µg)
Ciprofloxacin, CIP	0.004-0.016	30-40 (5µg)
Colistin, COL	0.25-2	11-17 (10µg)
Ertapenem, ERTA	0.004-0.015	29-36 (10µg)
Gentamicin, GEN	0.25-1	19-26 (10µg)
Imipenem, IMI	0.06-0.25	26-32 (10µg)
Meropenem, MERO	0.008-0.06	28-34 (10µg)
Nalidixic acid, NAL	1-4	22-28 (30µg)
Sulfisoxazole, FIS	8-32	15-23 (250/300µg)
Tetracycline, TET	0.5-2	18-25 (30µg)
Trimethoprim, TMP	0.5-2	21-28 (5µg)

MIC ranges and disc diffusion ranges are according to CLSI M100 S23 (range for ciprofloxacin 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)**
Chloramphenicol, CHL	1-8	1-4	None	None
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

Ranges are according to CLSI (VET01-S2)

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

Lab no.	Antimicrobial	Operator	Value	Low limit	High limit	Mark	Method
1	Ampicillin, AMP	=	4	2	8	1	MIC
1	Cefotaxime, CTX	<=	0.125	0.03	0.125	1	MIC
1	Chloramphenicol, CHL	=	4	2	8	1	MIC
1	Ciprofloxacin, CIP	<=	0.015	0.004	0.016	1	MIC
1	Colistin, COL	<=	1	0.25	2	1	MIC
1	Gentamicin, GEN	<=	0.5	0.25	1	1	MIC
1	Nalidixic acid, NAL	<=	4	1	4	1	MIC
1	Tetracycline, TET	<=	2	0.5	2	1	MIC
1	Trimethoprim, TMP	<=	1	0.5	2	1	MIC
2	Ampicillin, AMP	=	4	2	8	1	MIC
2	Cefotaxime, CTX	<=	0.06	0.03	0.125	1	MIC
2	Ceftazidime, CAZ	<=	0.25	0.06	0.5	1	MIC
2	Chloramphenicol, CHL	=	4	2	8	1	MIC
2	Ciprofloxacin, CIP	=	0.015	0.004	0.016	1	MIC
2	Colistin, COL	<=	2	0.25	2	1	MIC
2	Gentamicin, GEN	=	0.5	0.25	1	1	MIC
2	Nalidixic acid, NAL	<=	4	1	4	1	MIC
2	Sulfisoxazole, FIS	=	16	8	32	1	MIC
2	Tetracycline, TET	<=	1	0.5	2	1	MIC
2	Trimethoprim, TMP	<=	0.5	0.5	2	1	MIC
4	Ampicillin, AMP	=	8	2	8	1	MIC
4	Cefotaxime, CTX	=	0.06	0.03	0.125	1	MIC
4	Ceftazidime, CAZ	=	0.25	0.06	0.5	1	MIC
4	Chloramphenicol, CHL	=	8	2	8	1	MIC
4	Ciprofloxacin, CIP	=	0.015	0.004	0.016	1	MIC
4	Colistin, COL	=	2	0.25	2	1	MIC
4	Gentamicin, GEN	=	0.5	0.25	1	1	MIC
4	Nalidixic acid, NAL	=	4	1	4	1	MIC
4	Sulfisoxazole, FIS	=	32	8	32	1	MIC
4	Tetracycline, TET	=	2	0.5	2	1	MIC
4	Trimethoprim, TMP	=	0.5	0.5	2	1	MIC
6	Ampicillin, AMP	=	2	2	8	1	MIC
6	Cefotaxime, CTX	<	0.06	0.03	0.125	1	MIC
6	Ceftazidime, CAZ	<	0.25	0.06	0.5	1	MIC
6	Chloramphenicol, CHL	=	4	2	8	1	MIC
6	Ciprofloxacin, CIP	<	0.008	0.004	0.016	1	MIC
6	Gentamicin, GEN	=	0.5	0.25	1	1	MIC
6	Nalidixic acid, NAL	<	4	1	4	1	MIC
6	Tetracycline, TET	<	1	0.5	2	1	MIC
6	Trimethoprim, TMP	<	0.5	0.5	2	1	MIC
9	Ampicillin, AMP	=	4	2	8	1	MIC
9	Cefepime, FEP	=	0.06	0.015	0.125	1	MIC
9	Cefotaxime, CTX	=	0.06	0.03	0.125	1	MIC
9	Cefoxitin, FOX	=	4	2	8	1	MIC
9	Ceftazidime, CAZ	=	0.25	0.06	0.5	1	MIC
9	Chloramphenicol, CHL	=	4	2	8	1	MIC
9	Ciprofloxacin, CIP	=	0.008	0.004	0.016	1	MIC
9	Colistin, COL	=	0.5	0.25	2	1	MIC
9	Ertapenem, ERTA	=	0.008	0.004	0.016	1	MIC
9	Gentamicin, GEN	=	0.5	0.25	1	1	MIC
9	Imipenem, IMI	=	0.12	0.06	0.25	1	MIC
9	Meropenem, MER	=	0.015	0.008	0.06	1	MIC
9	Nalidixic acid, NAL	=	4	1	4	1	MIC
9	Sulfisoxazole, FIS	=	16	8	32	1	MIC
9	Tetracycline, TET	=	1	0.5	2	1	MIC
9	Trimethoprim, TMP	=	1	0.5	2	1	MIC

Lab no.	Antimicrobial	Operator	Value	Low limit	High limit	Mark	Method
11	Ampicillin, AMP	=	2	2	8	1	MIC
11	Cefotaxime, CTX	=	0.06	0.03	0.125	1	MIC
11	Ceftazidime, CAZ	<=	0.25	0.06	0.5	1	MIC
11	Chloramphenicol, CHL	<=	2	2	8	1	MIC
11	Ciprofloxacin, CIP	=	0.016	0.004	0.016	1	MIC
11	Colistin, COL	<=	0.5	0.25	2	1	MIC
11	Gentamicin, GEN	=	1	0.25	1	1	MIC
11	Nalidixic acid, NAL	=	4	1	4	1	MIC
11	Sulfisoxazole, FIS	<=	8	8	32	1	MIC
11	Tetracycline, TET	<=	1	0.5	2	1	MIC
11	Trimethoprim, TMP	=	0.5	0.5	2	1	MIC
12	Ampicillin, AMP	=	4	2	8	1	MIC
12	Cefotaxime, CTX	=	0.12	0.03	0.125	1	MIC
12	Cefoxitin, FOX	=	4	2	8	1	MIC
12	Ceftazidime, CAZ	=	0.5	0.06	0.5	1	MIC
12	Chloramphenicol, CHL	=	4	2	8	1	MIC
12	Ciprofloxacin, CIP	=	0.03	0.004	0.016	**0**	MIC
12	Colistin, COL	=	1	0.25	2	1	MIC
12	Gentamicin, GEN	=	1	0.25	1	1	MIC
12	Nalidixic acid, NAL	=	2	1	4	1	MIC
12	Tetracycline, TET	=	2	0.5	2	1	MIC
12	Trimethoprim, TMP	=	1	0.5	2	1	MIC
13	Ampicillin, AMP	=	8	2	8	1	MIC
13	Cefotaxime, CTX	<=	0.06	0.03	0.125	1	MIC
13	Ceftazidime, CAZ	<=	0.25	0.06	0.5	1	MIC
13	Chloramphenicol, CHL	=	8	2	8	1	MIC
13	Ciprofloxacin, CIP	=	0.015	0.004	0.016	1	MIC
13	Gentamicin, GEN	=	0.5	0.25	1	1	MIC
13	Nalidixic acid, NAL	<=	4	1	4	1	MIC
13	Sulfisoxazole, FIS	=	16	8	32	1	MIC
13	Tetracycline, TET	=	2	0.5	2	1	MIC
13	Trimethoprim, TMP	<=	0.5	0.5	2	1	MIC
15	Cefepime, FEP	=	36	31	37	1	DD
15	Cefotaxime, CTX	=	35	29	35	1	DD
15	Cefoxitin, FOX	=	29	23	29	1	DD
15	Ceftazidime, CAZ	=	32	25	32	1	DD
15	Chloramphenicol, CHL	=	26	21	27	1	DD
15	Colistin, COL	=	19	11	17	**0**	DD
15	Ertapenem, ERTA	=	36	29	36	1	DD
15	Gentamicin, GEN	=	26	19	26	1	DD
15	Nalidixic acid, NAL	=	25	22	28	1	DD
15	Sulfisoxazole, FIS	=	18	15	23	1	DD
15	Tetracycline, TET	=	25	18	25	1	DD
15	Trimethoprim, TMP	=	28	21	28	1	DD
16	Ampicillin, AMP	=	8	2	8	1	MIC
16	Cefotaxime, CTX	=	0.12	0.03	0.125	1	MIC
16	Ceftazidime, CAZ	=	0.25	0.06	0.5	1	MIC
16	Chloramphenicol, CHL	<=	4	2	8	1	MIC
16	Ciprofloxacin, CIP	=	0.015	0.004	0.016	1	MIC
16	Colistin, COL	=	1	0.25	2	1	MIC
16	Gentamicin, GEN	<=	0.5	0.25	1	1	MIC
16	Meropenem, MER	<=	0.12	0.008	0.06	1	MIC
16	Nalidixic acid, NAL	<=	2	1	4	1	MIC
16	Tetracycline, TET	<=	1	0.5	2	1	MIC
16	Trimethoprim, TMP	=	0.5	0.5	2	1	MIC

Lab no.	Antimicrobial	Operator	Value	Low limit	High limit	Mark	Method
17	Ampicillin, AMP	=	4	2	8	1	MIC
17	Cefotaxime, CTX	=	0.12	0.03	0.125	1	MIC
17	Ceftazidime, CAZ	<=	0.25	0.06	0.5	1	MIC
17	Chloramphenicol, CHL	=	8	2	8	1	MIC
17	Ciprofloxacin, CIP	=	0.015	0.004	0.016	1	MIC
17	Colistin, COL	<=	2	0.25	2	1	MIC
17	Gentamicin, GEN	=	0.5	0.25	1	1	MIC
17	Nalidixic acid, NAL	<=	4	1	4	1	MIC
17	Sulfisoxazole, FIS	=	32	8	32	1	MIC
17	Tetracycline, TET	<=	1	0.5	2	1	MIC
17	Trimethoprim, TMP	=	1	0.5	2	1	MIC
18	Ampicillin, AMP	=	4	2	8	1	MIC
18	Cefotaxime, CTX	=	0.12	0.03	0.125	1	MIC
18	Ceftazidime, CAZ	<=	0.25	0.06	0.5	1	MIC
18	Chloramphenicol, CHL	=	4	2	8	1	MIC
18	Ciprofloxacin, CIP	=	0.008	0.004	0.016	1	MIC
18	Colistin, COL	<=	2	0.25	2	1	MIC
18	Gentamicin, GEN	=	0.5	0.25	1	1	MIC
18	Nalidixic acid, NAL	<=	4	1	4	1	MIC
18	Sulfisoxazole, FIS	=	32	8	32	1	MIC
18	Tetracycline, TET	=	2	0.5	2	1	MIC
18	Trimethoprim, TMP	<=	0.5	0.5	2	1	MIC
19	Ampicillin, AMP	=	8	2	8	1	MIC
19	Cefotaxime, CTX	<=	0.06	0.03	0.125	1	MIC
19	Ceftazidime, CAZ	=	0.5	0.06	0.5	1	MIC
19	Chloramphenicol, CHL	=	4	2	8	1	MIC
19	Ciprofloxacin, CIP	=	0.015	0.004	0.016	1	MIC
19	Colistin, COL	<=	2	0.25	2	1	MIC
19	Gentamicin, GEN	=	0.5	0.25	1	1	MIC
19	Nalidixic acid, NAL	<=	4	1	4	1	MIC
19	Sulfisoxazole, FIS	=	64	8	32	**0**	MIC
19	Tetracycline, TET	=	2	0.5	2	1	MIC
19	Trimethoprim, TMP	=	1	0.5	2	1	MIC
20	Ampicillin, AMP	=	4	2	8	1	MIC
20	Cefepime, FEP	<=	1	0.015	0.125	1	MIC
20	Cefotaxime, CTX	<=	0.06	0.03	0.125	1	MIC
20	Cefoxitin, FOX	<=	4	2	8	1	MIC
20	Ceftazidime, CAZ	<=	0.25	0.06	0.5	1	MIC
20	Chloramphenicol, CHL	=	4	2	8	1	MIC
20	Ciprofloxacin, CIP	=	0.015	0.004	0.016	1	MIC
20	Colistin, COL	<=	2	0.25	2	1	MIC
20	Ertapenem, ERTA	=	0.5	0.004	0.016	**0**	MIC
20	Gentamicin, GEN	=	0.5	0.25	1	1	MIC
20	Imipenem, IMI	=	30	26	32	1	DD
20	Meropenem, MER	=	32	28	34	1	DD
20	Nalidixic acid, NAL	<=	4	1	4	1	MIC
20	Sulfisoxazole, FIS	=	32	8	32	1	MIC
20	Tetracycline, TET	<=	1	0.5	2	1	MIC
20	Trimethoprim, TMP	<=	0.5	0.5	2	1	MIC
21	Ampicillin, AMP	=	2	2	8	1	MIC
21	Cefotaxime, CTX	=	0.06	0.03	0.125	1	MIC
21	Ceftazidime, CAZ	=	0.25	0.06	0.5	1	MIC
21	Chloramphenicol, CHL	=	4	2	8	1	MIC
21	Ciprofloxacin, CIP	=	0.008	0.004	0.016	1	MIC
21	Colistin, COL	=	2	0.25	2	1	MIC
21	Gentamicin, GEN	=	0.5	0.25	1	1	MIC
21	Nalidixic acid, NAL	=	4	1	4	1	MIC
21	Sulfisoxazole, FIS	=	32	8	32	1	MIC
21	Tetracycline, TET	=	1	0.5	2	1	MIC
21	Trimethoprim, TMP	=	0.5	0.5	2	1	MIC

Lab no.	Antimicrobial	Operator	Value	Low limit	High limit	Mark	Method
22	Ampicillin, AMP	=	4	2	8	1	MIC
22	Cefotaxime, CTX	<	0.06	0.03	0.125	1	MIC
22	Ceftazidime, CAZ	<	0.25	0.06	0.5	1	MIC
22	Chloramphenicol, CHL	=	4	2	8	1	MIC
22	Ciprofloxacin, CIP	=	0.015	0.004	0.016	1	MIC
22	Colistin, COL	=	2	0.25	2	1	MIC
22	Gentamicin, GEN	=	0.5	0.25	1	1	MIC
22	Nalidixic acid, NAL	<	4	1	4	1	MIC
22	Sulfisoxazole, FIS	=	16	8	32	1	MIC
22	Tetracycline, TET	<	1	0.5	2	1	MIC
22	Trimethoprim, TMP	=	0.5	0.5	2	1	MIC
23	Ampicillin, AMP	=	2	2	8	1	MIC
23	Cefotaxime, CTX	=	0.06	0.03	0.125	1	MIC
23	Ceftazidime, CAZ	=	0.25	0.06	0.5	1	MIC
23	Chloramphenicol, CHL	=	4	2	8	1	MIC
23	Ciprofloxacin, CIP	=	0.008	0.004	0.016	1	MIC
23	Colistin, COL	<	2	0.25	2	1	MIC
23	Gentamicin, GEN	=	0.5	0.25	1	1	MIC
23	Nalidixic acid, NAL	=	4	1	4	1	MIC
23	Sulfisoxazole, FIS	=	32	8	32	1	MIC
23	Tetracycline, TET	=	1	0.5	2	1	MIC
23	Trimethoprim, TMP	=	1	0.5	2	1	MIC
25	Ampicillin, AMP	=	4	2	8	1	MIC
25	Cefotaxime, CTX	=	0.12	0.03	0.125	1	MIC
25	Ceftazidime, CAZ	<=	0.25	0.06	0.5	1	MIC
25	Chloramphenicol, CHL	=	8	2	8	1	MIC
25	Ciprofloxacin, CIP	=	0.015	0.004	0.016	1	MIC
25	Colistin, COL	<=	2	0.25	2	1	MIC
25	Gentamicin, GEN	=	0.5	0.25	1	1	MIC
25	Nalidixic acid, NAL	<=	4	1	4	1	MIC
25	Sulfisoxazole, FIS	<=	8	8	32	1	MIC
25	Tetracycline, TET	<=	1	0.5	2	1	MIC
25	Trimethoprim, TMP	<=	0.5	0.5	2	1	MIC
26	Ampicillin, AMP	=	2	2	8	1	MIC
26	Cefotaxime, CTX	=	0.12	0.03	0.125	1	MIC
26	Ceftazidime, CAZ	<=	0.25	0.06	0.5	1	MIC
26	Chloramphenicol, CHL	=	4	2	8	1	MIC
26	Ciprofloxacin, CIP	<=	0.008	0.004	0.016	1	MIC
26	Colistin, COL	<=	2	0.25	2	1	MIC
26	Gentamicin, GEN	=	0.5	0.25	1	1	MIC
26	Nalidixic acid, NAL	<=	4	1	4	1	MIC
26	Tetracycline, TET	<=	1	0.5	2	1	MIC
26	Trimethoprim, TMP	<=	0.5	0.5	2	1	MIC
29	Ampicillin, AMP	=	4	2	8	1	MIC
29	Cefotaxime, CTX	=	0.06	0.03	0.125	1	MIC
29	Ceftazidime, CAZ	=	0.5	0.06	0.5	1	MIC
29	Chloramphenicol, CHL	=	8	2	8	1	MIC
29	Ciprofloxacin, CIP	=	0.016	0.004	0.016	1	MIC
29	Gentamicin, GEN	=	0.5	0.25	1	1	MIC
29	Nalidixic acid, NAL	=	0.5	1	4	**0**	MIC
29	Tetracycline, TET	=	0.5	0.5	2	1	MIC
29	Trimethoprim, TMP	=	1	0.5	2	1	MIC

Lab no.	Antimicrobial	Operator	Value	Low limit	High limit	Mark	Method
30	Ampicillin, AMP	=	8	2	8	1	MIC
30	Cefepime, FEP	<=	1	0.015	0.125	1	MIC
30	Cefotaxime, CTX	=	0.12	0.03	0.125	1	MIC
30	Cefoxitin, FOX	<=	4	2	8	1	MIC
30	Ceftazidime, CAZ	<=	0.25	0.06	0.5	1	MIC
30	Chloramphenicol, CHL	=	4	2	8	1	MIC
30	Ciprofloxacin, CIP	=	0.015	0.004	0.016	1	MIC
30	Colistin, COL	<=	2	0.25	2	1	MIC
30	Gentamicin, GEN	=	1	0.25	1	1	MIC
30	Imipenem, IMI	<=	0.5	0.06	0.25	1	MIC
30	Meropenem, MER	<=	1	0.008	0.06	1	MIC
30	Nalidixic acid, NAL	<=	4	1	4	1	MIC
30	Sulfisoxazole, FIS	=	32	8	32	1	MIC
30	Tetracycline, TET	<=	1	0.5	2	1	MIC
30	Trimethoprim, TMP	<=	0.5	0.5	2	1	MIC
32	Ampicillin, AMP	=	4	2	8	1	MIC
32	Cefotaxime, CTX	<=	0.06	0.03	0.125	1	MIC
32	Ceftazidime, CAZ	<=	0.25	0.06	0.5	1	MIC
32	Chloramphenicol, CHL	=	4	2	8	1	MIC
32	Ciprofloxacin, CIP	<=	0.008	0.004	0.016	1	MIC
32	Colistin, COL	<=	2	0.25	2	1	MIC
32	Gentamicin, GEN	=	0.5	0.25	1	1	MIC
32	Meropenem, MER	=	0.008	0.008	0.06	1	MIC
32	Nalidixic acid, NAL	<=	4	1	4	1	MIC
32	Sulfisoxazole, FIS	=	16	8	32	1	MIC
32	Tetracycline, TET	<=	1	0.5	2	1	MIC
32	Trimethoprim, TMP	<=	0.5	0.5	2	1	MIC
33	Ampicillin, AMP	=	4	2	8	1	MIC
33	Cefotaxime, CTX	=	0.06	0.03	0.125	1	MIC
33	Ceftazidime, CAZ	=	0.5	0.06	0.5	1	MIC
33	Chloramphenicol, CHL	=	4	2	8	1	MIC
33	Ciprofloxacin, CIP	=	0.03	0.004	0.016	**0**	MIC
33	Colistin, COL	=	1	0.25	2	1	MIC
33	Gentamicin, GEN	=	0.5	0.25	1	1	MIC
33	Nalidixic acid, NAL	=	4	1	4	1	MIC
33	Tetracycline, TET	<=	1	0.5	2	1	MIC
33	Trimethoprim, TMP	=	0.5	0.5	2	1	MIC
34	Ampicillin, AMP	=	4	2	8	1	MIC
34	Cefotaxime, CTX	<=	0.06	0.03	0.125	1	MIC
34	Ceftazidime, CAZ	=	0.5	0.06	0.5	1	MIC
34	Chloramphenicol, CHL	=	4	2	8	1	MIC
34	Ciprofloxacin, CIP	=	0.015	0.004	0.016	1	MIC
34	Colistin, COL	<=	2	0.25	2	1	MIC
34	Gentamicin, GEN	=	0.5	0.25	1	1	MIC
34	Nalidixic acid, NAL	<=	4	1	4	1	MIC
34	Sulfisoxazole, FIS	=	128	8	32	**0**	MIC
34	Tetracycline, TET	<=	1	0.5	2	1	MIC
34	Trimethoprim, TMP	<=	0.5	0.5	2	1	MIC
36	Ampicillin, AMP	=	8	2	8	1	MIC
36	Cefotaxime, CTX	=	0.12	0.03	0.125	1	MIC
36	Ceftazidime, CAZ	<=	0.25	0.06	0.5	1	MIC
36	Chloramphenicol, CHL	=	4	2	8	1	MIC
36	Ciprofloxacin, CIP	=	0.03	0.004	0.016	**0**	MIC
36	Colistin, COL	<=	0.5	0.25	2	1	MIC
36	Gentamicin, GEN	=	0.5	0.25	1	1	MIC
36	Nalidixic acid, NAL	=	2	1	4	1	MIC
36	Sulfisoxazole, FIS	=	16	8	32	1	MIC
36	Tetracycline, TET	<=	1	0.5	2	1	MIC
36	Trimethoprim, TMP	=	0.5	0.5	2	1	MIC

Lab no.	Antimicrobial	Operator	Value	Low limit	High limit	Mark	Method
37	Ampicillin, AMP	=	4	2	8	1	AGA
37	Cefotaxime, CTX	<=	0.06	0.03	0.125	1	AGA
37	Ceftazidime, CAZ	=	0.5	0.06	0.5	1	AGA
37	Chloramphenicol, CHL	=	4	2	8	1	AGA
37	Ciprofloxacin, CIP	<=	0.008	0.004	0.016	1	AGA
37	Gentamicin, GEN	=	0.5	0.25	1	1	AGA
37	Nalidixic acid, NAL	<=	2	1	4	1	AGA
37	Tetracycline, TET	=	1	0.5	2	1	AGA
37	Trimethoprim, TMP	=	0.5	0.5	2	1	AGA
39	Ampicillin, AMP	=	4	2	8	1	MIC
39	Cefotaxime, CTX	=	0.12	0.03	0.125	1	MIC
39	Ceftazidime, CAZ	=	0.5	0.06	0.5	1	MIC
39	Chloramphenicol, CHL	=	4	2	8	1	MIC
39	Ciprofloxacin, CIP	=	0.016	0.004	0.016	1	MIC
39	Colistin, COL	<=	0.5	0.25	2	1	MIC
39	Gentamicin, GEN	=	0.5	0.25	1	1	MIC
39	Nalidixic acid, NAL	=	2	1	4	1	MIC
39	Tetracycline, TET	<=	1	0.5	2	1	MIC
39	Trimethoprim, TMP	=	0.5	0.5	2	1	MIC
40	Ampicillin, AMP	=	20	16	22	1	DD
40	Cefepime, FEP	=	32	31	37	1	DD
40	Cefotaxime, CTX	=	34	29	35	1	DD
40	Cefoxitin, FOX	=	28	23	29	1	DD
40	Ceftazidime, CAZ	=	30	25	32	1	DD
40	Chloramphenicol, CHL	=	24	21	27	1	DD
40	Ciprofloxacin, CIP	=	33	30	40	1	DD
40	Gentamicin, GEN	=	21	19	26	1	DD
40	Imipenem, IMI	=	31	26	32	1	DD
40	Meropenem, MER	=	30	28	34	1	DD
40	Nalidixic acid, NAL	=	24	22	28	1	DD
40	Sulfisoxazole, FIS	=	23	15	23	1	DD
40	Tetracycline, TET	=	23	18	25	1	DD
40	Trimethoprim, TMP	=	28	21	28	1	DD
41	Ampicillin, AMP	=	4	2	8	1	MIC
41	Cefotaxime, CTX	=	0.06	0.03	0.125	1	MIC
41	Ceftazidime, CAZ	=	0.25	0.06	0.5	1	MIC
41	Chloramphenicol, CHL	=	8	2	8	1	MIC
41	Ciprofloxacin, CIP	=	0.015	0.004	0.016	1	MIC
41	Colistin, COL	=	2	0.25	2	1	MIC
41	Gentamicin, GEN	=	0.5	0.25	1	1	MIC
41	Nalidixic acid, NAL	=	4	1	4	1	MIC
41	Tetracycline, TET	=	1	0.5	2	1	MIC
41	Trimethoprim, TMP	=	1	0.5	2	1	MIC
42	Ampicillin, AMP	=	4	2	8	1	MIC
42	Cefepime, FEP	<=	1	0.015	0.125	1	MIC
42	Cefotaxime, CTX	=	0.12	0.03	0.125	1	MIC
42	Cefoxitin, FOX	<=	4	2	8	1	MIC
42	Ceftazidime, CAZ	<=	0.25	0.06	0.5	1	MIC
42	Chloramphenicol, CHL	=	8	2	8	1	MIC
42	Ciprofloxacin, CIP	=	0.015	0.004	0.016	1	MIC
42	Colistin, COL	<=	2	0.25	2	1	MIC
42	Gentamicin, GEN	=	0.5	0.25	1	1	MIC
42	Imipenem, IMI	=	0.25	0.06	0.25	1	MIC
42	Meropenem, MER	<=	1	0.008	0.06	1	MIC
42	Nalidixic acid, NAL	<=	4	1	4	1	MIC
42	Sulfisoxazole, FIS	=	32	8	32	1	MIC
42	Tetracycline, TET	=	2	0.5	2	1	MIC
42	Trimethoprim, TMP	=	1	0.5	2	1	MIC

Lab no.	Antimicrobial	Operator	Value	Low limit	High limit	Mark	Method
44	Ampicillin, AMP	<=	8	2	8	1	AGA
44	Cefotaxime, CTX	<=	0.5	0.03	0.125	1	AGA
44	Cefoxitin, FOX	<=	8	2	8	1	AGA
44	Ceftazidime, CAZ	<=	1	0.06	0.5	1	AGA
44	Chloramphenicol, CHL	<=	8	2	8	1	AGA
44	Ciprofloxacin, CIP	<=	0.064	0.004	0.016	1	AGA
44	Colistin, COL	<=	2	0.25	2	1	AGA
44	Ertapenem, ERTA	<=	0.064	0.004	0.016	1	AGA
44	Gentamicin, GEN	<=	2	0.25	1	1	AGA
44	Imipenem, IMI	=	0.19	0.06	0.25	1	AGA
44	Meropenem, MER	=	0.008	0.008	0.06	1	AGA
44	Nalidixic acid, NAL	<=	16	1	4	1	AGA
44	Sulfisoxazole, FIS	<=	256	8	32	1	AGA
44	Tetracycline, TET	<=	8	0.5	2	1	AGA
44	Trimethoprim, TMP	<=	2	0.5	2	1	AGA
45	Ampicillin, AMP	=	14.6	16	22	0	DD
45	Cefotaxime, CTX	=	32.0	29	35	1	DD
45	Cefoxitin, FOX	=	23.6	23	29	1	DD
45	Ceftazidime, CAZ	=	27.8	25	32	1	DD
45	Chloramphenicol, CHL	=	26.3	21	27	1	DD
45	Ciprofloxacin, CIP	=	35.1	30	40	1	DD
45	Colistin, COL	=	13.8	11	17	1	DD
45	Gentamicin, GEN	=	18.6	19	26	0	DD
45	Meropenem, MER	=	32.4	28	34	1	DD
45	Nalidixic acid, NAL	=	25.5	22	28	1	DD
45	Sulfisoxazole, FIS	=	19.5	15	23	1	DD
45	Tetracycline, TET	=	22.9	18	25	1	DD
45	Trimethoprim, TMP	=	25.0	21	28	1	DD
56	Ampicillin, AMP	=	4	2	8	1	MIC
56	Cefepime, FEP	=	32	31	37	1	DD
56	Cefotaxime, CTX	<=	0.06	0.03	0.125	1	MIC
56	Cefoxitin, FOX	=	26	23	29	1	DD
56	Ceftazidime, CAZ	<=	0.25	0.06	0.5	1	MIC
56	Chloramphenicol, CHL	=	4	2	8	1	MIC
56	Ciprofloxacin, CIP	=	0.015	0.004	0.016	1	MIC
56	Colistin, COL	<	2	0.25	2	1	MIC
56	Gentamicin, GEN	=	0.5	0.25	1	1	MIC
56	Meropenem, MER	=	30	28	34	1	DD
56	Nalidixic acid, NAL	<=	4	1	4	1	MIC
56	Sulfisoxazole, FIS	=	32	8	32	1	MIC
56	Tetracycline, TET	<=	1	0.5	2	1	MIC
56	Trimethoprim, TMP	=	1	0.5	2	1	MIC
58	Ampicillin, AMP	=	4	2	8	1	MIC
58	Cefepime, FEP	=	0.094	0.015	0.125	1	MIC
58	Cefotaxime, CTX	<=	0.06	0.03	0.125	1	MIC
58	Cefoxitin, FOX	<=	4	2	8	1	MIC
58	Ceftazidime, CAZ	<=	0.25	0.06	0.5	1	MIC
58	Chloramphenicol, CHL	=	8	2	8	1	MIC
58	Ciprofloxacin, CIP	<=	0.008	0.004	0.016	1	MIC
58	Colistin, COL	<=	2	0.25	2	1	MIC
58	Ertapenem, ERTA	=	0.06	0.004	0.016	0	MIC
58	Gentamicin, GEN	=	0.5	0.25	1	1	MIC
58	Imipenem, IMI	=	0.5	0.06	0.25	0	MIC
58	Meropenem, MER	=	0.016	0.008	0.06	1	MIC
58	Nalidixic acid, NAL	<=	4	1	4	1	MIC
58	Sulfisoxazole, FIS	=	32	8	32	1	MIC
58	Tetracycline, TET	<=	1	0.5	2	1	MIC
58	Trimethoprim, TMP	<=	0.5	0.5	2	1	MIC

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, CIP	=	0.25	0,06	0,25	1	MIC	X	
1	Erythromycin, ERY	=	2	0,5	2	1	MIC	X	
1	Gentamicin, GEN	=	0.25	0,5	2	0	MIC	X	
1	Nalidixic acid, NAL	=	8	4	16	1	MIC	X	
1	Tetracycline, TET	=	2	0,25	2	1	MIC	X	
2	Ciprofloxacin, CIP	=	0.25	0,06	0,25	1	MIC	X	
2	Erythromycin, ERY	=	1	0,5	2	1	MIC	X	
2	Gentamicin, GEN	=	0.25	0,5	2	0	MIC	X	
2	Nalidixic acid, NAL	=	8	4	16	1	MIC	X	
2	Tetracycline, TET	=	1	0,25	2	1	MIC	X	
4	Ciprofloxacin, CIP	=	0.12	0,06	0,25	1	MIC	X	
4	Erythromycin, ERY	=	2	0,5	2	1	MIC	X	
4	Gentamicin, GEN	=	1	0,5	2	1	MIC	X	
4	Nalidixic acid, NAL	=	4	4	16	1	MIC	X	
4	Tetracycline, TET	=	2	0,25	2	1	MIC	X	
6	Ciprofloxacin, CIP	=	0.12	0,03	0,125	1	MIC		X
6	Erythromycin, ERY	<=	0.5	0,25	2	1	MIC		X
6	Gentamicin, GEN	=	1	0,25	2	1	MIC		X
6	Nalidixic acid, NAL	=	8	4	16	1	MIC		X
6	Tetracycline, TET	=	1	0,25	1	1	MIC		X
9	Ciprofloxacin, CIP	=	0.12	0,06	0,25	1	MIC	X	
9	Erythromycin, ERY	=	1	0,5	2	1	MIC	X	
9	Gentamicin, GEN	=	1	0,5	2	1	MIC	X	
9	Nalidixic acid, NAL	=	8	4	16	1	MIC	X	
9	Tetracycline, TET	=	0.5	0,25	2	1	MIC	X	
11	Ciprofloxacin, CIP	=	0.25	0,03	0,125	0	MIC		X
11	Erythromycin, ERY	<=	0.5	0,25	2	1	MIC		X
11	Gentamicin, GEN	=	1	0,25	2	1	MIC		X
11	Nalidixic acid, NAL	=	8	4	16	1	MIC		X
11	Tetracycline, TET	=	1	0,25	1	1	MIC		X
12	Ciprofloxacin, CIP	=	0.5	0,06	0,25	0	MIC	X	
12	Erythromycin, ERY	=	2	0,5	2	1	MIC	X	
12	Gentamicin, GEN	=	1	0,5	2	1	MIC	X	
12	Nalidixic acid, NAL	=	16	4	16	1	MIC	X	
12	Tetracycline, TET	=	1	0,25	2	1	MIC	X	
14	Ciprofloxacin, CIP	=	0.125	0,03	0,125	1	MIC		X
14	Erythromycin, ERY	<=	0.5	0,25	2	1	MIC		X
14	Gentamicin, GEN	=	1	0,25	2	1	MIC		X
14	Nalidixic acid, NAL	=	4	4	16	1	MIC		X
14	Tetracycline, TET	=	1	0,25	1	1	MIC		X
17	Ciprofloxacin, CIP	=	0.25	0,06	0,25	1	MIC	X	
17	Erythromycin, ERY	=	2	0,5	2	1	MIC	X	
17	Gentamicin, GEN	=	1	0,5	2	1	MIC	X	
17	Nalidixic acid, NAL	=	8	4	16	1	MIC	X	
17	Tetracycline, TET	=	0.5	0,25	2	1	MIC	X	
19	Ciprofloxacin, CIP	=	0.12	0,03	0,125	1	MIC		X
19	Erythromycin, ERY	<=	0.5	0,25	2	1	MIC		X
19	Gentamicin, GEN	=	1	0,25	2	1	MIC		X
19	Nalidixic acid, NAL	=	4	4	16	1	MIC		X
19	Tetracycline, TET	=	1	0,25	1	1	MIC		X

Lab no.	Antimicrobial	Operator	Value	Low limit	High limit	Mark	Method	36-37ºC/48h	42ºC/24h
20	Ciprofloxacin, CIP	=	0.25	0,06	0,25	1	MIC	X	
20	Erythromycin, ERY	=	1	0,5	2	1	MIC	X	
20	Gentamicin, GEN	=	1	0,5	2	1	MIC	X	
20	Nalidixic acid, NAL	=	8	4	16	1	MIC	X	
20	Tetracycline, TET	=	1	0,25	2	1	MIC	X	
21	Ciprofloxacin, CIP	=	0.25	0,03	0,125	0	MIC		X
21	Erythromycin, ERY	=	0.5	0,25	2	1	MIC		X
21	Gentamicin, GEN	=	0.12	0,25	2	0	MIC		X
21	Nalidixic acid, NAL	=	2	4	16	0	MIC		X
21	Tetracycline, TET	=	0.25	0,25	1	1	MIC		X
22	Ciprofloxacin, CIP	=	0.12	0,03	0,125	1	MIC		X
22	Erythromycin, ERY	=	1	0,25	2	1	MIC		X
22	Gentamicin, GEN	=	0.5	0,25	2	1	MIC		X
22	Nalidixic acid, NAL	=	8	4	16	1	MIC		X
22	Tetracycline, TET	=	1	0,25	1	1	MIC		X
23	Ciprofloxacin, CIP	=	0.12	0,03	0,125	1	MIC		X
23	Erythromycin, ERY	<	0.5	0,25	2	1	MIC		X
23	Gentamicin, GEN	=	1	0,25	2	1	MIC		X
23	Nalidixic acid, NAL	=	8	4	16	1	MIC		X
23	Tetracycline, TET	=	1	0,25	1	1	MIC		X
25	Ciprofloxacin, CIP	=	0.25	0,06	0,25	1	MIC	X	
25	Erythromycin, ERY	=	2	0,5	2	1	MIC	X	
25	Gentamicin, GEN	<=	0.25	0,5	2	0	MIC	X	
25	Nalidixic acid, NAL	=	8	4	16	1	MIC	X	
25	Tetracycline, TET	=	2	0,25	2	1	MIC	X	
26	Ciprofloxacin, CIP	=	0.12	0,06	0,25	1	MIC	X	
26	Erythromycin, ERY	=	1	0,5	2	1	MIC	X	
26	Gentamicin, GEN	=	1	0,5	2	1	MIC	X	
26	Nalidixic acid, NAL	=	8	4	16	1	MIC	X	
26	Tetracycline, TET	=	2	0,25	2	1	MIC	X	
29	Ciprofloxacin, CIP	=	0.06	0,06	0,25	1	MIC	X	
29	Erythromycin, ERY	=	1	0,5	2	1	MIC	X	
29	Gentamicin, GEN	=	2	0,5	2	1	MIC	X	
29	Nalidixic acid, NAL	=	4	4	16	1	MIC	X	
29	Tetracycline, TET	=	0.25	0,25	2	1	MIC	X	
30	Ciprofloxacin, CIP	=	0.25	0,06	0,25	1	MIC	X	
30	Erythromycin, ERY	=	1	0,5	2	1	MIC	X	
30	Gentamicin, GEN	=	0.5	0,5	2	1	MIC	X	
30	Nalidixic acid, NAL	=	8	4	16	1	MIC	X	
30	Tetracycline, TET	=	1	0,25	2	1	MIC	X	
32	Ciprofloxacin, CIP	=	0.125	0,06	0,25	1	MIC	X	
32	Erythromycin, ERY	=	1	0,5	2	1	MIC	X	
32	Gentamicin, GEN	=	0.5	0,5	2	1	MIC	X	
32	Nalidixic acid, NAL	=	8	4	16	1	MIC	X	
32	Tetracycline, TET	=	1	0,25	2	1	MIC	X	
33	Ciprofloxacin, CIP	=	0.25	0,06	0,25	1	MIC	X	
33	Erythromycin, ERY	=	1	0,5	2	1	MIC	X	
33	Gentamicin, GEN	=	1	0,5	2	1	MIC	X	
33	Nalidixic acid, NAL	=	8	4	16	1	MIC	X	
33	Tetracycline, TET	=	0.5	0,25	2	1	MIC	X	

Lab no.	Antimicrobial	Operator	Value	Low limit	High limit	Mark	Method	36-37ºC/48h	42ºC/24h
34	Ciprofloxacin, CIP	=	0.25	0,06	0,25	1	MIC	X	
34	Erythromycin, ERY	=	2	0,5	2	1	MIC	X	
34	Gentamicin, GEN	=	0.5	0,5	2	1	MIC	X	
34	Nalidixic acid, NAL	=	8	4	16	1	MIC	X	
34	Tetracycline, TET	=	2	0,25	2	1	MIC	X	
36	Ciprofloxacin, CIP	=	0.25	0,06	0,25	1	MIC	X	
36	Erythromycin, ERY	<=	0.5	0,5	2	1	MIC	X	
36	Gentamicin, GEN	=	0.5	0,5	2	1	MIC	X	
36	Nalidixic acid, NAL	=	8	4	16	1	MIC	X	
36	Tetracycline, TET	=	0.5	0,25	2	1	MIC	X	
37	Ciprofloxacin, CIP	=	0.25	0,12	1	1	AGA	X	
37	Erythromycin, ERY	=	1	1	8	1	AGA	X	
37	Gentamicin, GEN	=	1	0,5	2	1	AGA	X	
37	Nalidixic acid, NAL	=	8	NA	NA		AGA	X	
37	Tetracycline, TET	=	1	NA	NA		AGA	X	
40	Ciprofloxacin, CIP	=	0.12	0,03	0,125	1	MIC		X
40	Erythromycin, ERY	=	0.5	0,25	2	1	MIC		X
40	Gentamicin, GEN	=	0.25	0,25	2	1	MIC		X
40	Nalidixic acid, NAL	=	4	4	16	1	MIC		X
40	Tetracycline, TET	=	1	0,25	1	1	MIC		X
41	Ciprofloxacin, CIP	=	0.06	0,03	0,125	1	MIC		X
41	Erythromycin, ERY	=	0.5	0,25	2	1	MIC		X
41	Gentamicin, GEN	=	1	0,25	2	1	MIC		X
41	Nalidixic acid, NAL	=	4	4	16	1	MIC		X
41	Tetracycline, TET	=	0.5	0,25	1	1	MIC		X
42	Ciprofloxacin, CIP	=	0.12	0,06	0,25	1	MIC	X	
42	Erythromycin, ERY	=	1	0,5	2	1	MIC	X	
42	Gentamicin, GEN	=	0.25	0,5	2	**0**	MIC	X	
42	Nalidixic acid, NAL	=	8	4	16	1	MIC	X	
42	Tetracycline, TET	=	1	0,25	2	1	MIC	X	
44	Ciprofloxacin, CIP	<	1	0,12	1	1	AGA	X	
44	Erythromycin, ERY	<	4	1	8	1	AGA	X	
44	Gentamicin, GEN	<	1	0,5	2	1	AGA	X	
44	Nalidixic acid, NAL	<	16	NA	NA		AGA	X	
44	Tetracycline, TET	<	2	NA	NA		AGA	X	
45	Ciprofloxacin, CIP	=	0.12	0,06	0,25	1	MIC	X	
45	Erythromycin, ERY	=	1	0,5	2	1	MIC	X	
45	Gentamicin, GEN	=	1	0,5	2	1	MIC	X	
45	Nalidixic acid, NAL	=	8	4	16	1	MIC	X	
45	Tetracycline, TET	=	1	0,25	2	1	MIC	X	
56	Ciprofloxacin, CIP	=	0.12	0,03	0,125	1	MIC		X
56	Erythromycin, ERY	<=	0.5	0,25	2	1	MIC		X
56	Gentamicin, GEN	=	1	0,25	2	1	MIC		X
56	Nalidixic acid, NAL	=	8	4	16	1	MIC		X
56	Tetracycline, TET	=	1	0,25	1	1	MIC		X
58	Ciprofloxacin, CIP	=	0.12	0,03	0,125	1	MIC		X
58	Erythromycin, ERY	=	1	0,25	2	1	MIC		X
58	Gentamicin, GEN	=	1	0,25	2	1	MIC		X
58	Nalidixic acid, NAL	=	8	4	16	1	MIC		X
58	Tetracycline, TET	=	1	0,25	1	1	MIC		X

MIC: microbroth dilution
AGA: agar dilution
NA: Not available

Salmonella - expected and obtained interpretation

Antimicrobial	Strain	Expected	% R	% S	No. correct	No. incorrect
Ampicillin, AMP	EURL S-8.1	S	0	100	34	0
	EURL S-8.2	S	0	100	34	0
	EURL S-8.3	R	100	0	34	0
	EURL S-8.4	R	100	0	34	0
	EURL S-8.5	R	100	0	34	0
	EURL S-8.6	R	100	0	34	0
	EURL S-8.7	R	100	0	34	0
	EURL S-8.8	R	97	3	33	1
Cefotaxime, CTX	EURL S-8.1	S	0	100	34	0
	EURL S-8.2	S	0	100	34	0
	EURL S-8.3	S	0	100	34	0
	EURL S-8.4	R	100	0	34	0
	EURL S-8.5	R	100	0	34	0
	EURL S-8.6	R	100	0	34	0
	EURL S-8.7	R	100	0	34	0
	EURL S-8.8	S	3	97	33	1
Ceftazidime, CAZ	EURL S-8.1	S	0	100	33	0
	EURL S-8.2	S	0	100	33	0
	EURL S-8.3	S	0	100	33	0
	EURL S-8.4	R	100	0	34	0
	EURL S-8.5	S	6	94	31	2
	EURL S-8.6	R	100	0	34	0
	EURL S-8.7	R	100	0	34	0
	EURL S-8.8	S	3	97	32	1
Chloramphenicol, CHL	EURL S-8.1	S	0	100	34	0
	EURL S-8.2	S	0	100	34	0
	EURL S-8.3	S	3	97	33	1
	EURL S-8.4	S	0	100	34	0
	EURL S-8.5	S	0	100	34	0
	EURL S-8.6	R	100	0	34	0
	EURL S-8.7	S	0	100	34	0
	EURL S-8.8	R	97	3	33	1
Ciprofloxacin, CIP	EURL S-8.1	R	94	6	32	2
	EURL S-8.2	S	0	100	34	0
	EURL S-8.3	R	100	0	34	0
	EURL S-8.4	R	100	0	34	0
	EURL S-8.5	R	97	3	33	1
	EURL S-8.6	R	97	3	33	1
	EURL S-8.7	S	3	97	33	1
	EURL S-8.8	S	0	100	34	0
Colistin, COL	EURL S-8.1	S	0	100	30	0
	EURL S-8.2	S	7	93	28	2
	EURL S-8.3	S	3	97	29	1
	EURL S-8.4	S	0	100	30	0
	EURL S-8.5	S	0	100	30	0
	EURL S-8.6	S	0	100	30	0
	EURL S-8.7	S	0	100	30	0
	EURL S-8.8	S	3	97	29	1

Antimicrobial	Strain	Expected	% R	% S	No. correct	No. incorrect
Gentamicin, GEN	EURL S-8.1	S	0	100	34	0
	EURL S-8.2	S	0	100	34	0
	EURL S-8.3	R	100	0	34	0
	EURL S-8.4	R	100	0	34	0
	EURL S-8.5	S	3	97	33	1
	EURL S-8.6	R	100	0	34	0
	EURL S-8.7	S	0	100	34	0
	EURL S-8.8	S	0	100	34	0
Meropenem, MER	EURL S-8.1	S	0	100	14	0
	EURL S-8.2	S	0	100	13	0
	EURL S-8.3	S	0	100	15	0
	*EURL S-8.4**	*R*	*38*	*62*	*5*	*8*
	EURL S-8.5	S	0	100	14	0
	EURL S-8.6	S	0	100	14	0
	EURL S-8.7	S	0	100	15	0
	EURL S-8.8	S	0	100	14	0
Nalidixic acid, NAL	EURL S-8.1	S	0	100	34	0
	EURL S-8.2	S	0	100	34	0
	EURL S-8.3	R	100	0	34	0
	EURL S-8.4	R	97	3	33	1
	EURL S-8.5	R	97	3	33	1
	EURL S-8.6	R	100	0	34	0
	EURL S-8.7	S	0	100	34	0
	EURL S-8.8	S	0	100	34	0
Sulfamethoxazole, SMX	EURL S-8.1	S	6	94	31	2
	EURL S-8.2	S	0	100	33	0
	EURL S-8.3	R	100	0	33	0
	EURL S-8.4	R	100	0	33	0
	EURL S-8.5	S	6	94	31	2
	EURL S-8.6	R	100	0	33	0
	EURL S-8.7	S	3	97	32	1
	EURL S-8.8	R	97	3	32	1
Tetracycline, TET	EURL S-8.1	S	0	100	34	0
	EURL S-8.2	S	0	100	34	0
	EURL S-8.3	R	100	0	34	0
	EURL S-8.4	R	100	0	34	0
	EURL S-8.5	R	100	0	34	0
	EURL S-8.6	R	100	0	34	0
	EURL S-8.7	S	0	100	34	0
	EURL S-8.8	R	97	3	33	1
Trimethoprim, TMP	EURL S-8.1	S	0	100	34	0
	EURL S-8.2	S	0	100	34	0
	EURL S-8.3	S	0	100	34	0
	EURL S-8.4	S	0	100	34	0
	EURL S-8.5	S	0	100	34	0
	EURL S-8.6	R	100	0	34	0
	EURL S-8.7	S	0	100	34	0
	EURL S-8.8	R	97	3	33	1

*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-8.1	R	93%	7%	28	2
	EURL C-8.2	S	0%	100%	30	0
	EURL C-8.3	R	93%	7%	27	2
	EURL C-8.4	S	4%	96%	26	1
	EURL C-8.5	R	97%	3%	29	1
	EURL C-8.6	S	3%	97%	29	1
	EURL C-8.7	S	3%	97%	29	1
	EURL C-8.8	R	100%	0%	30	0
Erythromycin, ERY	EURL C-8.1	R	97%	3%	29	1
	EURL C-8.2	R	97%	3%	29	1
	EURL C-8.3	S	3%	97%	28	1
	EURL C-8.4	S	0%	100%	27	0
	EURL C-8.5	S	3%	97%	29	1
	EURL C-8.6	S	3%	97%	29	1
	EURL C-8.7	S	0%	100%	30	0
	EURL C-8.8	S	3%	97%	29	1
Gentamicin, GEN	EURL C-8.1	S	0%	100%	30	0
	EURL C-8.2	S	0%	100%	30	0
	EURL C-8.3	S	0%	100%	29	0
	EURL C-8.4	S	0%	100%	27	0
	EURL C-8.5	S	0%	100%	30	0
	EURL C-8.6	S	0%	100%	30	0
	EURL C-8.7	S	3%	97%	29	1
	EURL C-8.8	S	0%	100%	30	0
Nalidixic acid, NAL	EURL C-8.1	R	97%	3%	29	1
	EURL C-8.2	S	3%	97%	29	1
	EURL C-8.3	R	90%	10%	26	3
	EURL C-8.4	R	92%	8%	24	2
	EURL C-8.5	R	97%	3%	29	1
	EURL C-8.6	S	17%	83%	25	5
	EURL C-8.7	S	7%	93%	28	2
	EURL C-8.8	R	97%	3%	29	1
Streptomycin, STR	EURL C-8.1	R	97%	3%	29	1
	EURL C-8.2	S	7%	93%	28	2
	EURL C-8.3	S	3%	97%	28	1
	EURL C-8.4	S	4%	96%	26	1
	EURL C-8.5	S	3%	97%	29	1
	EURL C-8.6	R	100%	0%	30	0
	EURL C-8.7	S	7%	93%	28	2
	EURL C-8.8	R	100%	0%	30	0
Tetracycline, TET	EURL C-8.1	R	79%	21%	23	6
	EURL C-8.2	S	0%	100%	30	0
	EURL C-8.3	R	93%	7%	27	2
	EURL C-8.4	R	96%	4%	26	1
	EURL C-8.5	S	0%	100%	30	0
	EURL C-8.6	R	100%	0%	30	0
	EURL C-8.7	S	3%	97%	29	1
	EURL C-8.8	R	100%	0%	30	0

Deviations - *Salmonella*

Lab no.	Strain	Antimicrobial	Obtained interpretation	Obtained value	Expected interpretation	Expected MIC / ESBL conclusion	Method used
6	EURL S-8.7	ESBL test conclusion		Unusual pt		ESBL	MIC
11	EURL S-8.1	Ciprofloxacin, CIP	S	0.06	R	= 0.25	MIC
12	EURL S-8.7	Ciprofloxacin, CIP	R	0.12	S	= 0.03	MIC
15	EURL S-8.1	Ciprofloxacin, CIP	S	19	R	= 0.25	DD
15	EURL S-8.5	Ciprofloxacin, CIP	S		R	= 0.5	DD
15	EURL S-8.6	Ciprofloxacin, CIP	S		R	= 1	DD
18	EURL S-8.7	ESBL test conclusion		Unusual pt		ESBL	MIC
22	EURL S-8.3	ESBL test conclusion		Unusual pt		Not ESBL	MIC
23	EURL S-8.2	Colistin, COL	R	4	S	<= 1	MIC
23	EURL S-8.3	Colistin, COL	R	4	S	<= 1	MIC
26	EURL S-8.5	Nalidixic acid, NAL	S	<=4	R	> 64	MIC
30	EURL S-8.7	ESBL test conclusion		Unusual pt		ESBL	MIC
33	EURL S-8.4	Nalidixic acid, NAL	S	>128	R	> 64	MIC
39	EURL S-8.5	Ceftazidime, CAZ	R	1	S	= 1	MIC
40	EURL S-8.5	Sulfamethoxazole, SMX	R	15	S	<= 64	DD
41	EURL S-8.2	Colistin, COL	R	4	S	<= 1	MIC
41	EURL S-8.6	ESBL test conclusion		Unusual pt		ESBL	MIC
42	EURL S-8.8	Ampicillin,Â AMP	S	2	R	> 32	MIC
42	EURL S-8.8	Chloramphenicol, CHL	S	8	R	> 64	MIC
42	EURL S-8.8	Sulfamethoxazole, SMX	S	64	R	> 1024	MIC
42	EURL S-8.8	Tetracycline, TET	S	2	R	> 32	MIC
42	EURL S-8.8	Trimethoprim, TMP	S	<=0.05	R	> 32	MIC
45	EURL S-8.1	Sulfamethoxazole, SMX	R	16.9	S	<= 64	DD
45	EURL S-8.3	Chloramphenicol, CHL	R	0	S	= 8	DD
56	EURL S-8.1	Sulfamethoxazole, SMX	R	512	S	<= 64	DD
56	EURL S-8.7	ESBL test conclusion		Unusual pt		ESBL	DD
58	EURL S-8.1	ESBL test conclusion		pAmpC		Not ESBL	MIC
58	EURL S-8.2	ESBL test conclusion		ESBL		Not ESBL	MIC
58	EURL S-8.3	ESBL test conclusion		pAmpC		Not ESBL	MIC
58	EURL S-8.5	Ceftazidime, CAZ	R	>16	S	= 1	MIC
58	EURL S-8.5	ESBL test conclusion		Not ESBL		Unusual pt	MIC
58	EURL S-8.5	Gentamicin, GEN	R	16	S	<= 0.5	MIC
58	EURL S-8.5	Sulfamethoxazole, SMX	R	>1024	S	<= 64	MIC
58	EURL S-8.7	ESBL test conclusion		Not ESBL		ESBL	MIC
58	EURL S-8.7	Sulfamethoxazole, SMX	R	1024	S	<= 64	MIC
58	EURL S-8.8	Cefotaxime, CTX	R	>4	S	<= 0.12	MIC
58	EURL S-8.8	Ceftazidime, CAZ	R	>16	S	= 0.25	MIC
58	EURL S-8.8	Colistin, COL	R	4	S	<= 1	MIC
58	EURL S-8.8	ESBL test conclusion		pAmpC		Not ESBL	MIC

AGA Agar dilution
DD Disk diffusion
ET E-test
MIC Microbroth dilution

Deviations - *Campylobacter*

Lab no.	Strain	Antimicrobial	Obtained interpretation	Obtained value	Expected interpretation	Expected MIC	Method used
4	EURL C-8.6	Nalidixic acid, NAL	R	32	S	= 16	MIC
4	EURL C-8.8	Erythromycin, ERY	R	32	S	<= 0.5	MIC
6	EURL C-8.1	Tetracycline, TET	S	<= 2	R	= 8	MIC
6	EURL C-8.2	Streptomycin, STR	R	<= 4	S	= 2	MIC
6	EURL C-8.3	Nalidixic acid, NAL	S	<= 4	R	> 64	MIC
6	EURL C-8.3	Tetracycline, TET	S	<= 1	R	> 16	MIC
6	EURL C-8.3	Ciprofloxacin, CIP	S	<= 0.06	R	> 4	MIC
6	EURL C-8.3	Erythromycin, ERY	R	> 32	S	= 2	MIC
6	EURL C-8.6	Ciprofloxacin, CIP	R	<= 0.12	S	= 0.25	MIC
12	EURL C-8.1	Tetracycline, TET	S	16	R	= 8	MIC
12	EURL C-8.2	Streptomycin, STR	R	8	S	= 2	MIC
12	EURL C-8.6	Nalidixic acid, NAL	R	32	S	= 16	MIC
14	EURL C-8.1	Tetracycline, TET	S	1	R	= 8	MIC
14	EURL C-8.4	Nalidixic acid, NAL	S	16	R	= 64	MIC
17	EURL C-8.4	Nalidixic acid, NAL	S	16	R	= 64	MIC
20	EURL C-8.4	Streptomycin, STR	R	16	S	<= 1	MIC
21	EURL C-8.1	Tetracycline, TET	S	2	R	= 8	MIC
22	EURL C-8.3	Ciprofloxacin, CIP	S	=0.25	R	> 4	MIC
22	EURL C-8.3	Nalidixic acid, NAL	S	<2	R	> 64	MIC
22	EURL C-8.3	Streptomycin, STR	R	=8	S	<= 1	MIC
22	EURL C-8.4	Campylobacter type				C. jejuni	
22	EURL C-8.7	Nalidixic acid, NAL	R	>64	S	= 4	MIC
22	EURL C-8.7	Ciprofloxacin, CIP	R	=4	S	<= 0.06	MIC
22	EURL C-8.7	Tetracycline, TET	R	=16	S	= 0.5	MIC
22	EURL C-8.7	Streptomycin, STR	R	=16	S	<= 1	MIC
22	EURL C-8.7	Gentamicin, GEN	R	=16	S	= 0.25	MIC
23	EURL C-8.1	Campylobacter type				C. coli	
23	EURL C-8.2	Campylobacter type				C. coli	
23	EURL C-8.3	Campylobacter type				C. jejuni	
23	EURL C-8.4	Campylobacter type				C. jejuni	
23	EURL C-8.4	Ciprofloxacin, CIP	R	1	S	= 0.5	MIC
23	EURL C-8.5	Campylobacter type				C. jejuni	
23	EURL C-8.6	Campylobacter type				C. coli	
23	EURL C-8.7	Campylobacter type				C. coli	
23	EURL C-8.8	Campylobacter type				C. coli	
29	EURL C-8.3	Nalidixic acid, NAL	S	<1	R	> 64	MIC
29	EURL C-8.3	Tetracycline, TET	S	2	R	> 16	MIC
29	EURL C-8.5	Nalidixic acid, NAL	S	16	R	> 64	MIC
29	EURL C-8.5	Ciprofloxacin, CIP	S	1	R	> 4	MIC
29	EURL C-8.5	Streptomycin, STR	R	4	S	= 2	MIC
29	EURL C-8.8	Nalidixic acid, NAL	S	32	R	= 64	MIC
36	EURL C-8.5	Campylobacter type		C. coli		C. jejuni	
36	EURL C-8.6	Campylobacter type		C. jejuni		C. coli	
36	EURL C-8.6	Nalidixic acid, NAL	R	32	S	= 16	MIC
37	EURL C-8.1	Nalidixic acid, NAL	S	<=2	R	> 64	AGA
37	EURL C-8.1	Tetracycline, TET	S	<=0.125	R	= 8	AGA
37	EURL C-8.1	Ciprofloxacin, CIP	S	<=0.06	R	> 4	AGA
37	EURL C-8.1	Streptomycin, STR	S	4	R	> 16	AGA
37	EURL C-8.1	Erythromycin, ERY	S	4	R	> 32	AGA
37	EURL C-8.2	Erythromycin, ERY	S	4	R	> 32	AGA
40	EURL C-8.1	Tetracycline, TET	S	2	R	= 8	MIC
40	EURL C-8.6	Campylobacter type		C. jejuni		C. coli	
40	EURL C-8.7	Nalidixic acid, NAL	R	32	S	= 4	MIC
42	EURL C-8.6	Erythromycin, ERY	R	4	S	= 4	MIC
44	EURL C-8.1	Ciprofloxacin, CIP	S	<1	R	> 4	AGA
44	EURL C-8.4	Tetracycline, TET	S	<2	R	> 16	AGA
44	EURL C-8.6	Nalidixic acid, NAL	R	>16<32	S	= 16	AGA
44	EURL C-8.7	Streptomycin, STR	R	>4	S	<= 1	AGA
45	EURL C-8.6	Nalidixic acid, NAL	R	32	S	= 16	MIC
58	EURL C-8.2	Nalidixic acid, NAL	R	32	S	= 8	MIC
58	EURL C-8.5	Erythromycin, ERY	R	32	S	= 2	MIC

AGA Agar dilution
MIC Microbroth dilution

Genotypic characterization (optional)

Lab no.	Strain	Gene tested		Not detected	Primer used 5'→3'	Primer used 3'→5'	PCR-method	Reference
I	EURL S-8.4	VIM	-2					Whole genome sequencing
I	EURL S-8.5	CTX	M-9					Whole genome sequencing
I	EURL S-8.6	CTX	M-3					Whole genome sequencing
I	EURL S-8.7	TEM	-52					Whole genome sequencing
III	EURL S-8.4	TEM	-1				PCR (published)	Olesen et al., MDR 2004
III	EURL S-8.4	VIM	-2				PCR (published)	Dallene et al. JAC 2010
III	EURL S-8.4	ACC		X			PCR (published)	Perez-Perez JCM 2002
III	EURL S-8.4	ACT		X			PCR (published)	Perez-Perez JCM 2002
III	EURL S-8.4	CMY-2		X			PCR (published)	Zhao et al. AAC 2001
III	EURL S-8.4	CTX		X			PCR (published)	Bachelor et al. AAC 2005
III	EURL S-8.4	DHA		X			PCR (published)	Perez-Perez JCM 2002
III	EURL S-8.4	FOX		X			PCR (published)	Perez-Perez JCM 2002
III	EURL S-8.4	GES		X				Provided by EURL-AR, H. Hasman
III	EURL S-8.4	IMP		X			PCR (published)	Dallene et al. JAC 2010
III	EURL S-8.4	KPC		X			PCR (published)	Dallene et al. JAC 2010
III	EURL S-8.4	MOX		X			PCR (published)	Perez-Perez JCM 2002
III	EURL S-8.4	NDM		X			PCR (published)	Poirel et al. DMID 2011
III	EURL S-8.4	OXA		X				See comment (several families were tested)
III	EURL S-8.4	PER		X				Provided by EURL-AR, H. Hasman
III	EURL S-8.4	SHV		X			PCR (published)	Weill et al, JCM 2004
III	EURL S-8.4	VEB		X			PCR (published)	Provided by EURL-AR, H. Hasman
III	EURL S-8.5	CTX	M-9				PCR (published)	Paauw et al., EID 2006; see comments
III	EURL S-8.5	TEM	-1				PCR (published)	Olesen et al., MDR 2004
III	EURL S-8.5	ACC		X				See 8.4
III	EURL S-8.5	ACT		X				See 8.4
III	EURL S-8.5	CMY		X				See 8.4
III	EURL S-8.5	DHA		X				See 8.4
III	EURL S-8.5	FOX		X				See 8.4
III	EURL S-8.5	GES		X				See 8.4
III	EURL S-8.5	IMP		X				See 8.4
III	EURL S-8.5	KPC		X				See 8.4
III	EURL S-8.5	MOX		X				See 8.4
III	EURL S-8.5	NDM		X				See 8.4
III	EURL S-8.5	OXA		X				several families were tested see 8.4
III	EURL S-8.5	PER		X				See 8.4
III	EURL S-8.5	SHV		X				See 8.4
III	EURL S-8.5	VEB		X				See 8.4
III	EURL S-8.5	VIM		X				See 8.4
III	EURL S-8.6	CTX	M-3				PCR (published)	Carattoli et al., JCM 2008
III	EURL S-8.6	OXA	-30				PCR (published)	Guerra et al., AAC 2000
III	EURL S-8.6	ACC		X				
III	EURL S-8.6	ACT		X				
III	EURL S-8.6	CMY		X				
III	EURL S-8.6	DHA		X				
III	EURL S-8.6	FOX		X				
III	EURL S-8.6	GES		X				
III	EURL S-8.6	IMP		X				
III	EURL S-8.6	KPC		X				
III	EURL S-8.6	MOX		X				
III	EURL S-8.6	NDM		X				
III	EURL S-8.6	PER		X				
III	EURL S-8.6	SHV		X				
III	EURL S-8.6	TEM		X				
III	EURL S-8.6	VEB		X				

Lab no.	Strain	Gene tested		Not detected	Primer used 5'→3'	Primer used 3'→5'	PCR-method	Reference
III	EURL S-8.6	VIM		X				
III	EURL S-8.7	TEM	-52				PCR (published)	Olesen et al., MDR 2004
III	EURL S-8.7	ACC		X				
III	EURL S-8.7	ACT		X				
III	EURL S-8.7	CMY		X				
III	EURL S-8.7	CTX		X				
III	EURL S-8.7	DHA		X				
III	EURL S-8.7	FOX		X				
III	EURL S-8.7	GES		X				
III	EURL S-8.7	IMP		X				
III	EURL S-8.7	KPC		X				
III	EURL S-8.7	MOX		X				
III	EURL S-8.7	NDM		X				
III	EURL S-8.7	OXA		X				
III	EURL S-8.7	PER		X				
III	EURL S-8.7	SHV		X				
III	EURL S-8.7	VEB		X				
III	EURL S-8.7	VIM		X				
IV	EURL S-8.4	TEM	-1				PCR (published)	Dierikx, Vet Mic (2010);145:273-8
IV	EURL S-8.4	VIM					PCR (published)	Ellington, JAC (2007); 59:321-322
IV	EURL S-8.5	CTX	M-9				PCR (published)	Paauw A, EID 2006;12:807-12
IV	EURL S-8.6	CTX	M-3				PCR (published)	Carattoli A, JCM (2008);46:103-8
IV	EURL S-8.7	TEM	-52				PCR (published)	Dierikx, Vet Mic (2010);145:273-8
VI	EURL S-8.1	ACC-1		X	AGCCTCAGCAGCCGGTTAC	CCGGATCAACTAACGGCTTC	PCR (published)	J Clin Microbiol. 2002 Jun;40(6):2153-62
VI	EURL S-8.1	CMY		X	ATGCAACAACGACAATCC	CATCGTCATGCTGGCCAA	PCR (published)	. Antimicrob Agents Chemother 2006 50:618-24.
VI	EURL S-8.1	CMY		X	GCACTTAGCCACCTATACGGCAG	CCTGGCGCATTCTTGAAAAGC	PCR (published)	J. Antimicrob. Chemother. 2006 56:115-121
VI	EURL S-8.1	CTX		X	ATGTGCAGYACCAGTAARGTKATGGC	CCGCTSRTTCTGGTSACYTAYTTYACCCA	PCR (published)	Pediatr Infect Dis J. 28:814-818.2009
VI	EURL S-8.1	DHA-1		X	CTGATGAAAAAATCGTTATC	TATTTTGAGTGCACTGGAAT	PCR (published)	Journal of Antimicrobial Chemotherapy (2009) 64, 1
VI	EURL S-8.1	OXA-10		X	CGCCAGAGAAGTTGGCGAAGTAAG	CCGCAGTTAATCAAGTGGAGTTTC	PCR (published)	Int J Antimicrob Agents. 2011 Apr; 37 (4):356-9.
VI	EURL S-8.1	OXA-30		X	ATGAAAAACACAATACATATCAACTTCG	AATGCGATCACCCATTCTAAAGACAC	PCR (published)	Journal of Antimicrobial Chemotherapy (2009) 64, 1
VI	EURL S-8.1	SHV		X	TTATCTCCCTGTTAGCCACC	CCGAGCGAAATCAGCAAATC	PCR (published)	FEMS Microbiol Lett. 1997. 152:163-7.
VI	EURL S-8.1	TEM		X	GCGGAACCCCTATTTG	CTCACTGATTAAGCATTGGT	PCR (published)	Antimicrobial Agents and Chemotherapy. 2009. 53:17
VI	EURL S-8.2	ACC-1		X	AGCCTCAGCAGCCGGTTAC	CCGGATCAACTAACGGCTTC	PCR (published)	J Clin Microbiol. 2002 Jun;40(6):2153-62
VI	EURL S-8.2	CMY		X	ATGCAACAACGACAATCC	CATCGTCATGCTGGCCAA	PCR (published)	Antimicrob Agents Chemother 2006 50:618-24.
VI	EURL S-8.2	CMY		X	GCACTTAGCCACCTATACGGCAG	CCTGGCGCATTCTTGAAAAGC	PCR (published)	J. Antimicrob. Chemother. 2006 56:115-121
VI	EURL S-8.2	CTX		X	ATGTGCAGYACCAGTAARGTKATGGC	CCGCTSRTTCTGGTSACYTAYTTYACCCA	PCR (published)	Pediatr Infect Dis J. 28:814-818.2009
VI	EURL S-8.2	DHA-1		X	CTGATGAAAAAATCGTTATC	TATTTTGAGTGCACTGGAAT	PCR (published)	Journal of Antimicrobial Chemotherapy (2009) 64, 1
VI	EURL S-8.2	OXA-10		X	CGCCAGAGAAGTTGGCGAAGTAAG	CCGCAGTTAATCAAGTGGAGTTTC	PCR (published)	Int J Antimicrob Agents. 2011 Apr; 37 (4):356-9.
VI	EURL S-8.2	OXA-30		X	ATGAAAAACACAATACATATCAACTTCG	AATGCGATCACCCATTCTAAAGACAC	PCR (published)	Journal of Antimicrobial Chemotherapy (2009) 64
VI	EURL S-8.2	SHV		X	TTATCTCCCTGTTAGCCACC	CCGAGCGAAATCAGCAAATC	PCR (published)	FEMS Microbiol Lett. 1997. 152:163-7.
VI	EURL S-8.2	TEM		X	GCGGAACCCCTATTTG	CTCACTGATTAAGCATTGGT	PCR (published)	Antimicrobial Agents and Chemotherapy. 2009. 53:17
VI	EURL S-8.3	ACC-1		X	AGCCTCAGCAGCCGGTTAC	CCGGATCAACTAACGGCTTC	PCR (published)	J Clin Microbiol. 2002 Jun;40(6):2153-62
VI	EURL S-8.3	CMY		X	ATGCAACAACGACAATCC	CATCGTCATGCTGGCCAA	PCR (published)	Antimicrob Agents Chemother 2006 50:618-24.
VI	EURL S-8.3	CMY		X	GCACTTAGCCACCTATACGGCAG	CCTGGCGCATTCTTGAAAAGC	PCR (published)	J. Antimicrob. Chemother. 2006 56:115-121
VI	EURL S-8.3	CTX		X	ATGTGCAGYACCAGTAARGTKATGGC	CCGCTSRTTCTGGTSACYTAYTTYACCCA	PCR (published)	Pediatr Infect Dis J. 28:814-818.2009
VI	EURL S-8.3	DHA-1		X	CTGATGAAAAAATCGTTATC	TATTTTGAGTGCACTGGAAT	PCR (published)	Journal of Antimicrobial Chemotherapy (2009) 64, 1
VI	EURL S-8.3	OXA-10		X	CGCCAGAGAAGTTGGCGAAGTAAG	CCGCAGTTAATCAAGTGGAGTTTC	PCR (published)	Int J Antimicrob Agents. 2011 Apr; 37 (4):356-9.
VI	EURL S-8.3	OXA-30		X	ATGAAAAACACAATACATATCAACTTCG	AATGCGATCACCCATTCTAAAGACAC	PCR (published)	Journal of Antimicrobial Chemotherapy (2009) 64, 1
VI	EURL S-8.3	SHV		X	TTATCTCCCTGTTAGCCACC	CCGAGCGAAATCAGCAAATC	PCR (published)	FEMS Microbiol Lett. 1997. 152:163-7.
VI	EURL S-8.3	TEM		X	GCGGAACCCCTATTTG	CTCACTGATTAAGCATTGGT	PCR (published)	Antimicrobial Agents and Chemotherapy. 2009. 53:17
VI	EURL S-8.4	TEM	-1		GCGGAACCCCTATTTG	CTCACTGATTAAGCATTGGT	PCR (published)	Antimicrobial Agents and Chemotherapy. 2009. 53:17
VI	EURL S-8.4	ACC-1		X	AGCCTCAGCAGCCGGTTAC	CCGGATCAACTAACGGCTTC	PCR (published)	J Clin Microbiol. 2002 Jun;40(6):2153-62
VI	EURL S-8.4	CMY		X	ATGCAACAACGACAATCC	CATCGTCATGCTGGCCAA	PCR (published)	Antimicrob Agents Chemother 2006 50:618-24
VI	EURL S-8.4	CMY		X	GCACTTAGCCACCTATACGGCAG	CCTGGCGCATTCTTGAAAAGC	PCR (published)	J. Antimicrob. Chemother. 2006 56:115-121
VI	EURL S-8.4	CTX		X	ATGTGCAGYACCAGTAARGTKATGGC	CCGCTSRTTCTGGTSACYTAYTTYACCCA	PCR (published)	Pediatr Infect Dis J. 28:814-818.2009
VI	EURL S-8.4	DHA-1		X	CTGATGAAAAAATCGTTATC	TATTTTGAGTGCACTGGAAT	PCR (published)	Journal of Antimicrobial Chemotherapy (2009) 64, 1

Lab no.	Strain	Gene tested		Not detected	Primer used 5'→3'	Primer used 3'→5'	PCR-method	Reference
VI	EURL S-8.4	OXA-10		X	CGCCAGAGAAGTTGGCGAAGTAAG	CCGCAGTTAATCAAGTGGAGTTTC	PCR (published)	Int J Antimicrob Agents. 2011 Apr; 37 (4):356-9.
VI	EURL S-8.4	OXA-30		X	ATGAAAAACACAATACATATCAACTTCG	AATGCGATCACCCATTCTAAAGACAC	PCR (published)	Journal of Antimicrobial Chemotherapy (2009) 64, 1
VI	EURL S-8.4	SHV		X	TTATCTCCCTGTTAGCCACC	CCGAGCGAAATCAGCAAATC	PCR (published)	FEMS Microbiol Lett. 1997. 152:163-7.
VI	EURL S-8.5	CTX	M-9		ATGTGCAGYACCAGTAARGTKATGGC	CCGCTSRTTCTGGTSACYTAYTTYACCCA	PCR (published)	Pediatr Infect Dis J. 2009 28:814-818.
VI	EURL S-8.5	TEM	-1		GCGGAACCCCTATTTG	CTCACTGATTAAGCATTGGT	PCR (published)	Antimicrobial Agents and Chemotherapy. 2009. 53:17
VI	EURL S-8.5	ACC-1		X	AGCCTCAGCAGCCGGTTAC	CCGGATCAACTAACGGCTTC	PCR (published)	J Clin Microbiol. 2002 Jun;40(6):2153-62
VI	EURL S-8.5	CMY		X	ATGCAACAACGACAATCC	CATCGTCATGCTGGCCAA	PCR (published)	Antimicrob Agents Chemother 2006 50:618-24.
VI	EURL S-8.5	CMY		X	GCACTTAGCCACCTATACGGCAG	CCTGGCGCATTCTTGAAAAGC	PCR (published)	J. Antimicrob. Chemother. 2006 56:115-121
VI	EURL S-8.5	DHA-1		X	CTGATGAAAAAATCGTTATC	TATTTTGAGTGCACTGGAAT	PCR (published)	Journal of Antimicrobial Chemotherapy (2009) 64, 1
VI	EURL S-8.5	OXA-10		X	CGCCAGAGAAGTTGGCGAAGTAAG	CCGCAGTTAATCAAGTGGAGTTTC	PCR (published)	Int J Antimicrob Agents. 2011 Apr; 37 (4):356-9.
VI	EURL S-8.5	OXA-30		X	ATGAAAAACACAATACATATCAACTTCG	AATGCGATCACCCATTCTAAAGACAC	PCR (published)	Journal of Antimicrobial Chemotherapy (2009) 64, 1
VI	EURL S-8.5	SHV		X	TTATCTCCCTGTTAGCCACC	CCGAGCGAAATCAGCAAATC	PCR (published)	FEMS Microbiol Lett. 1997. 152:163-7.
VI	EURL S-8.6	CTX	M-3		ATGTGCAGYACCAGTAARGTKATGGC	CCGCTSRTTCTGGTSACYTAYTTYACCCA	PCR (published)	Pediatr Infect Dis J. 28:814-818.2009
VI	EURL S-8.6	OXA	-30		ATGAAAAACACAATACATATCAACTTCG	AATGCGATCACCCATTCTAAAGACAC	PCR (published)	Journal of Antimicrobial Chemotherapy (2009) 64, 1
VI	EURL S-8.6	ACC-1		X	AGCCTCAGCAGCCGGTTAC	CCGGATCAACTAACGGCTTC	PCR (published)	J Clin Microbiol. 2002 Jun;40(6):2153-62
VI	EURL S-8.6	CMY		X	ATGCAACAACGACAATCC	CATCGTCATGCTGGCCAA	PCR (published)	Antimicrob Agents Chemother 2006 50:618-24.
VI	EURL S-8.6	CMY		X	GCACTTAGCCACCTATACGGCAG	CCTGGCGCATTCTTGAAAAGC	PCR (published)	J. Antimicrob. Chemother.2006 56:115-121
VI	EURL S-8.6	DHA-1		X	CTGATGAAAAAATCGTTATC	TATTTTGAGTGCACTGGAAT	PCR (published)	Journal of Antimicrobial Chemotherapy (2009) 64, 1
VI	EURL S-8.6	OXA-10		X	CGCCAGAGAAGTTGGCGAAGTAAG	CCGCAGTTAATCAAGTGGAGTTTC	PCR (published)	Int J Antimicrob Agents. 2011 Apr; 37 (4):356-9.
VI	EURL S-8.6	SHV		X	TTATCTCCCTGTTAGCCACC	CCGAGCGAAATCAGCAAATC	PCR (published)	FEMS Microbiol Lett. 1997. 152:163-7.
VI	EURL S-8.6	TEM		X	GCGGAACCCCTATTTG	CTCACTGATTAAGCATTGGT	PCR (published)	Antimicrobial Agents and Chemotherapy. 2009. 53:17
VI	EURL S-8.7	TEM	-52		GCGGAACCCCTATTTG	CTCACTGATTAAGCATTGGT	PCR (published)	Antimicrobial Agents and Chemotherapy. 2009. 53:17
VI	EURL S-8.7	ACC-1		X	AGCCTCAGCAGCCGGTTAC	CCGGATCAACTAACGGCTTC	PCR (published)	J Clin Microbiol. 2002 Jun;40(6):2153-62
VI	EURL S-8.7	CMY		X	ATGCAACAACGACAATCC	CATCGTCATGCTGGCCAA	PCR (published)	Antimicrob Agents Chemother 2006 50:618-24
VI	EURL S-8.7	CMY		X	GCACTTAGCCACCTATACGGCAG	CCTGGCGCATTCTTGAAAAGC	PCR (published)	J. Antimicrob. Chemother. 2006 56:115-121
VI	EURL S-8.7	CTX		X	ATGTGCAGYACCAGTAARGTKATGGC	CCGCTSRTTCTGGTSACYTAYTTYACCCA	PCR (published)	Pediatr Infect Dis J. 28:814-818.2009
VI	EURL S-8.7	DHA-1		X	CTGATGAAAAAATCGTTATC	TATTTTGAGTGCACTGGAAT	PCR (published)	Journal of Antimicrobial Chemotherapy (2009) 64, 1
VI	EURL S-8.7	OXA-10		X	CGCCAGAGAAGTTGGCGAAGTAAG	CCGCAGTTAATCAAGTGGAGTTTC	PCR (published)	Int J Antimicrob Agents. 2011 Apr; 37 (4):356-9.
VI	EURL S-8.7	OXA-30		X	ATGAAAAACACAATACATATCAACTTCG	AATGCGATCACCCATTCTAAAGACAC	PCR (published)	Journal of Antimicrobial Chemotherapy (2009) 64,
VI	EURL S-8.7	SHV		X	TTATCTCCCTGTTAGCCACC	CCGAGCGAAATCAGCAAATC	PCR (published)	FEMS Microbiol Lett. 1997. 152:163-7.
VI	EURL S-8.8	ACC-1		X	AGCCTCAGCAGCCGGTTAC	CCGGATCAACTAACGGCTTC	PCR (published)	J Clin Microbiol. 2002 Jun;40(6):2153-62
VI	EURL S-8.8	CMY		X	ATGCAACAACGACAATCC	CATCGTCATGCTGGCCAA	PCR (published)	Antimicrob Agents Chemother 2006 50:618-24.
VI	EURL S-8.8	CMY		X	GCACTTAGCCACCTATACGGCAG	CCTGGCGCATTCTTGAAAAGC	PCR (published)	J. Antimicrob. Chemother.2006 56:115-121
VI	EURL S-8.8	CTX		X	ATGTGCAGYACCAGTAARGTKATGGC	CCGCTSRTTCTGGTSACYTAYTTYACCCA	PCR (published)	Pediatr Infect Dis J. 28:814-818.2009
VI	EURL S-8.8	DHA-1		X	CTGATGAAAAAATCGTTATC	ATTCCAGTGCACTCAAAATA	PCR (published)	Journal of Antimicrobial Chemotherapy (2009) 64, 1
VI	EURL S-8.8	OXA-10		X	CGCCAGAGAAGTTGGCGAAGTAAG	CCGCAGTTAATCAAGTGGAGTTTC	PCR (published)	Int J Antimicrob Agents. 2011 Apr; 37 (4):356-9.
VI	EURL S-8.8	OXA-30		X	ATGAAAAACACAATACATATCAACTTCG	AATGCGATCACCCATTCTAAAGACAC	PCR (published)	Journal of Antimicrobial Chemotherapy (2009) 64, 1
VI	EURL S-8.8	SHV		X	TTATCTCCCTGTTAGCCACC	CCGAGCGAAATCAGCAAATC	PCR (published)	FEMS Microbiol Lett. 1997. 152:163-7.
VI	EURL S-8.8	TEM		X	GCGGAACCCCTATTTG	CTCACTGATTAAGCATTGGT	PCR (published)	Antimicrobial Agents and Chemotherapy. 2009. 53:17

Lab no.	Strain	Gene tested		Not detected	Primer used 5'→3'	Primer used 3'→5'	PCR-method	Reference
VII	EURL S-8.4	SHV						
VII	EURL S-8.4	TEM					PCR (published)	Fang, H., F. Ataker, et al. (2008)
VII	EURL S-8.4	ACC		X				
VII	EURL S-8.4	ACT		X				
VII	EURL S-8.4	CMY		X				
VII	EURL S-8.4	CTXM-1		X			PCR (published)	Woodford, N., E. J. Fagan, et al. (2006)
VII	EURL S-8.4	CTXM-2		X				
VII	EURL S-8.4	CTXM-26		X				
VII	EURL S-8.4	CTXM-8		X				
VII	EURL S-8.4	CTXM-9		X				
VII	EURL S-8.4	DHA		X				
VII	EURL S-8.4	FOX		X				
VII	EURL S-8.4	MOX		X			PCR (published)	Perez-Perez, F. J. and N. D. Hanson (2002)
VII	EURL S-8.4	OXA		X				
VII	EURL S-8.5	CTX	M-9					
VII	EURL S-8.5	TEM						
VII	EURL S-8.5	ACC		X				
VII	EURL S-8.5	ACT		X				
VII	EURL S-8.5	CMY		X				
VII	EURL S-8.5	CTXM-1		X			PCR (published)	Woodford, N., E. J. Fagan, et al. (2006)
VII	EURL S-8.5	CTXM-2		X				
VII	EURL S-8.5	CTXM-26		X				
VII	EURL S-8.5	CTXM-8		X				
VII	EURL S-8.5	DHA		X				
VII	EURL S-8.5	FOX		X				
VII	EURL S-8.5	MOX		X			PCR (published)	Perez-Perez, F. J. and N. D. Hanson (2002)
VII	EURL S-8.5	OXA		X			PCR (published)	Fang, H., F. Ataker, et al. (2008)
VII	EURL S-8.5	SHV		X				
VII	EURL S-8.6	CTX	M-1				PCR (published)	Woodford, N., E. J. Fagan, et al. (2006).
VII	EURL S-8.6	OXA						
VII	EURL S-8.6	ACC		X				
VII	EURL S-8.6	ACT		X				
VII	EURL S-8.6	CMY		X				
VII	EURL S-8.6	CTXM-2		X				
VII	EURL S-8.6	CTXM-26		X				
VII	EURL S-8.6	CTXM-8		X				
VII	EURL S-8.6	CTXM-9		X				
VII	EURL S-8.6	DHA		X				
VII	EURL S-8.6	FOX		X				
VII	EURL S-8.6	MOX		X			PCR (published)	Perez-Perez, F. J. and N. D. Hanson (2002)
VII	EURL S-8.6	SHV		X			PCR (published)	Fang, H., F. Ataker, et al. (2008)
VII	EURL S-8.6	TEM		X				
VII	EURL S-8.7	TEM						
VII	EURL S-8.7	ACC		X				
VII	EURL S-8.7	ACT		X				
VII	EURL S-8.7	CMY		X				
VII	EURL S-8.7	CTXM-1		X			PCR (published)	Woodford, N., E. J. Fagan, et al. (2006)
VII	EURL S-8.7	CTXM-2		X				
VII	EURL S-8.7	CTXM-26		X				
VII	EURL S-8.7	CTXM-8		X				
VII	EURL S-8.7	CTXM-9		X				
VII	EURL S-8.7	DHA		X				
VII	EURL S-8.7	FOX		X				
VII	EURL S-8.7	MOX		X			PCR (published)	Perez-Perez, F. J. and N. D. Hanson (2002)
VII	EURL S-8.7	OXA		X				
VII	EURL S-8.7	SHV		X			PCR (published)	Fang, H., F. Ataker, et al. (2008)

Lab no.	Strain	Gene tested		Not detected	Primer used 5'→3'	Primer used 3'→5'	PCR-method	Reference
X	EURL S-8.4	TEM	-1				PCR (published)	JAC 2010; 65: 490–495;doi:10.1093/jac/dkp498
X	EURL S-8.4	VIM	-2				PCR (published)	JAC 2010; 65: 490–495;doi:10.1093/jac/dkp498
X	EURL S-8.5	CTX	M-9				PCR (published)	JAC 2010; 65: 490–495;doi:10.1093/jac/dkp498
X	EURL S-8.5	TEM	-1				PCR (published)	JAC 2010; 65: 490–495;doi:10.1093/jac/dkp498
X	EURL S-8.6	CTX	M-3				PCR (published)	JAC 2010; 65: 490–495;doi:10.1093/jac/dkp498
X	EURL S-8.6	OXA	-30				PCR (published)	JAC 2010; 65: 490–495;doi:10.1093/jac/dkp498
X	EURL S-8.7	TEM	-52				PCR (published)	JAC 2010; 65: 490–495;doi:10.1093/jac/dkp498
XI	EURL S-8.4	**CTX**					PCR (published)	
XI	EURL S-8.4	TEM	-1				PCR (published)	
XI	EURL S-8.5	CTX					PCR (published)	
XI	EURL S-8.5	TEM					PCR (published)	
XI	EURL S-8.6	CTX					PCR (published)	
XI	EURL S-8.6	OXA					PCR (published)	
XI	EURL S-8.7	**CTX**					PCR (published)	
XI	EURL S-8.7	TEM					PCR (published)	
XIV	EURL S-8.5	CTX	M-9				PCR (published)	Dallenne et al. 2010
XIV	EURL S-8.5	TEM	-1				PCR (published)	Dallenne et al. 2010
XIV	EURL S-8.6	CTX	**M-15**				PCR (published)	Dallenne et al. 2010
XIV	EURL S-8.6	OXA	-30				PCR (published)	Dallenne et al. 2010
XIV	EURL S-8.7	TEM	-52				PCR (published)	Dallenne et al. 2010

Legend:

Fields shaded grey indicate that the gene was expected

Genes in bold were detected but not expected

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