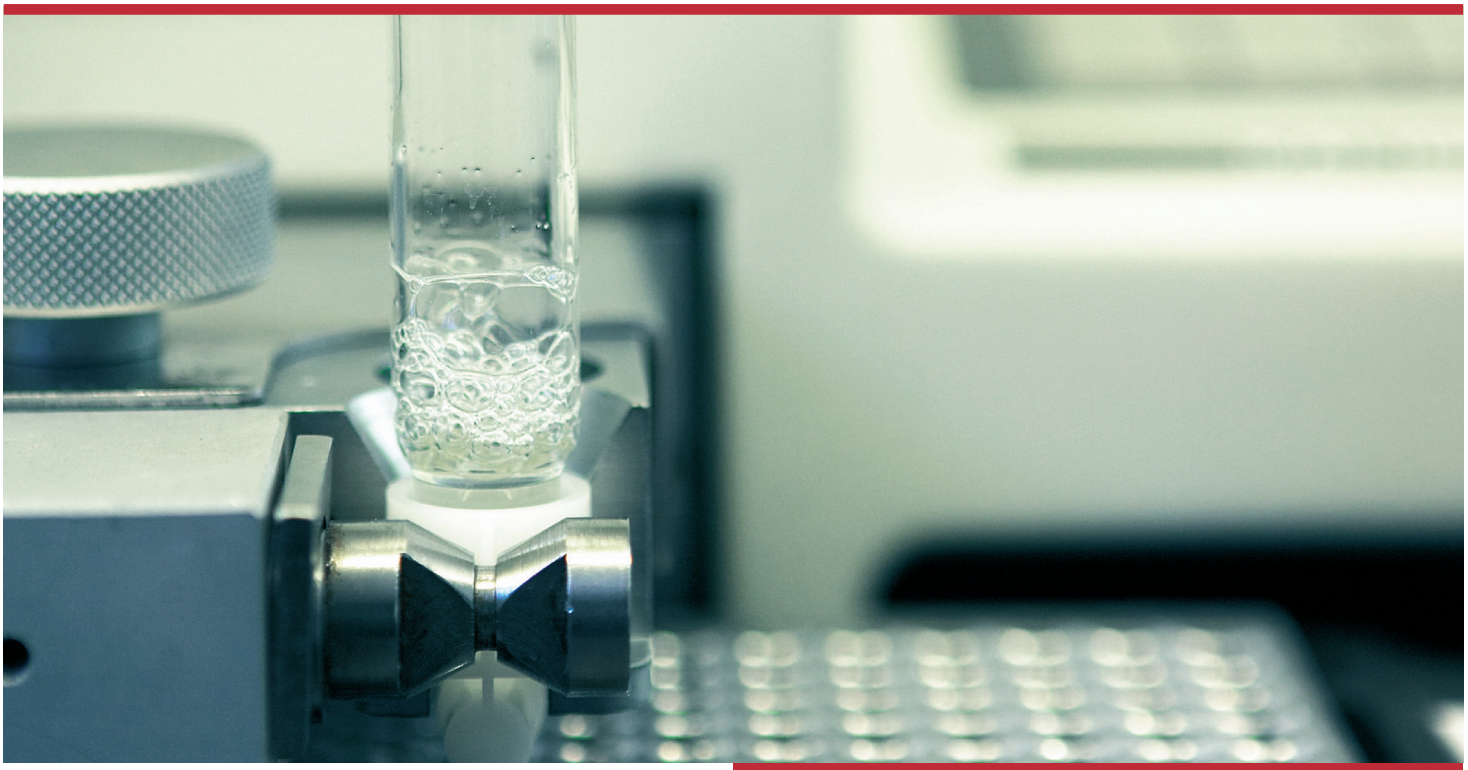
The 23rd EURL-AR Proficiency Test *Salmonella*, *Campylobacter* and genotypic characterisation 2017



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1. Introduction

This report describes and summarises results from the twenty-third 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 eleventh External Quality Assurance System (EQAS) conducted for these microorganisms (the first was EQAS 2006). In addition, the proficiency test includes categorisation of the relevant *Salmonella* strains as presumptive AmpC-, ESBL-, or carbapenemase producing organisms, and identification of the *Campylobacter* species as either *C. jejuni* or *C. coli*.

In addition, for the ninth time, an optional element was included, consisting of genotypic characterization of antimicrobial resistance genes by PCR and/or sequencing. This optional component included characterization of genes encoding AmpC, ESBL-, or carbapenemases in the *Salmonella* test strains.

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

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

1) Expected results were generated by performing Minimum Inhibitory Concentration (MIC) determinations for all test strains in two different occasions at the Technical University of Denmark, National Food Institute (DTU Food). These results were then verified by the Centers for Disease Control and Prevention, Georgia, US (*Salmonella*) and the United States Food and Drug Administration (FDA), Centre for Veterinary Medicine, Maryland, US (*Campylobacter*). Finally, a fourth MIC determination was performed at DTU Food after preparation of the agar stab culture/charcoal swab 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 Member States (MS) to report AST data to the European Food Safety Authority (EFSA), and complies with the main objective of this EQAS, i.e. to evaluate and improve the comparability of surveillance data on antimicrobial susceptibility of *Salmonella* and *Campylobacter* reported to EFSA by different laboratories, 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 including also considerations related to any corrective actions introduced in the laboratory. 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 categorising 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 categorised as susceptible or resistant. This result may be evaluated as correct based on the MIC-value produced but incorrect when the evaluation is based on the interpretation of the MIC value. This report is based on evaluation of AST interpretations, therefore some participants may find their results classified as incorrect even though the actual MIC they

reported is only a one-fold dilution away 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 cut offs 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 omitted 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 and 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 2017

A pre-notification (App. 1) to announce the EURL-AR EQAS on AST of *Salmonella* and *Campylobacter* was distributed on the 25th August 2017 by e-mail to the 44 laboratories in the EURL-AR-network including all EU countries and Iceland, the former Yugolsav Republic of Macedonia (FYROM), Norway, Serbia, Switzerland and Turkey. All EU MS as well as Iceland, Norway, and Switzerland were represented as participants for both *Salmonella* and *Campylobacter.* In addition to the AST of *Salmonella* and *Campylobacter*, an optional genotypic characterization by PCR/sequencing of antimicrobial resistance genes of the AmpC-, ESBL- and carbapenemase-producing *Salmonella* test strains was offered.

Appendix 2 shows that 29 of the 32 participating NRLs were appointed by the individual Member States' Competent Authority. Five additional laboratories were included; one from each of the following countries: Iceland, the Netherlands, Norway, Spain, and Switzerland. These were invited to take part in the EQAS 2017 on the basis of their participation in previous EQAS iterations and/or affiliation to the EU network. These laboratories were charged a fee for their participation in the EQAS, whereas the NRLs from EU Member States participated free of charge.

Figure 1 illustrates that of the 31 participating countries, all tested both *Salmonella* and *Campylobacter*. Thirteen laboratories participated in the optional genotypic characterisation of the ESC-resistant (Extended Spectrum Cephalosporin-resistant) *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. In total, results from 31 countries consisting of 31 laboratories submitting *Salmonella* results and 30 laboratories submitting *Campylobacter* results. Twelve sets of results in relation to the optional

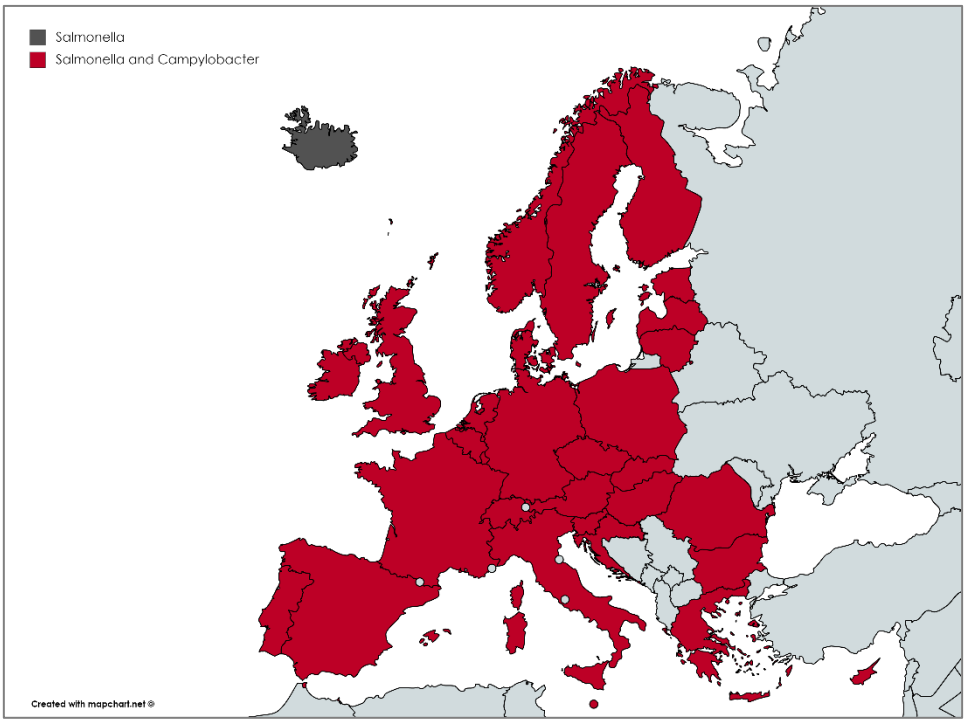

Figure 1: Participating countries that performed antimicrobial susceptibility testing of *Salmonella* and *Campylobacter* in 2017.

genotypic characterization is evaluated. Results from the two laboratories not designated by the MS but enrolled in the EQAS are not further presented or evaluated in this report.

2.2 Strains

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

Prior to distribution of the strains, AST was performed on the *Salmonella* and *Campylobacter* strains at DTU Food and verified by the Centers for Disease Control and Prevention (CDC), Georgia, US (*Salmonella*) and the United States Food and Drug Administration (FDA), Centre for Veterinary Medicine, Maryland, US (*Campylobacter*). When MIC-values were not in agreement but varied +/- one dilution-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 CDC for *Salmonella:* cefepime, cefotaxime, cefotaxime/clavulanic acid, ceftazidime, ceftazidime/clavulanic acid, colistin, ertapenem, imipenem, temocillin, tigecycline and trimethoprim, and results from the following antimicrobials were not verified by FDA for *Campylobacter*: streptomycin.

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

2.3 Antimicrobials

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

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

The method applied for the AST was the ISO standard, ISO 20776-1 “Clinical laboratory testing and *in vitro* diagnostic test system – Susceptibility testing of infectious agents and evaluation of performance of antimicrobial susceptibility test devices”, and, in addition, the following guidelines/standards from the Clinical and Laboratory Standards Institute (CLSI) were applied: Document M7-A10 (2015) “Methods for Dilution Antimicrobial Susceptibility Tests for Bacteria That Grow Aerobically; Approved Standard - Tenth Edition”; document M100S, 27th ed. (2017) “Performance Standards for Antimicrobial Susceptibility Testing” (CLSI Supplement M100S) and document VET01-A4 (2013) “Performance Standards for Antimicrobial Disk and Dilution Susceptibility Tests for Bacterial Isolated From Animals” (Approved Standard – Fourth Edition).

MIC results were interpreted by using the interpretative criteria listed in Decision 2013/652/EU. Where values were not available, the list of interpretative criteria was supplemented with CLSI-interpretative criteria as or tentative values as described and indicated in the protocol (App. 4). No interpretative criteria were available to determine the interpretation of MIC-values for cefepime. Results of ESC-resistance detection tests were interpreted according to the most recent EFSA recommendations also included as an appendix in the EQAS protocol (Appendix 4).

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

Minimum Inhibitory Concentration (MIC) determination of the *Salmonella* test strains was performed using the Sensititre system (EUVSEC and EUVSEC2) from Trek Diagnostic Systems Ltd, UK. The confirmatory tests for ESC-resistance included MIC determination by microbroth dilution.

For *Campylobacter* the following antimicrobials were included: ciprofloxacin (CIP), erythromycin (ERY), gentamicin (GEN), nalidixic acid (NAL), streptomycin (STR), and tetracycline (TET). MIC determination for the *Campylobacter* testing, was performed using the Sensititre systems (EUCAMP2) from Trek Diagnostic Systems Ltd, UK, according to guidelines from the CLSI document M45-A2 (2010) “Methods for Antimicrobial Dilution and Disk Susceptibility Testing of Infrequently Isolated or Fastidious Bacteria” (Approved Guideline – Second Edition) and VET01-S2 (2013) “Performance Standards for Antimicrobial Disk and Dilution Susceptibility Tests for Bacterial Isolated From Animals” (Second Informational Supplement). Participants of the *Campylobacter* EQAS were additionally requested to identify the species of the *Campylobacter* spp. as either *C. jejuni* or *C. coli*.

2.4 Distribution

On 30 October 2017, 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. The shipment (UN3373, biological substances category B) was sent according to International Air Transport Association (IATA) regulations.

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 at 4ºC (dark) and the freeze-dried strains cool and dark until performance of AST. Information related to the handling of the test strains and reference strains (App. 4b, c, d, e) was made available. Participants receiving an ATCC reference strain were requested to save and maintain this strain for future proficiency tests.

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

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

As regards the method for performing the antimicrobial susceptibility testing, the protocol referred to Decision 2013/652/EU and instructed participants to perform the international reference method for antimicrobial susceptibility testing. I.e. dilution methods performed according to the methods described by the European Committee on Antimicrobial Susceptibility Testing (EUCAST) and the Clinical and Laboratory Standards Institute (CLSI), accepted as the international reference method (ISO standard 20776-1:2006).

A mandatory part of the proficiency test was to detect ESC-resistant strains and interpret results according to the most recent EFSA recommendations as described in the protocol.

Results from QC reference strains would consist of MIC values for the reference strains *E. coli* (ATCC 25922) and *C. jejuni* (ATCC 33560). The results were evaluated towards the quality control ranges according to the relevant guidelines; i.e. the CLSI documents VET01-S2 (2013) or M100S, 27th ed. (2017) (App. 5).

For the optional genotypic characterisation of the genes encoding for resistance to extended-spectrum beta lactam antimicrobials in the *Salmonella* test strains, participating laboratories were requested to report the genes. The organizers, however, decided to include in the selection of isolates with none-ESC-resistant TEM-beta-lactamases encoded by $bla_{\text{TEM-1}}$ as an expected gene. 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 3.0 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.

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 January 3, 2018. After this date, the participants were invited to login to retrieve an individual, database-generated report which contained an evaluation of the submitted results including possible deviations from the expected interpretations. Deviations in the interpretation as resistant or susceptible were categorised as 'incorrect', as were also deviations concerning confirmation of an isolate as extended spectrum beta-lactamase- (ESBL-), ampC- or carbapenemase-producer.

3. Results

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

3.1 Data omitted from the report

As mentioned in the introduction, the EURL-AR network established that data should be examined and possibly omitted from the general analysis if there are less than 75% correct results based on strain/antimicrobial combination (see Appendix 7a and 7b for an overview of correct/incorrect results). In the present EQAS this occurred in three cases which have been examined and consequently omitted from the analysis; **1)** S-12.4/cefotaxime (expected interpretation was 'resistant', however, 42% (16 laboratories) found the strain susceptible in either panel 1 or panel 2. All but two of the deviating interpretations were based on MIC values one step from the expected; **2)** S-12.5/colistin (expected interpretation was 'resistant', however, 40% found the strain resistant to colistin. All but one of the deviating interpretations were based on MIC values one step from the expected; **3)** S-12.7/ceftazidime (expected interpretation was 'susceptible'), however, 26% (based on both panel 1 and panel 2) found the strain resistant to ceftazidime. All of the deviating interpretations were based on MIC values within one step from the expected.

For *Campylobacter*, it appeared that strain C-12.1 caused problems for six laboratories as the strain was expected to be fully susceptible, however, the six laboratories in question reported resistance to ciprofloxacin, nalidixic acid and tetracycline based on high MIC-values not close to the breakpoint. It was therefore concluded that the culture had likely contained a mixed culture and it was decided to exclude the results of the six laboratories in question in relation to C-12.1.

3.2 Methods

Results obtained by broth microdilution were accepted and evaluated together as they are both quantitative methods giving results corresponding to the MIC of the bacterial strain tested.

In the *Salmonella* as well as the *Campylobacter* trial, all 31 laboratories performed microbroth dilution.

With the aim to conclude on the strains' presumptive ESBL, AmpC or carbapenemase phenotype, two panels of antimicrobials were included in the testing of the *Salmonella* strains as also specified in the EU regulation 2013/652/EU. The test strains found resistant to cefotaxime, ceftazidime or meropenem on the

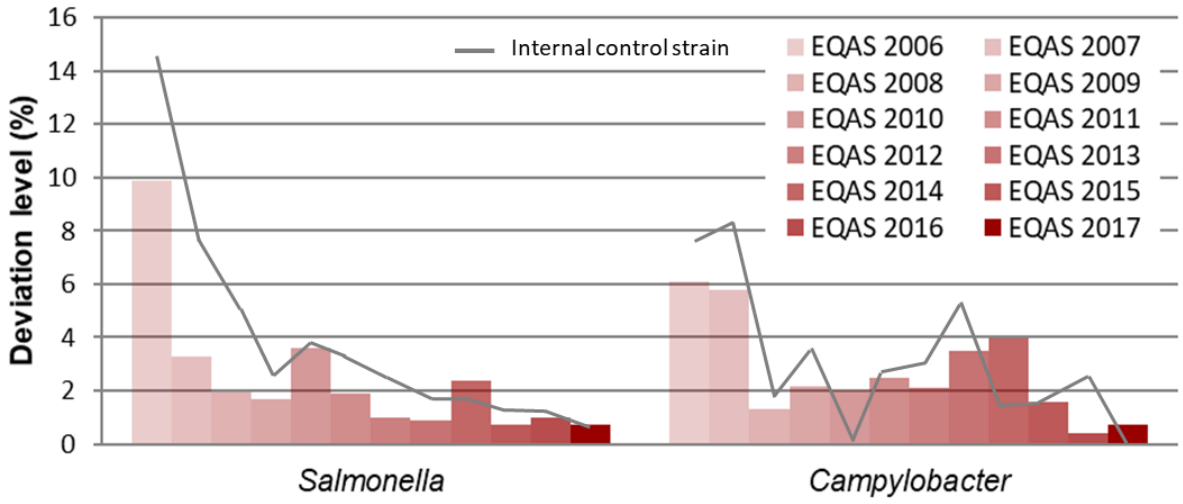

Figure 2: A comparison between the EURL-AR EQAS's since 2006, showing the total percentage of deviations for antimicrobial susceptibility testing performed by participating laboratories.

first panel (see 2013/652/EU, Table 1) were additionally tested on the second panel (see 2013/652/EU, Table 4) according to the protocol indications.

3.3 Deviations, overall

The list of deviations is presented in Appendix 8a and 8b. Figure 2 shows the total percentage of 2017 are acceptable for both the *Salmonella* and the *Campylobacter* trials.

3.3.1 *Salmonella* trial

For the *Salmonella* strains, 99.3% of the AST's were interpreted correctly. The number of AST's performed and the percentage of correct results for the individual strains in the EQAS, are listed in Table 1. Variations of obtained correct results ranged from 97.6-100% between the *Salmonella* strains. Table 2 illustrates the percentage of correct AST per antimicrobial by bacterial species. The level of correct AST was at 97.3% (ceftazidime) or above, for all the *Salmonella* test strains.

ESC-resistant *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

deviations from the expected results of AST performed by participating laboratories. The internal control strains mainly followed the trend in deviation level of the different EQAS trials (Figure 2), only, for 2017 the deviation level related to the *Campylobacter* internal control dropped to 0%. Overall, the deviation levels in

test for ESC-resistant isolates requires use of both cefotaxime (FOT) and ceftazidime (TAZ) alone and in combination with a β-lactamase inhibitor. The MIC value for either antimicrobial agent (FOT or TAZ) tested in combination with clavulanic acid should be compared to the corresponding MIC when tested alone. Synergy is indicated for one or both cephalosporins if a three dilution steps difference is observed between the two MIC values (i.e. if the FOT:CTX/Cl or TAZ:TAZ/Cl ratio ≥8) (CLSI M100S Table 2A; Enterobacteriaceae). Participants were instructed to test strains presenting resistance to cefotaxime (FOT), ceftazidime (TAZ or meropenem (MERO) on the second panel of antimicrobials.

The classification of the phenotypic results was based on the most recent EFSA recommendations indicating as indicated in the protocol (Appendix 4).

Table 1. The number of AST performed and the percentage of correct results for each strain of *Salmonella* (panel 1 and panel 2) and *Campylobacter*.

EQAS 2017 – *Salmonella*			EQAS 2017 – *Campylobacter*		
Test strain	AST in total	% correct	Test strain	AST in total	% correct
S-12.1	635	99.2	C-12.1 (*C. jejuni*)	138	100.0
S-12.2	635	99.2	C-12.2 (*C. jejuni*)	180	100.0
S-12.3	634	99.8	C-12.3 (*C. jejuni*)	180	98.9
S-12.4	540	97.6	C-12.4 (*C. jejuni*)	180	99.4
S-12.5	395	100.0	C-12.5 (*C. jejuni*)	180	98.3
S-12.6	426	100.0	C-12.6 (*C. coli*)	180	99.4
S-12.7	574	99.7	C-12.7 (*C. coli*)	180	98.3
S-12.8	635	98.9	C-12.8 (*C. jejuni*)	180	100.0

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

Antimicrobial	*Salmonella*	*Campylobacter*
Ampicillin	99.2	-
Azithromycin	99.5	-
Cefotaxime	100.0	-
Cefoxitin	98.3	-
Ceftazidime	97.3	-
Chloramphenicol	99.6	-
Ciprofloxacin	99.2	98.7
Colistin	100.0	-
Ertapenem	100.0	-
Erythromycin		100.0
Gentamicin	100.0	100.0
Imipenem	97.8	-
Meropenem	100.0	-
Nalidixic acid	100.0	99.1
Streptomycin		99.1
Sulphonamides	97.6	-
Temocillin	97.7	-
Tetracycline	100.0	98.7
Tigecycline	99.6	-
Trimethoprim	100.0	-

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

The strains S-12.1 and S-12.8 were carbapenemase producers, the strains S-12.2, S-12.3, and S-12.7 were ESBL-producers and strain S-12.4 which fell into the category of AmpC-phenotype. For strain S-12.4, the resistance mechanism is not known, and the phenotype is unusual (susceptibility to ampicillin) and therefore a categorisation as 'unusual phenotype' was also accepted.

In total, the categorisation as ESBL-, AmpC- or carbapenemase-producer was correct in 241 out of 248 reported results. The results that were considered incorrect were all related to strain S-12.4, as seven participants had indicated this strain as 'no ESBL, AmpC- or carbapenemase'-producer.

3.3.2 *Campylobacter* trial

For the *Campylobacter* strains, 99.3% of AST's were correctly tested. Table 1 presents that the variation in the obtained correct results ranged from 98.3-100% and Table 2 illustrates that the percentage of correct AST per antimicrobial were all above 98.7%.

The participants were requested to identify the *Campylobacter* species. All 30 laboratories delivered in total 233 results of which all were in accordance with the expected.

3.4 Deviations by laboratory

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

Table 3: Overview of ESBL-, AmpC- 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-, AmpC- and carbapenemase-producing *Salmonella* strains.
Fields shaded in grey with numbers in *italics* indicate an unexpected result.

Strain code		S-12.1	S-12.2	S-12.3	S-12.4	S-12.7	S-12.8
ESC-resistance genes harboured in the test strain		***bla*$_{NDM-1}$** ***bla*$_{CMY-16}$**	***bla*$_{CTX-M-9}$** ***bla*$_{TEM-1B}$**	***bla*$_{CTX-M-14b}$**	***Unknown resistance mechanism***	***bla*$_{CTX-M-14}$**	***bla*$_{NDM-1}$** ***bla*$_{CTX-M-15}$** ***bla*$_{DHA-1}$** ***bla*$_{OXA-1}$** ***bla*$_{OXA-9}$** ***bla*$_{OXA-10}$** ***bla*$_{TEM-1B}$**
ESBL-, AmpC- and carbapenemase-producing strain – expected results		carbapenemase	ESBL	ESBL	AmpC Unusual phenotype	ESBL	carbapenemase
Obtained results	Confirmed ESBL-producer	-	31/31 (100%)	31/31 (100%)	-	31/31 (100%)	-
	Confirmed ESBL + AmpC-producer	-	-	-	-	-	-
	Confirmed AmpC-producer	-	-	-	22/31 (71%)	-	-
	Confirmed carbapenemase-producer	31/31 (100%)	-	-	-	-	31/31 (100%)
	Confirmed unusual phenotype	-	-	-	2/31 (6%)	-	-
	Not ESBL-, AmpC- or carbapenemase-producing	-	-	-	*7/31 (23%)*	-	-

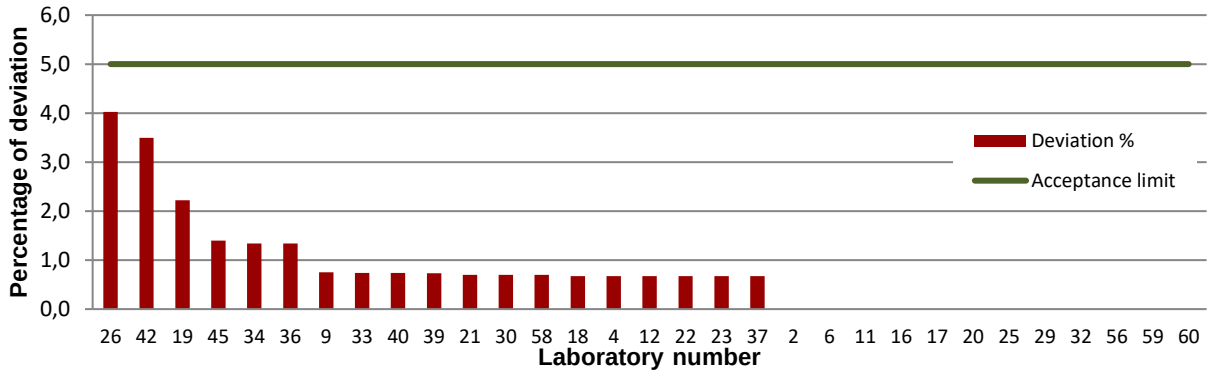

Figure 3: Individual participants' deviations in percent of their total number of *Salmonella* AST's.

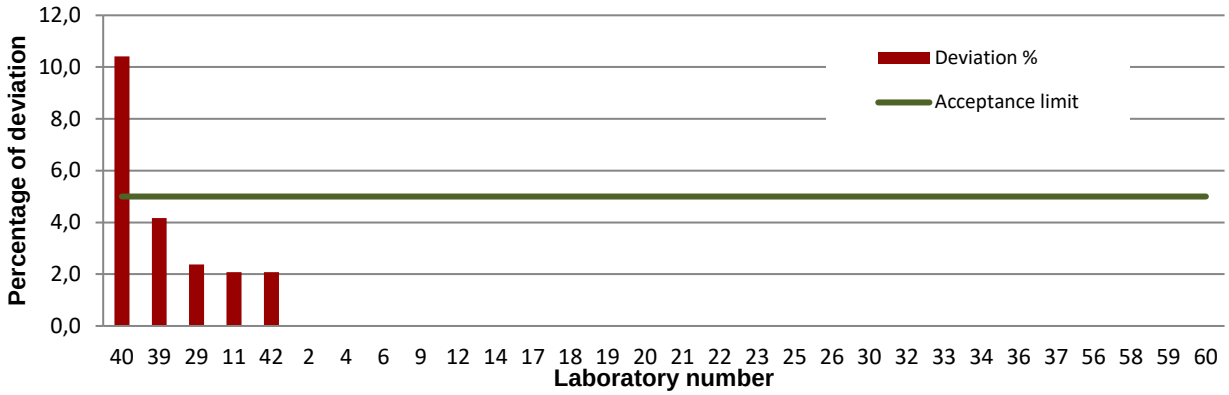

Figure 4: Individual participants' deviations in percent of their total number of *Campylobacter* AST's.

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

MIC determination *E. coli* ATCC 25922			
Antimicrobial	Proportion outside QC range	Obtained values in MIC steps (min/max)	
		Below lower QC limit	Above upper QC limit
Panel 1, AMP	0/31 (0%)	-	-
Panel 1, FOT	1/30 (3%)	-	1 step
Panel 1, TAZ	0/31 (0%)	-	-
Panel 1, CHL	0/31 (0%)	-	-
Panel 1, CIP	0/31 (0%)	-	-
Panel 1, COL	0/31 (0%)	-	-
Panel 1, GEN	1/31 (3%)	-	1 step
Panel 1, MER	0/31 (0%)	-	-
Panel 1, NAL	0/31 (0%)	-	-
Panel 1, SMX	1/30 (3%)	-	1 step
Panel 1, TET	0/31 (0%)	-	-
Panel 1, TGC	0/31 (0%)	-	-
Panel 1, TMP	2/31 (6%)	1 step	-
Panel 2, FEP	0/27 (0%)	-	-
Panel 2, FOT	0/26 (0%)	-	-
Panel 2, FOX	0/27 (0%)	-	-
Panel 2, TAZ	2/27 (7%)	1 step	-
Panel 2, ERT	0/27 (0%)	-	-
Panel 2, IMI	2/27 (7%)	1 step	-
Panel 2, MER	0/27 (0%)	-	-

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

MIC determination *C. jejuni* ATCC 33560			
Antimicrobial	Proportion outside QC range	Obtained values in MIC steps (min/max)	
		Below lower QC limit	Above upper QC limit
CIP	1/28 (4%)	-	1 step
ERY	0/28 (0%)	-	-
GEN	1/26 (4%)	1 step	-
NAL	2/27 (7%)	1 step	-
TET	1/27 (4%)	-	1 step

deviating results in the antimicrobial susceptibility tests.

3.4.1 *Salmonella* trial

All 31 participating laboratories obtained a result below the acceptance limit at 5% deviations for the *Salmonella* strains. The maximum percentage of deviations was at 4.0%, presenting a very good result across the EURL-AR network.

3.4.2 *Campylobacter* trial

In the *Campylobacter* trial, most laboratories performed very well. Applying the 5% acceptance threshold, 29 of 30 participating laboratories performed acceptably, with 25 laboratories having no deviations (Figure 4).

One laboratory presented a deviation level above the 5% acceptance level (#40). This laboratory was regarded as an outlier.

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).

Obtained values from the participants' testing of the QC strains are listed in Appendix 6a and 6b, and in Table 4 and 5. For the *Salmonella* and *Campylobacter* trial, 31 and 28 laboratories, respectively, uploaded data from QC-testing on the relevant reference strain.

Appendix 6a presents the results for the reference strain *E. coli* ATCC 25922. Nine laboratories each produced one value outside the QC-limit. Table 4 illustrates the obtained results which are fully presented in Appendix 6a.

Table 5 presents the proportion of the laboratories submitting AST-results for the *C. jejuni* reference strain ATCC 33560 with results below or above the QC interval. Five deviations were seen from four different laboratories.

3.6 Genotypic characterisation

For the optional genotypic characterisation of the ESC-resistant *Salmonella* test strains, 12 laboratories participated. In Appendix 9, information is presented on detected genes, primers used, and references for the method used. Three laboratories performed whole genome sequencing of the ESC-resistant *Salmonella* whereas the remaining eight laboratories indicated the use of various types of conventional PCR to identify the relevant genes.

Table 6 indicate the obtained results, both on gene and variant level. Moreover, Figure 5 indicates that six discordant results related to the genes and variant submitted by two different laboratories. These were related to the *bla*$_{CMY}$-gene and variants of the *bla*$_{OXA}$ and *bla*$_{CTX-M}$-genes.

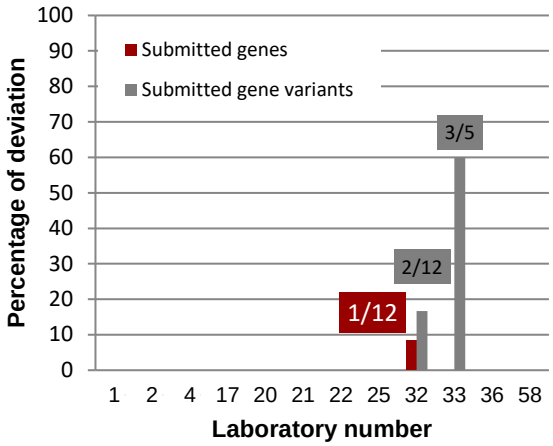

Figure 5: Individual participants' deviations in percent of their total number of results from the detected genes.

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

Strain code	Expected gene	Proportion of correct results (gene level)	Proportion of correct results (variant level)	Unexpected genes/variants identified
S-12.1	***bla*$_{NDM-1}$**	12/12 (100%)	7/7 (100%)	
	***bla*$_{CMY-16}$**	12/12 (100%)	6/6 (100%)	
S-12.2	***bla*$_{CTX-M-9}$**	12/12 (100%)	8/8 (100%)	
	***bla*$_{TEM-1/1B}$**	12/12 (100%)	6/6 (100%)	
S-12.3	***bla*$_{CTX-M-14b}$**	12/12 (100%)	7/8 (88%)	***bla*$_{CMY-16}$ (gene and variant: n=1)** ***bla*$_{CTX-M-9}$ (variant: n=1)**
S-12.4	***Unknown resistance mechanism***	-	-	
S-12.7	***bla*$_{CTX-M-14}$**	12/12 (100%)	7/8 (88%)	***bla*$_{CTX-M-9}$ (variant: n=1)**
S-12.8	***bla*$_{NDM-1}$**	12/12 (100%)	7/7 (100%)	***bla*$_{CTX-M-1}$ (variant: n=1)** ***bla*$_{OXA-17}$ (variant: n=1)**
	***bla*$_{CTX-M-15}$**	10/10 (100%)	6/7 (86%)	
	***bla*$_{DHA-1}$**	5/5 (100%)	2/2 (100%)	
	***bla*$_{OXA-1}$**	6/6 (100%)	5/5 (100%)	
	***bla*$_{OXA-9}$**	3/3 (100%)	3/3 (100%)	
	***bla*$_{OXA-10}$**	5/5 (100%)	4/5 (80%)	
	***bla*$_{TEM-1/1B}$**	8/8 (100%)	4/4 (100%)	

4. Discussion

In both 2016 and 2017, 31 laboratories participated in the *Salmonella* EQAS, whereas for the *Campylobacter* EQAS, 31 participated in 2016 and 30 in 2017. This allows for a fair comparison between the two EQAS periods.

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

This 2017 proficiency test is the fourth possibility of testing *Salmonella* and *Campylobacter* strains with the panels designed to follow the requirements of Decision 2013/652/EU.

4.1 *Salmonella* trial

Overall, the percentage of correct antimicrobial susceptibility test results of *Salmonella* was 99.3%. All (n=31) participants obtained satisfactory results according to the level of acceptance (<5% deviation). When comparing between the antimicrobials, the testing of ceftazidime appeared to cause most problems (97.3% correct results).

As indicated in Figure 2, the overall quality of the results in the 2017-EQAS would appear to be at the same high level as in 2015, also, the measure when comparing results obtained from testing the internal control strain indicates a steady and very good quality of *Salmonella* AST results.

As indicated by Figure 3, all laboratories exhibited very good results with deviation levels below 5%. Follow-up has therefore not been necessary based on these results, and none of the laboratories were defined as outliers.

For the *E. coli* reference strain, the obtained results were in general in agreement with the CLSI recommendations.

Follow up on previous EQAS results is not relevant as no laboratories had deviation levels for the AST results above the acceptance limit in EQAS 2016.

ESC-resistant *Salmonella* test strains

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

Of the six *Salmonella* test strains relevant for this component of the EQAS (S-12.1, S-12.2, S-12.3, S-12.4, S-12.7, and S-12.8), two were carbapenemase phenotypes and three were ESBL-phenotypes. In addition, one (S-12.4) was an AmpC-phenotype based on the criteria for interpretation of the ESBL-, AmpC- and carbapenemase indicated in the protocol. Only, this particular strain presented an unusual phenotype for an AmpC-producer, as it exhibited no resistance to ampicillin, which many participants noted as a comment for this strain. Currently, the resistance mechanism and the genetic background for it is not known. Close attention should be paid to strains with similar phenotypes/resistance mechanisms as they may be emerging in Europe.

The testing and interpretation of results for the ESBL- and carbapenemase-producing strains appeared not to cause difficulties for any of the participating laboratories. As for the S-12.4 which exhibited cefoxitin resistance and consequently fell into the category of AmpC-phenotype, indeed also was an unusual phenotype. In general, when observing antimicrobial resistance profiles that present unexpected resistance to extended spectrum cephalosporins or carbapenems, laboratories should be alert and perform relevant retesting to confirm the phenotype and may also consider to forward the strain for reference testing at the EURL-AR.

Even if no acceptance limit has been defined for this component of the EQAS, the overall result appears satisfactory.

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 99.3%. The performance varied from no deviations up to 10.4% deviations, with 29 laboratories performing satisfactorily according to the established acceptance range.

It appears that the level of deviations for the overall AST result is similar to the EQAS 2016, and in fact no deviations were observed in the results obtained from testing the internal control strain (Figure 2).

One laboratory (#40) obtained deviation levels above 5%. For this laboratory, however, the values obtained for the QC-strain did not indicate methodical issues to be the reason for the obtained deviations. The EURL-AR has been in contact with this laboratory to offer assistance in identifying the possible cause of this unsatisfactory performance and to improve the quality of results. Of the five obtained deviations that caused the 10.4% deviation level, three were related to one strain (C-12.7) caused by incorrect categorisations as 'resistant' and indicates switch of strains may have happened. The laboratory did not store strain C-12.7 and communicated that further follow-up has not been performed, i.e. the cause of the deviations has currently not been identified.

All participating laboratories except two (#4 and #42) uploaded data from tests performed on the *C. jejuni* reference strain and the proportion of results within the QC intervals was 96.3%.

All five values outside the QC intervals were one step below or above the QC-limits. It is suggested that these values are monitored over time to ensure that the tests render a reliable result for the particular antimicrobial.

In 2016, all laboratories obtained acceptable deviation levels for the AST results and therefore no follow-up is relevant.

4.3 Genotypic characterisation

The focus on genotypic characterization of microorganisms is increasing in the EU and worldwide. In EU, communication is ongoing to improve laboratory detection and confirmation of ESBL-, AmpC-, and carbapenemase-producing *Enterobacteriaceae* and also to identify the genetic mechanism conferring the resistance.

The optional genotypic characterisation is a supplementary component of this EQAS and should therefore be seen as an important possibility for the NRL-AR's to introduce or improve these methods in the laboratory. This year, twelve laboratories participated in the optional EQAS component and even though no acceptance limit has been defined, the 97% correct results (N=207) appears to be a satisfactory result.

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%. Again this year, this goal was reached for *Salmonella* and seems within reach for *Campylobacter*.

Compared to the EQAS 2016, the performance of the NRL's in 2017 appears to be at the same high level for *Salmonella* AST's (99.3% in 2017 and 98.9% in 2016) as well as for *Campylobacter* (99.3% in 2017 and 99.6% in 2016) (Figure 2). One outlier for the *Campylobacter* AST obtained 10.4% deviations and has been contacted to follow-up on the identification of the possible cause of this unsatisfactory performance with the purpose of improving the quality of results.

The test covering the identification of the phenotype of *Salmonella* test strains producing beta-lactamases of the ESBL-, AmpC, and

carbapenemase-type caused rendered seven deviations (97.2% correct categorisations). All deviations were related to an unusual AmpC-phenotype which was curiously susceptible to ampicillin. This is a priority area within the EURL-AR activities, and the focus on identifying AmpC-, ESBL-, and carbapenemase producing organisms – also those with unusual phenotypes – is encouraged.

Twelve NRLs participated in the EQAS component consisting of genotypic testing of ESBL-, AmpC- and carbapenemase-producing *Enterobacteriaceae* presenting satisfactory results.

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

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.

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G00-06-001/23.06.2017

EQAS 2017 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. Additionally, quality control (QC) strains *E. coli* ATCC 25922 (CCM 3954) and *C. jejuni* ATCC 33560 (CCM 6214) will be distributed to new participants.

It is the recipients' responsibility to comply with national legislation, rules and regulation regarding the correct use and handling of the provided strains and to possess the proper equipment and protocols to handle these strains.

This EQAS is specifically for NRL's on antimicrobial resistance (NRL-AR). Laboratories designated to be NRL-AR do not need to sign up to participate but are automatically regarded as participants. You may contact the EQAS-Coordinator if you wish to inform of changes in relation to your level of participation in compared to previous years. The EURL-AR will be able to cover the expenses for one parcel, only, per EU Member State. Therefore, countries with more than one laboratory registered on the EURL-AR contact-list will be contacted directly to confirm which laboratory will be included for participation free of charge.

The invitation to participate in the proficiency test is extended to additional participants besides official NRLs and to participants from laboratories which are involved in the network but are not designated NRLs (cost for participation will be 100 EUR).

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 2017. 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 18th 2017** 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.

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Next EQAS: The next EURL-AR EQAS that we will have is on isolation of ESBL- and AmpC-producing *E. coli* from caeca and meat samples which is expected to be carried out in November 2017 and for antimicrobial susceptibility testing, the next EQAS will be the testing of *E. coli*, staphylococci and enterococci which will be carried out in June 2018.

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

Sincerely,

Susanne Karlsmose Pedersen
EURL-AR EQAS-Coordinator

Participant list

Salmonella	*Campylobacter*	Genotypic characterisation	Institute	Country
X	X	X	Austrian Agency for Health and Food Safety	Austria
X	X	X	Institute of Public Health	Belgium
X	X	-	National Diagnostic and Research Veterinary Institute	Bulgaria
X	X	-	Croatian Veterinary Institut	Croatia
X	X	-	Veterinary Services	Cyprus
X	X	-	State Veterinary Institute Praha	Czech Republic
X*	X*	X	DTU National Food Institute	Denmark
X	X	-	Danish Veterinary and Food Administration, DVFA	Denmark
X	X	-	Estonian Veterinary and Food Laboratory	Estonia
X	X	-	Finnish Food Safety Authority EVIRA	Finland
X	-	-	Agence nationale de sécurité sanitaire ANSES - Fougères LERMVD	France
-	X	-	Agence nationale de sécurité sanitaire ANSES - Ploufragan - LERAP	France
X	X	X	Federal Institute for Risk Assessment	Germany
X	X	-	Veterinary Laboratory of Chalkis	Greece
X	X	-	Central Agricultural Office Veterinary Diagnostic Directorate	Hungary
X	X	-	University of Iceland	Iceland
X	X	X	Central Veterinary Research Laboratory	Ireland
X	X	X	Istituto Zooprofilattico Sperimentale delle Regioni Lazio e Toscana	Italy
X	X	X	Institute of Food Safety, Animal Health and Enviroment "BIOR"	Latvia
X	X	-	National Food and Veterinary Risk Assessment Institute	Lithuania
X	X	-	Laboratoire national de Santé	Luxembourg
X	X	-	Public Health Laboratory	Malta
X	X	X	Central Veterinary Institute of Wageningen UR	Netherlands
X*	X*	-	Food and Consumer Product Safety Authority (VWA)	Netherlands
X	X	X	Veterinærinstituttet	Norway
X	X	-	National Veterinary Research Institute	Poland
X	X	-	Laboratorio National de Investigacáo Veterinaria	Portugal
X*	X*	-	Institute for Hygiene and Veterinary Public Health	Romania
X	X	X	Institute for Diagnosis and Animal 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*	X*	Public Health England	United Kingdom
X	X	-	Animal Plant Health Agency	United Kingdom

Designated NRL-AR by the compentent authority of the member state
Non-NRL-AR enrolled by the EURL-AR
Not a Member State of the EU
* Submitted results were not included in the current report (allows for one dataset per country, only)

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

	Ampicillin AMP		Azithromycin AZI		Cefepime FEP		Cefotaxime FOT		Cefotaxime/clav F/C	F:F/C ratio	Cefoxitin FOX		Ceftazidime TAZ		Ceftazidime/clav T/C	T:T/C ratio	Chloramphenicol CHL		Ciprofloxacin CIP		Colistin COL		Ertapenem	
EURL S-12.1	>64	RESIST	>64	RESIST	32	NA	>64	RESIST	>64	<8	>64	RESIST	>128	RESIST	>128	<8	>128	RESIST	>8	RESIST	<=1	SUSC	1	RESIST
EURL S-12.2	>64	RESIST	8	SUSC	2	NA	16	RESIST	0.06	>=8	4	SUSC	1	SUSC	0.25	<8	<=8	SUSC	0.5	RESIST	<=1	SUSC	<=0.015	SUSC
EURL S-12.3	>64	RESIST	4	SUSC	>32	NA	>64	RESIST	0.12	>=8	4	SUSC	8	RESIST	0.5	>=8	<=8	SUSC	0.12	RESIST	<=1	SUSC	0.03	SUSC
EURL S-12.4	2	SUSC	8	SUSC	0.12	NA	1	RESIST	0.5	<8	32	RESIST	8	RESIST	4	<8	<=8	SUSC	0.03	SUSC	<=1	SUSC	<=0.015	SUSC
EURL S-12.5	2	SUSC	4	SUSC			<=0.25	SUSC					<=0.5	SUSC			<=8	SUSC	0.03	SUSC	4	RESIST		
EURL S-12.6	>64	RESIST	8	SUSC			<=0.25	SUSC					1	SUSC			<=8	SUSC	>8	RESIST	<=1	SUSC		
EURL S-12.7	>64	RESIST	>64	RESIST	8	NA	32	RESIST	0.12	>=8	8	SUSC	2	SUSC	0.25	>=8	>128	RESIST	0.03	SUSC	<=1	SUSC	<=0.015	SUSC
EURL S-12.8	>64	RESIST	>64	RESIST	>32	NA	>64	RESIST	>64	<8	>64	RESIST	>128	RESIST	>128	<8	64	RESIST	>8	RESIST	<=1	SUSC	>2	RESIST

	Gentamicin GEN		IMIPENEM IMI		MEROPENEM MER		Nalidixic acid NAL		Sulfamethoxazole SMX		TEMOCILLIN TRM		Tetracycline TETRA		TIGECYCLINE TGC		Trimethoprim TMP		ESBL-category	Relevant genes
EURL S-12.1	1	SUSC	2	RESIST	1	RESIST	>128	RESIST	>1024	RESIST	128	RESIST	>64	RESIST	0.5	SUSC	>32	RESIST	carbapenemase-phenotype	NDM-1 CMY-16
EURL S-12.2	<=0.5	SUSC	0.25	SUSC	<=0.03	SUSC	>128	RESIST	32	SUSC	4	SUSC	64	RESIST	<=0.25	SUSC	<=0.25	SUSC	ESBL-phenotype	CTX M-9 TEM-1B
EURL S-12.3	<=0.5	SUSC	0.25	SUSC	0.06	SUSC	>128	RESIST	>1024	RESIST	8	SUSC	>64	RESIST	0.5	SUSC	>32	RESIST	ESBL-phenotype	CTX M-14b
EURL S-12.4	<=0.5	SUSC	0.25	SUSC	0.06	SUSC	<=4	SUSC	64	SUSC	>128	RESIST	4	SUSC	0.5	SUSC	0.5	SUSC	AmpC	unknown
EURL S-12.5	<=0.5	SUSC			0.06	SUSC	8	SUSC	64	SUSC			4	SUSC	<=0.25	SUSC	0.5	SUSC	none	
EURL S-12.6	16	RESIST			<=0.03	SUSC	>128	RESIST	>1024	RESIST			64	RESIST	0.5	SUSC	<=0.25	SUSC	none	
EURL S-12.7	<=0.5	SUSC	0.25	SUSC	0.06	SUSC	<=4	SUSC	>1024	RESIST	8	SUSC	>64	RESIST	1	SUSC	>32	RESIST	ESBL-phenotype	CTX M-14
EURL S-12.8	>32	RESIST	8	RESIST	16	RESIST	>128	RESIST	>1024	RESIST	128	RESIST	4	SUSC	0.5	SUSC	0.5	SUSC	carbapenemase-phenotype	NDM-1 CTX-M15 DHA-1 OXA-1 OXA-9 OXA-10 TEM-1B

Resistant

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

Species	Code	Ciprofloxacin CIP		Erythromycin ERY		Gentamicin GEN		Nalidixic acid NAL		Streptomycin STR		Tetracycline TET	
C. jejuni	EURL C-12.1	<=0.12	SUSC	<= 1	SUSC	0.5	SUSC	8	SUSC	2	SUSC	<= 0.5	SUSC
C. jejuni	EURL C-12.2	>16	RESIST	128	RESIST	0.5	SUSC	>64	RESIST	>16	RESIST	64	RESIST
C. jejuni	EURL C-12.3	<=0.12	SUSC	<= 1	SUSC	0.5	SUSC	4	SUSC	>16	RESIST	8	RESIST
C. jejuni	EURL C-12.4	8	RESIST	<= 1	SUSC	<=0.12	SUSC	64	RESIST	0.5	SUSC	64	RESIST
C. jejuni	EURL C-12.5	4	RESIST	<= 1	SUSC	0.5	SUSC	64	RESIST	>16	RESIST	64	RESIST
C. coli	EURL C-12.6	16	RESIST	<= 1	SUSC	0.5	SUSC	>64	RESIST	2	SUSC	>64	RESIST
C. coli	EURL C-12.7	<=0.12	SUSC	<= 1	SUSC	0.5	SUSC	4	SUSC	2	SUSC	<= 0.5	SUSC
C. jejuni	EURL C-12.8	8	RESIST	<= 1	SUSC	0.25	SUSC	>64	RESIST	1	SUSC	64	RESIST

Resistant

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G00-06-001/23.06.2017

EURL-AR External Quality Assurance System 2017

- *Salmonella, Campylobacter* and optional genotypic characterisation

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

Kgs. Lyngby, October 2017

Dear «Name»,

Please find enclosed the bacterial strains for the EURL-AR EQAS 2017: eight *Salmonella spp.* and eight *Campylobacter* spp. Upon arrival to your laboratory, the strains should be stored in a dark place at 4°C for stabs, and in a dark and cool place for freeze-dried strains. Charcoal swabs must be subcultured upon arrival.

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

- Protocol for antimicrobial susceptibility testing of *Salmonella* and *Campylobacter* and test forms for reporting results
- Instructions for Opening and Reviving Lyophilised Cultures
- Subculture and Maintenance of Quality Control Strains

We ask you to test these *Salmonella* and *Campylobacter* strains for antimicrobial susceptibility. Detailed description of the procedures to follow for antimicrobial susceptibility testing, for optional genotypic characterization and for entering your results into the interactive web database can be found in the protocol. 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 **18th December 2017**.

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

Yours sincerely,

Susanne Karlsmose Pedersen
EURL-AR EQAS-Coordinator

Technical University of Denmark, National Food Institute, Søltofts Plads, Building 221, DK-2800 Kgs. Lyngby, Denmark
Ph: +45 3588 6601, e-mail: suska@food.dtu.dk

EU Reference Laboratory for Antimicrobial Resistance
External Quality Assurance System (EQAS) 2017

DTU Food
National Food Institute

PROTOCOL

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

1 INTRODUCTION

The organisation and implementation of an External Quality Assurance System (EQAS) on antimicrobial susceptibility testing (AST) of *Salmonella* and *Campylobacter* is among the tasks of the EU Reference Laboratory for Antimicrobial Resistance (EURL-AR). The *Salmonella*/*Campylobacter* EQAS 2017 will include AST of eight *Salmonella* and *Campylobacter* strains and AST of reference strains *E. coli* ATCC 25922 (CCM 3954) and *C. jejuni* ATCC 33560 (CCM 6214).

The reference strains are included in the parcel only for new participants of the EQAS who did not receive them previously. The reference strains are original CERTIFIED cultures provided free of charge, and should be used for future internal quality control for antimicrobial susceptibility testing in your laboratory. The reference strains will not be included in the years to come. Therefore, please

take proper care of these strains. Handle and maintain them as suggested in the manual 'Subculture and Maintenance of QC Strains' available on the EURL-AR website (see www.eurl-ar.eu).

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

2 OBJECTIVES

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

3 OUTLINE OF THE SALM/CAMP EQAS 2017

3.1 Shipping, receipt and storage of strains

In October 2017, the National Reference Laboratories for Antimicrobial Resistance (NRL-AR) will receive a parcel containing eight *Salmonella* and *Campylobacter* strains from the National Food Institute. This parcel will also contain reference strains, but only for participants who did not receive them previously.

All strains belong to UN3373, Biological substance, category B. Extended spectrum beta-lactamase (ESBL)-producing strains as well as carbapenemase producing strains are included in the selected material and are part of the optional EQAS-item, consisting of characterization of genes conferring ESBL- or carbapenemase production. It is the recipients' responsibility to comply with national legislation, rules and regulation regarding the correct use and handling of the provided strains and to possess the proper equipment and protocols to handle these strains.

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 QC reference strains

For a suggested procedure for reconstitution of the lyophilised, please refer to the document 'Instructions for opening and reviving lyophilised cultures' on the EURL-AR-website (see www.eurl-ar.eu).

Note that, for the testing of the *E. coli* ATCC25922 reference strain, the two compounds, sulfamethoxazole and sulfisoxazole, are regarded as comparable, i.e. the obtained MIC-value from

the testing of sulfamethoxazole will be evaluated against the acceptance range listed in CLSI M100 for sulfisoxazole.

3.3 Antimicrobial susceptibility testing

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

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

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

3.3.1 *Salmonella*

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

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

Antimicrobial	MIC (µg/mL) (R>)
Ampicillin (AMP)	8
Azithromycin (AZI)	16*
Cefotaxime (FOT)	0.5
Ceftazidime (TAZ)	2
Chloramphenicol (CHL)	16
Ciprofloxacin (CIP)	0.064
Colistin (COL)	2
Gentamicin (GEN)	2
Meropenem (MERO)	0.125
Nalidixic acid (NAL)	16
Sulfonamides (SMX)	256**
Tetracycline (TET)	8
Tigecycline (TGC)	1***
Trimethoprim (TMP)	2

* Tentative value
** CLSI M100 Table 2A
*** Data from EUCAST is available for *S.* Enteritidis, *S.* Typhimurium, *S.* Typhi and *S.* Paratyphi (for the purpose of this proficiency test, the ECOFF at 1 is applied)

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

Antimicrobial	MIC (µg/mL) (R>)
Cefepime, FEP	Not available*
Cefotaxime, FOT	0.5
Cefotaxime + clavulanic acid (F/C)	Not applicable
Cefoxitin, FOX	8
Ceftazidime, TAZ	2
Ceftazidime+ clavulanic acid (T/C)	Not applicable
Ertapenem, ETP	0.06
Imipenem, IMI	1
Meropenem, MERO	0.125
Temocillin, TRM	32**

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

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 should allow detection of plasmid-mediated quinolone resistant test strains.

Beta-lactam- and carbapenem resistance

Confirmatory tests for ESBL production are mandatory on all strains resistant to cefotaxime (FOT), ceftazidime (TAZ) and/or meropenem and should be performed by testing the second panel of antimicrobials (Table 2 in this document corresponding to Table 4 in Commission Implementing Decision 2013/652/EU).

Confirmatory test for AmpC-, ESBL- and carbapenemase production requires use of both cefotaxime (FOT) and ceftazidime (TAZ) 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. the MIC of the agent when tested alone (MIC FOT : FOT/Cl or TAZ : TAZ/Cl ratio ≥ 8) (CLSI M100 Table 3A, Tests for ESBLs). The presence of synergy indicates ESBL production.

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

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

The classification of the phenotypic results should be based on the most recent EFSA recommendations (available in The European Union summary report on antimicrobial resistance in zoonotic and indicator bacteria from humans, animals and food in 2015, EFSA Journal 2017;15(2):4694,212 pp. (page 43), and in the appendix to this protocol). It is important to notice that two cut-off values apply for cefotaxime and ceftazidime: the EUCAST cut-off values (ECOFFs: FOT>0.5 and TAZ>2), which are those used to define R/S, and the screening cut-off values (FOT>1 and TAZ>1), which are those applied to categorise bacterial phenotypes as ESBL, AmpC, carbapenemase, etc. based on panel 2 results (see Appendix).

3.3.2 *Campylobacter*

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

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

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

Identification of *Campylobacter* species

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

3.4 Optional genotypic characterisation

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

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 type (ACC-, ACT-, CARB-, 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 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 18th 2017.** After the deadline when all participants have uploaded results, you will be able to login to the database once again, and to view and print an automatically generated report evaluating your results. Results in agreement with the expected interpretation are categorised as 'correct', while results deviating from the expected interpretation are categorised as 'incorrect'.

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

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

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

Susanne Karlsmose Pedersen
National Food Institute,
Technical University of Denmark
Kemitorvet, Building 204, DK-2800 Lyngby
Denmark
Tel: +45 3588 6601
E-mail: suska@food.dtu.dk

5 HOW TO ENTER RESULTS IN THE INTERACTIVE DATABASE

Please read carefully this paragraph before entering the web page.

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

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

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

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

Click on "Start of Data Entry - Methods"

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

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

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

Click on "save and go to next page"

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

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

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

Click on "save and go to next page"

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

Click on "save".

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

Please complete the evaluation form.

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

If you have performed the optional genotypic characterisation:

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

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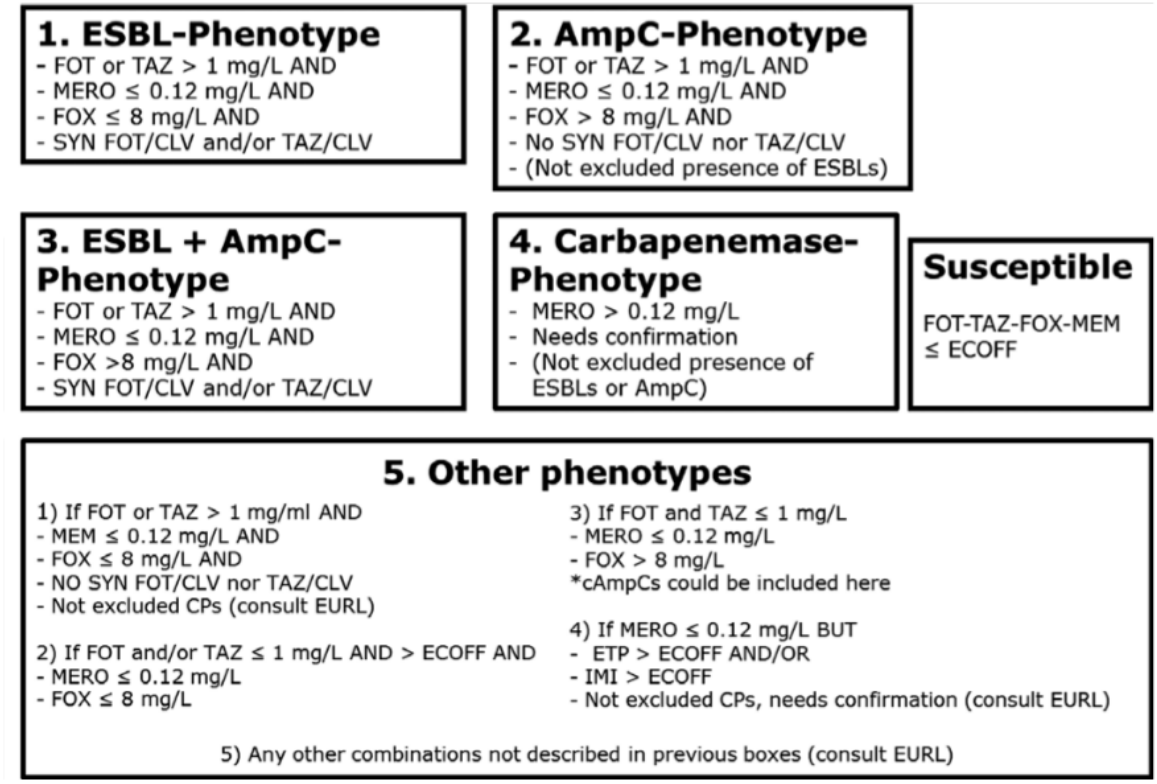
APPENDIX

Criteria for interpretation of *Salmonella*, panel 2 results



Please refer to: EFSA (European Food Safety Authority) and ECDC (European Centre for Disease Prevention and Control), 2017. The European Union summary report on antimicrobial resistance in zoonotic and indicator bacteria from humans, animals and food in 2015. EFSA Journal 2017;15(2):4694, 212 pp. doi:10.2903/j.efsa.2017.4694 (page 43).

Salmonella, *Campylobacter* and genetic characterisation

TEST FORMS

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

Comments:

TEST FORM

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

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

☐ Broth microdilution
☐ Agar dilution

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

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

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

Which method was followed for the preparation of the inoculum (please describe)

- Which standard was followed (TREK, CLSI…)
- Which solvent was used for the preparation of the 0.5 McFarland solution (water, saline)
- Please describe in detail how you prepared the dilution of the inoculum (including the volume in final MH-dilution and intended dilution level; e.g. diluted 1:1000 by adding 10µl of 0.5 McFarland solution in 10ml MH broth, for an expected inoculum of $1*10^5$ CFU/ml)

Comments or additional information:

TEST FORM

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

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

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

Brand of microbroth plates/agar:

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

Which method was followed for the preparation of the inoculum (please describe)

- Which standard was followed (TREK, CLSI…)
- Which solvent was used for the preparation of the 0.5 McFarland solution (water, saline)
- Please describe in detail how you prepared the dilution of the inoculum (including the volume in final MH-dilution and intended dilution level; e.g. diluted 1:1000 by adding 10µl of 0.5 McFarland solution in 10ml MH broth, for an expected inoculum of $1*10^5$ CFU/ml)

Comments or additional information:

TEST FORM

Strain	Antimicrobial	Results and interpretation		
		≤ / >	MIC-value (µg/ml)	S / R
Salmonella EURL S. 12.1	Ampicillin, AMP			
	Azithromycin, AZI			
	Cefotaxime, FOT			
	Ceftazidime, TAZ			
	Chloramphenicol, CHL			
	Ciprofloxacin CIP			
	Colistin, COL			
	Gentamicin, GEN			
	Meropenem, MERO			
	Nalidixic acid, NAL			
	Sulfamethoxazole, SMX			
	Tetracycline, TET			
	Tigecycline, TGC			
	Trimethoprim, TMP			

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

Strain	Antimicrobial	Results and interpretation		
		≤ / >	MIC-value (µg/ml)	S / R
Salmonella EURL S. 12.1	Cefepime, FEP			
	Cefotaxime, FOT			
	Cefotaxime + clavulanic acid (F/C)			
	Cefoxitin, FOX			
	Ceftazidime, TAZ			
	Ceftazidime+ clavulanic acid (T/C)			
	Ertapenem, ETP			
	Imipenem, IMI			
	Meropenem, MERO			
	Temocillin, TRM			

Interpretation of PANEL 2 results:

☐ Presumptive ESBL ☐ Presumptive AmpC ☐ Other phenotype
☐ Presumptive ESBL+ AmpC ☐ Presumptive Carbapenemase ☐ Susceptible

Comments (include optional genotype or other results):

TEST FORM

Strain	Antimicrobial	Results and interpretation		
		≤ / >	MIC-value (µg/ml)	S / R
Salmonella EURL S. 12.2	Ampicillin, AMP			
	Azithromycin, AZI			
	Cefotaxime, FOT			
	Ceftazidime, TAZ			
	Chloramphenicol, CHL			
	Ciprofloxacin CIP			
	Colistin, COL			
	Gentamicin, GEN			
	Meropenem, MERO			
	Nalidixic acid, NAL			
	Sulfamethoxazole, SMX			
	Tetracycline, TET			
	Tigecycline, TGC			
	Trimethoprim, TMP			

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

Strain	Antimicrobial	Results and interpretation		
		≤ / >	MIC-value (µg/ml)	S / R
Salmonella EURL S. 12.2	Cefepime, FEP			
	Cefotaxime, FOT			
	Cefotaxime + clavulanic acid (F/C)			
	Cefoxitin, FOX			
	Ceftazidime, TAZ			
	Ceftazidime+ clavulanic acid (T/C)			
	Ertapenem, ETP			
	Imipenem, IMI			
	Meropenem, MERO			
	Temocillin, TRM			

Interpretation of PANEL 2 results:

☐ Presumptive ESBL ☐ Presumptive AmpC ☐ Other phenotype
☐ Presumptive ESBL+ AmpC ☐ Presumptive Carbapenemase ☐ Susceptible

Comments (include optional genotype or other results):

TEST FORM

Strain	Antimicrobial	Results and interpretation		
		≤ / >	MIC-value (µg/ml)	S / R
Salmonella EURL S. 12.3	Ampicillin, AMP			
	Azithromycin, AZI			
	Cefotaxime, FOT			
	Ceftazidime, TAZ			
	Chloramphenicol, CHL			
	Ciprofloxacin CIP			
	Colistin, COL			
	Gentamicin, GEN			
	Meropenem, MERO			
	Nalidixic acid, NAL			
	Sulfamethoxazole, SMX			
	Tetracycline, TET			
	Tigecycline, TGC			
	Trimethoprim, TMP			

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

Strain	Antimicrobial	Results and interpretation		
		≤ / >	MIC-value (µg/ml)	S / R
Salmonella EURL S. 12.3	Cefepime, FEP			
	Cefotaxime, FOT			
	Cefotaxime + clavulanic acid (F/C)			
	Cefoxitin, FOX			
	Ceftazidime, TAZ			
	Ceftazidime+ clavulanic acid (T/C)			
	Ertapenem, ETP			
	Imipenem, IMI			
	Meropenem, MERO			
	Temocillin, TRM			

Interpretation of PANEL 2 results:

☐ Presumptive ESBL ☐ Presumptive AmpC ☐ Other phenotype
☐ Presumptive ESBL+ AmpC ☐ Presumptive Carbapenemase ☐ Susceptible

Comments (include optional genotype or other results):

TEST FORM

Strain	Antimicrobial	Results and interpretation		
		≤ / >	MIC-value (µg/ml)	S / R
Salmonella EURL S. 12.4	Ampicillin, AMP			
	Azithromycin, AZI			
	Cefotaxime, FOT			
	Ceftazidime, TAZ			
	Chloramphenicol, CHL			
	Ciprofloxacin CIP			
	Colistin, COL			
	Gentamicin, GEN			
	Meropenem, MERO			
	Nalidixic acid, NAL			
	Sulfamethoxazole, SMX			
	Tetracycline, TET			
	Tigecycline, TGC			
	Trimethoprim, TMP			

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

Strain	Antimicrobial	Results and interpretation		
		≤ / >	MIC-value (µg/ml)	S / R
Salmonella EURL S. 12.4	Cefepime, FEP			
	Cefotaxime, FOT			
	Cefotaxime + clavulanic acid (F/C)			
	Cefoxitin, FOX			
	Ceftazidime, TAZ			
	Ceftazidime+ clavulanic acid (T/C)			
	Ertapenem, ETP			
	Imipenem, IMI			
	Meropenem, MERO			
	Temocillin, TRM			

Interpretation of PANEL 2 results:

☐ Presumptive ESBL ☐ Presumptive AmpC ☐ Other phenotype
☐ Presumptive ESBL+ AmpC ☐ Presumptive Carbapenemase ☐ Susceptible

Comments (include optional genotype or other results):

TEST FORM

Strain	Antimicrobial	Results and interpretation		
		≤ / >	MIC-value (µg/ml)	S / R
Salmonella EURL S. 12.5	Ampicillin, AMP			
	Azithromycin, AZI			
	Cefotaxime, FOT			
	Ceftazidime, TAZ			
	Chloramphenicol, CHL			
	Ciprofloxacin CIP			
	Colistin, COL			
	Gentamicin, GEN			
	Meropenem, MERO			
	Nalidixic acid, NAL			
	Sulfamethoxazole, SMX			
	Tetracycline, TET			
	Tigecycline, TGC			
	Trimethoprim, TMP			

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

Strain	Antimicrobial	Results and interpretation		
		≤ / >	MIC-value (µg/ml)	S / R
Salmonella EURL S. 12.5	Cefepime, FEP			
	Cefotaxime, FOT			
	Cefotaxime + clavulanic acid (F/C)			
	Cefoxitin, FOX			
	Ceftazidime, TAZ			
	Ceftazidime+ clavulanic acid (T/C)			
	Ertapenem, ETP			
	Imipenem, IMI			
	Meropenem, MERO			
	Temocillin, TRM			

Interpretation of PANEL 2 results:

☐ Presumptive ESBL ☐ Presumptive AmpC ☐ Other phenotype
☐ Presumptive ESBL+ AmpC ☐ Presumptive Carbapenemase ☐ Susceptible

Comments (include optional genotype or other results):

TEST FORM

Strain	Antimicrobial	Results and interpretation		
		≤ / >	MIC-value (µg/ml)	S / R
Salmonella EURL S. 12.6	Ampicillin, AMP			
	Azithromycin, AZI			
	Cefotaxime, FOT			
	Ceftazidime, TAZ			
	Chloramphenicol, CHL			
	Ciprofloxacin CIP			
	Colistin, COL			
	Gentamicin, GEN			
	Meropenem, MERO			
	Nalidixic acid, NAL			
	Sulfamethoxazole, SMX			
	Tetracycline, TET			
	Tigecycline, TGC			
	Trimethoprim, TMP			

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

Strain	Antimicrobial	Results and interpretation		
		≤ / >	MIC-value (µg/ml)	S / R
Salmonella EURL S. 12.6	Cefepime, FEP			
	Cefotaxime, FOT			
	Cefotaxime + clavulanic acid (F/C)			
	Cefoxitin, FOX			
	Ceftazidime, TAZ			
	Ceftazidime+ clavulanic acid (T/C)			
	Ertapenem, ETP			
	Imipenem, IMI			
	Meropenem, MERO			
	Temocillin, TRM			

Interpretation of PANEL 2 results:

☐ Presumptive ESBL ☐ Presumptive AmpC ☐ Other phenotype
☐ Presumptive ESBL+ AmpC ☐ Presumptive Carbapenemase ☐ Susceptible

Comments (include optional genotype or other results):

TEST FORM

Strain	Antimicrobial	Results and interpretation		
		≤ / >	MIC-value (µg/ml)	S / R
Salmonella EURL S. 12.7	Ampicillin, AMP			
	Azithromycin, AZI			
	Cefotaxime, FOT			
	Ceftazidime, TAZ			
	Chloramphenicol, CHL			
	Ciprofloxacin CIP			
	Colistin, COL			
	Gentamicin, GEN			
	Meropenem, MERO			
	Nalidixic acid, NAL			
	Sulfamethoxazole, SMX			
	Tetracycline, TET			
	Tigecycline, TGC			
	Trimethoprim, TMP			

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

Strain	Antimicrobial	Results and interpretation		
		≤ / >	MIC-value (µg/ml)	S / R
Salmonella EURL S. 12.7	Cefepime, FEP			
	Cefotaxime, FOT			
	Cefotaxime + clavulanic acid (F/C)			
	Cefoxitin, FOX			
	Ceftazidime, TAZ			
	Ceftazidime+ clavulanic acid (T/C)			
	Ertapenem, ETP			
	Imipenem, IMI			
	Meropenem, MERO			
	Temocillin, TRM			

Interpretation of PANEL 2 results:

☐ Presumptive ESBL ☐ Presumptive AmpC ☐ Other phenotype
☐ Presumptive ESBL+ AmpC ☐ Presumptive Carbapenemase ☐ Susceptible

Comments (include optional genotype or other results):

TEST FORM

Strain	Antimicrobial	Results and interpretation		
		≤ >	MIC-value (µg/ml)	S / R
Salmonella EURL S. 12.8	Ampicillin, AMP			
	Azithromycin, AZI			
	Cefotaxime, FOT			
	Ceftazidime, TAZ			
	Chloramphenicol, CHL			
	Ciprofloxacin CIP			
	Colistin, COL			
	Gentamicin, GEN			
	Meropenem, MERO			
	Nalidixic acid, NAL			
	Sulfamethoxazole, SMX			
	Tetracycline, TET			
	Tigecycline, TGC			
	Trimethoprim, TMP			

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

Strain	Antimicrobial	Results and interpretation		
		≤ >	MIC-value (µg/ml)	S / R
Salmonella EURL S. 12.8	Cefepime, FEP			
	Cefotaxime, FOT			
	Cefotaxime + clavulanic acid (F/C)			
	Cefoxitin, FOX			
	Ceftazidime, TAZ			
	Ceftazidime+ clavulanic acid (T/C)			
	Ertapenem, ETP			
	Imipenem, IMI			
	Meropenem, MERO			
	Temocillin, TRM			

Interpretation of PANEL 2 results:

☐ Presumptive ESBL ☐ Presumptive AmpC ☐ Other phenotype
☐ Presumptive ESBL+ AmpC ☐ Presumptive Carbapenemase ☐ Susceptible

Comments (include optional genotype or other results):

TEST FORM

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

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

* for the testing of the *E. coli* ATCC25922 reference strain, sulfamethoxazole and sulfisoxazole, are regarded as comparable, i.e. the obtained MIC-value from the testing of sulfamethoxazole will be evaluated against the acceptance range listed in CLSI M100 for sulfisoxazole (CLSI M100, Table 3).

TEST FORM

Strain	Antimicrobial	Interpretation	
		MIC-value (µg/ml)	S / R
Campylobacter EURL C-12.1 ☐ *C. jejuni* ☐ *C. coli*	Ciprofloxacin		
	Erythromycin		
	Gentamicin		
	Nalidixic acid		
	Streptomycin		
	Tetracycline		
Campylobacter EURL C-12.2 ☐ *C. jejuni* ☐ *C. coli*	Ciprofloxacin		
	Erythromycin		
	Gentamicin		
	Nalidixic acid		
	Streptomycin		
	Tetracycline		
Campylobacter EURL C-12.3 ☐ *C. jejuni* ☐ *C. coli*	Ciprofloxacin		
	Erythromycin		
	Gentamicin		
	Nalidixic acid		
	Streptomycin		
	Tetracycline		
Campylobacter EURL C-12.4 ☐ *C. jejuni* ☐ *C. coli*	Ciprofloxacin		
	Erythromycin		
	Gentamicin		
	Nalidixic acid		
	Streptomycin		
	Tetracycline		

TEST FORM

Strain	Antimicrobial	Interpretation	
		MIC-value (µg/ml)	S / R
Campylobacter EURL C-12.5 ☐ *C. jejuni* ☐ *C. coli*	Ciprofloxacin		
	Erythromycin		
	Gentamicin		
	Nalidixic acid		
	Streptomycin		
	Tetracycline		
Campylobacter EURL C-12.6 ☐ *C. jejuni* ☐ *C. coli*	Ciprofloxacin		
	Erythromycin		
	Gentamicin		
	Nalidixic acid		
	Streptomycin		
	Tetracycline		
Campylobacter EURL C-12.7 ☐ *C. jejuni* ☐ *C. coli*	Ciprofloxacin		
	Erythromycin		
	Gentamicin		
	Nalidixic acid		
	Streptomycin		
	Tetracycline		
Campylobacter EURL C-12.8 ☐ *C. jejuni* ☐ *C. coli*	Ciprofloxacin		
	Erythromycin		
	Gentamicin		
	Nalidixic acid		
	Streptomycin		
	Tetracycline		

TEST FORM

Susceptibility testing of *Campylobacter jejuni* reference strain ATCC 33560

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

For Agar dilution:

Susceptibility testing of *Campylobacter jejuni* reference strain ATCC 33560

Strain	Antimicrobial	MIC-value (µg/ml)
C. jejuni ATCC 33560	Ciprofloxacin	
	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:	☐ Published method , reference:
	☐ In-house method
☐ Found	Primer used 5'→3':
☐ Tested, not found	Primer used 3'→5':
Gene:	☐ Published method , reference:
	☐ In-house method
☐ Found	Primer used 5'→3':
☐ Tested, not found	Primer used 3'→5':
Gene:	☐ Published method , reference:
	☐ In-house method
☐ Found	Primer used 5'→3':
☐ Tested, not found	Primer used 3'→5':
Gene:	☐ Published method , reference:
	☐ In-house method
☐ Found	Primer used 5'→3':
☐ Tested, not found	Primer used 3'→5':
Gene:	☐ Published method , reference:
	☐ In-house method
☐ Found	Primer used 5'→3':
☐ Tested, not found	Primer used 3'→5':
Gene:	☐ Published method , reference:
	☐ In-house method
☐ Found	Primer used 5'→3':
☐ Tested, not found	Primer used 3'→5':

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:

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

DTU Food
National Food Institute

INSTRUCTIONS FOR OPENING AND REVIVING LYOPHILISED CULTURES

Instructions adjusted from Czech Collection of Microorganisms (CCM) document 'Instructions for Opening and Reviving of Freeze-Dried Bacteria and Fungi' available on http://www.sci.muni.cz.

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 (see Figure 1)
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

Notes:

- Cultures should be grown on media and under conditions as recommended in the CCM catalogue (see http://www.sci.muni.cz)
- 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!

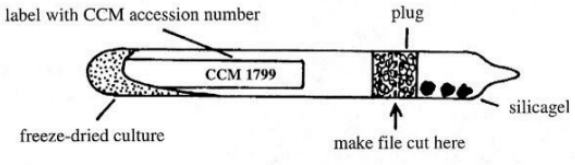


Figure 1: from CCM document 'Instructions for Opening and Reviving of Freeze-Dried Bacteria and Fungi' available on http://www.sci.muni.cz

SUBCULTURE AND MAINTENANCE OF QUALITY CONTROL STRAINS

1 PURPOSE AND REFERENCES

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

The following can be regarded as a summary of information that should be followed for subculturing and maintaining QC-strains when performing AST by broth dilution methods. For full information related to this subject, the following standards are relevant: M100 (Performance Standards for Antimicrobial Susceptibility Testing) and M7 (Methods for Dilution Antimicrobial Susceptibility Test for Bacteria That Grow Aerobically; Approved Standard).

2 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.

3 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 (after 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.

4 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.

5 FREQUENCY OF TESTING

Weekly vs. daily testing

Weekly testing is possible if the laboratory can demonstrate satisfactory performance with daily testing according to the descriptions in the CLSI guidelines.

- Documentation showing reference strain results from 20 or 30 consecutive test days were within the acceptable range.
- For each antimicrobial/organism combination, no more one out of 20 or three 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

If five acceptable QC results are available, no additional days of QC-testing are needed.

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

Repeat the 30 days validation before resuming weekly testing.

Quality Control ranges for ATCC reference strains

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

MIC ranges (µg/mL) are according to CLSI M100 27th edition (range for ciprofloxacin and ertapenem extended to include 0.016).

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

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

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

Lab no.	Panel	Antimicrobial	Operator	Value	Low limit	High limit	Mark	Method	Temperature	Time
2	1	Ampicillin	=	4	2	8	1	MIC	35±1	18-24
2	1	Ampicillin AMP	=	4	2	8	1	MIC	35±1	18-24
2	1	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	35±1	18-24
2	1	Ceftazidime TAZ	<=	0.5	0.06	0.5	1	MIC	35±1	18-24
2	1	Chloramphenicol CHL	<=	8	2	8	1	MIC	35±1	18-24
2	1	Ciprofloxacin CIP	<=	0.015	0.004	0.016	1	MIC	35±1	18-24
2	1	Colistin COL	<=	1	0.25	2	1	MIC	35±1	18-24
2	1	Gentamicin GEN	<=	0.5	0.25	1	1	MIC	35±1	18-24
2	1	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	35±1	18-24
2	1	Nalidixic acid NAL	<=	4	1	4	1	MIC	35±1	18-24
2	1	Sulfamethoxazole SMX	=	32	8	32	1	MIC	35±1	18-24
2	1	Tetracycline TET	<=	2	0.5	2	1	MIC	35±1	18-24
2	1	Tigecycline TGC	<=	0.25	0.03	0.25	1	MIC	35±1	18-24
2	1	Trimethoprim TMP	=	0.5	0.5	2	1	MIC	35±1	18-24
2	2	Cefepime FEP	<=	0.06	0.016	0.12	1	MIC	35±1	18-24
2	2	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	35±1	18-24
2	2	Cefoxitin FOX	=	4	2	8	1	MIC	35±1	18-24
2	2	Ceftazidime TAZ	<=	0.25	0.06	0.5	1	MIC	35±1	18-24
2	2	Ertapenem ETP	<=	0.015	0.004	0.016	1	MIC	35±1	18-24
2	2	Imipenem IMI	=	0.25	0.06	0.25	1	MIC	35±1	18-24
2	2	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	35±1	18-24
4	1	Ampicillin AMP	=	4	2	8	1	MIC	37°C	24
4	1	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	37°C	24
4	1	Ceftazidime TAZ	<=	0.5	0.06	0.5	1	MIC	37°C	24
4	1	Chloramphenicol CHL	<=	8	2	8	1	MIC	37°C	24
4	1	Ciprofloxacin CIP	<=	0.015	0.004	0.016	1	MIC	37°C	24
4	1	Colistin COL	<=	1	0.25	2	1	MIC	37°C	24
4	1	Gentamicin GEN	<=	0.5	0.25	1	1	MIC	37°C	24
4	1	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	37°C	24
4	1	Nalidixic acid NAL	<=	4	1	4	1	MIC	37°C	24
4	1	Sulfamethoxazole SMX	=	32	8	32	1	MIC	37°C	24
4	1	Tetracycline TET	<=	2	0.5	2	1	MIC	37°C	24
4	1	Tigecycline TGC	<=	0.25	0.03	0.25	1	MIC	37°C	24
4	1	Trimethoprim TMP	=	1	0.5	2	1	MIC	37°C	24
6	1	Ampicillin AMP	=	8	2	8	1	MIC	35	18
6	1	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	35	18
6	1	Ceftazidime TAZ	<=	0.5	0.06	0.5	1	MIC	35	18
6	1	Chloramphenicol CHL	<=	8	2	8	1	MIC	35	18
6	1	Ciprofloxacin CIP	<=	0.015	0.004	0.016	1	MIC	35	18
6	1	Colistin COL	<=	1	0.25	2	1	MIC	35	18
6	1	Gentamicin GEN	<=	0.5	0.25	1	1	MIC	35	18
6	1	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	35	18
6	1	Nalidixic acid NAL	<=	4	1	4	1	MIC	35	18
6	1	Sulfamethoxazole SMX	=	32	8	32	1	MIC	35	18
6	1	Tetracycline TET	<=	2	0.5	2	1	MIC	35	18
6	1	Tigecycline TGC	<=	0.25	0.03	0.25	1	MIC	35	18
6	1	Trimethoprim TMP	=	1	0.5	2	1	MIC	35	18
6	2	Cefepime FEP	<=	0.06	0.016	0.12	1	MIC	35	18
6	2	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	35	18
6	2	Cefoxitin FOX	=	4	2	8	1	MIC	35	18
6	2	Ceftazidime TAZ	<=	0.025	0.06	0.5	0	MIC	35	18
6	2	Ertapenem ETP	<=	0.015	0.004	0.016	1	MIC	35	18
6	2	Imipenem IMI	=	0.25	0.06	0.25	1	MIC	35	18
6	2	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	35	18
9	1	Ampicillin AMP	=	4	2	8	1	MIC	35+-1	20
9	1	Ceftazidime TAZ	<=	0.5	0.06	0.5	1	MIC	35+-1	20
9	1	Chloramphenicol CHL	<=	8	2	8	1	MIC	35+-1	20
9	1	Ciprofloxacin CIP	<=	0.015	0.004	0.016	1	MIC	35+-1	20
9	1	Colistin COL	<=	1	0.25	2	1	MIC	35+-1	20
9	1	Gentamicin GEN	<=	0.5	0.25	1	1	MIC	35+-1	20
9	1	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	35+-1	20
9	1	Nalidixic acid NAL	<=	4	1	4	1	MIC	35+-1	20
9	1	Sulfamethoxazole SMX	=	16	8	32	1	MIC	35+-1	20
9	1	Tetracycline TET	<=	2	0.5	2	1	MIC	35+-1	20
9	1	Tigecycline TGC	<=	0.25	0.03	0.25	1	MIC	35+-1	20
9	1	Trimethoprim TMP	=	1	0.5	2	1	MIC	35+-1	20
9	2	Cefepime FEP	<=	0.06	0.016	0.12	1	MIC	35+-1	20
9	2	Cefoxitin FOX	=	4	2	8	1	MIC	35+-1	20
9	2	Ceftazidime TAZ	<=	0.25	0.06	0.5	1	MIC	35+-1	20
9	2	Ertapenem ETP	<=	0.015	0.004	0.016	1	MIC	35+-1	20
9	2	Imipenem IMI	<=	0.12	0.06	0.25	1	MIC	35+-1	20
9	2	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	35+-1	20
11	1	Ampicillin AMP	=	2	2	8	1	MIC	35	18-20

Lab no.	Panel	Antimicrobial	Operator	Value	Low limit	High limit	Mark	Method	Temperature	Time
11	1	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	35	18-20
11	1	Ceftazidime TAZ	<=	0.5	0.06	0.5	1	MIC	35	18-20
11	1	Chloramphenicol CHL	<=	8	2	8	1	MIC	35	18-20
11	1	Ciprofloxacin CIP	<=	0.015	0.004	0.016	1	MIC	35	18-20
11	1	Colistin COL	<=	1	0.25	2	1	MIC	35	18-20
11	1	Gentamicin GEN	=	1	0.25	1	1	MIC	35	18-20
11	1	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	35	18-20
11	1	Nalidixic acid NAL	<=	4	1	4	1	MIC	35	18-20
11	1	Sulfamethoxazole SMX	=	16	8	32	1	MIC	35	18-20
11	1	Tetracycline TET	<=	2	0.5	2	1	MIC	35	18-20
11	1	Tigecycline TGC	<=	0.25	0.03	0.25	1	MIC	35	18-20
11	1	Trimethoprim TMP	=	0.5	0.5	2	1	MIC	35	18-20
11	2	Cefepime FEP	<=	0.06	0.016	0.12	1	MIC	35	18-20
11	2	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	35	18-20
11	2	Cefoxitin FOX	=	2	2	8	1	MIC	35	18-20
11	2	Ceftazidime TAZ	<=	0.05	0.06	0.5	0	MIC	35	18-20
11	2	Ertapenem ETP	<=	0.015	0.004	0.016	1	MIC	35	18-20
11	2	Imipenem IMI	<=	0.12	0.06	0.25	1	MIC	35	18-20
11	2	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	35	18-20
12	1	Ampicillin AMP	=	4	2	8	1	MIC	35	18-30
12	1	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	35	18-30
12	1	Ceftazidime TAZ	<=	0.5	0.06	0.5	1	MIC	35	18-30
12	1	Chloramphenicol CHL	<=	8	2	8	1	MIC	35	18-30
12	1	Ciprofloxacin CIP	<=	0.015	0.004	0.016	1	MIC	35	18-30
12	1	Colistin COL	<=	1	0.25	2	1	MIC	35	18-30
12	1	Gentamicin GEN	<=	0.5	0.25	1	1	MIC	35	18-30
12	1	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	35	18-30
12	1	Nalidixic acid NAL	<=	4	1	4	1	MIC	35	18-30
12	1	Sulfamethoxazole SMX	<=	8	8	32	1	MIC	35	18-30
12	1	Tetracycline TET	<=	2	0.5	2	1	MIC	35	18-30
12	1	Tigecycline TGC	<=	0.25	0.03	0.25	1	MIC	35	18-30
12	1	Trimethoprim TMP	=	1	0.5	2	1	MIC	35	18-30
12	2	Cefepime FEP	<=	0.06	0.016	0.12	1	MIC	35	18-30
12	2	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	35	18-30
12	2	Cefoxitin FOX	=	4	2	8	1	MIC	35	18-30
12	2	Ceftazidime TAZ	<=	0.25	0.06	0.5	1	MIC	35	18-30
12	2	Ertapenem ETP	<=	0.015	0.004	0.016	1	MIC	35	18-30
12	2	Imipenem IMI	<=	0.12	0.06	0.25	1	MIC	35	18-30
12	2	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	35	18-30
16	1	Ampicillin AMP	=	4	2	8	1	MIC	35	18-24
16	1	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	35	18-24
16	1	Ceftazidime TAZ	<=	0.5	0.06	0.5	1	MIC	35	18-24
16	1	Chloramphenicol CHL	<=	8	2	8	1	MIC	35	18-24
16	1	Ciprofloxacin CIP	<=	0.015	0.004	0.016	1	MIC	35	18-24
16	1	Colistin COL	<=	1	0.25	2	1	MIC	35	18-24
16	1	Gentamicin GEN	<=	0.5	0.25	1	1	MIC	35	18-24
16	1	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	35	18-24
16	1	Nalidixic acid NAL	<=	4	1	4	1	MIC	35	18-24
16	1	Sulfamethoxazole SMX	=	32	8	32	1	MIC	35	18-24
16	1	Tetracycline TET	<=	2	0.5	2	1	MIC	35	18-24
16	1	Tigecycline TGC	<=	0.25	0.03	0.25	1	MIC	35	18-24
16	1	Trimethoprim TMP	=	0.5	0.5	2	1	MIC	35	18-24
16	2	Cefepime FEP	<=	0.06	0.016	0.12	1	MIC	35	18-24
16	2	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	35	18-24
16	2	Cefoxitin FOX	=	4	2	8	1	MIC	35	18-24
16	2	Ceftazidime TAZ	<=	0.25	0.06	0.5	1	MIC	35	18-24
16	2	Ertapenem ETP	<=	0.015	0.004	0.016	1	MIC	35	18-24
16	2	Imipenem IMI	=	0.25	0.06	0.25	1	MIC	35	18-24
16	2	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	35	18-24
17	1	Ampicillin AMP	=	8	2	8	1	MIC	37	18
17	1	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	37	18
17	1	Ceftazidime TAZ	<=	0.5	0.06	0.5	1	MIC	37	18
17	1	Chloramphenicol CHL	<=	8	2	8	1	MIC	37	18
17	1	Ciprofloxacin CIP	<=	0.015	0.004	0.016	1	MIC	37	18
17	1	Colistin COL	<=	1	0.25	2	1	MIC	37	18
17	1	Gentamicin GEN	<=	0.5	0.25	1	1	MIC	37	18
17	1	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	37	18
17	1	Nalidixic acid NAL	<=	4	1	4	1	MIC	37	18
17	1	Sulfamethoxazole SMX	<=	8	8	32	1	MIC	37	18
17	1	Tetracycline TET	<=	2	0.5	2	1	MIC	37	18
17	1	Tigecycline TGC	<=	0.25	0.03	0.25	1	MIC	37	18
17	1	Trimethoprim TMP	<=	0.25	0.5	2	0	MIC	37	18
17	2	Cefepime FEP	<=	0.06	0.016	0.12	1	MIC	37	18
17	2	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	37	18
17	2	Cefoxitin FOX	=	8	2	8	1	MIC	37	18

Lab no.	Panel	Antimicrobial	Operator	Value	Low limit	High limit	Mark	Method	Temperature	Time
17	2	Ceftazidime TAZ	=	0.5	0.06	0.5	1	MIC	37	18
17	2	Ertapenem ETP	<=	0.015	0.004	0.016	1	MIC	37	18
17	2	Imipenem IMI	=	0.25	0.06	0.25	1	MIC	37	18
17	2	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	37	18
18	1	Ampicillin AMP	=	2	2	8	1	MIC	37	18
18	1	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	37	18
18	1	Ceftazidime TAZ	<=	0.5	0.06	0.5	1	MIC	37	18
18	1	Chloramphenicol CHL	<=	8	2	8	1	MIC	37	18
18	1	Ciprofloxacin CIP	<=	0.015	0.004	0.016	1	MIC	37	18
18	1	Colistin COL	<=	1	0.25	2	1	MIC	37	18
18	1	Gentamicin GEN	<=	0.5	0.25	1	1	MIC	37	18
18	1	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	37	18
18	1	Nalidixic acid NAL	<=	4	1	4	1	MIC	37	18
18	1	Sulfamethoxazole SMX	=	16	8	32	1	MIC	37	18
18	1	Tetracycline TET	<=	2	0.5	2	1	MIC	37	18
18	1	Tigecycline TGC	<=	0.25	0.03	0.25	1	MIC	37	18
18	1	Trimethoprim TMP	=	0.5	0.5	2	1	MIC	37	18
18	2	Cefepime FEP	<=	0.06	0.016	0.12	1	MIC	37	18
18	2	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	37	18
18	2	Cefoxitin FOX	=	2	2	8	1	MIC	37	18
18	2	Ceftazidime TAZ	<=	0.25	0.06	0.5	1	MIC	37	18
18	2	Ertapenem ETP	<=	0.015	0.004	0.016	1	MIC	37	18
18	2	Imipenem IMI	<=	0.12	0.06	0.25	1	MIC	37	18
18	2	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	37	18
19	1	Ampicillin AMP	=	4	2	8	1	MIC	35	18
19	1	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	35	18
19	1	Ceftazidime TAZ	<=	0.5	0.06	0.5	1	MIC	35	18
19	1	Chloramphenicol CHL	<=	8	2	8	1	MIC	35	18
19	1	Ciprofloxacin CIP	<=	0.015	0.004	0.016	1	MIC	35	18
19	1	Colistin COL	<=	1	0.25	2	1	MIC	35	18
19	1	Gentamicin GEN	<=	0.5	0.25	1	1	MIC	35	18
19	1	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	35	18
19	1	Nalidixic acid NAL	<=	4	1	4	1	MIC	35	18
19	1	Sulfamethoxazole SMX	=	32	8	32	1	MIC	35	18
19	1	Tetracycline TET	<=	2	0.5	2	1	MIC	35	18
19	1	Tigecycline TGC	<=	0.25	0.03	0.25	1	MIC	35	18
19	1	Trimethoprim TMP	=	0.5	0.5	2	1	MIC	35	18
19	2	Cefepime FEP	<=	0.06	0.016	0.12	1	MIC	35	18
19	2	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	35	18
19	2	Cefoxitin FOX	=	2	2	8	1	MIC	35	18
19	2	Ceftazidime TAZ	<=	0.25	0.06	0.5	1	MIC	35	18
19	2	Ertapenem ETP	<=	0.015	0.004	0.016	1	MIC	35	18
19	2	Imipenem IMI	<=	0.12	0.06	0.25	1	MIC	35	18
19	2	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	35	18
20	1	Ampicillin AMP	=	4	2	8	1	MIC	37C +/- 1C	20h +/- 2h
20	1	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	37C +/- 1C	20h +/- 2h
20	1	Ceftazidime TAZ	<=	0.5	0.06	0.5	1	MIC	37C +/- 1C	20h +/- 2h
20	1	Chloramphenicol CHL	<=	8	2	8	1	MIC	37C +/- 1C	20h +/- 2h
20	1	Ciprofloxacin CIP	<=	0.015	0.004	0.016	1	MIC	37C +/- 1C	20h +/- 2h
20	1	Colistin COL	<=	1	0.25	2	1	MIC	37C +/- 1C	20h +/- 2h
20	1	Gentamicin GEN	<=	0.5	0.25	1	1	MIC	37C +/- 1C	20h +/- 2h
20	1	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	37C +/- 1C	20h +/- 2h
20	1	Nalidixic acid NAL	<=	4	1	4	1	MIC	37C +/- 1C	20h +/- 2h
20	1	Sulfamethoxazole SMX	=	16	8	32	1	MIC	37C +/- 1C	20h +/- 2h
20	1	Tetracycline TET	<=	2	0.5	2	1	MIC	37C +/- 1C	20h +/- 2h
20	1	Tigecycline TGC	<=	0.25	0.03	0.25	1	MIC	37C +/- 1C	20h +/- 2h
20	1	Trimethoprim TMP	=	0.5	0.5	2	1	MIC	37C +/- 1C	20h +/- 2h
20	2	Cefepime FEP	<=	0.06	0.016	0.12	1	MIC	37C +/- 1C	20h +/- 2h
20	2	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	37C +/- 1C	20h +/- 2h
20	2	Cefoxitin FOX	=	2	2	8	1	MIC	37C +/- 1C	20h +/- 2h
20	2	Ceftazidime TAZ	<=	0.25	0.06	0.5	1	MIC	37C +/- 1C	20h +/- 2h
20	2	Ertapenem ETP	<=	0.015	0.004	0.016	1	MIC	37C +/- 1C	20h +/- 2h
20	2	Imipenem IMI	<=	0.12	0.06	0.25	1	MIC	37C +/- 1C	20h +/- 2h
20	2	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	37C +/- 1C	20h +/- 2h
21	1	Ampicillin AMP	=	4	2	8	1	MIC	36	24
21	1	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	36	24
21	1	Ceftazidime TAZ	<=	0.5	0.06	0.5	1	MIC	36	24
21	1	Chloramphenicol CHL	<=	8	2	8	1	MIC	36	24
21	1	Ciprofloxacin CIP	<=	0.015	0.004	0.016	1	MIC	36	24
21	1	Colistin COL	<=	1	0.25	2	1	MIC	36	24
21	1	Gentamicin GEN	<=	0.5	0.25	1	1	MIC	36	24
21	1	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	36	24
21	1	Nalidixic acid NAL	<=	4	1	4	1	MIC	36	24
21	1	Sulfamethoxazole SMX	=	16	8	32	1	MIC	36	24
21	1	Tetracycline TET	<=	2	0.5	2	1	MIC	36	24

Lab no.	Panel	Antimicrobial	Operator	Value	Low limit	High limit	Mark	Method	Temperature	Time
21	1	Tigecycline TGC	<=	0.25	0.03	0.25	1	MIC	36	24
21	1	Trimethoprim TMP	=	0.5	0.5	2	1	MIC	36	24
21	2	Cefepime FEP	<=	0.06	0.016	0.12	1	MIC	36	24
21	2	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	36	24
21	2	Cefoxitin FOX	=	4	2	8	1	MIC	36	24
21	2	Ceftazidime TAZ	<=	0.25	0.06	0.5	1	MIC	36	24
21	2	Ertapenem ETP	<=	0.015	0.004	0.016	1	MIC	36	24
21	2	Imipenem IMI	<=	0.12	0.06	0.25	1	MIC	36	24
21	2	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	36	24
22	1	Ampicillin AMP	=	4	2	8	1	MIC	36	20
22	1	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	36	20
22	1	Ceftazidime TAZ	<=	0.5	0.06	0.5	1	MIC	36	20
22	1	Chloramphenicol CHL	<=	8	2	8	1	MIC	36	20
22	1	Ciprofloxacin CIP	<=	0.015	0.004	0.016	1	MIC	36	20
22	1	Colistin COL	<=	1	0.25	2	1	MIC	36	20
22	1	Gentamicin GEN	=	1	0.25	1	1	MIC	36	20
22	1	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	36	20
22	1	Nalidixic acid NAL	<=	4	1	4	1	MIC	36	20
22	1	Sulfamethoxazole SMX	=	32	8	32	1	MIC	36	20
22	1	Tetracycline TET	<=	2	0.5	2	1	MIC	36	20
22	1	Tigecycline TGC	<=	0.25	0.03	0.25	1	MIC	36	20
22	1	Trimethoprim TMP	=	0.5	0.5	2	1	MIC	36	20
22	2	Cefepime FEP	<=	0.06	0.016	0.12	1	MIC	36	20
22	2	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	36	20
22	2	Cefoxitin FOX	=	2	2	8	1	MIC	36	20
22	2	Ceftazidime TAZ	<=	0.25	0.06	0.5	1	MIC	36	20
22	2	Ertapenem ETP	<=	0.015	0.004	0.016	1	MIC	36	20
22	2	Imipenem IMI	<=	0.12	0.06	0.25	1	MIC	36	20
22	2	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	36	20
23	1	Ampicillin AMP	=	4	2	8	1	MIC		
23	1	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC		
23	1	Ceftazidime TAZ	<=	0.5	0.06	0.5	1	MIC		
23	1	Chloramphenicol CHL	<=	8	2	8	1	MIC		
23	1	Ciprofloxacin CIP	<=	0.015	0.004	0.016	1	MIC		
23	1	Colistin COL	<=	1	0.25	2	1	MIC		
23	1	Gentamicin GEN	<=	0.5	0.25	1	1	MIC		
23	1	Meropenem MER	<=	0.03	0.008	0.06	1	MIC		
23	1	Nalidixic acid NAL	<=	4	1	4	1	MIC		
23	1	Sulfamethoxazole SMX	=	16	8	32	1	MIC		
23	1	Tetracycline TET	<=	2	0.5	2	1	MIC		
23	1	Tigecycline TGC	<=	0.25	0.03	0.25	1	MIC		
23	1	Trimethoprim TMP	=	0.5	0.5	2	1	MIC		
23	2	Cefepime FEP	=	0.06	0.016	0.12	1	MIC		
23	2	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC		
23	2	Cefoxitin FOX	=	2	2	8	1	MIC		
23	2	Ceftazidime TAZ	=	0.25	0.06	0.5	1	MIC		
23	2	Ertapenem ETP	=	0.015	0.004	0.016	1	MIC		
23	2	Imipenem IMI	=	0.25	0.06	0.25	1	MIC		
23	2	Meropenem MER	=	0.03	0.008	0.06	1	MIC		
25	1	Ampicillin AMP	=	4	2	8	1	MIC	35	16 - 20
25	1	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	35	16 - 20
25	1	Ceftazidime TAZ	<=	0.5	0.06	0.5	1	MIC	35	16 - 20
25	1	Chloramphenicol CHL	<=	8	2	8	1	MIC	35	16 - 20
25	1	Ciprofloxacin CIP	<=	0.015	0.004	0.016	1	MIC	35	16 - 20
25	1	Colistin COL	<=	1	0.25	2	1	MIC	35	16 - 20
25	1	Gentamicin GEN	=	2	0.25	1	0	MIC	35	16 - 20
25	1	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	35	16 - 20
25	1	Nalidixic acid NAL	<=	4	1	4	1	MIC	35	16 - 20
25	1	Sulfamethoxazole SMX	<=	8	8	32	1	MIC	35	16 - 20
25	1	Tetracycline TET	<=	2	0.5	2	1	MIC	35	16 - 20
25	1	Tigecycline TGC	<=	0.25	0.03	0.25	1	MIC	35	16 - 20
25	1	Trimethoprim TMP	=	0.5	0.5	2	1	MIC	35	16 - 20
25	2	Cefepime FEP	<=	0.06	0.016	0.12	1	MIC	35	16 - 20
25	2	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	35	16 - 20
25	2	Cefoxitin FOX	=	2	2	8	1	MIC	35	16 - 20
25	2	Ceftazidime TAZ	<=	0.25	0.06	0.5	1	MIC	35	16 - 20
25	2	Ertapenem ETP	<=	0.015	0.004	0.016	1	MIC	35	16 - 20
25	2	Imipenem IMI	=	0.25	0.06	0.25	1	MIC	35	16 - 20
25	2	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	35	16 - 20
26	1	Ampicillin AMP	=	2	2	8	1	MIC	37	18
26	1	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	37	18
26	1	Ceftazidime TAZ	<=	0.5	0.06	0.5	1	MIC	37	18
26	1	Chloramphenicol CHL	<=	8	2	8	1	MIC	37	18
26	1	Ciprofloxacin CIP	<=	0.015	0.004	0.016	1	MIC	37	18
26	1	Colistin COL	<=	1	0.25	2	1	MIC	37	18

Lab no.	Panel	Antimicrobial	Operator	Value	Low limit	High limit	Mark	Method	Temperature	Time
26	1	Gentamicin GEN	=	1	0.25	1	1	MIC	37	18
26	1	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	37	18
26	1	Nalidixic acid NAL	<=	4	1	4	1	MIC	37	18
26	1	Sulfamethoxazole SMX	=	64	8	32	0	MIC	37	18
26	1	Tetracycline TET	<=	2	0.5	2	1	MIC	37	18
26	1	Tigecycline TGC	<=	0.25	0.03	0.25	1	MIC	37	18
26	1	Trimethoprim TMP	=	0.5	0.5	2	1	MIC	37	18
29	1	Ampicillin AMP	=	4	2	8	1	MIC	37	18
29	1	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	37	18
29	1	Ceftazidime TAZ	<=	0.5	0.06	0.5	1	MIC	37	18
29	1	Chloramphenicol CHL	<=	8	2	8	1	MIC	37	18
29	1	Ciprofloxacin CIP	<=	0.015	0.004	0.016	1	MIC	37	18
29	1	Colistin COL	<=	1	0.25	2	1	MIC	37	18
29	1	Gentamicin GEN	<=	0.5	0.25	1	1	MIC	37	18
29	1	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	37	18
29	1	Nalidixic acid NAL	<=	4	1	4	1	MIC	37	18
29	1	Sulfamethoxazole SMX	=	16	8	32	1	MIC	37	18
29	1	Tetracycline TET	<=	2	0.5	2	1	MIC	37	18
29	1	Tigecycline TGC	<=	0.25	0.03	0.25	1	MIC	37	18
29	1	Trimethoprim TMP	=	1	0.5	2	1	MIC	37	18
29	2	Cefepime FEP	<=	0.06	0.016	0.12	1	MIC	37	18
29	2	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	37	18
29	2	Cefoxitin FOX	=	2	2	8	1	MIC	37	18
29	2	Ceftazidime TAZ	<=	0.25	0.06	0.5	1	MIC	37	18
29	2	Ertapenem ETP	<=	0.015	0.004	0.016	1	MIC	37	18
29	2	Imipenem IMI	<=	0.12	0.06	0.25	1	MIC	37	18
29	2	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	37	18
30	1	Ampicillin AMP	=	4	2	8	1	MIC		
30	1	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC		
30	1	Ceftazidime TAZ	<=	0.5	0.06	0.5	1	MIC		
30	1	Chloramphenicol CHL	<=	8	2	8	1	MIC		
30	1	Ciprofloxacin CIP	<=	0.015	0.004	0.016	1	MIC		
30	1	Colistin COL	<=	1	0.25	2	1	MIC		
30	1	Gentamicin GEN	<=	0.5	0.25	1	1	MIC		
30	1	Meropenem MER	<=	0.03	0.008	0.06	1	MIC		
30	1	Nalidixic acid NAL	<=	4	1	4	1	MIC		
30	1	Sulfamethoxazole SMX	=	16	8	32	1	MIC		
30	1	Tetracycline TET	<=	2	0.5	2	1	MIC		
30	1	Tigecycline TGC	<=	0.25	0.03	0.25	1	MIC		
30	1	Trimethoprim TMP	=	0.5	0.5	2	1	MIC		
30	2	Cefepime FEP	<=	0.06	0.016	0.12	1	MIC		
30	2	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC		
30	2	Cefoxitin FOX	=	2	2	8	1	MIC		
30	2	Ceftazidime TAZ	<=	0.25	0.06	0.5	1	MIC		
30	2	Ertapenem ETP	<=	0.015	0.004	0.016	1	MIC		
30	2	Imipenem IMI	<=	0.12	0.06	0.25	1	MIC		
30	2	Meropenem MER	<=	0.03	0.008	0.06	1	MIC		
32	1	Ampicillin AMP	=	8	2	8	1	MIC	37º +/- 1	18+/-2h
32	1	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	37º +/- 1	18+/-2h
32	1	Ceftazidime TAZ	<=	0.5	0.06	0.5	1	MIC	37º +/- 1	18+/-2h
32	1	Chloramphenicol CHL	<=	8	2	8	1	MIC	37º +/- 1	18+/-2h
32	1	Ciprofloxacin CIP	<=	0.15	0.004	0.016	1	MIC	37º +/- 1	18+/-2h
32	1	Colistin COL	<=	1	0.25	2	1	MIC	37º +/- 1	18+/-2h
32	1	Gentamicin GEN	<=	0.5	0.25	1	1	MIC	37º +/- 1	18+/-2h
32	1	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	37º +/- 1	18+/-2h
32	1	Nalidixic acid NAL	<=	4	1	4	1	MIC	37º +/- 1	18+/-2h
32	1	Sulfamethoxazole SMX	=	16	8	32	1	MIC	37º +/- 1	18+/-2h
32	1	Tetracycline TET	<=	2	0.5	2	1	MIC	37º +/- 1	18+/-2h
32	1	Tigecycline TGC	<=	0.25	0.03	0.25	1	MIC	37º +/- 1	18+/-2h
32	1	Trimethoprim TMP	=	0.5	0.5	2	1	MIC	37º +/- 1	18+/-2h
32	2	Cefepime FEP	<=	0.06	0.016	0.12	1	MIC	37º +/- 1	18+/-2h
32	2	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	37º +/- 1	18+/-2h
32	2	Cefoxitin FOX	=	8	2	8	1	MIC	37º +/- 1	18+/-2h
32	2	Ceftazidime TAZ	<=	0.25	0.06	0.5	1	MIC	37º +/- 1	18+/-2h
32	2	Ertapenem ETP	<=	0.015	0.004	0.016	1	MIC	37º +/- 1	18+/-2h
32	2	Imipenem IMI	<=	0.12	0.06	0.25	1	MIC	37º +/- 1	18+/-2h
32	2	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	37º +/- 1	18+/-2h
33	1	Ampicillin AMP	=	4	2	8	1	MIC	35	16-18
33	1	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	35	16-18
33	1	Ceftazidime TAZ	<=	0.5	0.06	0.5	1	MIC	35	16-18
33	1	Chloramphenicol CHL	<=	8	2	8	1	MIC	35	16-18
33	1	Ciprofloxacin CIP	<=	0.015	0.004	0.016	1	MIC	35	16-18
33	1	Colistin COL	<=	1	0.25	2	1	MIC	35	16-18
33	1	Gentamicin GEN	<=	0.5	0.25	1	1	MIC	35	16-18
33	1	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	35	16-18

Lab no.	Panel	Antimicrobial	Operator	Value	Low limit	High limit	Mark	Method	Temperature	Time
33	1	Nalidixic acid NAL	<=	4	1	4	1	MIC	35	16-18
33	1	Sulfamethoxazole SMX	=	32	8	32	1	MIC	35	16-18
33	1	Tetracycline TET	<=	2	0.5	2	1	MIC	35	16-18
33	1	Tigecycline TGC	<=	0.25	0.03	0.25	1	MIC	35	16-18
33	1	Trimethoprim TMP	=	1	0.5	2	1	MIC	35	16-18
33	2	Cefepime FEP	=	0.12	0.016	0.12	1	MIC	35	16-18
33	2	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	35	16-18
33	2	Cefoxitin FOX	=	4	2	8	1	MIC	35	16-18
33	2	Ceftazidime TAZ	<=	0.25	0.06	0.5	1	MIC	35	16-18
33	2	Ertapenem ETP	<=	0.015	0.004	0.016	1	MIC	35	16-18
33	2	Imipenem IMI	<=	0.012	0.06	0.25	0	MIC	35	16-18
33	2	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	35	16-18
34	1	Ampicillin AMP	=	4	2	8	1	MIC	37	24
34	1	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	37	24
34	1	Ceftazidime TAZ	<=	0.5	0.06	0.5	1	MIC	37	24
34	1	Chloramphenicol CHL	<=	8	2	8	1	MIC	37	24
34	1	Ciprofloxacin CIP	<=	0.015	0.004	0.016	1	MIC	37	24
34	1	Colistin COL	<=	1	0.25	2	1	MIC	37	24
34	1	Gentamicin GEN	<=	0.5	0.25	1	1	MIC	37	24
34	1	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	37	24
34	1	Nalidixic acid NAL	<=	4	1	4	1	MIC	37	24
34	1	Sulfamethoxazole SMX	=	16	8	32	1	MIC	37	24
34	1	Tetracycline TET	<=	2	0.5	2	1	MIC	37	24
34	1	Tigecycline TGC	<=	0.25	0.03	0.25	1	MIC	37	24
34	1	Trimethoprim TMP	=	0.5	0.5	2	1	MIC	37	24
34	2	Cefepime FEP	<=	0.06	0.016	0.12	1	MIC	37	24
34	2	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	37	24
34	2	Cefoxitin FOX	=	4	2	8	1	MIC	37	24
34	2	Ceftazidime TAZ	<=	0.25	0.06	0.5	1	MIC	37	24
34	2	Ertapenem ETP	<=	0.015	0.004	0.016	1	MIC	37	24
34	2	Imipenem IMI	<=	0.012	0.06	0.25	0	MIC	37	24
34	2	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	37	24
36	1	Ampicillin AMP	=	8	2	8	1	MIC	35	18-24
36	1	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	35	18-24
36	1	Ceftazidime TAZ	<=	0.5	0.06	0.5	1	MIC	35	18-24
36	1	Chloramphenicol CHL	<=	8	2	8	1	MIC	35	18-24
36	1	Ciprofloxacin CIP	<=	0.015	0.004	0.016	1	MIC	35	18-24
36	1	Colistin COL	<=	1	0.25	2	1	MIC	35	18-24
36	1	Gentamicin GEN	<=	0.5	0.25	1	1	MIC	35	18-24
36	1	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	35	18-24
36	1	Nalidixic acid NAL	<=	4	1	4	1	MIC	35	18-24
36	1	Sulfamethoxazole SMX	<=	8	8	32	1	MIC	35	18-24
36	1	Tetracycline TET	<=	2	0.5	2	1	MIC	35	18-24
36	1	Tigecycline TGC	<=	0.25	0.03	0.25	1	MIC	35	18-24
36	1	Trimethoprim TMP	=	1	0.5	2	1	MIC	35	18-24
36	2	Cefepime FEP	<=	0.06	0.016	0.12	1	MIC	35	18-24
36	2	Cefotaxime FOT	<=	0.06	0.03	0.12	1	MIC	35	18-24
36	2	Cefoxitin FOX	=	4	2	8	1	MIC	35	18-24
36	2	Ceftazidime TAZ	=	0.25	0.06	0.5	1	MIC	35	18-24
36	2	Ertapenem ETP	<=	0.015	0.004	0.016	1	MIC	35	18-24
36	2	Imipenem IMI	<=	0.12	0.06	0.25	1	MIC	35	18-24
36	2	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	35	18-24
37	1	Ampicillin AMP	=	4	2	8	1	MIC	37ºC	18-24hours
37	1	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	37ºC	18-24hours
37	1	Ceftazidime TAZ	<=	0.5	0.06	0.5	1	MIC	37ºC	18-24hours
37	1	Chloramphenicol CHL	<=	8	2	8	1	MIC	37ºC	18-24hours
37	1	Ciprofloxacin CIP	<=	0.015	0.004	0.016	1	MIC	37ºC	18-24hours
37	1	Colistin COL	<=	1	0.25	2	1	MIC	37ºC	18-24hours
37	1	Gentamicin GEN	=	1	0.25	1	1	MIC	37ºC	18-24hours
37	1	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	37ºC	18-24hours
37	1	Nalidixic acid NAL	<=	4	1	4	1	MIC	37ºC	18-24hours
37	1	Sulfamethoxazole SMX	=	32	8	32	1	MIC	37ºC	18-24hours
37	1	Tetracycline TET	<=	2	0.5	2	1	MIC	37ºC	18-24hours
37	1	Tigecycline TGC	<=	0.25	0.03	0.25	1	MIC	37ºC	18-24hours
37	1	Trimethoprim TMP	=	0.5	0.5	2	1	MIC	37ºC	18-24hours
39	1	Ampicillin AMP	=	4	2	8	1	MIC		
39	1	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC		
39	1	Ceftazidime TAZ	<=	0.5	0.06	0.5	1	MIC		
39	1	Chloramphenicol CHL	<=	8	2	8	1	MIC		
39	1	Ciprofloxacin CIP	<=	0.015	0.004	0.016	1	MIC		
39	1	Colistin COL	<=	1	0.25	2	1	MIC		
39	1	Gentamicin GEN	<=	0.5	0.25	1	1	MIC		
39	1	Meropenem MER	<=	0.03	0.008	0.06	1	MIC		
39	1	Nalidixic acid NAL	<=	4	1	4	1	MIC		
39	1	Sulfamethoxazole SMX	=	32	8	32	1	MIC		

Lab no.	Panel	Antimicrobial	Operator	Value	Low limit	High limit	Mark	Method	Temperature	Time
39	1	Tetracycline TET	<=	2	0.5	2	1	MIC		
39	1	Tigecycline TGC	<=	0.25	0.03	0.25	1	MIC		
39	1	Trimethoprim TMP	=	0.5	0.5	2	1	MIC		
39	2	Cefepime FEP	<=	0.06	0.016	0.12	1	MIC		
39	2	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC		
39	2	Cefoxitin FOX	=	4	2	8	1	MIC		
39	2	Ceftazidime TAZ	<=	0.25	0.06	0.5	1	MIC		
39	2	Ertapenem ETP	<=	0.015	0.004	0.016	1	MIC		
39	2	Imipenem IMI	<=	0.12	0.06	0.25	1	MIC		
39	2	Meropenem MER	<=	0.03	0.008	0.06	1	MIC		
40	1	Ampicillin AMP	=	2	2	8	1	MIC	37	20
40	1	Cefotaxime FOT	=	0.12	0.03	0.12	1	MIC	37	20
40	1	Ceftazidime TAZ	=	0.5	0.06	0.5	1	MIC	37	20
40	1	Chloramphenicol CHL	=	8	2	8	1	MIC	37	20
40	1	Ciprofloxacin CIP	=	0.015	0.004	0.016	1	MIC	37	20
40	1	Colistin COL	=	1	0.25	2	1	MIC	37	20
40	1	Gentamicin GEN	=	0.5	0.25	1	1	MIC	37	20
40	1	Meropenem MER	=	0.03	0.008	0.06	1	MIC	37	20
40	1	Nalidixic acid NAL	=	4	1	4	1	MIC	37	20
40	1	Sulfamethoxazole SMX	=	16	8	32	1	MIC	37	20
40	1	Tetracycline TET	=	2	0.5	2	1	MIC	37	20
40	1	Tigecycline TGC	=	0.25	0.03	0.25	1	MIC	37	20
40	1	Trimethoprim TMP	=	0.5	0.5	2	1	MIC	37	20
40	2	Cefepime FEP	=	0.06	0.016	0.12	1	MIC	37	20
40	2	Cefotaxime FOT	=	0.12	0.03	0.12	1	MIC	37	20
40	2	Cefoxitin FOX	=	4	2	8	1	MIC	37	20
40	2	Ceftazidime TAZ	=	0.5	0.06	0.5	1	MIC	37	20
40	2	Ertapenem ETP	=	0.015	0.004	0.016	1	MIC	37	20
40	2	Imipenem IMI	=	0.12	0.06	0.25	1	MIC	37	20
40	2	Meropenem MER	=	0.03	0.008	0.06	1	MIC	37	20
42	1	Ampicillin AMP	=	4	2	8	1	MIC	37°C	24 h
42	1	Cefotaxime FOT	=	0.25	0.03	0.12	0	MIC	37°C	24 h
42	1	Ceftazidime TAZ	<=	0.5	0.06	0.5	1	MIC	37°C	24 h
42	1	Chloramphenicol CHL	<=	8	2	8	1	MIC	37°C	24 h
42	1	Ciprofloxacin CIP	<=	0.015	0.004	0.016	1	MIC	37°C	24 h
42	1	Colistin COL	<=	1	0.25	2	1	MIC	37°C	24 h
42	1	Gentamicin GEN	<=	0.5	0.25	1	1	MIC	37°C	24 h
42	1	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	37°C	24 h
42	1	Nalidixic acid NAL	<=	4	1	4	1	MIC	37°C	24 h
42	1	Sulfamethoxazole SMX	=	8	8	32	1	MIC	37°C	24 h
42	1	Tetracycline TET	<=	2	0.5	2	1	MIC	37°C	24 h
42	1	Tigecycline TGC	<=	0.25	0.03	0.25	1	MIC	37°C	24 h
42	1	Trimethoprim TMP	=	0.5	0.5	2	1	MIC	37°C	24 h
42	2	Cefepime FEP	=	0.06	0.016	0.12	1	MIC	37°C	24 h
42	2	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	37°C	24 h
42	2	Cefoxitin FOX	=	4	2	8	1	MIC	37°C	24 h
42	2	Ceftazidime TAZ	<=	0.25	0.06	0.5	1	MIC	37°C	24 h
42	2	Ertapenem ETP	<=	0.015	0.004	0.016	1	MIC	37°C	24 h
42	2	Imipenem IMI	<=	0.12	0.06	0.25	1	MIC	37°C	24 h
42	2	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	37°C	24 h
45	1	Ampicillin AMP	=	8	2	8	1	MIC	36	18-22
45	1	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	36	18-22
45	1	Ceftazidime TAZ	<=	0.5	0.06	0.5	1	MIC	36	18-22
45	1	Chloramphenicol CHL	<=	8	2	8	1	MIC	36	18-22
45	1	Ciprofloxacin CIP	<=	0.015	0.004	0.016	1	MIC	36	18-22
45	1	Colistin COL	<=	1	0.25	2	1	MIC	36	18-22
45	1	Gentamicin GEN	<=	0.5	0.25	1	1	MIC	36	18-22
45	1	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	36	18-22
45	1	Nalidixic acid NAL	<=	4	1	4	1	MIC	36	18-22
45	1	Sulfamethoxazole SMX	=	16	8	32	1	MIC	36	18-22
45	1	Tetracycline TET	<=	2	0.5	2	1	MIC	36	18-22
45	1	Tigecycline TGC	<=	0.25	0.03	0.25	1	MIC	36	18-22
45	1	Trimethoprim TMP	=	0.5	0.5	2	1	MIC	36	18-22
45	2	Cefepime FEP	<=	0.06	0.016	0.12	1	MIC	36	18-22
45	2	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	36	18-22
45	2	Cefoxitin FOX	=	4	2	8	1	MIC	36	18-22
45	2	Ceftazidime TAZ	<=	0.25	0.06	0.5	1	MIC	36	18-22
45	2	Ertapenem ETP	<=	0.015	0.004	0.016	1	MIC	36	18-22
45	2	Imipenem IMI	<=	0.12	0.06	0.25	1	MIC	36	18-22
45	2	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	36	18-22
56	1	Ampicillin AMP	=	4	2	8	1	MIC	35	20
56	1	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	35	20
56	1	Ceftazidime TAZ	<=	0.5	0.06	0.5	1	MIC	35	20
56	1	Chloramphenicol CHL	<=	8	2	8	1	MIC	35	20
56	1	Ciprofloxacin CIP	<=	0.015	0.004	0.016	1	MIC	35	20

Lab no.	Panel	Antimicrobial	Operator	Value	Low limit	High limit	Mark	Method	Temperature	Time
56	1	Colistin COL	<=	1	0.25	2	1	MIC	35	20
56	1	Gentamicin GEN	<=	0.5	0.25	1	1	MIC	35	20
56	1	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	35	20
56	1	Nalidixic acid NAL	<=	4	1	4	1	MIC	35	20
56	1	Sulfamethoxazole SMX	=	16	8	32	1	MIC	35	20
56	1	Tetracycline TET	<=	2	0.5	2	1	MIC	35	20
56	1	Tigecycline TGC	<=	0.25	0.03	0.25	1	MIC	35	20
56	1	Trimethoprim TMP	=	0.5	0.5	2	1	MIC	35	20
56	2	Cefepime FEP	<=	0.06	0.016	0.12	1	MIC	35	20
56	2	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	35	20
56	2	Cefoxitin FOX	=	2	2	8	1	MIC	35	20
56	2	Ceftazidime TAZ	<=	0.25	0.06	0.5	1	MIC	35	20
56	2	Ertapenem ETP	<=	0.015	0.004	0.016	1	MIC	35	20
56	2	Imipenem IMI	<=	0.12	0.06	0.25	1	MIC	35	20
56	2	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	35	20
58	1	Ampicillin AMP	=	8	2	8	1	MIC	37	20
58	1	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	37	20
58	1	Ceftazidime TAZ	<=	0.5	0.06	0.5	1	MIC	37	20
58	1	Chloramphenicol CHL	<=	8	2	8	1	MIC	37	20
58	1	Ciprofloxacin CIP	<=	0.015	0.004	0.016	1	MIC	37	20
58	1	Colistin COL	<=	1	0.25	2	1	MIC	37	20
58	1	Gentamicin GEN	<=	0.5	0.25	1	1	MIC	37	20
58	1	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	37	20
58	1	Nalidixic acid NAL	<=	4	1	4	1	MIC	37	20
58	1	Sulfamethoxazole SMX	=	32	8	32	1	MIC	37	20
58	1	Tetracycline TET	<=	2	0.5	2	1	MIC	37	20
58	1	Tigecycline TGC	<=	0.25	0.03	0.25	1	MIC	37	20
58	1	Trimethoprim TMP	=	1	0.5	2	1	MIC	37	20
58	2	Cefepime FEP	<=	0.06	0.016	0.12	1	MIC	37	20
58	2	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	37	20
58	2	Cefoxitin FOX	=	4	2	8	1	MIC	37	20
58	2	Ceftazidime TAZ	<=	0.25	0.06	0.5	1	MIC	37	20
58	2	Ertapenem ETP	<=	0.015	0.004	0.016	1	MIC	37	20
58	2	Imipenem IMI	<=	0.12	0.06	0.25	1	MIC	37	20
58	2	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	37	20
59	1	Ampicillin AMP	=	4	2	8	1	MIC	35	18-24
59	1	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	35	18-24
59	1	Ceftazidime TAZ	<=	0.5	0.06	0.5	1	MIC	35	18-24
59	1	Chloramphenicol CHL	<=	8	2	8	1	MIC	35	18-24
59	1	Ciprofloxacin CIP	<=	0.015	0.004	0.016	1	MIC	35	18-24
59	1	Colistin COL	<=	1	0.25	2	1	MIC	35	18-24
59	1	Gentamicin GEN	<=	0.5	0.25	1	1	MIC	35	18-24
59	1	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	35	18-24
59	1	Nalidixic acid NAL	<=	4	1	4	1	MIC	35	18-24
59	1	Tetracycline TET	<=	2	0.5	2	1	MIC	35	18-24
59	1	Tigecycline TGC	<=	0.25	0.03	0.25	1	MIC	35	18-24
59	1	Trimethoprim TMP	=	0.5	0.5	2	1	MIC	35	18-24
59	2	Cefepime FEP	<=	0.06	0.016	0.12	1	MIC	35	18-24
59	2	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	35	18-24
59	2	Cefoxitin FOX	=	2	2	8	1	MIC	35	18-24
59	2	Ceftazidime TAZ	=	0.25	0.06	0.5	1	MIC	35	18-24
59	2	Ertapenem ETP	<=	0.015	0.004	0.016	1	MIC	35	18-24
59	2	Imipenem IMI	=	0.25	0.06	0.25	1	MIC	35	18-24
59	2	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	35	18-24
60	1	Ampicillin AMP	=	4	2	8	1	MIC	35-37	18-20
60	1	Cefotaxime FOT	<=	0.25	0.03	0.12	1	MIC	35-37	18-20
60	1	Ceftazidime TAZ	<=	0.5	0.06	0.5	1	MIC	35-37	18-20
60	1	Chloramphenicol CHL	<=	8	2	8	1	MIC	35-37	18-20
60	1	Ciprofloxacin CIP	<=	0.015	0.004	0.016	1	MIC	35-37	18-20
60	1	Colistin COL	<=	1	0.25	2	1	MIC	35-37	18-20
60	1	Gentamicin GEN	<=	0.5	0.25	1	1	MIC	35-37	18-20
60	1	Meropenem MER	<=	0.03	0.008	0.06	1	MIC	35-37	18-20
60	1	Nalidixic acid NAL	<=	4	1	4	1	MIC	35-37	18-20
60	1	Sulfamethoxazole SMX	<=	8	8	32	1	MIC	35-37	18-20
60	1	Tetracycline TET	<=	2	0.5	2	1	MIC	35-37	18-20
60	1	Tigecycline TGC	<=	0.25	0.03	0.25	1	MIC	35-37	18-20
60	1	Trimethoprim TMP	<=	0.25	0.5	2	0	MIC	35-37	18-20

MIC: Microbroth dilution
AGA: Agar dilution

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

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

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

MIC: Microbroth dilution
AGA: Agar dilution

Salmonella - expected and obtained interpretation

Antimicrobial	Strain	Panel	Expected	% R	% S	No. correct	No. incorrect
Ampicillin AMP	EURL S-12.1	Panel 1	R	100	0	31	0
	EURL S-12.2	Panel 1	R	100	0	31	0
	EURL S-12.3	Panel 1	R	100	0	31	0
	EURL S-12.4	Panel 1	S	3	97	30	1
	EURL S-12.5	Panel 1	S	0	100	31	0
	EURL S-12.6	Panel 1	R	100	0	31	0
	EURL S-12.7	Panel 1	R	100	0	31	0
	EURL S-12.8	Panel 1	R	97	3	30	1
Azithromycin AZI	EURL S-12.1	Panel 1	R	100	0	24	0
	EURL S-12.2	Panel 1	S	4	96	22	1
	EURL S-12.3	Panel 1	S	0	100	23	0
	EURL S-12.4	Panel 1	S	0	100	23	0
	EURL S-12.5	Panel 1	S	0	100	23	0
	EURL S-12.6	Panel 1	S	0	100	23	0
	EURL S-12.7	Panel 1	R	100	0	24	0
	EURL S-12.8	Panel 1	R	100	0	23	0
Cefotaxime FOT	EURL S-12.1	Panel 1	R	100	0	31	0
	EURL S-12.2	Panel 1	R	100	0	31	0
	*EURL S-12.4**	*Panel 1**	*R**	*40**	*60**	*18**	*12**
	EURL S-12.3	Panel 1	R	100	0	31	0
	EURL S-12.5	Panel 1	S	0	100	31	0
	EURL S-12.6	Panel 1	S	0	100	31	0
	EURL S-12.7	Panel 1	R	100	0	31	0
	EURL S-12.8	Panel 1	R	100	0	31	0
	EURL S-12.1	Panel 2	R	100	0	31	0
	EURL S-12.2	Panel 2	R	100	0	31	0
	EURL S-12.3	Panel 2	R	100	0	31	0
	*EURL S-12.4**	*Panel 2**	*R**	*56**	*44**	*14**	*11**
	EURL S-12.7	Panel 2	R	100	0	31	0
	EURL S-12.8	Panel 2	R	100	0	31	0
Cefoxitin FOX	EURL S-12.1	Panel 2	R	100	0	31	0
	EURL S-12.2	Panel 2	S	3	97	30	1
	EURL S-12.3	Panel 2	S	3	97	30	1
	EURL S-12.4	Panel 2	R	100	0	26	0
	EURL S-12.7	Panel 2	S	3	97	30	1
	EURL S-12.8	Panel 2	R	100	0	31	0
Ceftazidime TAZ	EURL S-12.1	Panel 1	R	100	0	31	0
	EURL S-12.2	Panel 1	S	3	97	30	1
	EURL S-12.3	Panel 1	R	100	0	31	0
	EURL S-12.4	Panel 1	R	80	20	24	6
	EURL S-12.5	Panel 1	S	0	100	31	0
	EURL S-12.6	Panel 1	S	0	100	31	0
	*EURL S-12.7**	*Panel 1**	*S**	*74**	*26**	*23**	*8**
	EURL S-12.8	Panel 1	R	100	0	31	0
	EURL S-12.1	Panel 2	R	100	0	31	0
	EURL S-12.2	Panel 2	S	0	100	31	0
	EURL S-12.3	Panel 2	R	100	0	31	0
	EURL S-12.4	Panel 2	R	88	12	22	3
	*EURL S-12.7**	*Panel 2**	*S**	*74**	*26**	*23**	*8**
	EURL S-12.8	Panel 2	R	100	0	31	0
Chloramphenicol CHL	EURL S-12.1	Panel 1	R	100	0	31	0
	EURL S-12.2	Panel 1	S	0	100	31	0
	EURL S-12.3	Panel 1	S	0	100	31	0
	EURL S-12.4	Panel 1	S	0	100	31	0
	EURL S-12.5	Panel 1	S	0	100	31	0
	EURL S-12.6	Panel 1	S	0	100	31	0
	EURL S-12.7	Panel 1	R	100	0	31	0
	EURL S-12.8	Panel 1	R	97	3	30	1

Antimicrobial	Strain	Panel	Expected	% R	% S	No. correct	No. incorrect
Ciprofloxacin CIP	EURL S-12.1	Panel 1	R	97	3	30	1
	EURL S-12.2	Panel 1	R	97	3	30	1
	EURL S-12.3	Panel 1	R	100	0	31	0
	EURL S-12.4	Panel 1	S	0	100	31	0
	EURL S-12.5	Panel 1	S	0	100	31	0
	EURL S-12.6	Panel 1	R	100	0	31	0
	EURL S-12.7	Panel 1	S	0	100	31	0
	EURL S-12.8	Panel 1	R	100	0	31	0
Colistin COL	EURL S-12.1	Panel 1	S	0	100	31	0
	EURL S-12.2	Panel 1	S	0	100	31	0
	EURL S-12.3	Panel 1	S	0	100	31	0
	EURL S-12.4	Panel 1	S	0	100	31	0
	*EURL S-12.5**	*Panel 1**	*R**	*40**	*60**	*18**	*12**
	EURL S-12.6	Panel 1	S	0	100	31	0
	EURL S-12.7	Panel 1	S	0	100	31	0
	EURL S-12.8	Panel 1	S	0	100	31	0
Ertapenem ETP	EURL S-12.1	Panel 2	R	100	0	31	0
	EURL S-12.2	Panel 2	S	0	100	31	0
	EURL S-12.3	Panel 2	S	0	100	31	0
	EURL S-12.4	Panel 2	S	0	100	26	0
	EURL S-12.7	Panel 2	S	0	100	31	0
	EURL S-12.8	Panel 2	R	100	0	31	0
Gentamicin GEN	EURL S-12.1	Panel 1	S	0	100	31	0
	EURL S-12.2	Panel 1	S	0	100	31	0
	EURL S-12.3	Panel 1	S	0	100	31	0
	EURL S-12.4	Panel 1	S	0	100	31	0
	EURL S-12.5	Panel 1	S	0	100	31	0
	EURL S-12.6	Panel 1	R	100	0	31	0
	EURL S-12.7	Panel 1	S	0	100	31	0
	EURL S-12.8	Panel 1	R	100	0	31	0
Imipenem IMI	EURL S-12.1	Panel 2	R	90	10	27	3
	EURL S-12.2	Panel 2	S	0	100	31	0
	EURL S-12.3	Panel 2	S	0	100	31	0
	EURL S-12.4	Panel 2	S	0	100	26	0
	EURL S-12.7	Panel 2	S	0	100	31	0
	EURL S-12.8	Panel 2	R	97	3	30	1
Meropenem MER	EURL S-12.1	Panel 1	R	100	0	31	0
	EURL S-12.2	Panel 1	S	0	100	31	0
	EURL S-12.3	Panel 1	S	0	100	30	0
	EURL S-12.4	Panel 1	S	0	100	31	0
	EURL S-12.5	Panel 1	S	0	100	31	0
	EURL S-12.6	Panel 1	S	0	100	31	0
	EURL S-12.7	Panel 1	S	0	100	31	0
	EURL S-12.8	Panel 1	R	100	0	31	0
	EURL S-12.1	Panel 2	R	100	0	31	0
	EURL S-12.2	Panel 2	S	0	100	31	0
	EURL S-12.3	Panel 2	S	0	100	31	0
	EURL S-12.4	Panel 2	S	0	100	26	0
	EURL S-12.7	Panel 2	S	0	100	31	0
	EURL S-12.8	Panel 2	R	100	0	31	0
Nalidixic acid NAL	EURL S-12.1	Panel 1	R	100	0	31	0
	EURL S-12.2	Panel 1	R	100	0	31	0
	EURL S-12.3	Panel 1	R	100	0	31	0
	EURL S-12.4	Panel 1	S	0	100	31	0
	EURL S-12.5	Panel 1	S	0	100	31	0
	EURL S-12.6	Panel 1	R	100	0	31	0
	EURL S-12.7	Panel 1	S	0	100	31	0
	EURL S-12.8	Panel 1	R	100	0	31	0

Antimicrobial	Strain	Panel	Expected	% R	% S	No. correct	No. incorrect
Sulfamethoxazole SMX	EURL S-12.1	Panel 1	R	100	0	31	0
	EURL S-12.2	Panel 1	S	0	100	31	0
	EURL S-12.3	Panel 1	R	100	0	31	0
	EURL S-12.4	Panel 1	S	10	90	28	3
	EURL S-12.5	Panel 1	S	0	100	31	0
	EURL S-12.6	Panel 1	R	100	0	31	0
	EURL S-12.7	Panel 1	R	100	0	31	0
	EURL S-12.8	Panel 1	R	90	10	28	3
Temocillin TRM	EURL S-12.1	Panel 2	R	96	4	22	1
	EURL S-12.2	Panel 2	S	4	96	22	1
	EURL S-12.3	Panel 2	S	0	100	23	0
	EURL S-12.4	Panel 2	R	100	0	17	0
	EURL S-12.7	Panel 2	S	0	100	23	0
	EURL S-12.8	Panel 2	R	96	4	22	1
Tetracycline TET	EURL S-12.1	Panel 1	R	100	0	31	0
	EURL S-12.2	Panel 1	R	100	0	31	0
	EURL S-12.3	Panel 1	R	100	0	31	0
	EURL S-12.4	Panel 1	S	0	100	31	0
	EURL S-12.5	Panel 1	S	0	100	31	0
	EURL S-12.6	Panel 1	R	100	0	31	0
	EURL S-12.7	Panel 1	R	100	0	31	0
	EURL S-12.8	Panel 1	S	0	100	31	0
Tigecycline TGC	EURL S-12.1	Panel 1	S	0	100	31	0
	EURL S-12.2	Panel 1	S	0	100	31	0
	EURL S-12.3	Panel 1	S	0	100	31	0
	EURL S-12.4	Panel 1	S	0	100	31	0
	EURL S-12.5	Panel 1	S	0	100	31	0
	EURL S-12.6	Panel 1	S	0	100	31	0
	EURL S-12.7	Panel 1	S	3	97	30	1
	EURL S-12.8	Panel 1	S	0	100	31	0
Trimethoprim TMP	EURL S-12.1	Panel 1	R	100	0	31	0
	EURL S-12.2	Panel 1	S	0	100	31	0
	EURL S-12.3	Panel 1	R	100	0	31	0
	EURL S-12.4	Panel 1	S	0	100	31	0
	EURL S-12.5	Panel 1	S	0	100	31	0
	EURL S-12.6	Panel 1	S	0	100	31	0
	EURL S-12.7	Panel 1	R	100	0	31	0
	EURL S-12.8	Panel 1	S	0	100	31	0

**Strain/antimicrobial-combination excluded from the evaluation*

Campylobacter - expected and obtained interpretation

Antimicrobial	Strain	Expected	% R	% S	No. correct	No. incorrect
Ciprofloxacin, CIP	EURL C-12.1*	S	0	100	23	0
	EURL C-12.2	R	100	0	30	0
	EURL C-12.3	S	0	100	30	0
	EURL C-12.4	R	97	3	29	1
	EURL C-12.5	R	97	3	29	1
	EURL C-12.6	R	100	0	30	0
	EURL C-12.7	S	3	97	29	1
	EURL C-12.8	R	100	0	30	0
Erythromycin, ERY	EURL C-12.1*	S	0	100	23	0
	EURL C-12.2	R	100	0	30	0
	EURL C-12.3	S	0	100	30	0
	EURL C-12.4	S	0	100	30	0
	EURL C-12.5	S	0	100	30	0
	EURL C-12.6	S	0	100	30	0
	EURL C-12.7	S	0	100	30	0
	EURL C-12.8	S	0	100	30	0
Gentamicin, GEN	EURL C-12.1*	S	0	100	23	0
	EURL C-12.2	S	0	100	30	0
	EURL C-12.3	S	0	100	30	0
	EURL C-12.4	S	0	100	30	0
	EURL C-12.5	S	0	100	30	0
	EURL C-12.6	S	0	100	30	0
	EURL C-12.7	S	0	100	30	0
	EURL C-12.8	S	0	100	30	0
Nalidixic acid, NAL	EURL C-12.1*	S	0	100	23	0
	EURL C-12.2	R	100	0	30	0
	EURL C-12.3	S	0	100	30	0
	EURL C-12.4	R	100	0	30	0
	EURL C-12.5	R	97	3	29	1
	EURL C-12.6	R	100	0	30	0
	EURL C-12.7	S	3	97	29	1
	EURL C-12.8	R	100	0	30	0
Streptomycin, STR	EURL C-12.1*	S	0	100	23	0
	EURL C-12.2	R	100	0	30	0
	EURL C-12.3	R	100	0	30	0
	EURL C-12.4	S	0	100	30	0
	EURL C-12.5	R	97	3	29	1
	EURL C-12.6	S	3	97	29	1
	EURL C-12.7	S	0	100	30	0
	EURL C-12.8	S	0	100	30	0
Tetracycline, TET	EURL C-12.1*	S	0	100	23	0
	EURL C-12.2	R	100	0	30	0
	EURL C-12.3	R	93	7	28	2
	EURL C-12.4	R	100	0	30	0
	EURL C-12.5	R	100	0	30	0
	EURL C-12.6	R	100	0	30	0
	EURL C-12.7	S	3	97	29	1
	EURL C-12.8	R	100	0	30	0

**Results excluded for six users that appear to have been testing a contamination*

Deviations - *Salmonella*

Lab no.	Strain	Panel	Antimicrobial	Obtained MIC value	Expected MIC-value	Obtained interpretation	Expected interpretation
2	EURL S-12.4		ESBL-categorization			None	Presumptive AmpC
4	EURL S-12.7	1	Tigecycline TGC	2	1	R	S
9	EURL S-12.1	2	Imipenem IMI	1	2	S	R
12	EURL S-12.4	1	Sulfamethoxazole SMX	1024	64	R	S
18	EURL S-12.4	1	Sulfamethoxazole SMX	> 1024	64	R	S
19	EURL S-12.2	2	Cefoxitin FOX	2	4	R	S
19	EURL S-12.3	2	Cefoxitin FOX	4	4	R	S
19	EURL S-12.7	2	Cefoxitin FOX	4	8	R	S
21	EURL S-12.4	1	Ceftazidime TAZ	1	4	S	R
21	EURL S-12.4		ESBL-categorization			None	Presumptive AmpC
22	EURL S-12.2	1	Ceftazidime TAZ	1	1	R	S
23	EURL S-12.8	1	Sulfamethoxazole SMX	256	> 1024	S	R
26	EURL S-12.1	2	Imipenem IMI	= 0.5	2	S	R
26	EURL S-12.1	2	Temocillin TRM	32	64	S	R
26	EURL S-12.4	1	Sulfamethoxazole SMX	512	64	R	S
26	EURL S-12.8	1	Chloramphenicol CHL	16	64	S	R
26	EURL S-12.8	2	Imipenem IMI	1	8	S	R
26	EURL S-12.8	2	Temocillin TRM	32	> 128	S	R
30	EURL S-12.4	1	Ceftazidime TAZ	<= 0.5	4	S	R
30	EURL S-12.4		ESBL-categorization			None	Presumptive AmpC
33	EURL S-12.4	2	Ceftazidime TAZ	2	4	S	R
34	EURL S-12.4	1	Ceftazidime TAZ	2	4	S	R
34	EURL S-12.4	2	Ceftazidime TAZ	2	4	S	R
34	EURL S-12.4		ESBL-categorization			None	Presumptive AmpC
36	EURL S-12.4	2	Ceftazidime TAZ	4	4	S	R
36	EURL S-12.8	1	Sulfamethoxazole SMX	<= 8	> 1024	S	R
37	EURL S-12.8	1	Ampicillin AMP	> 64	> 64	S	R
39	EURL S-12.1	2	Imipenem IMI	1	2	S	R
40	EURL S-12.4	1	Ampicillin AMP	64	2	R	S
42	EURL S-12.1	1	Ciprofloxacin CIP	8	> 8	S	R
42	EURL S-12.2	1	Ciprofloxacin CIP	= 0.25	= 0.5	S	R
42	EURL S-12.2	2	Temocillin TRM	4	4	R	S
42	EURL S-12.4	1	Ceftazidime TAZ	2	4	S	R
42	EURL S-12.4		ESBL-categorization			None	Presumptive AmpC
42	EURL S-12.8	1	Sulfamethoxazole SMX	<= 8	> 1024	S	R
45	EURL S-12.2	1	Azithromycin AZI	4	8	R	S
45	EURL S-12.4	1	Ceftazidime TAZ	2	4	S	R
45	EURL S-12.4		ESBL-categorization			None	Presumptive AmpC
58	EURL S-12.4	1	Ceftazidime TAZ	<= 0.5	4	S	R
58	EURL S-12.4		ESBL-categorization			None	Presumptive AmpC

Deviations - *Campylobacter*

Lab no.	Strain	Antimicrobial	Obtained MIC value	Expected MIC-value	Obtained interpretation	Expected interpretation
11	EURL C-12.3	Tetracycline TET	<= 0.5	8	S	R
42	EURL C-12.3	Tetracycline TET	16	8	S	R
29	EURL C-12.4	Ciprofloxacin CIP	8	8	S	R
39	EURL C-12.5	Ciprofloxacin CIP	4	4	S	R
39	EURL C-12.5	Nalidixic acid NAL	16	64	S	R
40	EURL C-12.5	Streptomycin STR	<= 0.25	> 16	S	R
40	EURL C-12.6	Streptomycin STR	16	2	R	S
40	EURL C-12.7	Ciprofloxacin CIP	16	<= 0.12	R	S
40	EURL C-12.7	Nalidixic acid NAL	64	4	R	S
40	EURL C-12.7	Tetracycline TET	> 64	<= 0.5	R	S

Genotypic characterization (optional); genes detected in the ESBL-, AmpC, and carbapenemase producing *Salmonella* strains

Labno	Strain	Genetype	Gene number	Method	Reference	Primer 5 3	Primer 3 5
1	EURL S-12.1	CMY	-16	Whole genome sequenced			
1	EURL S-12.2	CTX	M-9	Whole genome sequenced			
1	EURL S-12.2	TEM	-1B	Whole genome sequenced			
1	EURL S-12.3	CTX	M-14	Whole genome sequenced			
1	EURL S-12.7	CTX	M-14	Whole genome sequenced			
1	EURL S-12.8	CTX	M-15	Whole genome sequenced			
1	EURL S-12.8	NDM	-1	Whole genome sequenced			
1	EURL S-12.8	OXA	-10	Whole genome sequenced			
1	EURL S-12.8	OXA	-9	Whole genome sequenced			
1	EURL S-12.8	OXA	-1	Whole genome sequenced			
1	EURL S-12.8	TEM	-1B	Whole genome sequenced			
2	EURL S-12.1	CMY					
2	EURL S-12.1	NDM					
2	EURL S-12.2	CTX					
2	EURL S-12.2	TEM					
2	EURL S-12.3	CTX					
2	EURL S-12.7	CTX					
2	EURL S-12.8	DHA					
2	EURL S-12.8	NDM					
4	EURL S-12.1	CMY	-16	PCR (published)			
4	EURL S-12.1	NDM	-1	PCR (published)			
4	EURL S-12.2	CTX	M-9	PCR (published)			
4	EURL S-12.2	TEM		PCR (published)			
4	EURL S-12.3	CTX	M-14	PCR (published)			
4	EURL S-12.7	CTX	M-14	PCR (published)			
4	EURL S-12.8	NDM	-1	PCR (published)			
17	EURL S-12.1	CMY	-16	Whole genome sequenced	ResFinder 3.0		
17	EURL S-12.1	CMY		PCR (published)	Zhao et al. (2001)		
17	EURL S-12.1	NDM	-1	Whole genome sequenced	ResFinder 3.0		
17	EURL S-12.1	NDM	-1	PCR (published)	Poirel et al. (2011)		
17	EURL S-12.2	CTX	M-9	PCR (published)	Batchelor et al. (2005)		
17	EURL S-12.2	CTX	M-9	Whole genome sequenced	ResFinder 3.0		
17	EURL S-12.2	TEM	-1B	Whole genome sequenced	ResFinder 3.0		
17	EURL S-12.2	TEM		PCR (published)	Guerra et al. (2001)		
17	EURL S-12.3	CTX	M-14	PCR (published)	Roschanski et al. [2014]		
17	EURL S-12.3	CTX	M-14	Whole genome sequenced	ResFinder 3.0		
17	EURL S-12.7	CTX	M-14	Whole genome sequenced	ResFinder 3.0		
17	EURL S-12.7	CTX	M-14	PCR (published)	Roschanski et al. [2014]		
17	EURL S-12.8	CTX	M-15	Whole genome sequenced	Resfinder 3.0		
17	EURL S-12.8	CTX	M-15	PCR (published)	Batchelor et al (2005)		
17	EURL S-12.8	DHA	-1	Whole genome sequenced	Resfinder 3.0		
17	EURL S-12.8	NDM	-1	PCR (published)	Poirel et al. (2011)		
17	EURL S-12.8	NDM	-1	Whole genome sequenced	Resfinder 3.0		
17	EURL S-12.8	OXA	-10	Whole genome sequenced	Resfinder 3.0		

Labno	Strain	Genetype	Gene number	Method	Reference	Primer 5 3	Primer 3 5
17	EURL S-12.8	OXA	-10	PCR (published)	Guerra et al. (2000)		
17	EURL S-12.8	OXA	-9	Whole genome sequenced	Resfinder 3.0		
17	EURL S-12.8	OXA	-1	Whole genome sequenced	Resfinder 3.0		
17	EURL S-12.8	TEM	-1	Whole genome sequenced	Resfinder 3.0		
17	EURL S-12.8	TEM		PCR (published)	Olesen et al. (2004)		
20	EURL S-12.1	CMY	-16	Whole genome sequenced	Resfinder		
20	EURL S-12.1	NDM	-1	Whole genome sequenced	Resfinder		
20	EURL S-12.2	CTX	M-9	Whole genome sequenced	resfinder		
20	EURL S-12.2	TEM	-1B	Whole genome sequenced	resfinder		
20	EURL S-12.3	CTX	M-14	Whole genome sequenced	Resfinder		
20	EURL S-12.7	CTX	M-14	Whole genome sequenced	resfinder		
20	EURL S-12.8	CTX	M-15	Whole genome sequenced	resfinder		
20	EURL S-12.8	NDM	-1	Whole genome sequenced	resfinder		
20	EURL S-12.8	OXA	-10	Whole genome sequenced	resfinder		
20	EURL S-12.8	OXA	-9	Whole genome sequenced	resfinder		
20	EURL S-12.8	OXA	-1	Whole genome sequenced	resfinder		
21	EURL S-12.1	CMY		PCR (published)	Wiesner M 2009	taaccacccagtcacgc	cagtagcgagactgcgca
21	EURL S-12.1	NDM		PCR (published)	Poirel L 2011	ggtttggcgatctgggttttc	cggaatggctcatcacgatc
21	EURL S-12.2	CTX		PCR (published)	Carattoli A 2008	cccatggttaaaaaatcactgc	cagcgcttttgccgtctaag
21	EURL S-12.3	CTX		PCR (published)	Carattoli A 2008	cccatggttaaaaaatcactgc	cagcgcttttgccgtctaag
21	EURL S-12.7	CTX		PCR (published)	Carattoli A 2008	cccatggttaaaaaatcactgc	cagcgcttttgccgtctaag
21	EURL S-12.8	CTX		PCR (published)	Carattoli A 2008	cccatggttaaaaaatcactgc	cagcgcttttgccgtctaag
21	EURL S-12.8	NDM		PCR (published)	Poirel L 2011	ggtttggcgatctgggttttc	cggaatggctcatcacgatc
22	EURL S-12.1	CMY		PCR (published)	Kim et al., 2009	AGC GAT CCG GTC ACG AAA TA	CCC GTT TTA TGC ACC CAT GA
22	EURL S-12.1	NDM		PCR (published)	Poirel et al., 2011	GGT TTG GCG ATC TGG TTT TC	CGG AAT GGC TCA TCA CGA TC
22	EURL S-12.2	CTX		PCR (published)	Kim et al., 2009	GAC AAA GAG AGT GCA ACG GAT G	TCA GTG CGA TCC AGA CGA AA
22	EURL S-12.2	TEM		PCR (published)	Kim et al., 2009	AGT GCT GCC ATA ACC ATG AGT G	CTG ACT CCC CGT CGT GTA GAT A
22	EURL S-12.3	CTX		PCR (published)	Kim et al., 2009	GAC AAA GAG AGT GCA ACG GAT G	TCA GTG CGA TCC AGA CGA AA
22	EURL S-12.7	CTX		PCR (published)	Kim et al., 2009	GAC AAA GAG AGT GCA ACG GAT G	TCA GTG CGA TCC AGA CGA AA
22	EURL S-12.8	CTX		PCR (published)	Kim et al., 2009	TCC AGA ATA AGG AAT CCC ATG G	TGC TTT ACC CAG CGT CAG AT
22	EURL S-12.8	DHA		PCR (published)	Kim et al., 2009	GTG GTG GAC AGC ACC ATT AAA	CCT GCG GTA TAG GTA GCC AGA T
22	EURL S-12.8	NDM		PCR (published)	Poirel et al., 2011	GGT TTG GCG ATC TGG TTT TC	CGG AAT GGC TCA TCA CGA TC
22	EURL S-12.8	OXA		PCR (published)	Kim et al., 2009	ATT ATC TAC AGC AGC GCC AGT G	TGC ATC CAC GTC TTT GGT G
22	EURL S-12.8	TEM		PCR (published)	Kim et al., 2009	AGT GCT GCC ATA ACC ATG AGT G	CTG ACT CCC CGT CGT GTA GAT A
25	EURL S-12.1	CMY	-16	PCR (in-house)			
25	EURL S-12.1	NDM	-1	PCR (published)			
25	EURL S-12.2	CTX	M-9	PCR (published)			
25	EURL S-12.2	TEM	-1B	PCR (published)			
25	EURL S-12.3	CTX	M-14	PCR (published)			
25	EURL S-12.7	CTX	M-14	PCR (published)			
25	EURL S-12.8	CTX	M-15	PCR (published)			
25	EURL S-12.8	DHA	-1	PCR (published)			
25	EURL S-12.8	NDM	-1	PCR (published)			
25	EURL S-12.8	TEM	-1B	PCR (published)			
32	EURL S-12.1	CMY	-16	PCR (published)	A.AGE.CHEM2006.ClinMicr1999-37		
32	EURL S-12.1	NDM	-1	PCR (published)	L. Poirel et al 2011		

Labno	Strain	Genetype	Gene number	Method	Reference	Primer 5 3	Primer 3 5
32	EURL S-12.2	CTX	M-9	PCR (published)	PediatrInfectDisJ28:814-818		
32	EURL S-12.2	TEM	-1	PCR (published)	AntimicrAgentsChemotherap2009		
32	EURL S-12.3	CMY	-16	PCR (published)	A.AGE.CHEM2006.ClinMicr1999-37		
32	EURL S-12.3	CTX	M-14	PCR (published)	PediatrInfectDisJ28:814-818		
32	EURL S-12.7	CTX	M-14	PCR (published)	PediatrInfectDisJ28:814-818		
32	EURL S-12.8	CTX	M-15	PCR (published)	PediatrInfectDisJ28:814-818		
32	EURL S-12.8	NDM	-1	PCR (published)	L. Poirel et al 2011		
32	EURL S-12.8	OXA	-17	PCR (published)	Voets et al. 2011		
32	EURL S-12.8	OXA	-1	PCR (published)	J. Antimic.Chemothe(2009) 64		
32	EURL S-12.8	TEM	-1	PCR (published)	AntimicrAgentsChemotherap2009		
33	EURL S-12.1	CMY		PCR (published)	Perez-Perez, F. J. and N. D. Hanson (2002). Detection of plasmid-mediated AmpC beta-lactamase genes in clinical isolates by using multiplex PCR, J Clin Microbiol 40(6): 2153-62.	TGGCCAGAACTGACAGGCAAA	TTTCTCCTGAACGTGGCTGGC
33	EURL S-12.1	NDM		PCR (published)	Poirel et al.(2011)"Multiplex PCR for detection of acquired carbapenemase genes", Diagnostic Microbiology & Infectious Disease, 70(1), 119-123, 2011	GGTTTGGCGATCTGGTTTTC	CGGAATGGCTCATCACGATC
33	EURL S-12.2	CTX	M-9	PCR (published)	Woodford, N., E. J. Fagan, et al. (2006). Multiplex PCR for rapid detection of genes encoding CTX-M extended-spectrum ß-lactamases. J Antimicrob Chemother 57(1): 154-5.	CAAAGAGARTGCAACGGATG	ATTGGAAAGCGTTCATCACC
33	EURL S-12.2	TEM		PCR (published)	Fang, H., F. Ataker, et al. (2008). J Clin Microbiol 46(2): 707-12.	CGCCGCATACACTATTCTCAGAATGA	ACGCTCACCGGCTCCAGATTTAT
33	EURL S-12.3	CTX	M-9	PCR (published)	Woodford, N., E. J. Fagan, et al. (2006). Multiplex PCR for rapid detection of genes encoding CTX-M extended-spectrum ß-lactamases. J Antimicrob Chemother 57(1): 154-5.	CAAAGAGARTGCAACGGATG	ATTGGAAAGCGTTCATCACC
33	EURL S-12.7	CTX	M-9	PCR (published)	Woodford, N., E. J. Fagan, et al. (2006). Multiplex PCR for rapid detection of genes encoding CTX-M extended-spectrum ß-lactamases. J Antimicrob Chemother 57(1): 154-5.	CAAAGAGARTGCAACGGATG	ATTGGAAAGCGTTCATCACC
33	EURL S-12.8	CTX	M-1	PCR (published)	Woodford, N., E. J. Fagan, et al. (2006). Multiplex PCR for rapid detection of genes encoding CTX-M extended-spectrum ß-lactamases. J Antimicrob Chemother 57(1): 154-5.	AAAAATCACTGCGYCAGTTC	AGCTTATTCATCGCCACGTT
33	EURL S-12.8	DHA		PCR (published)	Perez-Perez, F. J. and N. D. Hanson (2002). Detection of plasmid-mediated AmpC beta-lactamase genes in clinical isolates by using multiplex PCR, J Clin Microbiol 40(6): 2153-62.	AACTTTCACAGGTGTGCTGGGT	CCGTACGCATACTGGCTTTGC
33	EURL S-12.8	NDM		PCR (published)	Poirel et al.(2011)"Multiplex PCR for detection of acquired carbapenemase genes", Diagnostic Microbiology & Infectious Disease, 70(1), 119-123, 2011	GGTTTGGCGATCTGGTTTTC	CGGAATGGCTCATCACGATC
33	EURL S-12.8	OXA	-1	PCR (published)	Fang, H., F. Ataker, et al. (2008). J Clin Microbiol 46(2): 707-12.	ACACAATACATATCAACTTCGC	AGTGTGTTTAGAATGGTGATC
33	EURL S-12.8	TEM		PCR (published)	Fang, H., F. Ataker, et al. (2008). J Clin Microbiol 46(2): 707-12.	CGCCGCATACACTATTCTCAGAATGA	ACGCTCACCGGCTCCAGATTTAT
36	EURL S-12.1	NDM	-1	PCR (published)	S.Mushtaq et. al. J. Antimicrob. Chemother. (2011) 66 (9): 2002-2005. doi: 10.1093/jac/dkr226	GGGCAGTCGCTTCCAACGGT	GTAGTGCTCAGTGTCGGCAT
36	EURL S-12.2	CTX	M-9	PCR (published)	Hasman et al. J Antimicrob Chemother. 2005 Jul;56(1):115-21.	ATGTGCAGYACCAGTAARGTKATGGC	TGGGTRAARTARGTSACCAGAAYCAGCGG

Labno	Strain	Genetype	Gene number	Method	Reference	Primer 5 3	Primer 3 5
36	EURL S-12.2	TEM	-1B	PCR (published)	Briñas et al. Antimicrob Agents Chemother. 2002 Oct;46(10):3156-63.	TTCTTGAAGACGAAAGGGC	ACGCTCAGTGGAACGAAAAC
36	EURL S-12.3	CTX	M-14	PCR (published)	Hasman et al. J Antimicrob Chemother. 2005 Jul;56(1):115-21.	ATGTGCAGYACCAGTAARGTKATGGC	TGGGTRAARTARGTSACCAGAAYCAGCGG
36	EURL S-12.7	CTX	M-14	PCR (published)	Hasman et al. J Antimicrob Chemother. 2005 Jul;56(1):115-21.	ATGTGCAGYACCAGTAARGTKATGGC	TGGGTRAARTARGTSACCAGAAYCAGCGG
36	EURL S-12.8	NDM	-1	PCR (published)	S.Mushtaq et. al. J. Antimicrob. Chemother. (2011) 66 (9): 2002-2005. doi: 10.1093/jac/dkr226	GGGCAGTCGCTTCCAACGGT	GTAGTGCTCAGTGTCGGCAT
58	EURL S-12.1	CMY		PCR (published)	EURL protocol	5'-ATGATGAAAAAATCGTTATGCTGC-3'	5'-GCTTTTCAAGAATGCGCCAGG-3'
58	EURL S-12.1	NDM		PCR (published)	EURL protocol	5'-GGTTTGGCGATCTGGTTTTC-3'	5'-CGGAATGGCTCATCACGATC-3'
58	EURL S-12.2	CTX		PCR (published)	EURL protocol	5'-ATGTGCAGYACCAGTAARGTKATGGC-3'	5'-TGGGTRAARTARGTSACCAGAAYSAGCGG-3'
58	EURL S-12.2	TEM		PCR (published)	EURL protocol	5'-GCGGAACCCCTATTTG-3'	5'-ACCAATGCTTAATCAGTGAG-3'
58	EURL S-12.3	CTX		PCR (published)	EURL protocol	5'-ATGTGCAGYACCAGTAARGTKATGGC-3'	5'-TGGGTRAARTARGTSACCAGAAYSAGCGG-3'
58	EURL S-12.7	CTX		PCR (published)	EURL protocol	5'-ATGTGCAGYACCAGTAARGTKATGGC-3'	5'-TGGGTRAARTARGTSACCAGAAYSAGCGG-3'
58	EURL S-12.8	CTX		PCR (published)	EURL protocol	5'-ATGTGCAGYACCAGTAARGTKATGGC-3'	5'-TGGGTRAARTARGTSACCAGAAYSAGCGG-3'
58	EURL S-12.8	NDM		PCR (published)	EURL protocol	5'-GGTTTGGCGATCTGGTTTTC-3'	5'-CGGAATGGCTCATCACGATC-3'
58	EURL S-12.8	TEM		PCR (published)	EURL protocol	5'-GCGGAACCCCTATTTG-3'	5'-ACC AAT GCT TAA TCA GTG AG-3'

Legend:

Fields shaded grey indicate that the gene was expected

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

Note: TEM-1 does not confer ESBL-production and is as such not included as an expected result. TEM-1 or TEM-1B was, however, present in S-12.2 and S-12.8

Genotypic characterization (optional); comments by participants

Labno	Strain	Comment
1	EURL S-12.2	blaTEM-1b coding for TEM-1
1	EURL S-12.3	blaCTX-M-14b coding for CTX-M-14
1	EURL S-12.6	blaTEM-1b coding for TEM-1
1	EURL S-12.8	blaTEM-1b coding for TEM-1;partial blaDHA gene detected
17	EURL S-12.3	blaCTX-M-14b (100.00%, 876/876)
17	EURL S-12.8	DHA partially detected: blaDHA-1 (100.00%, 1140/796), blaTEM-1A (99.88%, 861/861)
25	EURL S-12.4	Despite resistance against cefotaxime and ceftazidime no resistance genes could be detected with microarray (CT103).
32	EURL S-12.1	SPM Gene tested for/not detected (L. Poirel et al 2011) IMP Gene: Gene Number should be blank , the gene has not been detected (we can´t change it in the database)
32	EURL S-12.2	SPM Gene tested for/not detected (L. Poirel et al 2011)
32	EURL S-12.3	SPM Gene tested for/not detected (L. Poirel et al 2011)
32	EURL S-12.4	SPM Gene tested for/not detected (L. Poirel et al 2011)
32	EURL S-12.7	SPM Gene tested for/not detected (L. Poirel et al 2011)
32	EURL S-12.8	SPM Gene tested for/not detected (L. Poirel et al 2011)
33	EURL S-12.1	If suspected for ESBL isolates are tested for CTX-M-1, -2 -9 -8 -25, SHV, TEM, OXA-1 groups If suspected for ampC isolates are tested for the above mentioned gene-groups and the following genegroups MOX, CIT, DHA, ACC, ACT and FOX For supected carbapenemase we test for the following genes: NDM, KPC, OXA-48, VIM, IMP
33	EURL S-12.2	If suspected for ESBL isolates are tested for CTX-M-1, -2 -9 -8 -25, SHV, TEM, OXA-1 groups If suspected for ampC isolates are tested for the above mentioned gene-groups and the following genegroups MOX, CIT, DHA, ACC, ACT and FOX For supected carbapenemase we test for the following genes: NDM, KPC, OXA-48, VIM, IMP
33	EURL S-12.3	If suspected for ESBL isolates are tested for CTX-M-1, -2 -9 -8 -25, SHV, TEM, OXA-1 groups If suspected for ampC isolates are tested for the above mentioned gene-groups and the following genegroups MOX, CIT, DHA, ACC, ACT and FOX For supected carbapenemase we test for the following genes: NDM, KPC, OXA-48, VIM, IMP
33	EURL S-12.4	If suspected for ESBL isolates are tested for CTX-M-1, -2 -9 -8 -25, SHV, TEM, OXA-1 groups If suspected for ampC isolates are tested for the above mentioned gene-groups and the following genegroups MOX, CIT, DHA, ACC, ACT and FOX For supected carbapenemase we test for the following genes: NDM, KPC, OXA-48, VIM, IMP
33	EURL S-12.7	If suspected for ESBL isolates are tested for CTX-M-1, -2 -9 -8 -25, SHV, TEM, OXA-1 groups If suspected for ampC isolates are tested for the above mentioned gene-groups and the following genegroups MOX, CIT, DHA, ACC, ACT and FOX For supected carbapenemase we test for the following genes: NDM, KPC, OXA-48, VIM, IMP
33	EURL S-12.8	If suspected for ESBL isolates are tested for CTX-M-1, -2 -9 -8 -25, SHV, TEM, OXA-1 groups If suspected for ampC isolates are tested for the above mentioned gene-groups and the following genegroups MOX, CIT, DHA, ACC, ACT and FOX For supected carbapenemase we test for the following genes: NDM, KPC, OXA-48, VIM, IMP
58	EURL S-12.1	We performed for mcr1 and mcr2 genes and the genes were not detected. We also performed for CTX-M1 gene and CTX-M9 gene and the genes were not detected. For OXA gene, we performed for OXA-48.
58	EURL S-12.2	We also performed for CTX-M9 gene with EURL primers and the gene was detected. We performed for CTX-M1 gene with EURL primers and the gene was not detected. We performed for mcr1 and mcr2 genes with EURL primers and the genes were not detected. For OXA gene, we performed for OXA-48.
58	EURL S-12.3	We also performed for CTX-M9 gene with EURL primers and the gene was detected. We performed for CTX-M1 gene with EURL primers and the gene was not detected. We performed for mcr1 and mcr2 genes with EURL primers and the genes were not detected. For OXA gene, we performed for OXA-48 with EURL primers.
58	EURL S-12.4	We also performed for CTX-M1 gene and CTX-M9 gene with EURL primers and the genes were not detected. We performed for mcr1 and mcr2 genes with EURL primers and the genes were not detected. For gene OXA we performed for OXA-48 gene with EURL primers and the gene was not detected.
58	EURL S-12.5	We performed for mcr1 and mcr2 genes with EURL primers and the genes were not detected. We also performed for CTX-M1 gene and CTX-M9 gene with EURL primers. For OXA gene, we performed for OXA-48 with EURL primers.

Labno	Strain	Comment
58	EURL S-12.6	We performed for mcr1 and mcr2 genes with EURL primers and the genes were not detected. We also performed for CTX-M1 gene and CTX-M9 gene with EURL primers and the genes were not detected. For gene OXA, we performed for OXA-48 gene with EURL primers.
58	EURL S-12.7	For gene CTX-M, we performed with EURL primers and the gene was detected. We also performed for CTX-M9 gene with EURL primers and the gene was detected. We also performed for CTX-M1 gene and the gene was nor detected. We performed for mcr1 and mcr2 genes with EURL primers and the genes were not detected. For gene OXA, we performed for OXA-48 with EURL primers.
58	EURL S-12.8	We performed for CTX-M1 gene with EURL primers and it was detected. We performed for CTX-M9 gene with EURL primers and it was not detected. We performed for mcr1 and mcr2 genes with EURL primers and the genes were not detected. For OXA gene we performed for OXA-48 gene with EURL primers.

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