TECHNICAL REPORT

Second external quality assurance scheme for *Salmonella* typing

European Food- and Waterborne Diseases and Zoonoses Network

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Main contractor:
KA Mooijman, RIVM, Laboratory for Zoonoses and Environmental Microbiology, 3720 BA Bilthoven, Netherlands

Authors:
W.F. Jacobs-Reitsma (RIVM), H. Maas (RIVM), E. de Pinna (HPA), D. Mevius (CVI) and K.A. Mooijman (RIVM)

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Contents

Abbreviations and symbols

Abbreviations

AMP	Ampicillin
AST	Antimicrobial susceptibility testing
ATCC	American Type Culture Collection
BGA	Brilliant green agar
CAMHB	Cation-adjusted Mueller-Hinton broth
CHL	Chloramphenicol
CIP	Ciprofloxacin
CLSI	Clinical and Laboratory Standards Institute
CTX	Cefotaxime
CVI	Central Veterinary Institute
DD	Disk diffusion
DSN	Dedicated surveillance network
DT	Definitive type
EEA	European Economic Area
ECDC	European Centre for Disease Prevention and Control
ESBL	Extended-spectrum beta-lactamase
EFSA	European Food Safety Authority
EQA	External quality assurance
EU	European Union
EUCAST	European Committee on Antimicrobial Susceptibility Testing
EU-RL-*Salmonella*	EU reference laboratory for *Salmonella*
EU-RL-AST	EU reference laboratory for antimicrobial resistance
FWD-Net	Food- and Waterborne Diseases and Zoonoses Network
GEN	Gentamicin
HPA	Health Protection Agency
I	Intermediate
LGP	Laboratory of Gastrointestinal Pathogens, London
LZO	Laboratory for Zoonoses and Environmental Microbiology, Bilthoven, Netherlands
MH agar	Mueller-Hinton agar
MIC	Minimal inhibition concentration
NAL	Nalidixic acid
NCCLS	National Committee for Clinical Laboratory Standards
NI	Not indicated
NRLs-*Salmonella*	National reference laboratories for *Salmonella*
NT	Not typable
PT	Phage type
R	Resistant
RDNC	Reacts with phages but does not confirm to a recognised pattern
RIVM	Dutch National Institute for Public Health and the Environment
S	Susceptible
SE	*Salmonella* Enteritidis
STM	*Salmonella* Typhimurium
STR	Streptomycin
SUL	Sulfonamides
TET	Tetracycline
TMP	Trimethoprim
TSA	Trypticase soy agar
TSEs	Transmissible spongiform encephalopathies

UK	United Kingdom
XLD	Xylose lysine desoxycholate

Symbols

–	No reaction
±	5–20 plaques
+	21–40 plaques
++	41–80 plaques
+++	81–100 plaques
<<	Merging plaques towards semi-confluent lysis
CL	Confluent clear lysis
OL	Confluent opaque lysis
SCL	Semi-confluent lysis

Summary

Thirty-five laboratories of the Food- and Waterborne Diseases and Zoonoses Network (FWD-Net), 28 from EU/EEA countries, participated in the second international external quality assurance (EQA) scheme for the typing of *Salmonella*.

Main findings

- All participating laboratories (including those in the EU/EEA) typed 99% of the samples correctly for O antigens. The participating EU/EEA laboratories also typed 93% of the samples correctly for H antigens, compared with 94% for all participants. Both EU/EEA and non-EU/EEA laboratories were able to assign the correct serovar names to 93% of the samples.
  In this second EQA scheme, more laboratories produced deviating serotyping results then in March 2009 during the first EQA scheme, but the number of deviations for every individual laboratory was generally lower.
- The phage-typing results showed that EU/EEA laboratories correctly phage-typed 84% of the *S.* Enteritidis strains (all laboratories: 85% correct). For *S.* Typhimurium, 89% of the strains were phage-typed correctly by the EU/EEA laboratories (overall correct rate: 91%). All in all, the phage typing results in the second EQA scheme were reassuring although there were slightly more deviations in the results for *S.* Enteritidis when compared with the first scheme (March 2009).
  The results for *S.* Typhimurium, when compared with the first EQA scheme, show that there were fewer deviations in the second scheme.
- Except for two laboratories (one EU, one non-EU/EEA), all participants produced ≤10% deviations for the interpretation of antimicrobial susceptibility tests. 72% of the EU/EEA laboratories and 71% of the total participants produced ≤5% deviations, which demonstrates a reasonably high level of performance.
  Overall, 96% of the 2443 evaluated tests were categorised in agreement with the reference method and interpretive criteria, compared with 95% of the 2849 evaluated tests in the first EQA scheme.

In December 2009, the second international external quality assurance (EQA) scheme for the typing of *Salmonella* spp. was launched. The study included the laboratories that form the Food- and Waterborne Diseases and Zoonoses Network and was carried out by the laboratory for Zoonoses and Environmental Microbiology (LZO) of the National Institute for Public Health and the Environment (RIVM, Bilthoven, Netherlands) in collaboration with the Salmonella Reference Unit of the Laboratory of Gastrointestinal Pathogens of the Health Protection Agency (HPA) in London and the Central Veterinary Institute of Wageningen University and Research Centre (CVI), Department of Bacteriology and TSEs, in Lelystad, Netherlands.

Three procedures for the typing of *Salmonella* spp. were tested in this second EQA scheme: serotyping, phage-typing, and antimicrobial susceptibility testing. The main objective of the EQA scheme was to evaluate whether typing of *Salmonella* strains by different laboratories within and outside the European Union was carried out uniformly and whether comparable results were obtained.

In total, 35 laboratories participated in this study, though one laboratory did not return its results. Twenty-eight EU/EEA laboratories and seven non-EU/EEA laboratories participated.

A total of 20 strains of the species *Salmonella enterica* subspecies *enterica* were selected by RIVM for serotyping. Thirty-two participants, including 25 EU/EEA laboratories, carried out serotyping the 20 strains. Under the rules of the scheme, strains had to be typed with the main method routinely used in each laboratory. The detected H and O antigens and serovar names (according to the White-Kauffmann-Le Minor scheme) had to be reported. Most problems were encountered in typing the H antigens: while the EU/EEA laboratories (as well as the non-EU/EEA labs) typed the O antigens correctly for 99% of the samples, the EU/EEA laboratories typed only 93% of the samples correctly for H antigens (overall correct rate: 94%). Both EU/EEA and non-EU/EEA laboratories were able to assign the correct serovar names to 93% of all samples. Fifteen of the 25 (60%) EU/EEA laboratories, and 16 of the 32 (50%) total participating laboratories correctly identified all 20 serovars. Two serovars, *S.* Stanley and *S.* Typhimurium, were correctly typed by all participants.

The HPA selected 20 strains for phage typing. Ten strains were of the serovar *Salmonella* Enteritidis and ten strains of the serovar *Salmonella* Typhimurium. Twenty laboratories carried out phage typing of the *S.* Enteritidis strains, 16 of these were from the EU/EEA. Two laboratories did not carry out phage typing on *S.* Typhimurium strains, therefore only 18 laboratories provided results on phage typing on *S.* Typhimurium (14 EU/EEA laboratories). Overall, 84% of the *S.* Enteritidis strains were phage-typed correctly by the EU/EEA laboratories, corresponding to 85% for all laboratories. For *S.* Typhimurium, 89% of the strains were phage-typed correctly by the EU/EEA laboratories (overall correct rate: 91%).

Ten strains of various *Salmonella* serovars were selected by CVI for antimicrobial susceptibility testing. These strains were tested by the participating laboratories for their susceptibility to a panel of ten antibiotics. Thirty-one laboratories participated in the antimicrobial susceptibility testing of the strains, 25 of these were EU/EEA laboratories. Eleven laboratories used a quantitative method that yielded minimum inhibitory concentrations (MIC values); twenty laboratories conducted a qualitative disk diffusion test, whose zone diameters serve as interpretive criteria. The laboratories categorised the results as susceptible (S), intermediate (I) or resistant (R), based on their own interpretive criteria. Minor deviations for the interpretation of the susceptibility tests were found in 3% of 1983 evaluated results (EU/EEA laboratories), and 1% of these results showed major deviations, which means that 96% of the antibiotic susceptibility testing data were correctly interpreted. The same percentages were found regarding the 2443 evaluated tests from all participating laboratories. Errors were mainly made on a number of strains with borderline susceptibility or as the result of applying inadequate interpretive criteria.

Except for one EU and one non-EU/EEA laboratory, all participants produced ≤10% deviations. Eighteen of the 25 EU/EEA laboratories (72%) and 22 of the 31 total participants (71%) produced ≤5% deviations, which demonstrates that the general performance level of antimicrobial susceptibility tests is very high.

1 Introduction

1.1 Background

The European Centre for Disease Prevention and Control (ECDC) is a European Union agency with a mandate to operate dedicated surveillance networks (DSNs) and to identify, assess, and communicate current and emerging threats to human health from communicable diseases. Within its mission, ECDC shall

> foster the development of sufficient capacity within the Community for the diagnosis, detection, identification and characterisation of infectious agents which may threaten public health. The Centre shall maintain and extend such cooperation and support the implementation of quality assurance schemes.
> *– Regulation (EC) No. 851/2004, Article 5.3*

External quality assurance (EQA), as a part of quality management system, evaluates the performance of laboratories by commissioning a third party which distributes a series of samples and also supplies all laboratory testing supplies. ECDC's disease-specific networks organised a series of EQA schemes for EU/EEA countries. In some instances, these networks also include non-EU/EEA countries, which then also participate in ECDC's EQA activities. ECDC's EQA schemes are designed to identify areas for improvement in laboratory diagnostic capacities relevant to disease surveillance as listed in Decision No 2119/98/EC[1] and ensure the comparability of results between laboratories in EU/EEA countries. The main purposes of external quality assurance schemes include the:

- assessment of the general standard of performance;
- assessment of the effects of analytical procedures (method principle, instruments, reagents, calibration);
- evaluation of individual laboratory performance;
- identification and justification of problem areas;
- provision of continuing education; and
- identification of needs for training activities.

1.2 ECDC programme, the role of EQA, and specific objectives

Over the years of its existence, Enter-net, an international surveillance network of national reference laboratories and surveillance centres on selected human gastrointestinal infections, was funded by the European Commission. Since 2 October 2007 the Enter-net network has been subsumed into the ECDC disease programme for Food- and Waterborne Diseases and Zoonoses. In 2008, a framework contract on external quality assurance for *Salmonella* and verocytotoxin-producing *E. coli* (VTEC) was put in place for the years 2008 to 2011. The Salmonella EQA contract was won by a consortium led by the Laboratory for Zoonoses and Environmental Microbiology of the National Institute for Public Health and the Environment (RIVM, Bilthoven, Netherlands), in collaboration with the Salmonella Reference Unit of the Laboratory of Gastrointestinal Pathogens of the Health Protection Agency (HPA) in London and the Central Veterinary Institute of Wageningen University and Research Centre, Department of Bacteriology and TSEs (Lelystad, Netherlands). The consortium arranges annual EQA audits for national reference laboratories in EU/EEA countries on serotyping, phage-typing and antimicrobial resistance testing (AST) for salmonellae. EU candidate countries are also invited to participate at cost. Non-EU/EEA countries can also participate at their own expense.

The main objective of the EQA scheme on typing of salmonellae is to evaluate whether typing of *Salmonella* strains by different laboratories within and outside the European Union is carried out uniformly and whether comparable results are obtained.

[1] Decision No 2119/98/EC of the European Parliament and of the Council of 24 September 1998 setting up a network for the epidemiological surveillance and control of communicable diseases in the Community

2 Materials and methods

2.1 Organisation of the study

The second EQA scheme on typing of *Salmonella* spp was organised for the laboratories of the Food- and Waterborne Diseases and Zoonoses Network (FWD-Net). An invitation letter was sent to national EU/EEA reference laboratories for serotyping, phage-typing and antimicrobial resistance testing for *Salmonella*. One EU candidate country, which had responded to an invitation to the first study, was again invited to participate. Non-EU/EEA countries were invited to participate at their own expense. Participating laboratories were given a choice of employing either all or only selected typing methods. A full list of participants is given in Annex 1.

All participants were assigned laboratory code F1-F36, which, at the request of ECDC, was identical to the code used in first EQA scheme.

Three weeks before the start of the study the laboratories received the protocol and a test report form (including a questionnaire) via e-mail. The protocol and test report form are reproduced in Annex 2 and Annex 3.

All samples were packed and classified as UN3373 (Biological Substance, Category B) and transported by door-to-door courier service. The parcels containing the strains for serotyping, phage typing, and/or antimicrobial susceptibility testing were sent by RIVM-LZO on 23 November 2009.

2.2 *Salmonella* strains for serotyping

A total of 20 strains of the species *Salmonella enterica* subspecies *enterica* were selected by RIVM for serotyping. These *Salmonella* strains originated from the collection of the National Salmonella Centre (RIVM) in the Netherlands. The strains were typed once again by LZO before mailing. The antigenic formula of the 20 serovars, according to the most recent White-Kauffmann-Le Minor scheme (Grimont and Weill, 2007), are shown in Table 1.

Table 1: Antigenic formulas of the 20 *Salmonella* strains according to the White-Kauffmann-Le Minor scheme used in the second EQA scheme on *Salmonella* typing

No.	Serovar	O antigens	H antigens
S1	*S.* Llandoff	1,3,19	z_{29}:[z_6]
S2	*S.* London	3,{10}{15}	l,v:1,6
S3	*S.* Infantis	6,7,14	r:1,5
S4	*S.* Bardo	8	e,h:1,2
S5	*S.* Stanley	1,4,[5],12,[27]	d:1,2
S6	*S.* Enteritidis	1,9,12	g,m:-
S7	*S.* Derby	1,4,[5],12	f,g:[1,2]
S8	*S.* Hadar	6,8	z_{10}:e,n,x
S9	*S.* Virchow	6,7,14	r:1,2
S10	*S.* Stockholm	3,{10}{15}	y:z_6
S11	*S.* Agona	1,4,[5],12	f,g,s:[1,2]
S12	*S.* Typhimurium	1,4,[5],12	i:1,2
S13	*S.* Brandenburg	4,[5],12	l,v:e,n,z_{15}
S14	*S.* Kapemba	9,12	l,v:1,7
S15	*S.* Mississippi	1,13,23	b:1,5
S16	*S.* Winslow	13,22	z:1,5
S17	*S.* Ohio	6,7,14	b:l,w
S18	*S.* Thompson	6,7,14	k:1,5
S19	*S.* Lagos	1,4,[5],12	i:1,5
S20	*S.* Altona	8,20	r,[i]:z_6

The evaluation of the serotyping results is described in Table 2.

Due to the recently reported possibility of colonial form variation which may occur with the expression of the O:61 antigen by some serogroup C2 serovars (Hendriksen et al., 2009), it was decided to accept this colonial form variation and to consider the serovar pairs *S.* Newport/*S.* Bardo and *S.* Hadar/*S.* Istanbul not as distinct serovars for the purposes of this second EQA scheme.

Table 2: Evaluation of serotyping results

Results of serotyping	Evaluation
Auto agglutination or incomplete set of antisera (outside the range of antisera)	**nt = not typable**
Partly typable due to incomplete set of antisera or part of the formula (for the name of the serovar)	**+/− = partly correct**
Wrong serovar or mixed sera formula	**− = incorrect**

2.3 *Salmonella* strains for phage typing

The *Salmonella* strains for phage typing were obtained from the collection of the Salmonella Reference Unit of the Laboratory of Gastrointestinal Pathogens, Health Protection Agency (HPA), London, UK. Ten strains of *Salmonella* Enteritidis and 10 strains of *Salmonella* Typhimurium were selected. After selection, the phage reactions of the strains were checked before forwarding them to RIVM for distribution to the participating laboratories. A set of strains for distribution were returned to the Salmonella Reference Unit and the phage reactions were again checked.

Table 3: Phage reactions of the *Salmonella* Enteritidis strains used in the second EQA scheme on *Salmonella* typing

		Phage reactions at routine test dilution (*S.* Enteritidis)																
Strain no.	**Phage type**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	**15**	**16**	**17**
E1	6	-	SCL	-	OL	-	SCL	-	OL	<OL	OL	-	-	-	-	-	-	<OL
E2	22	OL	-	-	SCL	-	+++	-	OL	OL	OL	-	-	-	CL	-	-	SCL
E3	59	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	<OL
E4	1	OL	SCL	CL	OL	CL	SCL	CL	OL	OL	OL	CL	CL	CL	CL	-	-	SCL
E5	3	OL	-	-	-	-	++	-	OL	-	OL	-	-	-	CL	-	-	-
E6	4	-	SCL	CL	OL	CL	SCL	CL	OL	OL	OL	CL	CL	CL	-	-	-	<OL
E7	14b	-	-	-	±	-	SCL	-	-	±	-	-	-	-	-	-	-	OL
E8	1b	OL	SCL	CL	OL	CL	SCL	CL	OL	<OL	<OL	CL	CL	CL	CL	<OL	CL	<OL
E9	21	OL	SCL	-	<OL	-	SCL	-	OL	OL	OL	-	-	-	CL	-	-	<OL
E10	14c	-	-	-	-	-	+++	-	-	-	-	-	-	-	-	-	-	-

−	=	no reaction
+	=	5-20 plaques
+	=	21-40 plaques
++	=	41-80 plaques
+++	=	81-100 plaques
SCL	=	semi-confluent lysis
CL	=	confluent clear lysis
OL	=	confluent opaque lysis
<<	=	merging plaques towards semi-confluent lysis

Table 4: Phage reactions of the *Salmonella* Typhimurium strains used in the second EQA scheme on *Salmonella* typing

		Phage reactions at routine test dilution (*S.* Typhimurium)																
Strain no.	**Phage type**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**10**	**11**	**12**	**13**	**14**	**15**	**16**	**17**	**18**	**19**
T11	10	-	-	-	-	-	-	-	-	CL	OL	CL	CL	-	-	<CL	-	-	-
T12	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
T13	208	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
T14	36	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL
T15	195	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
T16	104	-	-	-	-	-	-	-	-	-	-	SCL	SCL	-	-	-	-	++	-
T17	1	CL	CL	CL	OL	CL	CL	CL	-	CL	OL	CL	CL	CL	CL	CL	CL	SCL	CL
T18	193	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
T19	8	-	-	-	-	-	-	-	+++	SCL	CL	-	-	-	-	+++	-	-	-
T20	40	CL	CL	CL	CL	CL	CL	CL	-	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL

		Phage reactions at routine test dilution (*S.* Typhimurium)												Additional phages						
Strain no.	**Phage type**	**20**	**21**	**22**	**23**	**24**	**25**	**26**	**27**	**28**	**29**	**32**	**35**	**1**	**2**	**3**	**10**	**10 var 2**	**10 var 3**	**18**
T11	10	<CL	-	OL	CL	-	++	+	-	-	CL	CL	-	+	+	+	OL	OL	OL	-
T12	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OL	-
T13	208	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	SCL	SCL	SCL	SCL
T14	36	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	+++	++	+++	OL	OL	OL	OL
T15	195	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+++	-	-	-	-
T16	104	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OL	OL	OL	-
T17	1	CL	CL	CL	CL	CL	CL	CL	CL	-	CL	CL	OL	+++	++	+++	OL	OL	OL	OL
T18	193	-	-	-	-	-	-	-	-	-	-	-	-	+++	+++	+++	-	-	-	-
T19	8	SCL	-	SCL	SCL	-	++	+	-	-	CL	SCL	-	+	+	+	<OL	OL	OL	-
T20	40	CL	CL	CL	CL	CL	CL	CL	CL	-	CL	CL	OL	+	+	+	OL	OL	OL	OL

For notations see Table 3.

2.4 Strains and antibiotics for antimicrobial susceptibility testing (AST)

The *Salmonella* strains used for the antimicrobial susceptibility testing originated from the collection of the Central Veterinary Institute of Wageningen UR (CVI), Department of Bacteriology and TSEs (Lelystad, Netherlands). The ten strains were numbered A1 through A10. The strains were selected based on their resistance phenotype. *S.* Corvallis (strain A2) was selected because of its conventional quinolone resistance phenotype (reduced susceptibility to CIP; NAL susceptible), typical for its qnr-S1 gene. *S.* Kentucky (strain A4) displays a high-level resistance to ciprofloxacin. Strain A8 was selected because it shows the typical ACSSuT resistance profile of *S.* Typhimurium DT104, and strain A9 (*S.* Indiana) was included as an ESBL producer harbouring the blaTEM-52 gene. Two variants of *S.* Paratyphi B var. Java were included (strains A3 and A7) based on their multidrug resistance patterns.

In contrast to the first EQA strain collection used for AST, the aim of the second EQA scheme was to include fewer isolates with susceptibility patterns close to the breakpoints in order to reduce the numbers of results showing artificial deviation.

A summary of the serotypes and sources of strains A1 to A10 is given in Table 5.

Table 5: Serotypes and sources of AST-strains

AST strains	Source	Serotype	Resistance determinants
A1	Human faeces	*S.* subsp. enterica 4,[5],12:i:-	
A2	Human faeces	*S.* Corvallis	Harbouring qnr-S1 gene
A3	Poultry meat product	*S.* Paratyphi B var. Java	Multi-drug resistance pattern
A4	Human faeces	*S.* Kentucky	High level R to CIP
A5	Human blood	*S.* Dublin	
A6	Human faeces	*S.* Typhimurium	
A7	Poultry meat product	*S.* Paratyphi B var. Java	Multidrug resistance pattern
A8	Human faeces	*S.* Typhimurium DT104	ACSSuT resistance profile
A9	Broiler caeca	*S.* Indiana	ESBL producer harbouring blaTEM-52
A10	Human faeces	*S.* Enteritidis Pt4	

The strains were tested in duplicate at CVI for their susceptibility by broth microdilution method using *Sensititre* plates (Trek Diagnostic systems, UK) according to ISO-20776-1:2006. Based on the results of the first EQA trial and in order to meet EFSA's proposal for a harmonised monitoring scheme of antimicrobial resistance in *Salmonella* (EFSA, 2007[2]), amoxicillin-clavulanic acid, ceftazidime, kanamycin, neomycin, florfenicol and trimethoprim/sulfamethoxazole were excluded from the panel in the second EQA trial.

[2] European Food Safety Authority. Report of the Task Force of Zoonoses Data Collection including a proposal for a harmonized monitoring scheme of antimicrobial resistance in *Salmonella* in fowl (*Gallus gallus*), turkeys, and pigs and *Campylobacter jejuni* and *C. coli* in broilers. EFSA Journal, 2007, 96:1–46. Available from: http://www.efsa.europa.eu/fr/efsajournal/doc/96r.pdf.

E. coli ATCC 25922 was used as control strain. The MIC values determined for the prescribed panel of antibiotics and the categories 'resistant (R)' and 'susceptible (S)', based on CLSI breakpoints (M100–S20), are shown in Table 6. Ciprofloxacin isolates with MICs varying from 0.25–0.5 mg/L were classified as 'reduced susceptibility'.

Table 6: MIC results (in µg/ml) of AST strains and of control strain *E. coli* ATCC 25922 determined with a prescribed panel of antibiotics by CVI; inhibition zones of the disk diffusion test are also given for *E. coli* ATCC 25922

Strain number	Antibiotic									
	AMP	**CTX**	**CHL**	**CIP**	**GEN**	**NAL**	**STR**	**SUL**	**TET**	**TMP**
A-1	>32 (R)	0.12 (S)	8 (S)	0.015 (S)	0.5 (S)	≤4 (S)	>128 (R)	>1024 (R)	>64 (R)	≤0.5 (S)
A-2	1 (S)	≤0.06 (S)	4 (S)	0.5 (I)	1 (S)	16 (S)	4 (S)	≤8 (S)	≤1 (S)	≤0.5 (S)
A-3	1 (S)	0.12 (S)	8 (S)	0.03 (S)	≤0.25 (S)	≤4 (S)	128 (R)	>1024 (R)	>64 (R)	>32 (R)
A-4	>32 (R)	0.12 (S)	8 (S)	8 (R)	1 (S)	>64 (R)	16 (S)	≤8 (S)	2 (S)	≤0.5 (S)
A-5	1 (S)	≤0.06 (S)	4 (S)	0.015 (S)	0.5 (S)	≤4 (S)	16 (S)	≤8 (S)	2 (S)	≤0.5 (S)
A-6	>32 (R)	0.25 (S)	8 (S)	0.03 (S)	0.5 (S)	≤4 (S)	16 (S)	≤8 (S)	2 (S)	≤0.5 (S)
A-7	2 (S)	0.12 (S)	8 (S)	0.25 (I)	16 (R)	>64 (R)	128 (R)	>1024 (R)	4 (S)	>32 (R)
A-8	>32 (R)	≤0.06 (S)	>64 (R)	0.015 (S)	0.5 (S)	≤4 (S)	128 (R)	>1024 (R)	64 (R)	≤0.5 (S)
A-9	>32 (R)	>4 (R)	4 (S)	0.015 (S)	0.5 (S)	≤4 (S)	16 (S)	≤8 (S)	≤1 (S)	≤0.5 (S)
A-10	>32 (R)	≤0.06 (S)	8 (S)	0.25 (I)	0.5 (S)	>64 (R)	4 (S)	≤8 (S)	2 (S)	≤0.5 (S)
E. coli (MIC)	2-8	0.03-0.12	2-8	0.004-0.015	0.25-1	1-4	No CLSI QC-range	8-32	0.5-2	0.5-2
E. coli (disk)[1]	(10) 16-22	(30) 29-35	(30) 21-27	(5) 30-40	(10) 19-26	(30) 22-28	(10) 12-20	(300) 15-23	(30) 18-25	(5) 21-28

Dark grey cells = resistant (R); light grey cells = reduced susceptibility (I); white cells = susceptible (S); 1: disc load in µg between brackets, zone diameter in mm.

The participating laboratories were asked to use their standard method for susceptibility testing. If a disk diffusion test was used, the following antibiotics and concentrations in the disks were requested:

- Ampicillin (10 µg)
- Cefotaxime (30 µg)
- Chloramphenicol (30 µg)
- Ciprofloxacin (5 µg)
- Gentamicin (10 µg)
- Nalidixic acid (30 µg)
- Streptomycin (10 µg)
- Sulfonamides (250 or 300 µg)
- Tetracycline (30 µg)
- Trimethoprim (5 µg)

Laboratories that did not have the disks with the required amount of antibiotics were asked to omit that antibiotic from their list. In order to determine MICs, the participants were asked to test the same antibiotics as for the diffusion tests.

Participants using a quantitative method were asked to record the determined MIC values. All participants were asked to categorise their results as susceptible (S), intermediate (I) or resistant (R) according to their own breakpoint criteria. The deviations from the categories determined by CVI (Table 6) were classified as minor or major deviations. For example, an R-I (i.e. a resistant strain was classified as intermediate or vice versa) or an S-I deviation was classified as a 'minor deviation', while an S-R or an R-S deviation constituted a 'major deviation'.

The CLSI clinical breakpoints, which are most commonly used by the majority of the participating laboratories, were used as the reference interpretative criteria. The CLSI clinical breakpoints for MICs according to guideline M100–S20 (CLSI, January 2010) and interpretive criteria for disk diffusion according to guideline M100–S20/M31–A3 (CLSI, 2010/CLSI, 2008) are shown in Table 7. For cefotaxime and other cefalosporins, CLSI has substantially changed the interpretive criteria and breakpoints. Specific low breakpoints for sensitive ESBL-detection including confirmatory tests is not advised anymore by CLSI. However, the use of CLSI guideline M100–S20 of January 2010 was of no consequence for the interpretation of results compared with CLSI guideline M100–S19 (see section 3.5.1).

Table 7: CLSI interpretive criteria in mg/L for MIC and mm for disk diffusion

	MIC (M100–S20) (mg/L)		Disk diffusion (M100–S20/M31–A3) (mm)	
Antibiotics	**Susceptible**	**Resistant**	**Susceptible**	**Resistant**
Ampicillin (AMP)	≤8	≥32	≥17	≤13
Cefotaxime (CTX)	≤1	≥4	≥26	≤22
Chloramphenicol (CHL)	≤8	≥32	≥18	≤12
Ciprofloxacin (CIP)	≤1	≥4	≥21	≤15
Gentamicin (GEN)	≤4	≥16	≥15	≤12
Nalidixic Acid (NAL)	≤16	≥32	≥19	≤13
Streptomycin (STR)	≤ 16	≥32[#]	≥15	≤11
Sulfonamides* (SUL)	≤ 256	≥512	≥17	≤ 12
Tetracycline (TET)	≤4	≥16	≥19	≤14
Trimethoprim (TMP)	≤8	≥16	≥16	≤10

** CLSI breakpoints for sulfisoxazole used.*
 # EURL-AST breakpoint used.

3 Results

3.1 Overview of participation and results

Overall, thirty-five laboratories participated in the second EQA scheme, though one laboratory did not return its results. Twenty-eight laboratories of the participating laboratories were located in the Member States of the European Union (EU) or in countries of the European Economic Area (EEA), the remaining seven were from countries outside the EU/EEA.

An overview of the number of laboratories scoring 100% according to intended results and number of laboratories participating by test (laboratories in EU/EEA countries and all participating laboratories) is given in Table 8.

Table 8: Number of laboratories scoring 100% according to intended results and number of laboratories participating by test; EU/EEA countries and all participating laboratories

Tests	EU/EEA		All laboratories	
	All correct	Participating	All correct	Participating
Serotyping (20 strains)				
O antigens	22	25	26	32
H antigens	15	25	17	32
Serovar name	15	25	16	32
Phage typing				
S. Enteritidis (10 strains)	6	16	6	20
S. Typhimurium (10 strains)	7	14	10	18
Antimicrobial susceptibility testing (9 antimicrobials, 10 strains*)	3	25	3	31

** Except for A4 for ampicillin and A9 for cefotaxime*

3.2 Questionnaire results

3.2.1 General questions

In this section the questions and answers of the questionnaire are summarised. For details please refer to Annex 4, Table 1.

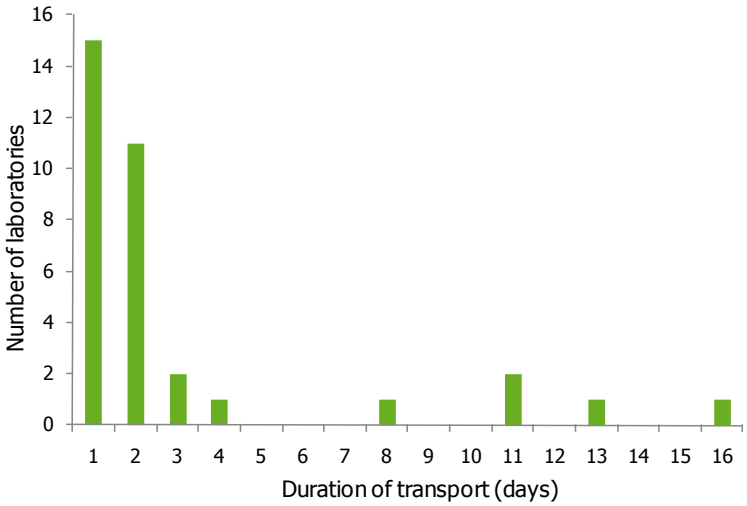
Question 1: Was your parcel damaged at arrival?

All parcels were received in a perfect state and no damage was reported.

Question 2: What was the date of receipt at your laboratory?

Figure 1 shows the duration of shipment. Most laboratories received the parcels in the same week they were sent (week 48/2009). For countries outside the EU/EEA, the parcels took more than four days to arrive (five laboratories; 8, 11 [2 laboratories], 13, and 16 days).

Figure 1: Duration of transport (parcels with samples shipped to laboratories)



Question 3: What kind of medium did you use for sub-culturing the strains?

The laboratories used a variety of media from various manufacturers for the subculturing of the *Salmonella* strains (see Table 1, Annex 4). Nutrient agar and TSA were the most commonly used media.

3.2.2 Questions regarding serotyping

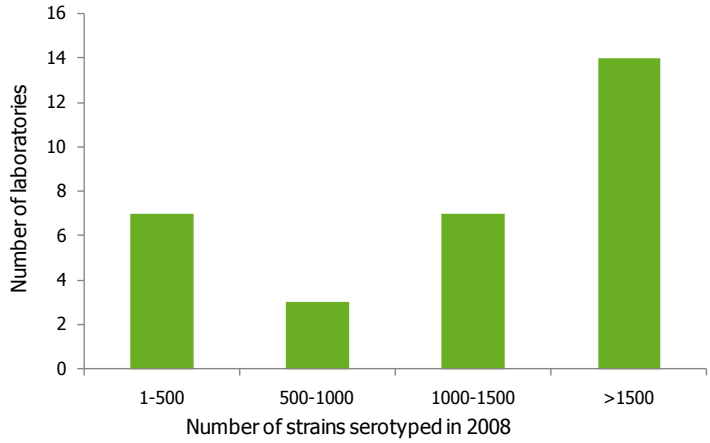
Details regarding serotyping are given in Annex 4, Table 2. A summary is given below.

Question 4: What was the frequency of **Salmonella** *serotyping at your laboratory in 2008?*

The majority of the laboratories (n=25) indicated that samples were serotyped daily. One laboratory serotypes twice a week, two laboratories serotype thrice a week, and three laboratories type weekly. One (non-EU/EEA) laboratory only serotypes on demand.

Question 5: How many **Salmonella** *strains did your laboratory (approximately) serotype in 2008?*

Figure 2: Frequency distribution of the number of strains serotyped by the laboratories in 2008



Question 6: What kind of sera do you use?

Table 9: Number of laboratories using sera from one or more manufacturers

Sera obtained from:	Number of laboratories
One manufacturer	8
Two manufacturers	5
Three manufacturers	8
Four manufacturers	6
Five or more manufacturers	5

Table 10: Number of laboratories using sera from one or more manufacturers and/or in-house prepared sera

Manufacturer	Number of laboratories
Bio-Rad	12
Dade Behring	2
Denka Seiken	5
Difco	2
Lucron	2
Mast Assure	2
Prolab	3
Reagensia AB	3
Remel	4
Sifin	13
SSI	26
Own lab	13
Other	6

Question 7: Were the strains in the EQA scheme typed in your own laboratory?

All strains were typed in their own laboratories.

3.2.3 Questions regarding phage typing

Details regarding phage typing are given in Annex 4, Table 3. A summary is given below.

Question 8: Does your laboratory perform phage typing?

Twenty laboratories carry out phage typing of *Salmonella* Enteritidis, and eighteen laboratories carry out phagetyping of *Salmonella* Typhimurium.

Question 9: If yes, which **Salmonella** *strains do you phage type?*

In addition to *S.* Enteritidis and *S.* Typhimurium, the most commonly phage-typed strains are *S.* Typhi (10x), *S.* Paratyphi B (7x), *S.* Hadar (6x) and *S.* Virchow (5x).

Question 10: Which typing system is used for **Salmonella** *Enteritidis?*

Sixteen laboratories cite the Health Protection Agency, HPA Colindale, London, as the source of their typing system for *S.* Enteritidis ('HPA/Colindale'). Four labs quote 'Ward's system', which is identical to the HPA's typing system. One country uses its own national system in addition to Ward's.

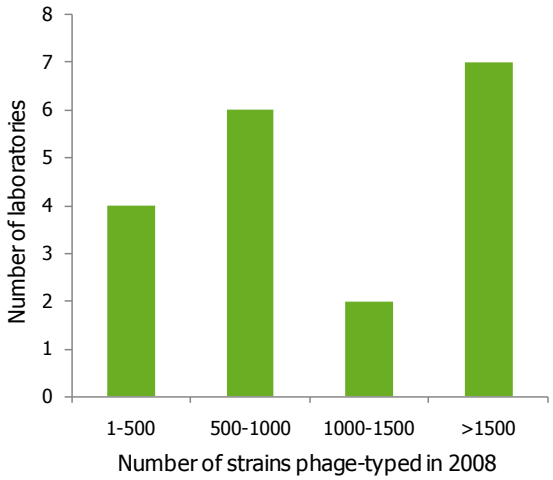
Question 11: Which typing system is used for **Salmonella** *Typhimurium?*

Twelve laboratories give HPA/Colindale as their typing system for *S.* Typhimurium. Four labs list 'Anderson's system', and one country uses Felix-Callow's in addition to Ward's, which is the same as the HPA/Colindale system.

Question 12: How many strains did your laboratory (approximately) phage type in 2008?

Figure 3 shows the frequency distribution of the number of strains that were phage-typed by the laboratories in 2008.

Figure 3: Frequency distribution of the number of strains phage-typed by the laboratories in 2008



3.2.4 Questions regarding antimicrobial susceptibility testing

Details regarding antimicrobial susceptibility testing in the questionnaire are given in Annex 4, Tables 4 and 5. A summary is given below.

Question 13: What method do you use for antimicrobial susceptibility testing?

A total of 20 laboratories, including three from non-EU/EEA countries, used a disk-diffusion method, and 11 laboratories, including three non-EU/EEA ones, used an MIC method for antimicrobial susceptibility testing.

Question 14: Which control strain (S) do you use with routine analysis?

All but two laboratories used the *E. coli* ATTC 25922 strain as control strain. Some laboratories also used additional strains, e.g. *E.* faecalis or *Salmonella*.

Question 15: Which agar/broth medium do you use?

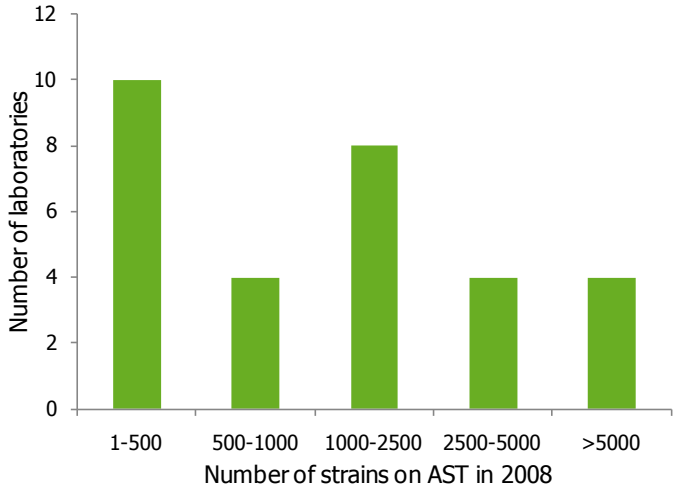
Mueller-Hinton agar was by far the most commonly used agar/broth medium.

Question 16: What is the concentration of the inoculum in bacteria per ml?

Eighteen out of the 20 laboratories that test by disk diffusion used an inoculum of ca. 1 x 10^8 cfu/ml (0.5 McFarland). Laboratories testing by MIC more commonly used a lower inoculum of about 10^5–10^6 cfu/ml.

Question 17: How many strains were (approximately) tested for antimicrobial susceptibility in your laboratory in 2008?

Figure 4: Frequency distribution showing the number of strains tested for antimicrobial susceptibility; participating laboratories in 2008



Question 18: Which antibiotics did you use in this EQA scheme?
The majority of laboratories tested the entire range of antibiotics as indicated by the study. Some laboratories omitted one or more of these antibiotics; see overview Annex 4, Table 5.

3.3 Serotyping results

3.3.1 Serotyping results for EU/EEA laboratories

Exact numbers on the correct or incorrect identification of O and H antigens and serovars (EU/EEA laboratories) are given in Annex 5 and summarised in Figures 5, 6, and 7.

Generally, the identification of H antigen produced more deviations than O antigen detection. Six laboratories incorrectly identified one to three serotype names, one laboratory listed ten incorrect serovars, and one laboratory provided twelve incorrect results (total: 20 serotypes).

Figure 5: Distribution of deviations in O antigen typing; EU/EEA laboratories

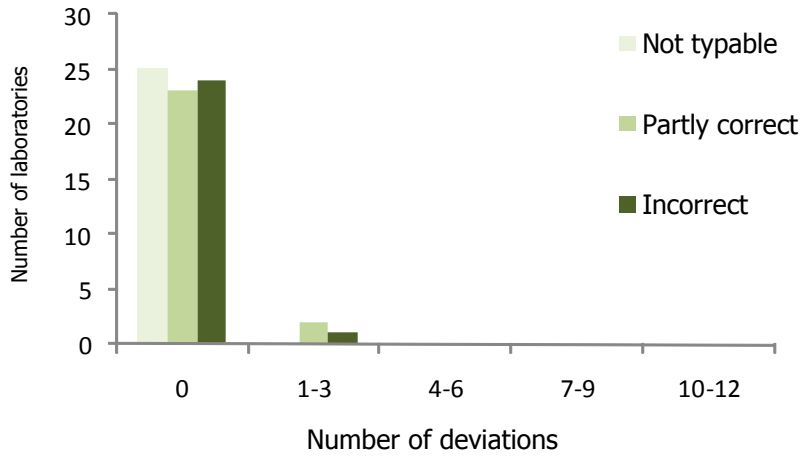


Figure 6: Distribution of deviations in H antigen typing; EU/EEA laboratories

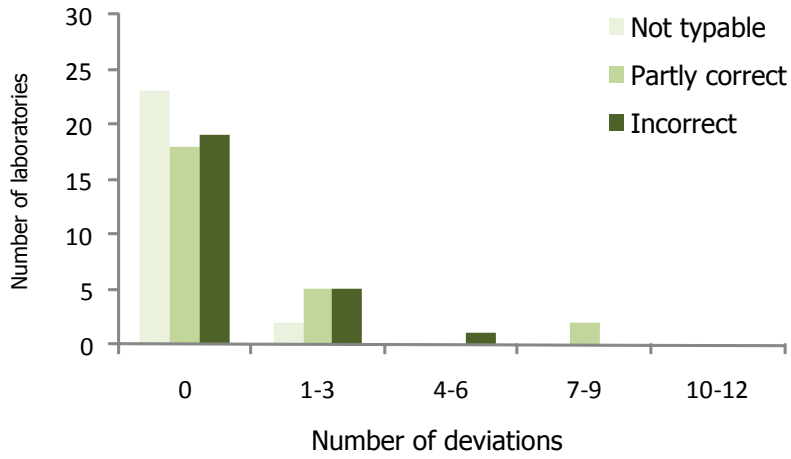


Figure 7: Distribution of deviations in serovar names; EU/EEA laboratories

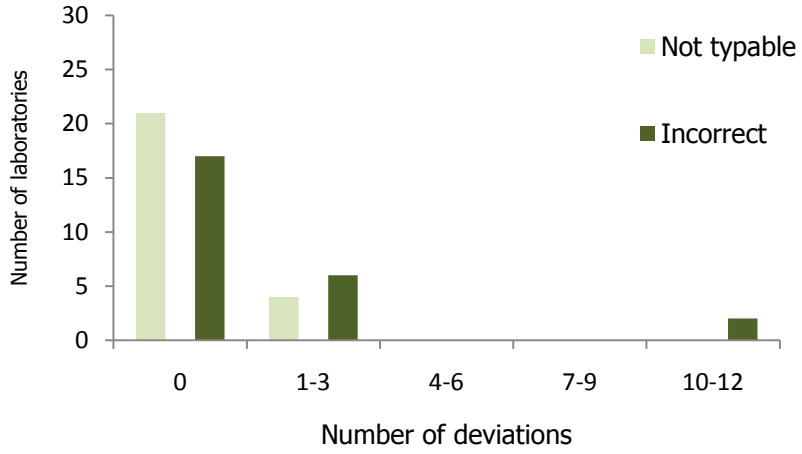
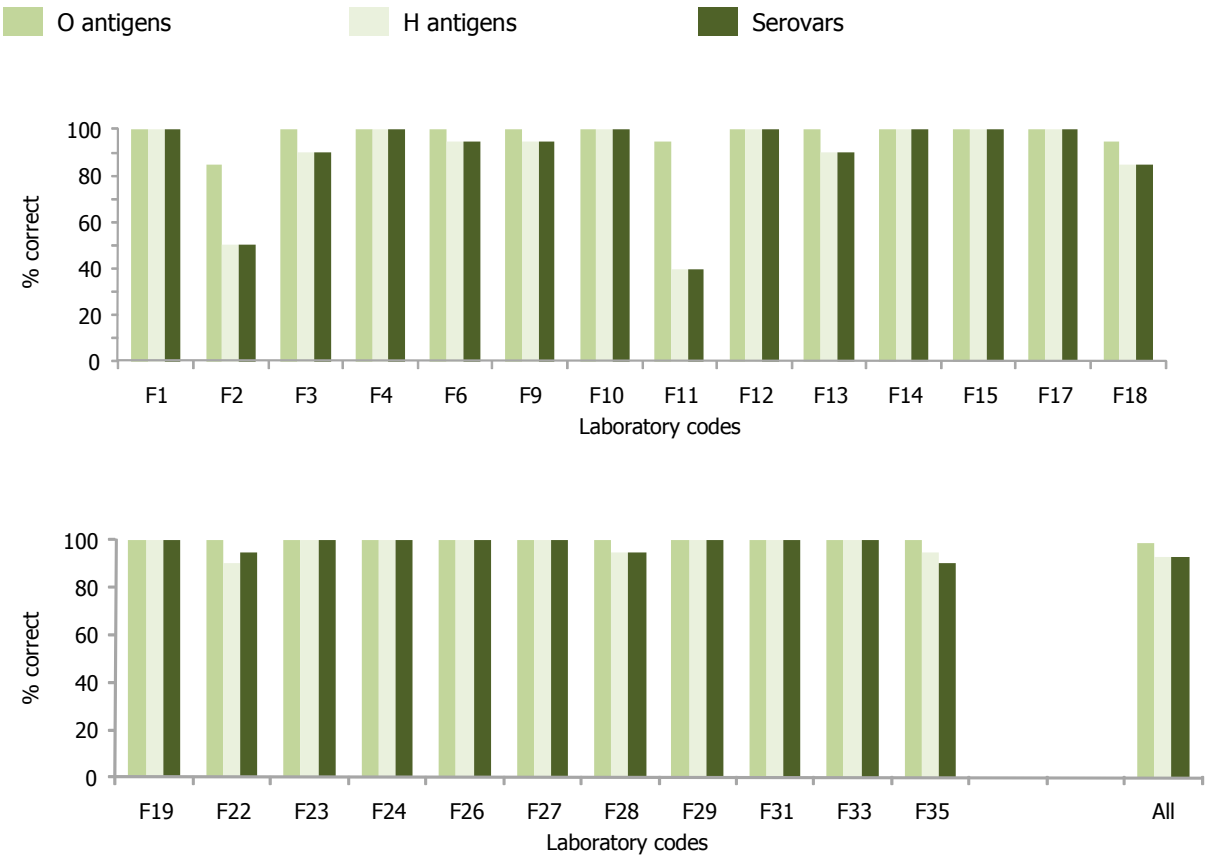


Figure 8 provides the percentage of correct identifications for O and H antigens and serovars for EU/EEA laboratories.

Twenty-two of the 25 participating EU/EEA laboratories (88%) typed all O antigens correctly. This corresponds to 99% of the total amount of strains.

Fifteen (60%) EU/EEA laboratories typed all H antigens correctly, corresponding to 93% of the total amount of supplied strains. Fifteen (60%) EU/EEA laboratories identified all serovar names correctly, corresponding to 93% of all strains.

Figure 8: Correctly serotyped samples in percent; EU/EEA laboratories



3.3.2 Serotyping results for all participants

Numbers on the detection of O and H antigens as well as serovar identification for all participating laboratories are available in Annex 6. These results are summarised in Figures 9, 10, and 11.

Generally, H antigen detection produced more deviations than O antigen detection. Ten laboratories incorrectly identified one to three serotype names, one laboratory listed ten incorrect serovars, and one laboratory provided twelve incorrect results (total: 20 serotypes).

Figure 9: Distribution of deviations in O antigen detection; all laboratories

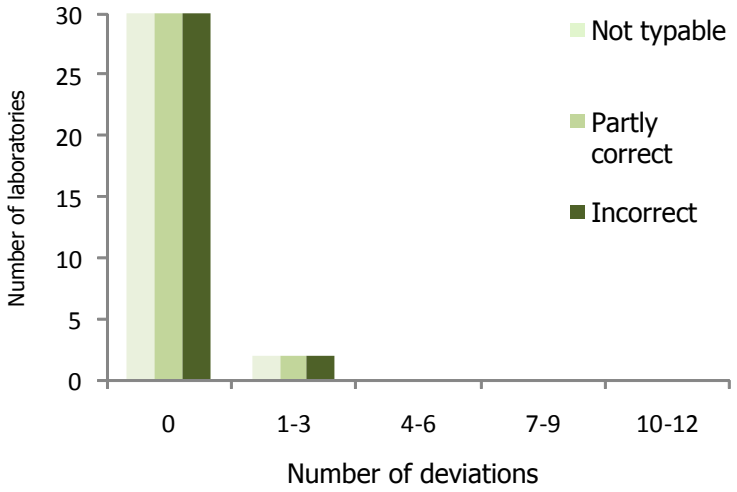


Figure 10: Distribution of deviations in H antigen detection; all laboratories

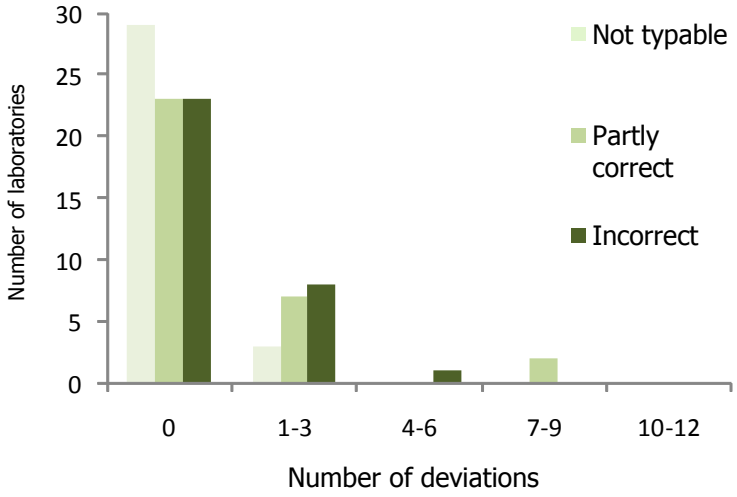
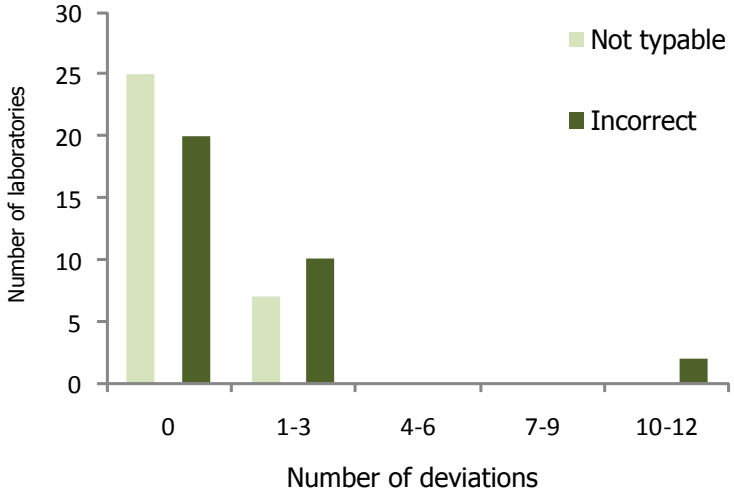
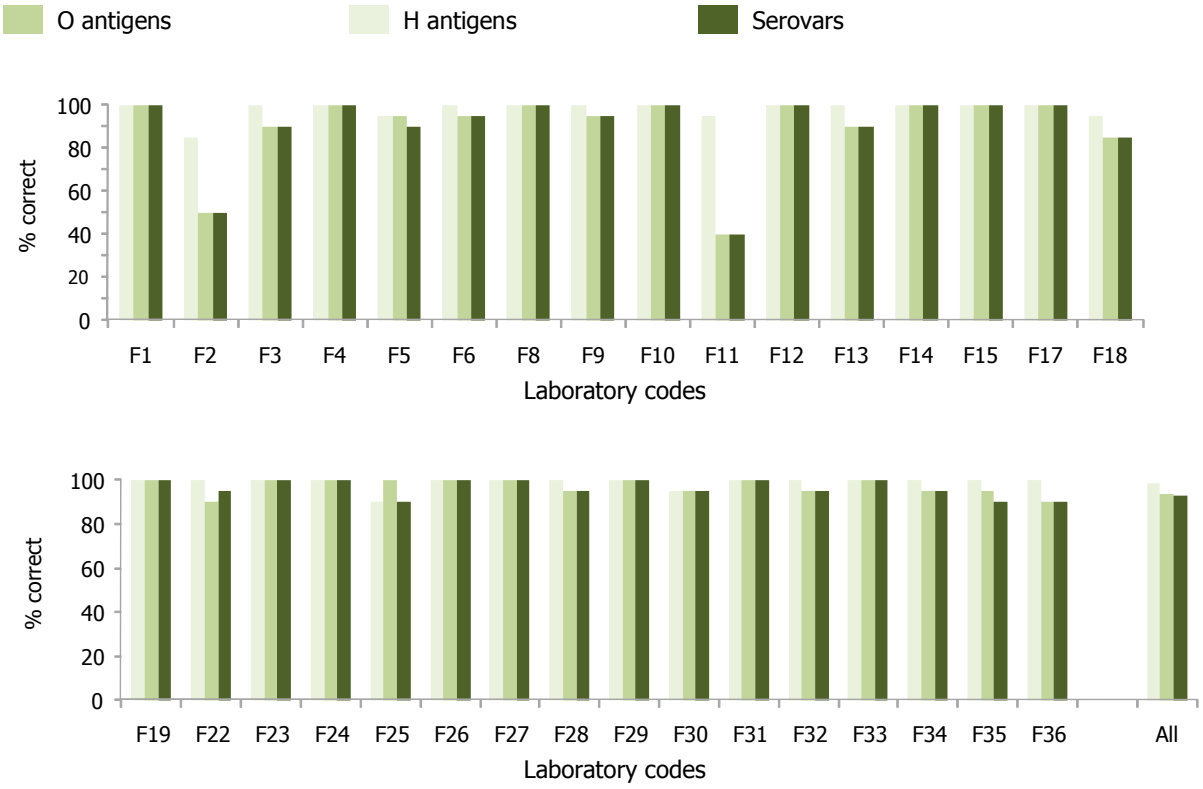


Figure 11: Distribution of deviations in serovar names; all laboratories



The percentages correctness of the detection of O and H antigens and identification of the strains for all laboratories are given in Figure 12. Twenty-six of the thirty-two participating laboratories (81%) typed all O antigens correctly. This corresponds to 99% of the total amount of strains. Seventeen (53%) laboratories typed all H antigens correctly, corresponding to 94% of the total amount of strains. Sixteen laboratories (50%) identified all serovar names correctly, corresponding to 93% of all strains.

Figure 12: Correctly serotyped samples in percent; all laboratories



3.3.3 Results of serotyping by strain

Results for each strain and each laboratory are given in Table 11.

All laboratories correctly identified *S.* Stanley (S5) and *S.* Typhimurium (S12).

Most problems (11 laboratories) occurred with serovar *S.* Llandoff (S1). Serovars *S.* Infantis (S 3), *S.* Stockholm (S10), and *S.* Winslow (S16) caused problems in four laboratories. Strains that caused problems in serotyping by the laboratories are shown in Table 12. Serotyping problems could not be directly linked to the use of a particular brand of sera (also see section 3.2.2).

Table 11: Test results of serotyping; by strain for all laboratories

Lab	S1	S2	S3	S4	S5	S6	S7	S8	S9	S10	S11	S12	S13	S14	S15	S16	S17	S18	S19	S20	
RIVM	Llandoff	London	Infantis	Bardo/ Newport	Stanley	Enteritidis	Derby	Hadar/ Istanbul	Virchow	Stockholm	Agona	Typhimurium	Brandenburg	Kapemba	Mississippi	Winslow	Ohio	Thompson	Lagos	Altona	Y
F1	Llandoff	London	Infantis	Bardo	Stanley	Enteritidis	Derby	Hadar	Virchow	Stockholm	Agona	Typhimurium	Brandenburg	Kapemba	Mississippi	Winslow	Ohio	Thompson	Lagos	Altona	0
F2	Llandoff	Give	Grampian	Edmonton	Stanley	Hillingdon	Kalamu	Hadar	Virchow	London	Agona	Typhimurium	Brandenburg	Kapemba	Poona	Winslow	Kotte	Thompson	Farsta	Hindmarsh	10
F3	Llandoff	London	Infantis	Bardo	Stanley	Enteritidis	Derby	Hadar	Virchow	Amager	Agona	Typhimurium	Brandenburg	Kapemba	Mississippi	S. spp. salamae	Ohio	Thompson	Lagos	Altona	2
F4	Llandoff	London	Infantis	Bardo	Stanley	Enteritidis	Derby	Hadar	Virchow	Stockholm	Agona	Typhimurium	Brandenburg	Kapemba	Mississippi	Winslow	Ohio	Thompson	Lagos	Altona	0
F5	Tomelilla	London	S. I ser rough :r:1,5	Newport	Stanley	Enteritidis	Derby	Hadar	Virchow	Stockholm	Agona	Typhimurium	Brandenburg	Kapemba	Mississippi	Winslow	Ohio	Thompson	Lagos	Altona	2
F6	Accra	London	Infantis	Newport	Stanley	Enteritidis	Derby	Hadar	Virchow	Stockholm	Agona	Typhimurium	Brandenburg	Kapemba	Mississippi	Winslow	Ohio	Thompson	Lagos	Altona	1
F8	Llandoff	London	Infantis	Bardo	Stanley	Enteritidis	Derby	Hadar	Virchow	Stockholm	Agona	Typhimurium	Brandenburg	Kapemba	Mississippi	Winslow	Ohio	Thompson	Lagos	Altona	0
F9	Llandoff	London	Infantis	Newport	Stanley	Enteritidis	Derby	Hadar	Virchow	Stockholm	Agona	Typhimurium	Brandenburg	Kapemba	Mississippi	Unnamed	Ohio	Thompson	Lagos	Altona	1
F10	Llandoff	London	Infantis	Bardo	Stanley	Enteritidis	Derby	Hadar	Virchow	Stockholm	Agona	Typhimurium	Brandenburg	Kapemba	Mississippi	Winslow	Ohio	Thompson	Lagos	Altona	0
F11	Senftenberg	London	Virchow	Bardo	Stanley	Enteritidis	S. Paratyphi B var. Java	Hadar	Colindale	Amager	Brandenburg	Typhimurium	Bredeney	Dublin	Worthington	Roodepoort	Colorado	Thompson	Lagos	Goldcoast	12
F12	Llandoff	London	Infantis	Bardo	Stanley	Enteritidis	Derby	Hadar	Virchow	Stockholm	Agona	Typhimurium	Brandenburg	Kapemba	Mississippi	Winslow	Ohio	Thompson	Lagos	Altona	0
F13	Lerum	London	Bareilly	Bardo	Stanley	Enteritidis	Derby	Hadar	Virchow	Stockholm	Agona	Typhimurium	Brandenburg	Kapemba	Mississippi	Winslow	Ohio	Thompson	Lagos	Altona	2
F14	Llandoff	London	Infantis	Newport	Stanley	Enteritidis	Derby	Hadar	Virchow	Stockholm	Agona	Typhimurium	Brandenburg	Kapemba	Mississippi	Winslow	Ohio	Thompson	Lagos	Altona	0
F15	Llandoff	London	Infantis	Newport	Stanley	Enteritidis	Derby	Hadar	Virchow	Stockholm	Agona	Typhimurium	Brandenburg	Kapemba	Mississippi	Winslow	Ohio	Thompson	Lagos	Altona	0
F17	Llandoff	London	Infantis	Newport	Stanley	Enteritidis	Derby	Hadar	Virchow	Stockholm	Agona	Typhimurium	Brandenburg	Kapemba	Mississippi	Winslow	Ohio	Thompson	Lagos	Altona	0
F18		London	Infantis	Bardo	Stanley	Enteritidis	Derby	Hadar	Virchow	Stockholm	Agona	Typhimurium	Brandenburg	Kapemba	Mississippi	II		Thompson	Lagos	Altona	3
F19	Llandoff	London	Infantis	Bardo	Stanley	Enteritidis	Derby	Hadar	Virchow	Stockholm	Agona	Typhimurium	Brandenburg	Kapemba	Mississippi	Winslow	Ohio	Thompson	Lagos	Altona	0
F22	Serogroup 4	London	Infantis	Bardo	Stanley	Enteritidis	Derby	Istanbul	Virchow	Stockholm	Agona	Typhimurium	Brandenburg	Kapemba	Mississippi	Winslow	Ohio	Thompson	Lagos	Altona	1
F23	Llandoff	London	Infantis	Bardo	Stanley	Enteritidis	Derby	Hadar	Virchow	Stockholm	Agona	Typhimurium	Brandenburg	Kapemba	Mississippi	Winslow	Ohio	Thompson	Lagos	Altona	0
F24	Llandoff	London	Infantis	Bardo	Stanley	Enteritidis	Derby	Hadar	Virchow	Stockholm	Agona	Typhimurium	Brandenburg	Kapemba	Mississippi	Winslow	Ohio	Thompson	Lagos	Altona	0
F25	Llandoff	London	Infantis	Bardo	Stanley	Enteritidis	Derby	S. ssp1, OR:z10:e,n,x	S. ssp, OR:r:1,2	Stockholm	Agona	Typhimurium	Brandenburg	Kapemba	Mississippi	Winslow	Ohio	Thompson	Lagos	Altona	2
F26	Llandoff	London	Infantis	Bardo	Stanley	Enteritidis	Derby	Hadar	Virchow	Stockholm	Agona	Typhimurium	Brandenburg	Kapemba	Mississippi	Winslow	Ohio	Thompson	Lagos	Altona	0
F27	Llandoff	London	Infantis	Bardo	Stanley	Enteritidis	Derby	Hadar	Virchow	Stockholm	Agona	Typhimurium	Brandenburg	Kapemba	Mississippi	Winslow	Ohio	Thompson	Lagos	Altona	0
F28	Senftenberg	London	Infantis	Bardo	Stanley	Enteritidis	Derby	Hadar	Virchow	Stockholm	Agona	Typhimurium	Brandenburg	Kapemba	Mississippi	Winslow	Ohio	Thompson	Lagos	Altona	1
F29	Llandoff	London	Infantis	Bardo	Stanley	Enteritidis	Derby	Hadar	Virchow	Stockholm	Agona	Typhimurium	Brandenburg	Kapemba	Mississippi	Winslow	Ohio	Thompson	Lagos	Altona	0
F30	Llandoff	London	Infantis	Bardo	Stanley	Enteritidis	Derby	Hadar	Virchow	Stockholm	Agona	Typhimurium	Brandenburg	Kapemba	Mississippi	Winslow	Ohio	Thompson	Lagos	Thompson	1
F31	Llandoff	London	Infantis	Bardo	Stanley	Enteritidis	Derby	Hadar	Virchow	Stockholm	Agona	Typhimurium	Brandenburg	Kapemba	Mississippi	Winslow	Ohio	Thompson	Lagos	Altona	0
F32	Taksony	London	Infantis	Bardo	Stanley	Enteritidis	Derby	Hadar	Virchow	Stockholm	Agona	Typhimurium	Brandenburg	Kapemba	Mississippi	Winslow	Ohio	Thompson	Lagos	Altona	1
F33	Llandoff	London	Infantis	Bardo	Stanley	Enteritidis	Derby	Hadar	Virchow	Stockholm	Agona	Typhimurium	Brandenburg	Kapemba	Mississippi	Winslow	Ohio	Thompson	Lagos	Altona	0
F34	1,3,19:-:-	London	Infantis	Bardo	Stanley	Enteritidis	Derby	Hadar	Virchow	Stockholm	Agona	Typhimurium	Brandenburg	Kapemba	Mississippi	Winslow	Ohio	Thompson	Lagos	Altona	1
F35	Senftenberg	London	Infantis	Bardo	Stanley	Enteritidis	Derby	Hadar	Virchow	Yoruba	Agona	Typhimurium	Brandenburg	Kapemba	Mississippi	Winslow	Ohio	Thompson	Lagos	Altona	2
F36	Senftenberg	London	Infantis	Bardo	Stanley	Enteritidis	Derby	Hadar	Virchow	Stockholm	Agona	Typhimurium	Brandenburg	Kapemba	Mississippi	Winslow	Ohio	Bareilly	Lagos	Altona	2
X	11	1	4	1	0	1	2	1	2	4	1	0	1	1	2	4	3	1	1	3	

X: number of deviating laboratories by strain; Y: number of deviating strains by laboratory

Table 12: Identifications causing problems with serotyping; all laboratories, by strain

Strain	O antigens	H antigens	Serovar	Lab code
S1	**1,3,19**	**z_{29}:[z_6]:[z_{37}]**	***S.* Llandoff**	**RIVM**
	19	l,z28 : 1,7	*S.* Tomelilla	F5
	3,19	b:z6	*Salmonella* Accra	F6
	1,3,19	g,s,t:-	S. Senftenberg	F11
	1,3,19	z:1,7	S. Lerum	F13
	1,3,19	Z29:-	*S.* Llandoff *(rough)	F17
	1, 3, 19			F18
	1,3,19	-	Serogroup E4*	F22
	1,3,19	g,t	*S.* Senftenberg	F28
	3,19	i, z6	*S.* Taksony	F32
	1,3,19	z45	*S.* Senftenberg	F35
	1,3,19	- : -	1,3,19:-:-	F34
	1, 3, 19	g, s, t; - [z27], [z34], [z45]	*S.* Senftenberg	F36
S2	**3,{10}{15}**	**l,v:1,6**	***S.* London**	**RIVM**
	3{10}{15}{15,34}	l,v:1,7	Give	F2
S3	**6,7,14**	**r:1,5**	***S.* Infantis**	**RIVM**
	6,7	r:l,w	Grampian	F2
	rough	r : 1,5	*S.* I ser rough:r:1,5	F5
	6,7,14	r:1,2	S. Virchow	F11
	7,14	y:1,5	S. Bareilly	F13
S4	**8**	**e,h:1,2**	***S.* Bardo**	**RIVM**
	6,8	l,v:e,n,z15	Edmonton	F2
	6,8	e,h : 1,2	*S.* Newport	F5
	8	e,h:1,2	*Salmonella* Newport	F6
	6,8	e,h : 1,2	Newport	F9
	6,8	e,h:1,2	Newport	F14
	6,8	e,h:2	Newport	F15
	6,8	e,h:1,2	*S.* Newport	F17
S6	**1,9,12**	**g,m:-**	***S.* Enteritidis**	**RIVM**
	9,46	g,m:-	Hillingdon	F2
	9	m, t, s	Enteritidis	F18
S7	**1,4,[5],12**	**f,g:[1,2]**	***S.* Derby**	**RIVM**
	1,4,[5],12	z4,z24:-	Kalamu	F2
	1,4,5,12	b:1,2	S. Paratyphi B var. Java	F11
S8	**6,8**	**z_{10}:e,n,x**	***S.* Hadar**	**RIVM**
	8	e,n,x	Istanbul	F22
	organism rough	z10:e,n,x	S. ssp1, OR:z10:e,n,x	F25
S9	**6,7,14**	**r:1,2**	***S.* Virchow**	**RIVM**
	6,7	r:1,7	S. Colindale	F11
	organism rough	r:1,2	S. ssp1, OR:r:1,2	F25
S10	**3,{10}{15}**	**y:z_6**	***S.* Stockholm**	**RIVM**
	3,{10},{15}	l,v:1,6	London	F2
	3,10	y:1,2	*S.*Amager	F3
	3,10,15	y:1,2	S. Amager	F11
	3,10	y : z6	*S.* Yoruba	F35
S11	**1,4,[5],12**	**f,g,s:[1,2]:[z_{27}],[z_{45}]**	***S.* Agona**	**RIVM**
	4,5,12	l,v: enz15	S. Brandenburg	F11
S13	**4,[5],12**	**l,v:e,n,z_{15}**	***S.* Brandenburg**	**RIVM**
	1,4,12,27	l,v:1,7	S. Bredeney	F11
S14	**9.12**	**l,v:1,7**	***S.* Kapemba**	**RIVM**

Strain	O antigens	H antigens	Serovar	Lab code
	1,9,12	g,p:-	S. Dublin	F11
S15	**1,13,23**	**b:1,5**	***S.* Mississippi**	**RIVM**
	1,13,22	z:1,6	Poona	F2
	1,13,23	z:l,w	S. Worthington	F11
S16	**13.22**	**z:1,5**	***S.* Winslow**	**RIVM**
	13,22	1,5	*S.spp.salamae*	F3
	13,22	- : 1,5	Unnamed	F9
	1,13,22	z10:1,5	S. Roodepoort	F11
	6, 7	z: 1, 5	II	F18
S17	**6,7,14**	**b:l,w:[z_{59}]**	***S.* Ohio**	**RIVM**
	6,7	b:z35	Kotte	F2
	6,7	l,w:1,5	S. Colorado	F11
	6, 7	b		F18
S18	**6,7,14**	**k:1,5**	***S.* Thompson**	**RIVM**
	6, 7	y; 1, 5	*S.* Bareilly	F36
S19	**1,4,[5],12**	**i:1,5**	***S.* Lagos**	**RIVM**
	4,12	i:e,n,x	Farsta	F2
S20	**8,20**	**r,[i]:z_6**	***S.* Altona**	**RIVM**
	8,20	r:1,5	Hindmarsh	F2
	6,8	r:l,w	S. Goldcoast	F11
	6,7	k:1,5	Thompson	F30

3.4 Phage typing results

3.4.1 Phage typing results for the EU/EEA laboratories

Fourteen laboratories carried out phage typing of both *Salmonella* Enteritidis and *Salmonella* Typhimurium. Two further laboratories only carried out phage typing of *S.* Enteritidis. Separate notations by phage type and by laboratory are given in Annex 7. The phage typing results of the EU/EEA laboratories were evaluated by strain and by laboratory. Results for *S.* Enteritidis are shown in Table 13 and data for *S.* Typhimurium are shown in Table 14.

Table 13: Results of *Salmonella* Enteritidis phage typing; EU/EEA laboratories

	E1	E2	E3	E4	E5	E6	E7	E8	E9	E10	Y
HPA	**6**	**22**	**59**	**1**	**3**	**4**	**14b**	**1b**	**21**	**14c**	
F1	6	22	59	1	3	4	14b	1b	21	14c	0
F2	6	22	59	1a	21b	4	14b	1b	21	14c	2
F4	6	22	59	1	3	4	14b	1b	21	14c	0
F6	6c	22	59	37	3a	4	14b	1b	3	14c	4
F7	6c	22	59	1	3	4	14b	1b	21c	14c	2
F13	6	22	59	44	3a	4	14b	1b	3	14c	3
F14	6	22	59	44	3	4	14b	1b	21c	14c	2
F17	6	22	14b	1	21	4b	14b	1b	21c	55	5
F19	6	22	59	1	unstable	4	14b	1b	21	14c	1
F23	6	22	59	1	3	4	14b	1b	21	14c	0
F24	6	22	59	37	3	8	14b	9b	2	14c	4
F26	6	22	59	1	3	4	14b	1b	21	14c	0
F27	6	22	59	1	3	4	14b	1b	21	14c	0
F29	6	22	59	1	21	4	14b	1b	21c	14c	2
F31	6	22	59	1	3	4	14b	1b	21	14c	0
F35	6	22	59	1	21	4	14b	1b	21	14c	1
X	2	0	1	5	7	2	0	1	7	1	26

Grey cells = deviating results

X: number of deviating laboratories by strain

Y: number of deviating strains by laboratory

Table 14: Results of *Salmonella* Typhimurium phage typing; EU/EEA laboratories

	T11	T12	T13	T14	T15	T16	T17	T18	T19	T20	Y
HPA	**10**	**U311**	**208**	**36**	**195**	**104**	**1**	**193**	**8**	**40**	
F1	10	U311	208	36	195	104	1	193	8	40	0
F2	10	U311	208	36	195	104	1	193	8	40	0
F4	10	U311	208	36	195	104	1	193	8	40	0
F6	10	U311	U302	36	195	104	1	193	8	40	1
F7	10	U311	208	36	195	104	1	193	8	41	1
F13	10	U311	208	36	195	110B	U320	193	8	40	2
F14	10	U311	208	36	195	104	1	193	8	40	0
F19	10	U311	208	36	rough	104	1	193	8	40	1
F23	10	U311	208	36	195	104	1	193	8	40	0
F24	67	U311	U302	104C	99	12	104	193	U302	40	7
F27	10	U311	208	36	NT	104	1	193	8	40	1
F29	10	U311	208	36	195	104	1	193	8	40	0
F31	67	U311	U302	36	195	104	1	193	8	40	2
F35	10	U311	208	36	195	104	1	193	8	40	0
X	2	0	3	1	3	2	2	0	1	1	15

Grey cells = deviating results

X: number of deviating laboratories by strain

Y: number of deviating strains by laboratory

Figure 13 displays the distribution of deviations for phage typing *S.* Enteritidis and *S.* Typhimurium for the EU/EEA laboratories. Correct phage types for the EU/EEA laboratories (in per cent) are shown in Figure 14.

Figure 13: Distribution of deviations in phage typing of *S.* Enteritidis and *S.* Typhimurium; EU/EEA laboratories

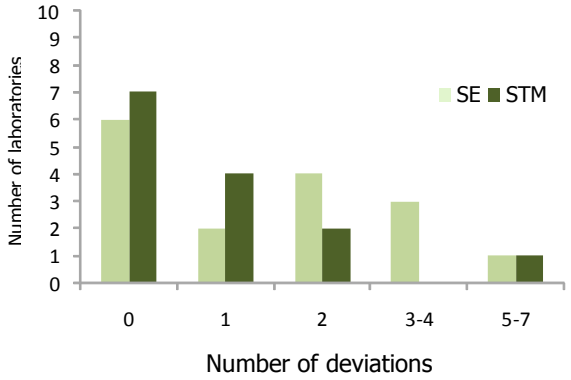
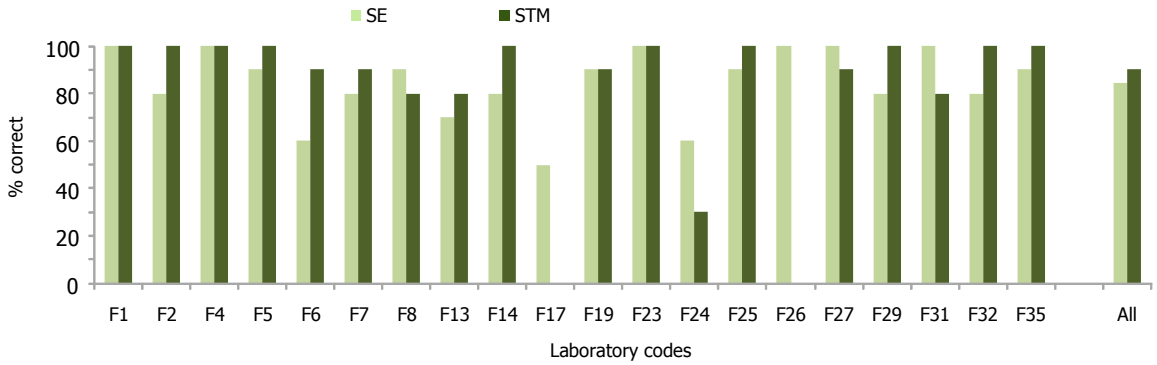


Figure 14: Percentage of strains correctly phage-typed; EU/EEA laboratories



3.4.2 *S.* Enteritidis phage typing results for the EU/EEA laboratories

Six out of 16 laboratories identified the correct phage type for all ten strains of *S.* Enteritidis. Six laboratories showed one to two deviations each from the correct results. Three laboratories produced three to four deviations, while one laboratory reported five deviations from the correct results (Figure 13).

Table 13 shows that two of the ten *S.* Enteritidis strains were phage-typed correctly by all participating laboratories, namely PT22 (strain E2) and PT14b (strain E7).

The *S.* Enteritidis strains that were most difficult to identify were PT3 (strain E5) and PT21 (strain E9), which both were incorrectly phage-typed by seven laboratories.

Three laboratories incorrectly phage-typed PT3 (strain E5) as PT21, and one laboratory typed it as PT21b. As PT3 is related to PT21 and PT21b (PT21b is a variant of PT21), the reason for the incorrect results is probably the inoculum size of the broth culture used for the phage typing. Two laboratories typed this strain as PT3a because they did not obtain a reading with phage 6. This suggests that the dilution of this phage was incorrect. One laboratory did not give a phage type for this strain; they did not obtain a reaction with phage 6, but the reactions with all the other phages were correct.

Four laboratories all typed PT21 (strain E9) as PT21c.The difference between these two phage types is the reaction of PT21c with phage 16. Phage type 21 either shows no reaction with this phage or a very weak reaction. PT21c produces a strong reaction with phage 16. The results suggest that the laboratories that typed this strain as PT21c either used phage 16 at the wrong dilution or misinterpreted the reaction they obtained from this phage. Two laboratories incorrectly phage-typed PT21 as PT3. Phage types 21 and 3 are related, with PT3 reacting with fewer phages. A possible reason for this result is that the inoculum size of the broth culture used for the phage typing was incorrect. A heavy inoculum is required for the phage typing of *S.* Enteritidis. One laboratory phage-typed PT21 as PT2; they did not obtain a phage reaction with phage 2 but did observe a reaction with phage 4 (PT21 does not react with this phage). The reactions they obtained with the other phages were correct.

Five laboratories incorrectly phage-typed PT1 (strain E4). Two laboratories typed this strain as PT37 and two other laboratories as PT44. The reason for the incorrect result for both PT37 and PT44 was no or weak reactions with phages 2, 4, and 9. This was probably due to the inoculum size of the broth culture used for the phage typing, as most of these laboratories correctly typed strain E8 (PT1b), which produces a strong reaction with all phages, suggesting that the dilution of the phages was correct. One laboratory incorrectly typed this strain as PT1a. This was probably due to the misinterpretation of the reaction obtained with phage 14. PT1 gives a high reaction with phage 14 and PT1a gives a +++ reaction but the phage plaques are very small and can only be observed using a hand lens.

PT6 (strain E1) and PT4 (strain E6) were each incorrectly phage-typed by two laboratories. PT6 was typed as PT6c by two laboratories. Both laboratories obtained a reaction with phage 16, and PT6 does not react with this phage. This suggests that the dilution of this phage was incorrect. PT4 was incorrectly typed as PT4b by one laboratory because the laboratory obtained a reaction with phage 16. PT4 does not react with this phage so this suggests that the dilution of the phage was incorrect. Another laboratory typed this strain as PT8 because they did not obtain any reactions with phages 2 and 13.

Strains E8 and E10 were both incorrectly phage-typed by one laboratory. PT1b (strain E8) was typed as PT9b by one laboratory, which failed to obtain reactions with several of the phages. PT1b produces a strong reaction with all phages. PT14c (strain E10) was typed as PT55 by one laboratory. This laboratory obtained the correct phage reactions but indicated the incorrect phage type.

3.4.3 *S.* Typhimurium phage typing results for the EU/EEA laboratories

Seven out of 14 laboratories assigned the correct phage type for all ten strains of *S.* Typhimurium. Six laboratories produced one to two deviations each from the intended results, while one laboratory showed seven deviations from the intended results (Figure 13).

Table 14 shows that two of the ten *S.* Typhimurium strains were phage-typed correctly by all participating laboratories, PT U311 (strain T12) and DT 193 (strain T18).

The *S.* Typhimurium strain that caused most problems was DT208 (strain T13). This strain was typed as PT U302 by three laboratories. This was due to no or only a very weak reaction with additional phage 18.

Strain DT195 (strain T15) was also incorrectly phage-typed by three laboratories. One laboratory identified this strain to be rough and did not allocate a phage type, but they obtained the correct phage reactions. Another laboratory typed this strain as DT99 because they obtained a reaction with phage 11. This suggests that the dilution of this phage was incorrect. A third laboratory did not allocate a phage type for this strain as they did not obtain a phage reaction with additional phage 3, suggesting that the dilution of this phage was incorrect.

Strains T11, T16 and T17 were each incorrectly phage-typed by two laboratories. Strain DT10 (strain T11) was typed as DT67 by two laboratories. Both laboratories failed to obtain a reaction with phage 11, suggesting that this phage was incorrectly diluted. Strain DT104 (strain T16) was typed as DT110b by one laboratory, as no reaction was obtained with phage 12. Another laboratory typed this strain as DT12 because the laboratory did not obtain a reaction with phage 18. Strain DT1 (strain T17) was phage-typed as PT U320 by one laboratory, as some of the reactions were slightly weaker than would be expected for DT1. The incorrect result may have been due to a misinterpretation of the reactions obtained. Another laboratory incorrectly typed this strain as DT104. As this laboratory produced several incorrect results this could indicate that strains were mixed up.

Three strains, T14, T19, and T20 were each incorrectly phage-typed by one laboratory. Another laboratory typed strain DT36 (strain T14) as DT104c, and strain DT8 (strain T19) as PT U302. The same laboratory had problems with other strains, which could indicate that strains were mixed up.

One laboratory incorrectly typed strain DT40 (strain T20) as DT41. This was due to not obtaining any reaction with phage 13, suggesting that the dilution of this phage was incorrect.

3.4.4 Phage typing results for all participants

Overall, eighteen participants carried out phage typing of both *Salmonella* Enteritidis and *Salmonella* Typhimurium. Two laboratories (EU/EEA) only phage-typed *S.* Enteritidis. Separate notations by phage type and laboratory are given in Annex 7. The phage typing results were evaluated for all laboratories and strains. Data for *S.* Enteritidis and *S.* Typhimurium are shown in Tables 15 and 16, respectivelyTyphimurium.

Figure 15 displays the distribution of deviations for phage typing *S.* Enteritidis and *S.* Typhimurium for all participating laboratories. The percentage of correctly identified phage types (all participating laboratories) is shown in Figure 16.

Six out of 20 laboratories identified the correct phage type for all ten strains of *S.* Enteritidis. Ten laboratories produced one to two deviations each from the correct results. Three laboratories showed three to four deviations, while one laboratory produced five deviations (Figure 15).

Figure 15: Distribution of deviations in phage typing of *S.* Enteritidis and *S.* Typhimurium; all participants

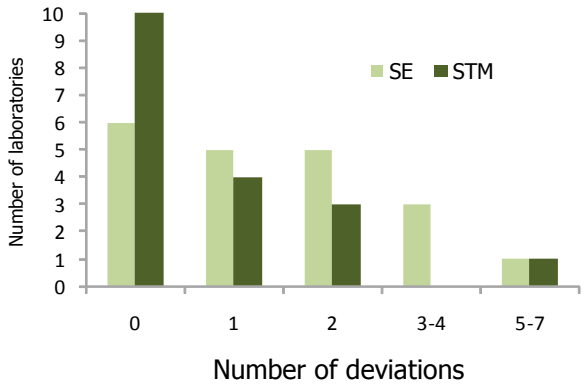


Figure 16: Percentages of strains correctly phage-typed; all participants

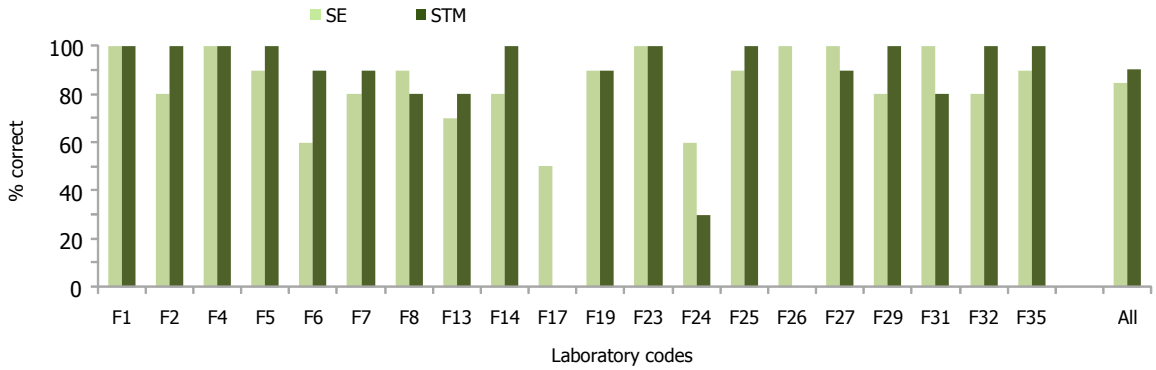


Table 15 shows that two of the ten *S.* Enteritidis strains were phage-typed correctly by all participating laboratories, namely PT22 (strain E2) and PT14b (strain E7).

Ten out of 18 laboratories identified the correct phage type for all ten strains of *S.* Typhimurium. Seven laboratories produced one to two deviations each from the intended results, while one laboratory showed seven deviations from the intended results (Figure 15).

Table 16 shows that two of the ten *S.* Typhimurium strains were phage-typed correctly by all participating laboratories, namely PT U311 (strain T12) and DT 193 (strain T18).

Table 15: Results of *Salmonella* Enteritidis phage typing; all participants

	E1	E2	E3	E4	E5	E6	E7	E8	E9	E10	Y
HPA	**6**	**22**	**59**	**1**	**3**	**4**	**14b**	**1b**	**21**	**14c**	
F1	6	22	59	1	3	4	14b	1b	21	14c	0
F2	6	22	59	1a	21b	4	14b	1b	21	14c	2
F4	6	22	59	1	3	4	14b	1b	21	14c	0
F5	6	22	59	1	3	4	14b	1b	21c	14c	1
F6	6c	22	59	37	3a	4	14b	1b	3	14c	4
F7	6c	22	59	1	3	4	14b	1b	21c	14c	2
F8	6	22	59	1	3	4	14b	1b	21c	14c	1
F13	6	22	59	44	3a	4	14b	1b	3	14c	3
F14	6	22	59	44	3	4	14b	1b	21c	14c	2
F17	6	22	14b	1	21	4b	14b	1b	21c	55	5
F19	6	22	59	1	unstable	4	14b	1b	21	14c	1
F23	6	22	59	1	3	4	14b	1b	21	14c	0
F24	6	22	59	37	3	8	14b	9b	2	14c	4
F25	6	22	59	1	3	4	14b	1b	21c	14c	1
F26	6	22	59	1	3	4	14b	1b	21	14c	0
F27	6	22	59	1	3	4	14b	1b	21	14c	0
F29	6	22	59	1	21	4	14b	1b	21c	14c	2
F31	6	22	59	1	3	4	14b	1b	21	14c	0
F32	6	22	23	1	3	4	14b	1b	21c	14c	2
F35	6	22	59	1	21	4	14b	1b	21	14c	1
X	2	0	2	5	7	2	0	1	11	1	31

Grey cells = deviating results

X: number of deviating laboratories by strain

Y: number of deviating strains by laboratory

Table 16: Results of *Salmonella* Typhimurium phage typing; all participants

	T11	T12	T13	T14	T15	T16	T17	T18	T19	T20	Y
HPA	**10**	**U311**	**208**	**36**	**195**	**104**	**1**	**193**	**8**	**40**	
F1	10	U311	208	36	195	104	1	193	8	40	0
F2	10	U311	208	36	195	104	1	193	8	40	0
F4	10	U311	208	36	195	104	1	193	8	40	0
F5	10	U311	208	36	195	104	1	193	8	40	0
F6	10	U311	U302	36	195	104	1	193	8	40	1
F7	10	U311	208	36	195	104	1	193	8	41	1
F8	10	U311	U302	36	195	104	1	193	66A	40	2
F13	10	U311	208	36	195	110B	U320	193	8	40	2
F14	10	U311	208	36	195	104	1	193	8	40	0
F19	10	U311	208	36	rough	104	1	193	8	40	1
F23	10	U311	208	36	195	104	1	193	8	40	0
F24	67	U311	U302	104C	99	12	104	193	U302	40	7
F25	10	U311	208	36	195	104	1	193	8	40	0
F27	10	U311	208	36	NT	104	1	193	8	40	1
F29	10	U311	208	36	195	104	1	193	8	40	0
F31	67	U311	U302	36	195	104	1	193	8	40	2
F32	10	U311	208	36	195	104	1	193	8	40	0
F35	10	U311	208	36	195	104	1	193	8	40	0
X	2	0	4	1	3	2	2	0	2	1	17

Grey cells = deviating results

X: number of deviating laboratories by strain

Y: number of deviating strains by laboratory

3.5 Antimicrobial susceptibility testing results

3.5.1 Results by antibiotic

As in the first EQA, AST strains were tested for susceptibility to antibiotics by 31 participating laboratories. Eleven laboratories (eight from the EU/EEA) determined MICs, while 20 laboratories (17 EU/EEA) determined zone diameters by disk diffusion. MICs were determined by broth microdilution according to CLSI/ISO standards, Etest (mostly for confirmation), and automated systems (VITEK2, Sensititre ARIS, MIDITECH) and a breakpoint method with antibiotics dissolved in agar (see section 3.2.4 or Annex 4). Of the laboratories using disk diffusion, 18 carried out the tests according to CLSI guidelines and two according to national guidelines.

Only CLSI criteria were accepted for the interpretation of the reference MICs (determined earlier by CVI), which implied the use of broth microdilution according to ISO-20776-1:2006. As EUCAST does not yet provide interpretive criteria for disk diffusion, CLSI criteria were also used for the interpretation of the zone diameters.

CVI participated in the ring trial and used EUCAST epidemiological cut-off values as prescribed for EU National Reference Laboratories on antimicrobial resistance by the European Food Safety Authority (EFSA) for surveillance purposes.

The interpretive criteria used by the participating laboratories varied substantially, although this differed by antibiotic (see Annex 8). For cefotaxime, CLSI has recently updated its criteria for the interpretation of both MICs and zone diameters. These new CLSI criteria (CLSI, January 2010) are specifically aimed at the detection of resistance against the different third- and fourth-generation cephalosporins, but were not yet implemented by many of the participants (Annex 8). However, the use of CLSI guideline M100–S20 of January 2010 did not influence the interpretation of results compared with the previous CLSI guideline (M100–S19) (see section on cefotaxime). The study also used EUCAST clinical breakpoints and epidemiological cut-off values, which produced a substantial range of differences in the results (Annex 8). As in 2009, substantial differences in the results were also recorded for ciprofloxacin. Some laboratories applied EUCAST expert rules for the interpretation of certain phenotypes. Because of these differences in methods, criteria and interpretations, quantifying the deviating results for ciprofloxacin was not appropriate.

This section describes the results for each antibiotic, while keeping in mind the characteristics of the isolates and the range of differences as mentioned above.

The results for all laboratories by antibiotic are shown in Annex 8. For those laboratories that determined MICs, the concentration is given in mg/L. For the laboratories using disk diffusion, the zone diameters are given in millimetres.

Ampicillin

Ampicillin susceptibility was detected accurately by 27 of the 31 participating laboratories. The results of strain A4 were excluded from the interpretation because the A4 strain sent to the participants was either a mixed culture with a susceptible variant or lost the plasmid that harbours blaTEM-1. Six laboratories classified it 'correctly' as R and all others as S. Only two deviations were recorded for the other strains that harboured a beta-lactamase (A1, A6, A8, A9, A10). Two laboratories incorrectly classified the blaTEM-52 (A9) as S. However, one laboratory also classified this isolate S for cefotaxime, indicating that the A9 isolate may have lost its plasmid or was somehow replaced by a different *Salmonella*. Four minor errors were produced: two on A7 by F5, and F29. One laboratory produced three additional minor errors by applying local interpretive criteria.

Cefotaxime

For this ring trial, blaTEM-52 (A9), a cefotaxime-resistant strain, was included in the panel. All other strains including those harbouring blaTEM-1 (A1, A6, A10) or blaPSE-1 (A8), were susceptible and showed low MICs.

Deviating results were only reported for the ESBL-producing A9. The susceptible isolates were classified correctly by all laboratories. Two laboratories classified A9 as S (major error) and 15 as I (minor error). Except for one, these intermediate classifications were all based on disk diffusion and the interpretation of the zone diameters or MICs did not adhere to CLSI M100–S20. If CLSI M100–S20 criteria had been used, all isolates would have been classified correctly. Because of the transition from S19 to S20 at the time of the second EQA scheme, the results of strain A9 were excluded from the overall evaluation of minor and major deviations in this EQA.

Chloramphenicol

One chloramphenicol-resistant strain (A8) was included in the panel: a DT104 strain harbouring the floR gene.

All isolates were correctly classified by all laboratories. This is at least partially due to the fact that no isolates with susceptibility patterns close to the breakpoint MICs were included in this second EQA.

Ciprofloxacin

As in the first EQA, various breakpoints and interpretive criteria were used for ciprofloxacin, which made quantifying the results (deviations) difficult and let to the exclusion of ciprofloxacin from the overall evaluation.

Moreover, the interpretation of the reference MICs according to CLSI criteria showed that these criteria are not always adequate.

Strains A2, A7, A10 with reduced susceptibility (MIC 0.25 – 0.5 mg/L) were classified S applying the CLSI criteria. Strain A4 with MIC 8 mg/L was classified R, and strains A1, A3, A5, A6, A8, A9 were classified *S.*

Strain A2 was a qnrS1-positive *S.* Corvallis, showing a typical 'qnr phenotype' with reduced susceptibility to ciprofloxacin (0.5 mg/L) and continued susceptibility to nalidixic acid (16 mg/L). Nineteen laboratories classified A2 as S, 5 as I, and 6 as R, indicating the necessity of a more harmonised approach for the interpretation.

Similar variations in the results were produced for isolates A7 and A10, which both harbour a single-point mutation in the gyrA gene. The susceptible isolates and the high-level resistant isolate A4 were classified correctly by almost all laboratories.

Gentamicin

Only one gentamicin-resistant isolate (A7) was included in the panel.

Except for one laboratory that misclassified A7 as S using an agar dilution breakpoint method, the results of all laboratories were correct.

Nalidixic acid

Three nalidixic acid-resistant strains (A4, A7, A10) were included, as was the qnrS1-positive A2 isolate, which shows reduced susceptibility (MIC 16 mg/L) compared with the fully susceptible isolates (MICs ≤4 mg/L). As in the first EQA, most deviations were produced for A2 because of its borderline susceptibility pattern. The NAL MIC is slightly elevated, which resulted in zone diameters varying from 14 to 17 mm – clearly smaller than those for the susceptible strains and clearly wider than those for the fully resistant ones. These reduced zone diameters in combination with reduced ciprofloxacin susceptibility can be used as an indicator for the presence of qnr genes.

CLSI criteria only provide an 'intermediate' area for the disk diffusion method for nalidixic acid, which implies that all isolates classified as I will inevitably be considered a minor deviation from the reference MIC.

Two laboratories produced minor deviations for the susceptible isolates A1, A3, and A9. It appears that one laboratory applied a different methodology to these isolates as results consistently showed a smaller zone diameter than other laboratories.

Streptomycin

Streptomycin is a difficult antibiotic to test due to the many variations of susceptibility patterns, which result from the various combinations of resistance genes. MIC breakpoints have not been defined by CLSI. For the purpose of this ring trial, the EU reference laboratory breakpoint was used (Table 7). In this ring trial, strains A1, A3, A7, and A8 were high-level resistant (MIC ≥128 mg/L). Strains A4, A5, A6 and A9 showed borderline MICs (16 mg/L).

Inclusion of streptomycin in the test panel is aimed at the detection of DT104 and has no clinical purposes. Therefore an intermediate criterion is not necessary. This again will lead to minor deviations for those that use disk diffusion because of the criteria for intermediate resistance provided by CLSI.

The susceptible isolates A2 and A10 (MIC 4 mg/L) were classified correctly by all laboratories. Among resistant isolates, four minor deviations were produced by a laboratory that used a breakpoint agar dilution method. With regard to the borderline strains with MIC 16 mg/L, 16 minor and two major errors were produced.

Sulphamethoxazole

Strains A1, A3, A7, and A8 were high-level sulphonamide resistant (MI >1024 mg/L). The other isolates were S (MIC ≤8 mg/L). The resistant isolates were classified correctly by all laboratories, while for the S isolates 13 major and nine minor deviations were produced. This is likely to be due to the difficulties determining end-points for sulphonamides because of the presence of antagonists in the broth or agar.

Tetracycline

Strains A1, A3, and A8 were tetracycline resistant (MIC ≥64 mg/L). The other strains were susceptible (MIC ≤1 – 4 mg/L). As to the resistant A8 isolate, four minor errors were produced based on either the method (breakpoint MIC in agar dilution; one laboratory) or the applied criteria (two laboratories).

One laboratory used non-CLSI criteria and misclassified most susceptible strains as intermediate.

Trimethoprim

By and large, trimethoprim causes little or no confusion when salmonellae are tested for susceptibility. No deviating results were produced.

3.5.2 AST results for participating EU/EEA laboratories

The numbers of deviating results are summarised in Table 17. Figure 17 gives percentage points.

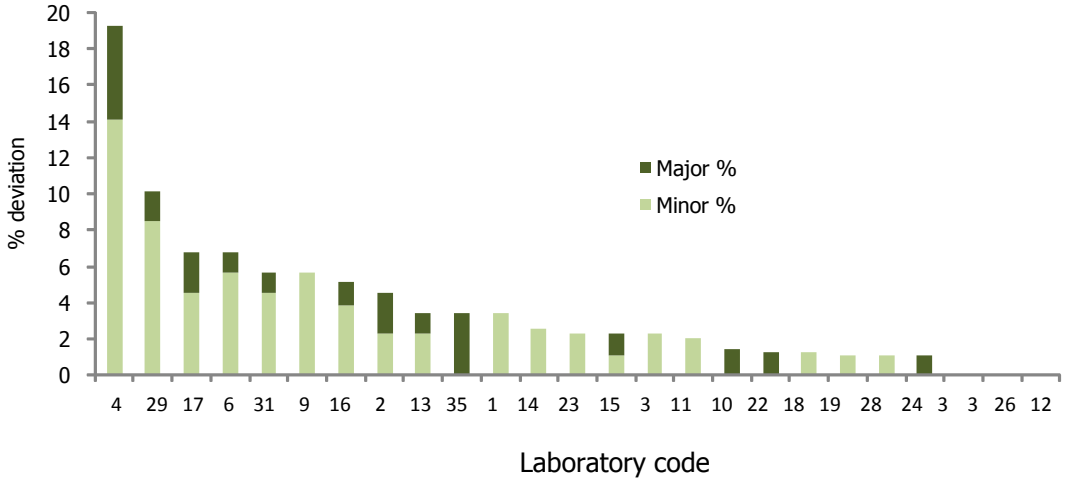
Keeping in mind the complexity of certain isolate–antibiotic combinations and the wide variety of applied methods and interpretive criteria, one can expect a certain number of deviations. After the exclusion of two problematic strains (ampicillin for strain A4, cefotaxime for strain A9) and ciprofloxacin for all strains, all EU/EEA laboratories, save one (96%), produced ≤10% deviating results, while 18 of the 25 laboratories (72%) produced ≤5% deviating results.

Minor deviations for the interpretation of the susceptibility tests were found in 3% of the 1983 evaluated results from the EU/EEA laboratories, and an additional one per cent showed major deviations. This resulted in a total of 96% of correctly interpreted antibiotic susceptibility testing data.

Table 17: Numbers of minor and major deviations recorded for EU/EEA laboratories; all strains except A4 for ampicillin and A9 for cefotaxime, and all antibiotics except ciprofloxacin

Laboratory code	No. of tests (N)	Minor deviations (N)	Major deviations (N)
F1	88	3	0
F2	88	2	2
F3	88	2	0
F4	78	11	4
F6	88	5	1
F9	88	5	0
F10	70	0	1
F11	48	1	0
F12	38	0	0
F13	88	2	1
F14	78	2	0
F15	88	1	1
F16	78	3	1
F17	88	4	2
F18	78	1	0
F19	88	1	0
F22	78	0	1
F23	88	2	0
F24	88	0	1
F26	88	0	0
F28	88	1	0
F29	59	5	1
F31	88	4	1
F33	58	0	0
F35	88	0	3

Figure 17: Percentages of minor and major deviations recorded for EU/EEA laboratories; all strains except A4 for ampicillin and A9 for cefotaxime, and all antibiotics except ciprofloxacin



3.5.3 AST results for all participants

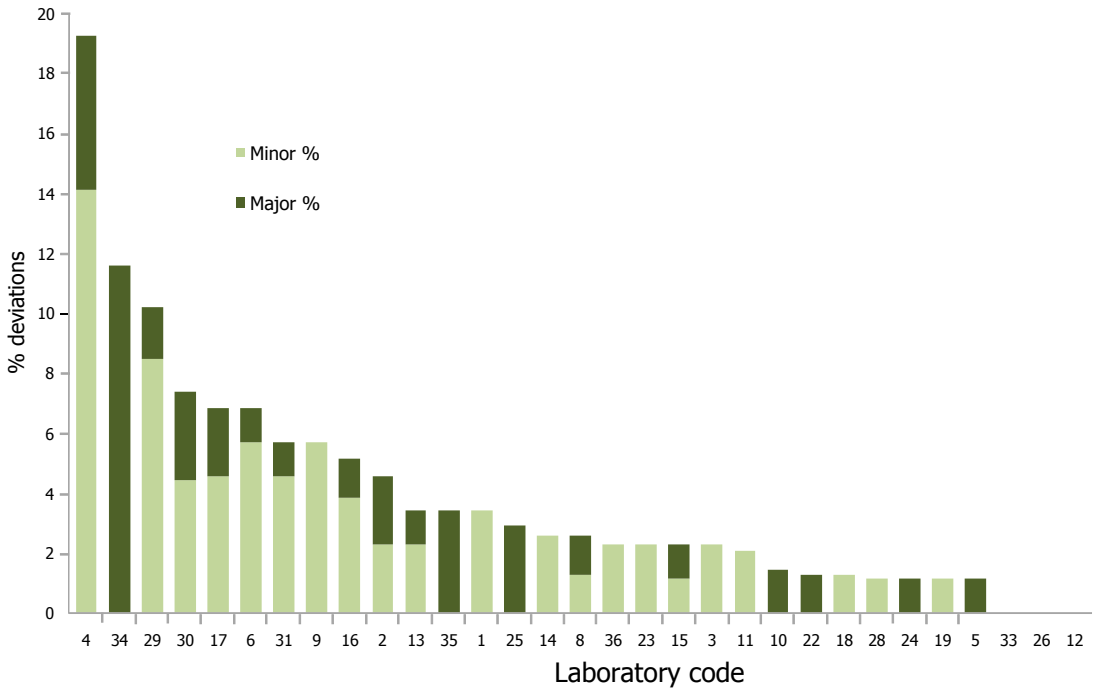
The numbers of deviating results for non-EU/EEA laboratories are summarised in Table 18 and presented as percentages in Figure 18. After exclusion of two problematic strains (A4 for ampicillin and A9 for cefotaxime) and ciprofloxacin for all strains, four of the six non-EU/EEA laboratories produced ≤5% deviations, and five of the six laboratories experienced ≤10% deviations.

Minor deviations for the interpretation of the susceptibility tests were found in 3% of the 2443 evaluated results from all participating laboratories. One per cent of the results showed major deviations. This resulted in a total of 96% of correctly interpreted antibiotic susceptibility testing data.

Table 18: Minor and major deviations recorded for non-EU/EEA laboratories; all strains except A4 for ampicillin and A9 for cefotaxime, and all antibiotics except ciprofloxacin

Laboratory code	No. of tests (N)	Minor deviations (N)	Major deviations (N)
F5	88	0	1
F8	78	1	1
F25	69	0	2
F30	68	3	2
F34	69	0	8
F36	88	2	0

Figure 18: Percentages of minor and major deviations recorded for all participating laboratories (for all strains except A4 for ampicillin and A9 for cefotaxime, and all antibiotics except ciprofloxacin)



3.5.4 Comparison between MIC and disk diffusion

Figure 19 shows the percentages of minor and major deviations for laboratories that either determine MICs or use disk diffusion. The two laboratories that produced the highest proportion of deviating results (>10%) used MICs, as did the three laboratories that produced no deviations. Of the 11 laboratories that determined MICs, six (55%) produced less than 2% deviations. Of the 20 laboratories using disk diffusion, five (25%) produced less than 2% deviations. Overall, the nine laboratories using MICs produced 2% minor and 2% major deviations, compared with 3% minor and 1% major deviations produced by the 20 laboratories using disk diffusion.

Figure 19-a: Percentages of minor and major deviations recorded for laboratories that determined MICs

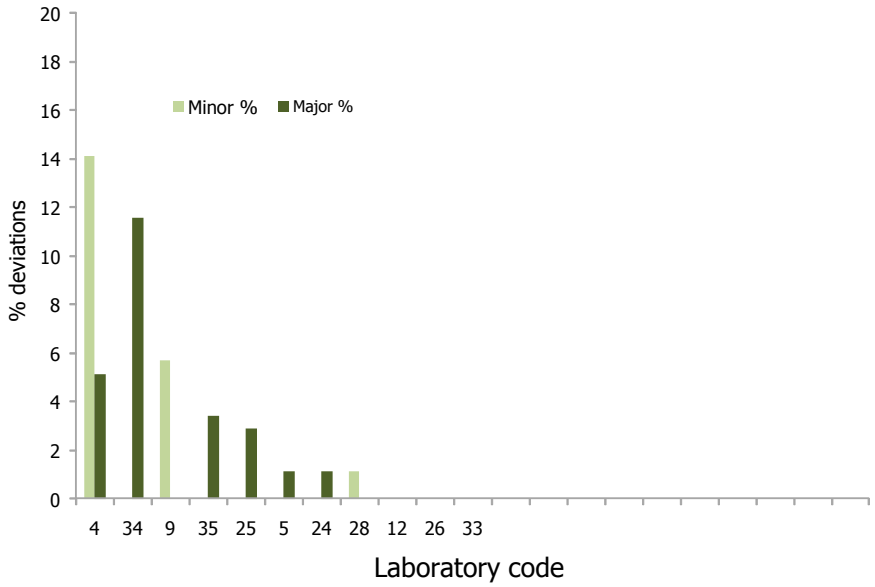
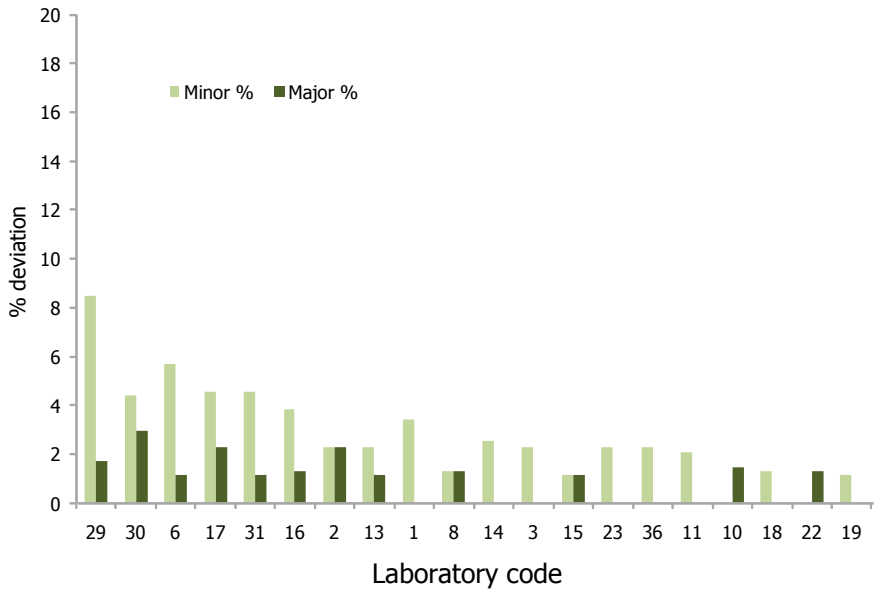


Figure 19-b: Percentages of minor and major deviations recorded for laboratories using disk diffusion



4 Discussion

4.1 Serotyping

A total of 20 strains of the species *Salmonella* enterica subspecies enterica were selected for serotyping by RIVM. Thirty-two participants carried out serotyping of the strains, 25 of which were EU/EEA laboratories. The laboratories had to report the detected H and O antigens and the serovar names according to the White-Kauffmann-Le Minor scheme.

The incorrect typing of H antigens is still the most frequently occurring problem. The majority of laboratories did not encounter any difficulties with correctly serotyping the O antigens. Problems with serotyping could not be directly linked to the use of a particular brand of culture medium or preparation. An overview of the results as obtained in the first and second EQA scheme is given in Table 19. A comparison of the percentages of correctly named serovars by laboratory in the first and second EQA scheme is shown is Figure 20.

In the second EQA, only two serovars, *S.* Stanley and *S.* Typhimurium, were correctly typed by all participants. In the first EQA, nine serovars were correctly identified: *S.* Dublin, *S.* Heidelberg, *S.* Coeln, *S.* Brandenburg, *S.* Bredeney, *S.* Virchow, *S.* Infantis, *S.* Enteritidis, and *S.* Typhimurium, with the latter four also being included in the second EQA.

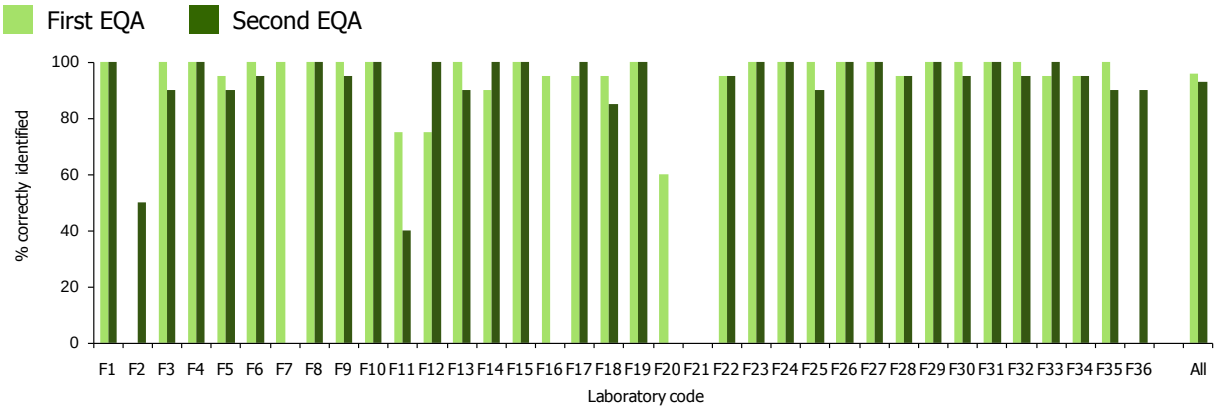
Overall, the second EQA scheme showed more laboratories having deviating serotyping results, but the number of deviations by laboratory were generally lower than in the first EQA.

Table 19: Overview of the serotyping results for EU/EEA laboratories and the total number of laboratories participating in the first and second EQA scheme

	First EQA: EU/EEA	Second EQA: EU/EEA	First EQA: all labs	Second EQA: all labs
O antigens, laboratories	21/28 (75%)*	22/25 (88%)	25/34 (74%)	26/32 (81%)
O antigens, strains	547/560 (98%)	495/500 (99%)	665/680 (98%)	631/640 (99%)
H antigens, laboratories	19/28 (68%)	15/25 (58%)	25/34 (74%)	17/32 (53%)
H antigens, strains	539/560 (96%)	465/500 (93%)	659/680 (97%)	599/640 (94%)
Serovar names, laboratories	16/28 (57%)	15/25 (58%)	20/34 (59%)	16/32 (50%)
Serovar names, strains	528/560 (94%)	465/500 (93%)	646/680 (95%)	596/640 (93%)

** Number correct/total number (%)*

Figure 20: Results for all participating laboratories in the first and second EQA serotyping scheme: correctly identified strains, in percent



4.2 Phage typing

Ten strains of *S.* Enteritidis and ten strains of *S.* Typhimurium were selected for this study by the Salmonella Reference Unit of the Health Protection Agency, London.

Two strains of *S.* Enteritidis, PT14b and PT22, were correctly phage-typed by all participating laboratories. Two strains of *S.* Typhimurium, DT193 and PT U311, were also correctly phage-typed by all participating laboratories.

In this study, phage typing the *S.* Enteritidis strains proved more difficult than for the *S.* Typhimurium strains, both for the subgroup of EU/EEA laboratories (n=16) and the group of all participating laboratories (n=20).

There are three probable reasons for the deviations in the phage typing results. One is the inoculum size of the broth culture used for phage typing. For *S.* Enteritidis, a heavy inoculum is needed to obtain the correct phage reactions, while for *S.* Typhimurium a lighter inoculum is required. To obtain the correct inoculum size the incubation conditions for the broth cultures in the phage-typing procedure should be followed.

The second reason is dilution: phages are supplied as a concentrate and must be diluted before use. It is important that the titre of the diluted phage solution is correct. The titre of the phages can also change during storage. The phages should be checked by observing the reactions obtained on strains with a known phage type. For *S.* Enteritidis this is PT 1b and DT 36 for *S.* Typhimurium.

Finally, some deviations were due to the misinterpretation of the reactions obtained with the phages. Misinterpretation of results may be due to lack of experience in phage typing, new staff in the laboratory, or the laboratory may not phage-type many different strains and thus be unfamiliar with some of the phage types.

On the whole, the results for *S.* Enteritidis were good, with 85% of the strains being correctly phage-typed. The results for *S.* Typhimurium were better: 91% of the total strains were correctly phage-typed. The results for the EU/EEA laboratories were comparable with the results for all 20 participants.

S. Enteritidis: 84% of the strains were correctly identified. Eleven of the participating laboratories produced one or no deviations. Six laboratories had acceptable results with two to three deviations, and three laboratories produced four or more deviations. Typhimurium

S. Typhimurium: 89% were correctly phage-typed.Typhimurium Fourteen laboratories produced one or no deviations. Three laboratories had two to three deviations, and one laboratory produced four or more deviations.

TyphimuriumOne laboratory had four or more deviations for *S.* Enteridis and *S.* Typhimurium.

An overview of the phage typing results as obtained in the first and second EQA scheme, both for EU/EEA laboratories and all participants is given in Table 20. A comparison by laboratory of the percentages of correctly phage-typed strains in the first and the second EQA scheme is shown in Figure 21.

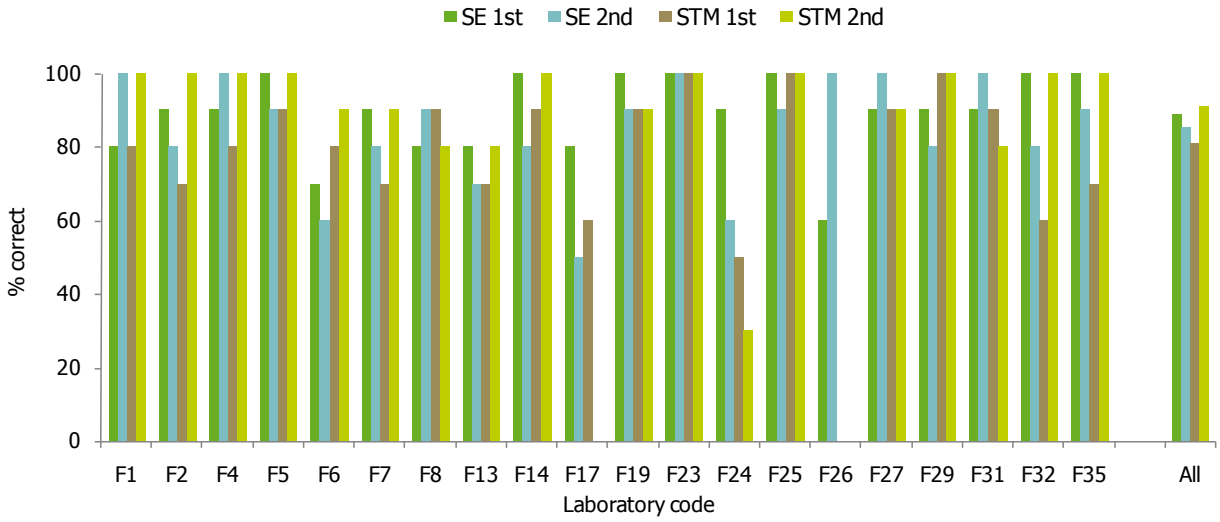
In general, phage typing results in the second EQA scheme were good although there were slightly more deviations in the results for *S.* Enteritidis when compared with the first scheme (March 2009). The results for *S.* Typhimurium show fewer deviations in the second scheme when compared with the first EQA scheme.

Table 20: Overview of the correct phage typing results in the first and second EQA scheme

	First EQA: EU/EEA	Second EQA: EU/EEA	First EQA: all labs	Second EQA: all labs
S. Enteritidis, laboratories	4/16 (25%)*	6/16 (38%)	7/20 (35%)	6/20 (30%)
S. Enteritidis, strains	140/160 (88%)	134/160 (84%)	178/200 (89%)	169/200 (85%)
S. Typhimurium, laboratories	2/15 (13%)	7/14 (50%)	3/19 (16%)	10/18 (56%)
S. Typhimurium, strains	119/150 (79%)	125/140 (89%)	153/190 (81%)	163/180 (91%)

** Number correct/total number (%)*

Figure 21: Results for all participating laboratories in the first and second EQA phage scheme: correctly identified strains, in percent



4.3 Antimicrobial susceptibility testing

The second EQA tested the susceptibility of ten strains against a panel of ten antibiotics. In contrast to the first EQA, four antibiotics were excluded for various reasons: inconclusive results, inadequate criteria, and or low participation rates.

The participating laboratories were asked to use their standard method for susceptibility testing: deployed test methods included broth microdilution, breakpoint-MIC determination with antibiotics dissolved in agar, MICs obtained with Etest, or automated methods. Inhibition zone diameters were obtained with the disk diffusion test according to CLSI or local guidelines. An additional source of variation in the results was the wide variety in interpretive criteria used for some antibiotics (e.g. ciprofloxacin).

For the purpose of this ring trial only CLSI criteria, still most commonly used by the majority of the participating laboratories, could be applied to determine the reference values. The results show that CLSI criteria are not always adequate and up-to-date (e.g. ciprofloxacin, nalidixic acid, streptomycin). Current clinical breakpoints or interpretive criteria will fail to detect some mechanisms of acquired resistance to ciprofloxacin that result in reduced susceptibility to ciprofloxacin, with MICs varying from 0.25 to 1 mg/L. This is of particular concern because EUCAST expert rules state that there is 'evidence for clinical failure of fluoroquinolones in case of resistance to nalidixic acid due to the acquisition of at least one target mutation in gyrA'. If the existing criteria for ciprofloxacin are applied, isolates with a single-point mutation will be classified as susceptible. Because these isolates will then, by definition, be resistant to nalidixic acid, we advocate that nalidixic acid be included in the panel of antibiotics. All *Salmonella* isolates classified R to nalidixic acid should be reported to be resistant to all fluoroquinolones (http://www.eucast.org).

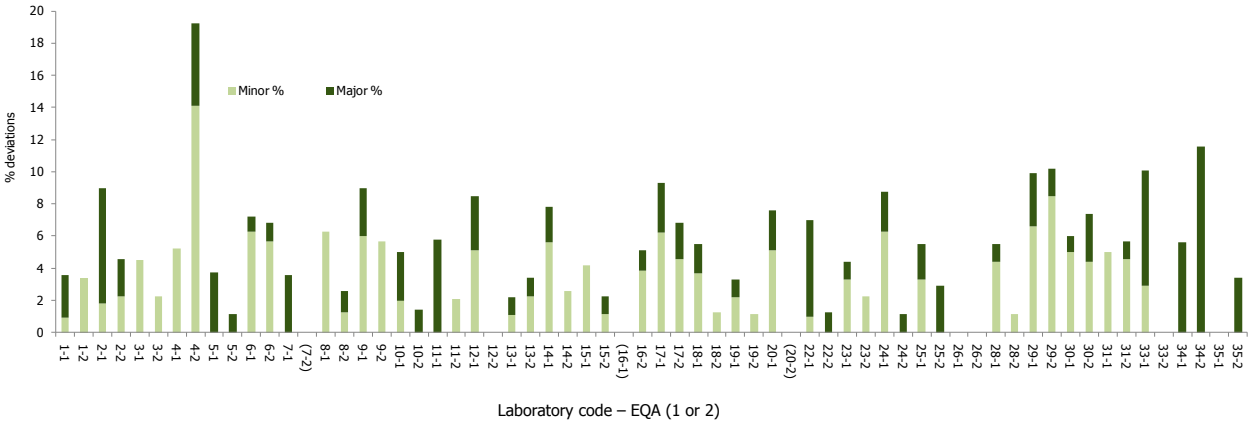
The three laboratories that produced no deviations used broth microdilution or an automated method (VITEK). In this study the determination of MICs was slightly better in quality than disk diffusion. Some of the deviations when using disk diffusion were caused by obvious differences in interpretive criteria for MIC and zone diameters.

In addition to the qualitative analysis of the numbers of recorded deviations, each laboratory should carefully compare its results (MICs or millimeters) with those obtained by laboratories using identical methods. This could reveal information on systematic or occasional differences in methodologies, which could have caused errors or deviations.

If, as in the first EQA scheme, a threshold of 90% accuracy would be used, all laboratories but two would have been approved. Seventy-one percent of all participating laboratories produced ≤5% deviations, which demonstrates that the general level of test performance is high.

A comparison of the percentages of minor and major deviations in AST for every laboratory in the first and the second EQA scheme is shown is Figure 22. Overall, 96% of the 2443 evaluated test results were typed correctly in the second EQA scheme, corresponding to 3% minor deviations and 1% major deviations. In the first EQA scheme, 95% of the 2849 evaluated test results were typed correctly, which corresponds to 3% minor deviations and 2% major deviations.

Figure 22: Percentages of minor and major deviations in AST in the first and second EQA typing scheme, all participants



5 Conclusions

5.1 Serotyping

The serotyping results showed that the correct serovar names were identified for 93% of the samples (EU/EEA laboratories and all participating laboratories). In this second EQA scheme, more laboratories had deviating serotyping results compared to the first scheme (March 2009), but the number of deviations for every laboratory were generally lower.

- The participating laboratories must ensure that they follow the proper procedures for serotyping as described in the manufacturers' instructions, and they should be aware that instructions may differ significantly between the various manufacturers of sera and serum substitutes. In general, serotyping problems could not be directly linked to the use of a particular brand of sera.

5.2 Phage typing

The results for the phage typing of *S.* Enteritidis and *S.* Typhimurium in the second EQA scheme were good. There was an improvement in the results for *S.* Typhimurium compared with the results of the first EQA scheme. There were more deviations with the phage typing of *S.* Enteritidis when compared with the first EQA scheme.

- Participating laboratories must ensure that they follow the published procedures for phage typing in order to obtain consistent results.
- It is important that the titres of the phage solutions are verified on strains with a known phage type to ensure the correct phage reactions are obtained.
- If new laboratory staff lack experience in phage typing, it is essential they are given adequate training in the technique and the interpretation of results.

5.3 Antimicrobial susceptibility testing

Except for one EU laboratory and one non-EU/EEA laboratory, all participants produced ≤10% deviations in the interpretation of the antimicrobial susceptibility tests. 72% of the EU/EEA laboratories and 71% of all participants produced ≤5% deviations, which demonstrates that the general level of performance of the antimicrobial susceptibility tests was high. In the second EQA scheme, 96% of the 2443 evaluated tests were categorised in agreement with the reference method, compared to 95% of the 2849 evaluated tests in the first EQA scheme.

- In addition to the qualitative analysis of the numbers of recorded deviations, each laboratory should carefully compare its results (MIC values or inhibition zones) with those obtained by other laboratories using identical methods. This could reveal information about systematic or occasional differences in methodologies, which could have caused errors or deviations.
- The current discussion on the global acceptance of the forthcoming European disk diffusion test (based on CLSI) and a set of interpretive criteria derived from EUCAST MIC breakpoints, as ISO (S)tandard, will be a very important step towards the standardisation and harmonisation of AST results.

5.4 ECDC comment on the results of EU/EEA laboratories in the second round of the external quality assurance (EQA) scheme for *Salmonella* typing and antimicrobial susceptibility testing

Serotyping is the basic phenotypic typing method for *Salmonella* in order to separate this large genus into smaller entities. The reference for the nomenclature is the White-Kauffman-Le Minor scheme, but for the typing method itself an international standard is yet only in the development stage. For salmonellosis, serotyping represents the foundation for surveillance, outbreak detection, and linkage to suspected sources. Consequently, correct serotyping in the national reference laboratories is a key quality priority in EU/EEA countries. Serotyping scores in the second EQA was acceptable, with 93% of all strains correctly serotyped, and 15 out of 25 laboratories producing 100% correct results. If the acceptance threshold was set to 90% correct results or higher, 22 out of 25 laboratories would pass. Considering that over 100 000 salmonellosis cases are reported to ECDC annually, this would mean that about 7 000 cases could potentially be reported with the wrong serotype. The problems mainly lie in the typing of H antigens with subsequent misnaming of the serotypes. In addition, two EU laboratories produced serotyping results in the 40 to 50% range, misclassifying some of the more common serotypes.

Phage typing for the EQA was carried out by 16 EU/EEA laboratories. Phage typing has proven very useful as a subtyping method for common serotypes, for example when linking human cases and food sources. The drawback of the method is that a lot of training is required to apply the correct inoculum size, the correct dilution and to correctly interpret the results. An international standard for the methodology is also still lacking. Overall, 84% and 89%, respectively, of the *S.* Enteritidis and *S.* Typhimurium strains were correctly phage-typed. It is notable, however, that a phage type like PT21 for *S.* Enteritidis, which is among the five most common phage types in the EU/EEA, was misclassified by 44% of the participating laboratories. The phage typing of *S.* Typhimurium generally resulted in fewer errors; however one laboratory only classified three out of ten *S.* Typhimurium strains correctly.

The antimicrobial susceptibility testing results achieved by the participating laboratories were satisfactory with all but one EU/EEA laboratory providing more than 10% deviations. Seventeen out of 25 EU/EEA laboratories used a disk diffusion method and eight a dilution method (either agar dilution or broth dilution). It is obvious that the absence of a standard for method and interpretative criteria makes it difficult to compare the results and also causes many misclassifications. Since countries only report interpreted results to ECDC, mostly by clinical breakpoints but also by EUCAST-defined epidemiological cut-off values, this is a major deficiency.

ECDC supports the use of EUCAST methods and interpretive criteria. The EQA showed that disk diffusion gave comparable results to MIC dilution. It is thus important that EUCAST continues the development of disk diffusion critical zone size diameters corresponding to breakpoints for more antimicrobials for *Salmonella* spp.

Comparing the results of the second round of EQA with those of the first, improvements were observed in the phage typing, with fewer laboratories showing deviations to the intended results, especially for *S.* Typhimurium. The antimicrobial susceptibility testing results were also better in the second round, but this could be an effect of fewer strains with borderline susceptibility being included. Also, four problematic antimicrobials were excluded in the second round. No clear improvements were observed in serotyping between the two rounds: while the typing of antigen O improved, the typing of antigen H worsened, making the proportion of correct final serotyping results equal in both rounds. The number of laboratories with deviations also increased, but the number of deviations per laboratory decreased, which may indicate that the serotypes in the second round were generally more difficult to type.

EQA schemes provide a useful tool for the identification of problematic areas in the typing of *Salmonella* strains in the national reference laboratories. The results from the second EQA round highlight the continuous need for EQA schemes for *Salmonella* serotyping and the need to develop and implement standard phage typing and antimicrobial susceptibility testing procedures and interpretation criteria.

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Regulation (EC) No 882/2004 of the European Parliament and of the Council of 29 April 2004 on official controls performed to ensure the verification of compliance with feed and food law, animal health and animal welfare rules.

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Annex 1. List of participants

Participating laboratories from EU/EEA countries

Country	*Institute/city*
Austria	AGES, Institute for Medical Microbiology and Hygiene, Graz
Belgium	Institute of Public Health, Brussels
Cyprus	Nicosia General Hospital, Nicosia
Czech Republic	National Institute of Public Health, Brno
Denmark	Statens Serum Institute, Copenhagen
Estonia	Health Protection Inspectorate, Tallinn
Finland	National Institute for Health and Welfare, Helsinki
France	Institut Pasteur Paris, Paris
Germany	Robert Koch Institute, Wernigerode Branch, Wernigerode
Greece	Central Public Health Laboratory, Vari, Attiki
Hungary	National Centre for Epidemiology, Budapest
Ireland	Galway UH, Medical Microbiology Department, Galway
Italy	Istituto Superiore di Sanità, Rome
Latvia	Infectology Center of Latvia, Riga
Lithuania	National Public Health Surveillance Laboratory, Vilnius
Luxembourg	Laboratoire National de Santé, Luxembourg
Malta	Mater Dei Hospital, Pathology Department, Malta
Netherlands	RIVM/CVI, Bilthoven/Lelystad
Norway	Norwegian Institute of Public Health, Oslo
Poland	National Institute of Public Health, National Institute of Hygiene, Warsaw
Portugal (no results returned)	Instituto Nacional de Saúde, Lisbon
Romania	National Institute of Research-Development for Microbiology and Immunology Cantacuzino, Bucharest
Slovak Republic	Public Health Authority of the Slovak Republic, Bratislava
Slovenia	National Institute of Public Health, Ljubljana
Spain	Instituo de Salud Carlos III, Madrid
Sweden	Smittskyddsinstitutet (SMI), Solna
United Kingdom – England	Health Protection Agency, London
United Kingdom – Scotland	Stobhill Hospital, Microbiology Department, Glasgow

List of participants: Participating laboratories from non-EU/EEA countries

Country	*Institute/City*
Australia	University of Melbourne, Department of Microbiology and Immunology, Melbourne, Victoria
Canada	Canadian Science Centre for Human and Animal Health, Winnipeg, Manitoba
Japan	National Institute of Infectious Diseases, Tokyo
New Zealand	Institute of Environmental Science & Research Limited, Wallaceville, Upper Hutt
South Africa	National Institute for Communicable Diseases, Johannesburg
Switzerland	Universität Zürich, Institut für Lebensmittelsicherheit und Hygiene, Zürich
Turkey	Refik Saydam National Public Health Agency, Ankara

Annex 2. Results questionnaire

Table 1: Details on general questions

Lab code	Parcel damaged	Date of arrival	Duration of transport (days)	Medium for subculture	Manufacturer
F1	no	24/11/2009	1	Bi, Br, DC, R	In-house
F2	no	25/11/2009	2	ADCL/nutrient agar	Merck/Difco
F3	no	24/11/2009	1	Nutrient agar	Bioprepare
F4	no	26/11/2009	3	Endo agar	Oxoid
F5*	no	07/12/2009	14	Nutrient agar	Oxoid
F6	no	24/11/2009	1	XLD	International Medical
F7	no	25/11/2009	2	BGA	Oxoid
F8*	no	09/12/2009	16	Nutrient agar	BD
F9	no	24/11/2009	1	Nutrient broth no. 2 (CM0067); agar SKW	Oxoid
F10	no	25/11/2009	2	XLT4	In-house
F11	no	24/11/2009	1	SS, TSA, BSA	BD
F12	no	26/11/2009	3	Nutrient agar	Sifin
F13	no	24/11/2009	1	TSA	Oxoid
F14	no	25/11/2009	2	TSA	Oxoid
F15	no	24/11/2009	1	MacConkey agar	Difco
F16	no	24/11/2009	1	Endo agar	Lab M
F17	no	25/11/2009	2	Blood agar/TSI	Merck/bioMérieux
F18	no	25/11/2009	2	Blood agar no. 2, BHI agar	Oxoid
F19	no	25/11/2009	2	Nutrient agar	LIP
F22	no	24/11/2009	1	TSA	bioMérieux
F23	no	24/11/2009	1	Agar L11	Oxoid
F24	no	25/11/2009	2	Nutrient agar	Merck
F25*	no	04/12/2009	11	MacConkey agar, 5% blood agar	Difco
F26	no	24/11/2009	1	Heart infusion agar with sheep blood	Difco
F27	no	24/11/2009	1	Nutrient agar	Karolinska
F28	no	24/11/2009	1	Nutrient agar	SSI
F29	no	24/11/2009	1	Lactose agar/nutrient agar/swarm agar	Biolife/Oxoid/SSI
F30*	no	27/11/2009	4	TSI agar	In-house
F31	no	24/11/2009	1	Drigalski-Conradi agar	In-house
F32*	no	01/12/2009	8	TSA	Fort Richard
F33	no	25/11/2009	2	MacConkey agar/nutrient agar	Fluka/mast
F34*	no	04/12/2009	11	Columbia agar	Selecta media
F35	no	25/11/2009	2	MacConkey agar without salt	Oxoid
F36*	no	25/11/2009	2	XLD	Oxoid

Non-EU/EEA country

Table 2: Details on the questions regarding serotyping

Lab code	Frequency of serotyping	Number of strains serotyped in 2008	Strains of second EQA typed by:
F1	Daily	2090	Own lab
F2	Thrice a week	492	Own lab
F3	Thrice a week	700	Own lab
F4	Daily	5266	Own lab
F5*	Daily	4050	Own lab
F6	Daily	4761	Own lab
F8*	On demand	50	Own lab
F9	Daily	7500	Own lab
F10	Daily	7500	Own lab
F11	Daily	1019	Own lab
F12	Twice a week	175	Own lab
F13	Weekly	250	Own lab
F14	Daily	6419	Own lab
F15	Daily	150	Own lab
F17	Weekly	No information	Own lab
F18	Daily	1039	Own lab
F19	Daily	1400	Own lab
F22	Daily	301	Own lab
F23	Daily	5655	Own lab
F24	Daily	573	Own lab
F25*	Daily	1209	Own lab
F26	Weekly	3500	Own lab
F27	Daily	1302	Own lab
F28	Daily	2341	Own lab
F29	Daily	2633	Own lab
F30*	Daily	1500	Own lab
F31	Daily	2750	Own lab
F32*	Daily	3000	Own lab
F33	Daily	164	Own lab
F34*	Daily	2568	Own lab
F35	Daily	1400	Own lab
F36*	Daily	800	Own lab

** Non-EU/EEA country*

Table 3: Details on questions regarding phage typing

				Phage typing of strains other than SE and STM				
Lab code[1]	**Number of strains phage-typed in 2008**	**Typing system used for *Salmonella* Enteritidis**	**Typing system used for *Salmonella* Typhi-murium**	**Typhi**	**Paratyphi B**	**Virchow**	**Hadar**	**Other**
F1	2500	Ward's scheme + country-based	Felix-Callow's scheme + Anderson	yes	yes			yes
F2	383	Ward/Rowe typing system	Anderson's typing system	yes	yes			yes
F4	2883	Ward	Extended Anderson	yes	yes	yes	yes	yes
F5*	4600	Colindale	Colindale	yes	yes	yes	yes	yes
F6	150	HPA	HPA			yes	yes	
F7	998	Colindale	Colindale					
F8*	500	HPA	HPA	yes				yes
F13	200	HPA/Colindale	HPA/Colindale					
F14	4379	HPA	HPA	yes		yes	yes	
F17	No information	HPA	N/A					
F19	522	Colindale	Colindale					
F23	3650	Colindale	Colindale	yes	yes	yes	yes	
F24	518	Ward et al. 1987	Andersen et al. 1977	yes	yes			
F25*	4716	Colindale	Colindale				yes	
F26	1000	UK	N/A					
F27	555	Colindale	Colindale					
F29	410	HPA	HPA	yes	yes			
F31	1450	Colindale	Colindale	yes				
F32*	1604	Colindale	Colindale					
F35	900	Colindale	Colindale					

[1] *Lab codes of the laboratories that perform phage typing*

** Non-EU/EEA country*

Table 4: Details on questions regarding antimicrobial susceptibility testing, general

Lab code	Disk/MIC	Method	Control strains	Agar/broth	Concentration	Number of strains tested in 2008
F1	Disk	CLSI 2009	*E. coli* ATCC 25922	Mueller-Hinton agar	0.5 McFarland	195
F2	Disk	CLSI M100-S19; vol. 29 No. 3, January 2009	*E. coli* ATCC 25922	Mueller-Hinton agar	0.5 McFarland	492
F3	Disk	CLSI	*E. coli* ATCC 25922	Mueller-Hinton agar	1.5 x 10^8 cfu/ml	640
F6	Disk	CLSI	*E. coli* ATCC 25922	Mueller-Hinton agar	0.5 McFarland	871
F8*	Disk	Disk diffusion	*E. coli* ATCC 25922	Agar	0.5 McFarland	500
F10	Disk	CA-SFM	*E. coli* ATCC 25922	Mueller-Hinton agar	10^8 cfu/ml	1000
F11	Disk	Disk diffusion	*E. coli*	Mueller-Hinton agar	1.5 x 10^8 cfu/ml	1850
F13	Disk	Disk diffusion	*E. coli* ATCC 25922	Mueller-Hinton agar	1.5 x 10^8 cfu/ml	300
F14	Disk	CLSI (2007 criteria)	*E. coli* ATCC 25922	Mueller-Hinton agar	0.5 McFarland	1824
F15	Disk	Disk diffusion	*E. coli* ATCC 25922	Mueller-Hinton agar	0.5 McFarland	400
F16	Disk	Disk diffusion	*E. coli* ATCC 25922	Mueller-Hinton agar	1.5 x 10^8 cfu/ml	421
F17	Disk	Disk diffusion	*E. coli* ATCC 25922	Mueller-Hinton agar	0.5 McFarland	No information
F18	Disk	Disk diffusion	*E. coli* ATCC 25922	Mueller-Hinton agar	0.5 McFarland	1039
F19	Disk	CLSI	*E. coli* ATCC 25922	Mueller-Hinton agar	0.5 McFarland	1400
F22	Disk	CLSI	*E. coli* ATCC 25922	Mueller-Hinton agar	0.5 McFarland	301
F23	Disk	CLSI	*E. coli* ATCC 25922		10^6 cfu/ml	5655
F29	Disk	BD Sensi-Disc, country-specific interpretation	*E. coli* ATCC 25922	Mueller-Hinton II agar	ca. 1 x 10^5 cfu/ml	2325
F30*	Disk	Kirby Bauer according to CLSI	*E. coli* ATCC 25922	Mueller-Hinton agar	0.5 McFarland	0
F31	Disk	CLSI, FiRe	*E. coli* ATCC 25922 + own S Virchow for MIC	Mueller-Hinton II agar	ca. 1 x 10^8 cfu/ml (0.5 McFarland)	2870
F36*	Disk	CLSI	*E. coli* ATCC 25922	Mueller-Hinton agar	10^8 cfu/ml (0.5 McFarland)	800
F4	MIC	MIC, DIN, ISO	*E. coli* ATCC 25922	Mueller-Hinton agar	5 x 10^5 cfu/ml	5000
F5*	MIC	CLSI (NCCLS) agar dilution	In-house wild strains	DSNB (as for phage typing)	as per CLSI	6700
F9	MIC	Agar breakpoint	*S.*Typhimurium 42R500, *E. coli* 1R713 K12m	Iso-Sensitest (Oxoid)	10^4 - 10^5 cfu/ml	14400
F12	MIC	CLSI	*E. coli* ATCC 25922 + others**	No information	180 x 10^6 cfu/ml	6
F24	MIC	Microdilution CLSI	*E. coli* ATCC 25922, 27853, 700603	Mueller-Hinton agar	0,5 x 10^6 cfu/ml	400
F25*	MIC	Sensititre (CLSI)	*E. coli* ATCC 25922	Col. 5% sheep blood agar/CAMHB	1,5 x 10^8 cfu/ml	3300
F26	MIC	Sensititre plates (ISO 20776)	*E. coli* ATCC 25922 + E. faecalis ATCC 29212	CAMHB from Trek	ca. 5 x 10^5 cfu/ml	2000 (*Salmonella*)
F28	MIC	CLSI	*E. coli* ATCC 25922	Mueller-Hinton agar	5 x 10^5 cfu/ml	3519
F33	MIC	CLSI	*E. coli* ATCC 25922	Mueller-Hinton agar	0.5 McFarland	164
F34*	MIC		*E. coli* ATCC 25922	Mueller-Hinton agar	1 x 10^8 cfu/ml	4335
F35	MIC		*E. coli* ATCC 25922 + in-house S control strains	Iso-Sensitest (Oxoid)	1/1000 dilution of 4-h broth culture	2000 (*Salmonella*)

** Non-EU/EEA country*

Table 5: Details on questions regarding antimicrobial susceptibility testing and tested antibiotics. Disk load in µg for disk diffusion method; concentration range tested in mg/L for MIC method

Lab code	Method	Manufacturer	AMP	CEF	CHL	CIP	GEN	NAL	STR	SUL	TET	TMP
F1	Disk	Oxoid	10	30	30	5	10	30	10	300	30	5
F2	Disk	Oxoid	10	30	30	5	10	30	10	300	30	5
F3	Disk	Biorad	10	30	30	5	10	30	10	300	30	5
F6	Disk	Biorad	10	30	30	5	10	30	10	300	30	5
F8*	Disk	BD	10	30	30	5	10	30	10	250	30	nt[#]
F10	Disk	Biorad	nt	nt	30	5	15	30	10	200	30	5
F11	Disk	Biorad	No information	No information	No information	No information	No information	nt	nt	nt	No information	nt
F13	Disk	BD	10	30	30	5	10	30	10	0,25	30	5
F14	Disk	Oxoid	10	30	30	5	10	30	10	300	30	nt
F15	Disk	Oxoid	10	30	30	5	10	30	10	300	30	5
F16	Disk	Oxoid	10	30	30	5	10	30	10	nt	30	5
F17	Disk	BBL/Oxoid	10	30	30	5	10	30	10	300	30	5
F18	Disk	Oxoid	10	30	30	5	10	30	10	nt	30	5
F19	Disk	Oxoid	10	30	30	5	10	30	10	300	30	5
F22	Disk	12A/BD	10	30	30	5/1-4	10	30	10	(200)	30	5
F23	Disk	Oxoid	10	30	30	5	10	30	10	300	30	5
F29	Disk	BD (S)ensi-Disc	10	nt	30	530	nt	30	10	250	30	nt
F30*	Disk	BD/Oxoid/bioMérieux	10	30	30	5	10	30	10	nt	30	nt
F31	Disk	Oxoid	10	30	30	5/0.002-32	10	30	10	300	30	5
F36*	Disk	Oxoid	10	30	30	5	10	30	10	300	30	5
F4	MIC	No information	1-16	1-16	4-32	0.0625-64	0.5-8	4-32	4-64	32-512	0.5-8	nt
F5*	MIC	Media Prep Unit	16	1	16	0.06 and 2	8	16	8 and 32	512	8	8
F9	MIC	Sigma	No information	No information	No information	No information	No information	No information	No information	No information	No information	No information
F12	MIC	VITEK2, bioMérieux	2-32	1-64	nt	0.25-4	1-16	nt	nt	nt	1-16	nt
F24	MIC	No information	0.5-64	0.25-32	0.25-32	0.03-4	0.25-32	2-128	1-64	64-512	0.125-16	0.5-16
F25*	MIC	Sensititre	1-32	nt	2-32	0.015-4	0.25-16	0.5-32	32-64	16-256	4-32	nt
F26	MIC	Sensititre	0.5-32	0.06-4	2-64	0.008-8	0.25-32	4-64	2-128	8-1024	1-64	0.5-32
F28	MIC	Trek Diagnostic system	1-32	0.125-4	2-64	0.015-4	0.5-16	4-64	8-128	64-1024	2-32	1-32
F33	MIC	bioMérieux	0.016-256	0.016-256	0.016-256	0.002-32	0.016-256	0.016-256	nt	nt	0.016-256	nt
F34*	MIC	AB bioMérieux	0.016-256	nt	0.016-256	0.002-32	nt	0.016-256	0.064-1024	nt	0.016-256	0.002-32
F35	MIC	In-house	No information	No information	No information	No information	No information	No information	No information	No information	No information	No information

** Non-EU/EEA country*

[#] nt = not tested

Annex 3. Identification of O and H antigens and correct serovar names; EU/EEA laboratories

Figure 1: Evaluation of serotyping of O antigens; EU/EEA laboratories

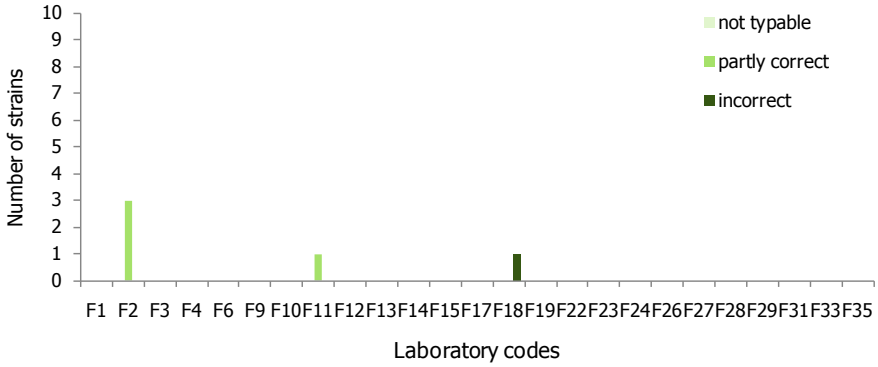


Figure 2: Evaluation of serotyping of H antigens; EU/EEA laboratories

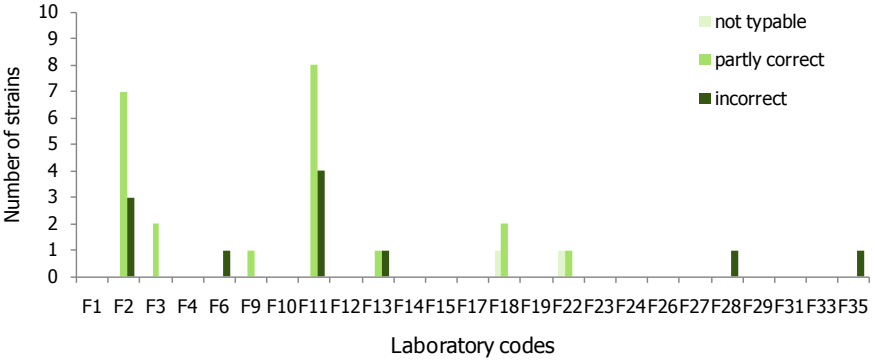
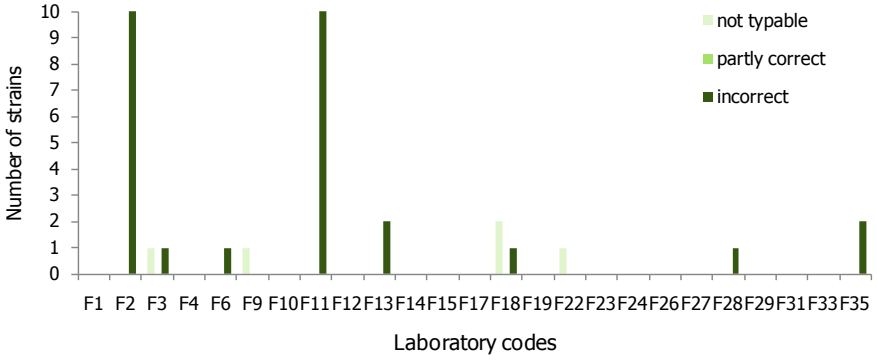


Figure 3: Evaluation of the correct serovar names; EU/EEA laboratories



Annex 4. Identification of O and H antigens and correct serovar names; all participants

Figure 1: Evaluation of serotyping of O antigens; all participants

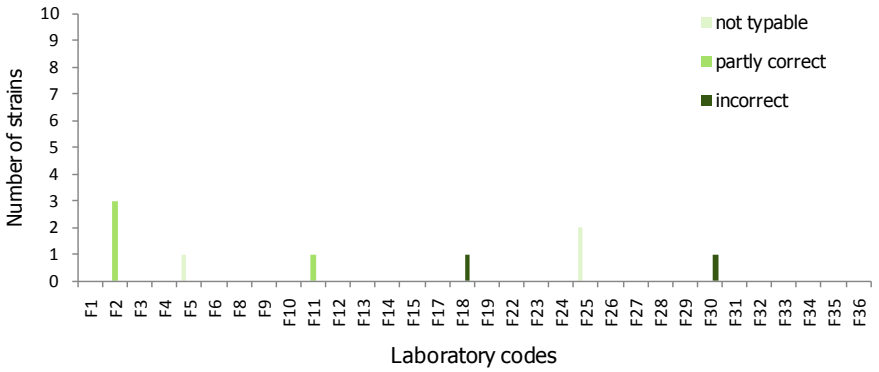


Figure 2: Evaluation of serotyping of H antigens; all participants

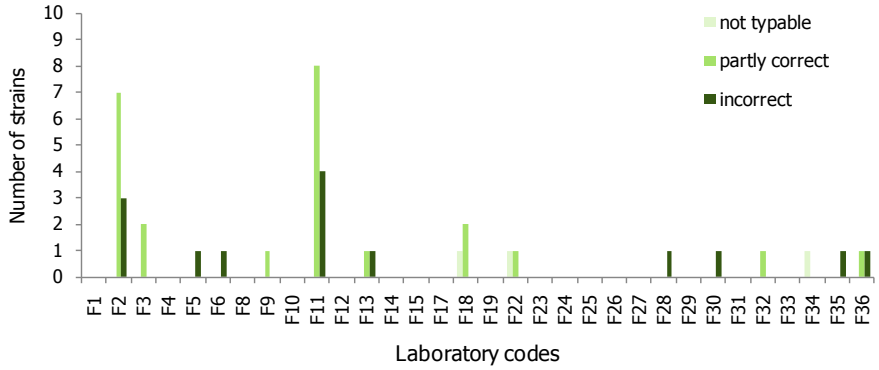
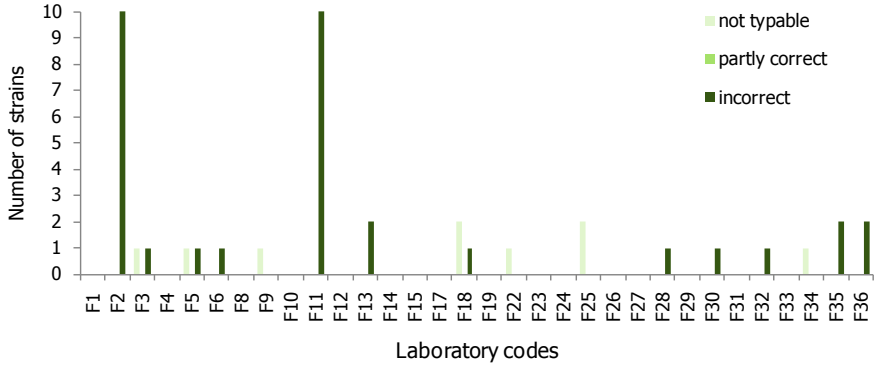


Figure 3: Evaluation of the correct serovar names; all participants



Annex 5. Test results of phage typing by strain for all participating laboratories

Strain E1		Phage reactions at routine test dilution (*S.* Enteritidis)																
Lab code	**Phage type**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	**15**	**16**	**17**
HPA	**6**	-	SCL	-	OL	-	SCL	-	OL	<OL	OL	-	-	-	-	-	-	<OL
F1	**6**	-	SCL	-	SCL	-	SCL	-	CL	SCL	+++	-	-	-	-	-	-	+++
F2	**6**	-	CL	-	OL	-	OL	-	OL	OL	OL	-	-	-	-	-	-	OL
F4	**6**	-	SCL	-	+++	-	+++	-	SCL	+++	SCL	-	-	-	-	-	-	<SCL
F5	**6**	-	SCL	-	SCL	-	+++	-	OL	SCL	+++	-	-	-	-		-	SCL
F6	**6c**	-	SCL	-	+++	-	+++	-	SCL	SCL	+++	-	-	-	-	-	+++	SCL
F7	**6c**	-	SCL	-	SCL	-	SCL	-	OL	OL	OL	-	-	-	-		CL	OL
F8	**6**	-	OL	-	OL	-	OL	-	OL	OL	OL	-	-	-	-	-	-	OL
F13	**6**	-	++	-	++	-	++	-	OL	+	+++	-	-	-	-	-	-	+++
F14	**6**	-	SCL	-	<SCL	-	<SCL	-	OL	SCL	OL	-	-	-	-	-	-	SCL
F17	**6**	-	SCL	-	SCL	-	SCL	-	OL	<OL	OL	-	-	-	-		-	SCL
F19	**6**	-	SCL	-	OL	-	SCL	-	SCL	OL	SCL	-	-	-	-	-	-	OL
F23	**6**	-	SCL	-	SCL	-	+++	-	<OL	<OL	<OL	-	-	-	-	-	-	OL
F24	**6**	-	CL	-	SCL	-	SCL	-	SCL	SCL	SCL	-	-	-	-	-	-	OL
F25	**6**	-	<OL	-	OL	-	SCL	-	OL	OL	OL	-	-	-	-	-	-	OL
F26	**6**	-	SCL	-	SCL	-	SCL	-	OL	OL	OL	-	-	-	-	-	-	OL
F27	**6**	-	<CL	-	OL	-	SCL	-	OL	OL	OL	-	-	-	-	-	-	OL
F29	**6**	2	SCL	-	SCL	-	+++	-	OL	SCL	OL	-	-	-	±	-	-	SCL
F31	**6**	-	+++	-	+++	-	+++	-	OL	OL	OL	-	-	-	-	-	-	+++
F32	**6**	-	<CL	-	<OL	-	<OL	-	OL	+++	OL	-	-	-	-	-	-	OL
F35	**6**	-	SCL	-	SCL	-	+++	-	OL	OL	OL	-	-	-	-	-	-	CL

Strain E2		Phage reactions at routine test dilution (*S.* Enteritidis)																
Lab code	**Phage type**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	**15**	**16**	**17**
HPA	**22**	OL	-	-	SCL	-	+++	-	OL	OL	OL	-	-	-	CL	-	-	SCL
F1	**22**	CL	-	-	++	-	SCL	-	SCL	+++	SCL	-	-	-	CL	-	-	++
F2	**22**	OL	-	-	OL	-	<CL	-	OL	<CL	OL	-	-	-	CL	-	-	SCL
F4	**22**	OL	-	-	+++	-	+++	-	OL	+++	OL	-	-	-	SCL	-	-	SCL
F5	**22**	CL	-	-	SCL	-	+++	-	OL	SCL	<CL	-	-	-	SCL		-	SCL
F6	**22**	SCL	-	-	SCL	-	+++	-	SCL	SCL	SCL	-	-	-	SCL	-	-	SCL
F7	**22**	OL	-	-	SCL	-	SCL	-	OL	OL	OL	-	-	-	CL	-	-	SCL
F8	**22**	OL	-	-	OL	-	OL	-	OL	OL	OL	-	-	-	CL	-	-	OL
F13	**22**	SCL	-	-	+++	-	+	-	OL	++	SCL	-	-	-	+++	-	-	+++
F14	**22**	OL	-	-	SCL	-	<SCL	-	OL	SCL	OL	-	-	-	<CL	-	-	SCL
F17	**22**	OL	-	-	SCL	-	SCL	-	OL	<OL	OL	-	-	-	CL		-	SCL
F19	**22**	OL	-	-	OL	-	+++	-	OL	<OL	OL	-	-	-	CL	-	-	<OL
F23	**22**	OL	-	-	<OL	-	<SCL	-	OL	<OL	OL	-	-	-	CL	-	-	OL
F24	**22**	OL	-	-	SCL	-	<SCL	-	OL	OL	OL	-	-	-	OL	-	-	SCL
F25	**22**	OL	-	1	OL	-	SCL	-	OL	OL	OL	-	-	-	OL	-	-	OL
F26	**22**	OL	-	-	SCL	-	SCL	-	OL	OL	OL	-	-	-	CL	-	-	SCL
F27	**22**	OL	-	-	OL	-	SCL	-	OL	OL	OL	-	-	-	CL	-	-	OL
F29	**22**	OL	-	-	SCL	-	+++	-	OL	SCL	OL	-	-	-	CL	-	-	SCL
F31	**22**	OL	-	-	+++	-	SCL	-	OL	+++	SCL	-	-	-	CL	-	-	+++
F32	**22**	OL	-	-	<OL	-	SCL	-	OL	OL	<OL	-	-	-	<CL	-	-	OL
F35	**22**	CL	-	-	SCL	-	++	-	OL	OL	OL	-	-	-	CL	-	-	CL

Strain E3		Phage reactions at routine test dilution (*S.* Enteritidis)																
Lab code	**Phage type**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	**15**	**16**	**17**
HPA	**59**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	<OL
F1	**59**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+++
F2	**59**	-	-	-	+	-	-	-	-	±	-	-	-	-	-	-	-	SCL
F4	**59**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	SCL
F5	**59**	-	-	-	±	-	-	-	-	±	-	-	-	-	-		-	SCL
F6	**59**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	SCL
F7	**59**	-	-	-	-	-	-	-	-	-	-	-	-	-	-		-	SCL
F8	**59**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OL
F13	**59**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+++
F14	**59**	-	-	-	4	-	-	-	-	5	-	-	-	-	-	-	-	SCL
F17	**14b**	-	-	-	+	-	OL	-	-	+	-	-	-	-	-		-	SCL
F19	**59**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	<OL
F23	**59**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	<OL
F24	**59**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OL
F25	**59**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	<OL
F26	**59**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	SCL
F27	**59**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OL
F29	**59**	-	-	-	1	-	-	-	-	1	-	-	-	-	-	-	-	+++
F31	**59**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+++
F32	**23**	-	-	-	<SCL	-	-	-	-	SCL	-	-	-	-	-	-	-	OL
F35	**59**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	CL

Strain E4		Phage reactions at routine test dilution (*S.* Enteritidis)																
Lab code	**Phage type**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	**15**	**16**	**17**
HPA	**1**	OL	SCL	CL	OL	CL	SCL	CL	OL	OL	OL	CL	CL	CL	CL	-	-	SCL
F1	**1**	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	-	-	+++
F2	**1a**	OL	SCL	CL	OL	CL	OL	CL	OL	OL	OL	CL	CL	CL	+++	-	-	<OL
F4	**1**	OL	+++	<CL	++	<CL	+++	OL	SCL	+++	SCL	SCL	<CL	OL	SCL	-	-	+++
F5	**1**	<SCL	+++	CL	++	CL	+++	<CL	<CL	++	++	CL	CL	CL	SCL		-	++
F6	**37**	SCL	-	SCL	-	SCL	+++	SCL	SCL	-	SCL	SCL	SCL	SCL	SCL	-	-	+
F7	**1**	OL	SCL	CL	SCL	CL	SCL	CL	OL	OL	OL	CL	CL	CL	CL	-	-	SCL
F8	**1**	OL	SCL	CL	OL	CL	OL	CL	OL	OL	OL	CL	CL	CL	CL	-	-	OL
F13	**44**	+++	+	±	-	++	++	SCL	OL	-	<SCL	SCL	SCL	SCL	+++	-	-	-
F14	**44**	OL	++	CL	±	CL	+++	<CL	SCL	2	OL	CL	CL	CL	<CL	2	2	4
F17	**1**	OL	SCL	CL	OL	CL	SCL	CL	OL	OL	OL	CL	CL	CL	CL		-	SCL
F19	**1**	OL	SCL	CL	CL	CL	SCL	CL	SCL	OL	SCL	CL	CL	CL	CL	-	-	<OL
F23	**1**	OL	<SCL	CL	<OL	CL	<SCL	CL	OL	<OL	OL	CL	CL	CL	CL	-	-	<OL
F24	**37**	OL	-	CL	-	OL	SCL	SCL	SCL	-	SCL	CL	CL	CL	CL	-	-	-
F25	**1**	OL	OL	<CL	OL	<CL	<SCL	<CL	OL	OL	OL	<CL	<CL	<CL	OL	-	-	OL
F26	**1**	OL	SCL	CL	<OL	CL	SCL	CL	OL	OL	OL	CL	CL	CL	CL	-	-	OL
F27	**1**	OL	<CL	CL	OL	CL	<SCL	CL	OL	OL	OL	CL	CL	CL	OL	-	-	OL
F29	**1**	OL	+++	OL	+++	OL	+++	OL	OL	+++	OL	OL	OL	OL	OL	-	-	+
F31	**1**	+++	+++	CL	++	CL	+++	SCL	+++	+++	+++	SCL	CL	CL	SCL	-	-	+++
F32	**1**	OL	<CL	<CL	OL	<CL	<CL	SCL	<CL	OL	OL	<CL	<CL	<CL	<CL	-	-	OL
F35	**1**	CL	CL	CL	SCL	CL	++	CL	OL	OL	OL	CL	CL	CL	CL	-	-	CL

Strain E5		Phage reactions at routine test dilution (*S.* Enteritidis)																
Lab code	**Phage type**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	**15**	**16**	**17**
HPA	**3**	OL	-	-	-	-	++	-	OL	-	OL	-	-	-	CL	-	-	-
F1	**3**	CL	-	-	-	-	±	-	CL	-	CL	-	-	-	CL	-	-	-
F2	**21b**	OL	<OL	-	SCL	-	SCL	-	OL	OL	OL	-	-	-	SCL	-	-	++
F4	**3**	SCL	-	-	-	-	±	-	SCL	-	SCL	-	-	-	++	-	-	-
F5	**3**	CL	-	-	-	-	-	-	CL	-	CL	-	-	-	<CL		-	-
F6	**3a**	OL	-	-	-	-	-	-	OL	-	OL	-	-	-	SCL	-	-	-
F7	**3**	OL	-	-	-	-	++	-	OL	-	OL	-	-	-	CL		-	-
F8	**3**	OL	-	-	-	-	+	-	OL	-	OL	-	-	-	CL	-	-	-
F13	**3a**	-	-	-	-	-	-	-	<OL	-	<SCL	-	-	-	+++	-	-	-
F14	**3**	OL	+++	-	±	-	+	-	OL	±	OL	-	-	-	<CL	-	-	±
F17	**21**	OL	SCL	-	<OL	-	SCL	-	OL	OL	OL	-	-	-	CL		-	SCL
F19	**NT**	OL	-	-	-	-	-	-	OL	-	OL	-	-	-	OL	-	-	-
F23	**3**	OL	-	-	-	-	++	-	OL	-	OL	-	-	-	CL	-	-	-
F24	**3**	<CL	-	-	-	-	SCL	-	OL	-	SCL	-	-	-	CL	-	-	-
F25	**3**	OL	-	-	-	-	-	-	OL	-	OL	-	-	-	SCL	-	-	-
F26	**3**	OL	-	-	-	-	-	-	OL	-	OL	-	-	-	CL	-	-	-
F27	**3**	OL	-	-	-	-	-	-	OL	-	OL	-	-	-	OL	-	-	-
F29	**21**	OL	+++	-	+	-	++	-	OL	++	OL	-	-	-	OL	+	-	+
F31	**3**	OL	-	-	-	-	+++	-	OL	-	OL	-	-	-	CL	-	-	+++
F32	**3**	<CL	-	-	-	-	++	-	OL	-	<OL	-	-	-	CL	-	-	±
F35	**21**	OL	++	-	++	-	+	-	OL	++	OL	-	-	-	CL	-	-	CL

Strain E6		Phage reactions at routine test dilution (*S.* Enteritidis)																
Lab code	**Phage type**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	**15**	**16**	**17**
HPA	**4**	-	SCL	CL	OL	CL	SCL	CL	OL	OL	OL	CL	CL	CL	-	-	-	<OL
F1	**4**	-	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	-	-	-	+++
F2	**4**	-	CL	<CL	OL	CL	SCL	CL	OL	OL	OL	CL	CL	CL	-	-	-	OL
F4	**4**	-	SCL	OL	SCL	OL	+++	OL	SCL	SCL	SCL	SCL	OL	SCL	-	-	-	SCL
F5	**4**	-	+++	CL	+++	CL	SCL	SCL	OL	<CL	<CL	CL	CL	CL	-		-	SCL
F6	**4**	-	SCL	SCL	+++	SCL	++	SCL	SCL	SCL	SCL	SCL	SCL	SCL	SCL	-	-	SCL
F7	**4**	-	SCL	CL	SCL	CL	SCL	CL	OL	OL	OL	CL	CL	CL	-	-	-	SCL
F8	**4**	-	OL	CL	OL	CL	OL	CL	OL	OL	OL	CL	CL	CL	-	-	-	OL
F13	**4**	-	+++	+++	+++	SCL	++	SCL	OL	++	SCL	SCL	SCL	SCL	-	-	-	++
F14	**4**	3	CL	<CL	OL	CL	SCL	<CL	OL	SCL	OL	CL	CL	CL	-	-	-	OL
F17	**4b**	-	SCL	CL	SCL	CL	SCL	CL	OL	OL	OL	CL	CL	CL	-		SCL	OL
F19	**4**	-	+++	CL	OL	CL	SCL	CL	CL	OL	SCL	CL	CL	CL	-	-	-	<OL
F23	**4**	-	SCL	CL	OL	CL	<SCL	CL	OL	OL	OL	CL	CL	CL	-	-	-	OL
F24	**8**	-	-	<CL	SCL	CL	SCL	<CL	OL	OL	SCL	SCL	SCL	-	-	-	-	OL
F25	**4**	-	OL	<CL	OL	<CL	<SCL	<CL	OL	OL	OL	<CL	<CL	<CL	-	-	-	OL
F26	**4**	-	CL	CL	SCL	CL	SCL	CL	OL	OL	OL	CL	CL	CL	-	-	-	OL
F27	**4**	-	CL	CL	OL	<CL	SCL	CL	OL	SCL	OL	<CL	CL	CL	-	-	-	OL
F29	**4**	4	CL	CL	OL	CL	+++	CL	OL	+++	OL	CL	CL	CL	3	-	-	SCL
F31	**4**	-	+++	SCL	+++	CL	SCL	CL	OL	OL	OL	CL	CL	CL	-	-	-	<OL
F32	**4**	-	<CL	<CL	OL	<CL	SCL	<CL	OL	OL	<OL	<CL	<CL	<CL	-	-	-	OL
F35	**4**	-	CL	CL	CL	CL	+++	CL	OL	OL	OL	CL	CL	CL	-	-	-	CL

Strain E7		Phage reactions at routine test dilution (*S.* Enteritidis)																
Lab code	**Phage type**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	**15**	**16**	**17**
HPA	**14b**	-	-	-	±	-	SCL	-	-	±	-	-	-	-	-	-	-	OL
F1	**14b**	-	-	-	-	-	CL	-	-	-	-	-	-	-	-	-	-	+++
F2	**14b**	-	-	-	±	-	<CL	-	-	±	-	-	-	-	-	-	-	<OL
F4	**14b**	-	-	-	3	-	+++	-	-	-	-	-	-	-	-	-	-	SCL
F5	**14b**	-	-	-	+	-	SCL	-	-	±	-	-	-	-	-		-	SCL
F6	**14b**	-	-	-	+	-	SCL	-	-	+	-	-	-	-	-	-	-	+++
F7	**14b**	-	-	-	+	-	SCL	-	-	+	-	-	-	-	-		-	SCL
F8	**14b**	-	-	-	-	-	OL	-	-	-	-	-	-	-	-	-	-	OL
F13	**14b**	-	-	-	-	-	++	-	-	-	-	-	-	-	-	-	-	++
F14	**14b**	-	-	-	+	-	SCL	-	-	±	-	-	-	-	-	-	-	SCL
F17	**14b**	-	-	-	+	-	OL	-	-	+	-	-	-	-	-		-	SCL
F19	**14b**	-	-	-	-	-	+++	-	-	-	-	-	-	-	-	-	-	<OL
F23	**14b**	-	-	-	±	-	<SCL	-	-	±	-	-	-	-	-	-	-	<OL
F24	**14b**	-	-	-	-	-	SCL	-	-	-	-	-	-	-	-	-	-	OL
F25	**14b**	-	-	-	-	-	<SCL	-	1	2	-	-	-	-	-	-	-	OL
F26	**14b**	-	-	-	+	-	SCL	-	-	+	-	-	-	-	-	-	-	OL
F27	**14b**	-	-	-	-	-	SCL	-	-	-	-	-	-	-	-	-	-	OL
F29	**14b**	-	-	-	2	-	++	-	2	-	-	-	-	-	-	-	-	+++
F31	**14b**	-	-	-	-	-	SCL	-	-	-	-	-	-	-	-	-	-	OL
F32	**14b**	-	-	-	-	-	SCL	-	-	+	-	-	-	-	-	-	-	OL
F35	**14b**	-	-	-	-	-	++	-	-	-	-	-	-	-	-	-	-	CL

Strain E8		Phage reactions at routine test dilution (*S.* Enteritidis)																
Lab code	**Phage type**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	**15**	**16**	**17**
HPA	**1b**	OL	SCL	CL	OL	CL	SCL	CL	OL	<OL	<OL	CL	CL	CL	CL	<OL	CL	<OL
F1	**1b**	+++	CL	CL	CL	CL	CL	CL	+++	CL	±	CL	CL	CL	CL	CL	CL	+++
F2	**1b**	OL	CL	<CL	OL	CL	OL	CL	OL	OL	OL	CL	CL	CL	SCL	OL	OL	OL
F4	**1b**	SCL	SCL	OL	+++	OL	+++	OL	SCL	SCL	SCL	SCL	OL	SCL	+++	SCL	SCL	SCL
F5	**1b**	+++	SCL	CL	+++	CL	<SCL	<SCL	OL	SCL	CL	CL	CL	<CL	CL		CL	SCL
F6	**1b**	+++	+++	SCL	SCL	SCL	+++	SCL	+++	+++	+++	SCL	SCL	SCL	SCL	SCL	SCL	+++
F7	**1b**	OL	SCL	CL	OL	CL	SCL	CL	OL	OL	OL	CL	CL	CL	CL	CL	CL	SCL
F8	**1b**	OL	SCL	CL	OL	CL	OL	CL	OL	OL	OL	CL	CL	CL	OL	OL	OL	OL
F13	**1b**	<SCL	+++	+	++	+	++	<SCL	OL	++	<OL	SCL	SCL	SCL	+++	SCL	SCL	++
F14	**1b**	OL	<SCL	CL	<SCL	<SCL	CL	<CL	SCL	SCL	<CL	CL	CL	CL	<CL	<CL	<OL	SCL
F17	**1b**	OL	SCL	CL	OL	CL	SCL	CL	OL	OL	OL	CL	CL	CL	CL		OL	SCL
F19	**1b**	SCL	<OL	CL	OL	CL	SCL	CL	SCL	OL	SCL	CL	CL	CL	CL	SCL	SCL	<OL
F23	**1b**	OL	SCL	CL	OL	CL	<SCL	CL	<OL	<OL	<OL	CL	CL	CL	CL	<OL	<OL	OL
F24	**9b**	-	-	OL	-	OL	-	OL	-	-	-	<SCL	CL	CL	-	-	OL	-
F25	**1b**	OL	SCL	<CL	OL	<CL	<SCL	<CL	OL	OL	OL	<CL	<CL	<CL	OL	<CL	<CL	OL
F26	**1b**	OL	CL	CL	OL	CL	SCL	CL	OL	OL	OL	CL	CL	CL	CL	SCL	SCL	OL
F27	**1b**	OL	<CL	CL	OL	<CL	SCL	CL	OL	OL	OL	CL	CL	CL	CL	SCL	SCL	OL
F29	**1b**	OL	+++	CL	++	CL	SCL	SCL	OL	SCL	OL	CL	CL	CL	CL	SCL	SCL	++
F31	**1b**	+++	SCL	CL	+++	CL	SCL	SCL	+++	OL	+++	SCL	CL	CL	CL	++	CL	+++
F32	**1b**	<OL	<CL	<CL	<OL	<CL	SCL	<CL	OL	OL	<OL	<CL	<OL	<CL	CL	<CL	<CL	OL
F35	**1b**	OL	CL	CL	CL	CL	+++	CL	OL	OL	OL	CL	CL	CL	CL	CL	CL	CL

Strain E9		Phage reactions at routine test dilution (*S.* Enteritidis)																
Lab code	**Phage type**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	**15**	**16**	**17**
HPA	**21**	OL	SCL	-	<OL	-	SCL	-	OL	OL	OL	-	-	-	CL	-	-	<OL
F1	**21**	CL	CL	-	CL	-	CL	-	CL	CL	CL	-	-	-	CL	++	+	+++
F2	**21**	OL	CL	-	OL	-	OL	-	OL	<OL	OL	-	-	-	CL	-	-	<OL
F4	**21**	<CL	SCL	-	+++	-	+++	-	OL	+++	SCL	-	-	-	SCL	-	3	<SCL
F5	**21c**	CL	SCL	-	SCL	-	++	-	OL	SCL	SCL	-	-	-	SCL		+++	SCL
F6	**3**	SCL	+	-	-	-	++	-	SCL	-	SCL	-	-	-	SCL	+++	+++	++
F7	**21c**	OL	SCL	-	OL	-	SCL	+	OL	OL	OL	-	-	-	CL	CL	CL	SCL
F8	**21c**	OL	SCL	-	OL	-	OL	-	OL	OL	OL	-	-	-	OL	+++	OL	OL
F13	**3**	SCL	-	-	-	-	+	-	OL	-	SCL	-	-	-	+++	-	+	-
F14	**21c**	OL	SCL	2	<SCL	-	SCL	-	OL	SCL	OL	-	-	-	<CL	SCL	++	SCL
F17	**21c**	OL	SCL	-	OL	-	SCL	-	OL	OL	OL	-	-	-	CL		<CL	SCL
F19	**21**	CL	SCL	-	OL	-	SCL	-	OL	<OL	OL	-	-	-	CL	++	+	<OL
F23	**21**	OL	SCL	-	OL	-	SCL	-	OL	<OL	OL	-	-	-	CL	-	-	ol
F24	**2**	OL	-	CL	SCL	<CL	SCL	SCL	OL	OL	SCL	<SCL	OL	-	CL	-	-	<OL
F25	**21c**	OL	<CL	-	OL	-	SCL	-	OL	OL	OL	-	-	-	<CL	+++	OL	OL
F26	**21**	OL	SCL	-	SCL	-	SCL	-	OL	<OL	OL	-	-	-	CL	+	+	<OL
F27	**21**	OL	<OL	-	OL	-	SCL	-	OL	SCL	OL	-	-	-	OL	-	-	OL
F29	**21c**	OL	SCL	1	SCL	-	+++	-	OL	+++	OL	-	1	-	CL	+++	++	SCL
F31	**21**	OL	+++	-	+++	-	SCL	-	OL	OL	SCL	-	-	-	CL	+	+++	OL
F32	**21c**	OL	SCL	-	SCL	-	SCL	-	OL	<OL	<OL	-	-	-	CL	++	+++	OL
F35	**21**	CL	SCL	-	SCL	-	++	-	OL	OL	OL	-	-	-	SCL	-	-	CL

Strain E10		Phage reactions at routine test dilution (*S.* Enteritidis)																
Lab code	**Phage type**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	**15**	**16**	**17**
HPA	**14c**	-	-	-	-	-	+++	-	-	-	-	-	-	-	-	-	-	-
F1	**14c**	-	-	-	-	-	+++	-	-	-	-	-	-	-	-	-	-	-
F2	**14c**	-	-	-	-	-	SCL	-	-	-	-	-	-	-	-	-	-	-
F4	**14c**	-	-	-	-	-	+++	-	-	-	-	-	-	-	-	-	-	-
F5	**14c**	-	-	-	-	-	+++	-	-	-	-	-	-	-	-	-	-	-
F6	**14c**	-	-	-	-	-	+++	-	-	-	-	-	-	-	-	-	-	-
F7	**14c**	-	-	-	-	-	SCL	-	-	-	-	-	-	-	-		-	-
F8	**14c**	-	-	-	-	-	OL	-	-	-	-	-	-	-	-	-	-	-
F13	**14c**	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-
F14	**14c**	-	-	-	-	-	SCL	-	-	-	-	-	-	-	-	-	-	-
F17	**55**	-	-	-	-	-	SCL	-	-	-	-	-	-	-	-		-	-
F19	**14c**	-	-	-	-	-	+++	-	-	-	-	-	-	-	-	-	-	-
F23	**14c**	-	-	-	-	-	<SCL	-	-	-	-	-	-	-	-	-	-	-
F24	**14c**	-	-	-	-	-	SCL	-	-	-	-	-	-	-	-	-	-	-
F25	**14c**	-	-	-	-	-	<SCL	-	-	-	-	-	-	-	-	-	-	-
F26	**14c**	-	-	-	-	-	SCL	-	-	-	-	-	-	-	-	-	-	-
F27	**14c**	-	-	-	-	-	SCL	-	-	-	-	-	-	-	-	-	-	-
F29	**14c**	-	-	-	1	-	++	-	-	-	-	-	-	-	-	-	-	-
F31	**14c**	-	-	-	-	-	+++	-	-	-	-	-	-	-	-	-	-	-
F32	**14c**	-	-	-	-	-	SCL	-	-	-	-	-	-	-	-	-	-	-
F35	**14c**	-	-	-	-	-	++	-	-	-	-	-	-	-	-	-	-	-

Strain T11		Phage reactions at routine test dilution (*S.* Typhimurium)																	
Lab code	**Phage type**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**10**	**11**	**12**	**13**	**14**	**15**	**16**	**17**	**18**	**19**
HPA	**10**	-	-	-	-	-	-	-	-	CL	OL	CL	CL	-	-	<CL	-	-	-
F1	**10**	-	-	-	-	-	-	-	-	++	CL	CL	CL	-	-	CL	-	-	-
F2	**10**	-	-	-	-	-	-	-	-	<CL	SCL	CL	CL	-	-	SCL	-	-	-
F4	**10**	-	-	-	-	-	-	-	-	OL	SCL	OL	OL	-	-	SCL	-	-	-
F5	**10**	-	-	-	-	-	-	-	-	<CL	CL	CL	CL	-	-	<CL	-	-	-
F6	**10**	-	-	-	-	-	-	-	-	SCL	SCL	SCL	-	-	-	SCL	-	-	-
F7	**10**	-	-	-	-	-	-	-	-	CL	CL	CL	CL	-	-	SCL	-	-	-
F8	**10**	-	-	-	-	-	-	-	-	++	CL	CL	CL	-	-	SCL	-	-	-
F13	**10**	-	-	-	-	-	-	-	-	CL	SCL	<OL	SCL	-	-	SCL	-	-	-
F14	**10**	-	-	-	-	-	-	-	-	CL	OL	CL	CL	-	±	<CL	-	-	-
F19	**10**	-	-	-	-	-	-	-	-	SCL	SCL	CL	CL	-	-	SCL	-	-	-
F23	**10**	-	-	-	-	-	-	-	-	CL	CL	CL	CL	-	-	<SCL	-	-	-
F24	**67**	-	-	-	-	-	-	-	-	SCL	-	CL	CL	-	-	<<	-	-	-
F25	**10**	-	-	-	-	-	-	-	-	<CL	<CL	<CL	CL	-	-	<SCL	-	-	-
F27	**10**	-	-	-	-	-	-	-	-	CL	SCL	CL	CL	-	-	SCL	-	-	-
F29	**10**	-	-	-	-	-	-	-	-	CL	OL	CL	CL	-	-	++	-	-	-
F31	**67**	-	-	-	-	-	-	-	-	++	-	CL	CL	-	-	++	-	-	-
F32	**10**	-	-	-	-	-	-	-	-	<CL	SCL	<CL	<CL	-	-	±	-	-	-
F35	**10**	-	-	-	-	-	-	-	-	CL	CL	CL	CL	-	-	CL	-	-	-

Strain T11		Phage reactions at routine test dilution (*S.* Typhimurium)											Additional phages						
Lab code	**Phage type**	**20**	**21**	**22**	**23**	**24**	**25**	**26**	**27**	**28**	**29**	**32**	**35**	**1**	**2**	**3**	**10**	**10VAR2**	**10VAR3**	**18**
HPA	**10**	<CL	-	OL	CL	-	++	+	-	-	CL	CL	-	+	+	+	OL	OL	OL	-
F1	**10**	++	-	+	++	-	±	-	-	-	CL	++	-	++	+	++	CL	CL	CL	-
F2	**10**	SCL	-	SCL	SCL	-	+	±	-	-	CL	CL	-	±	++	+	+	OL	OL	-
F4	**10**	SCL	-	SCL	SCL	-	+	-	-	-	OL	OL	-							
F5	**10**	<SCL	-	<CL	<CL	-	<SCL	+	-	-	CL	CL	-							
F6	**10**	SCL	-	SCL	SCL	-	+	+	-	-	SCL	SCL	-	-	+	+++	SCL	SCL	SCL	-
F7	**10**	CL	-	CL	CL	-	+	+	-	-	CL	SCL	-							
F8	**10**	CL	-	++	CL	-	-	-	-	-	CL	+	-	-	+	-	OL	OL	OL	-
F13	**10**	SCL	-	SCL	SCL	-	SCL	++	-	-	SCL	SCL	-	-	-	-	OL	OL	OL	-
F14	**10**	CL	-	CL	CL	±	+	±	-	-	CL	CL	-	-	±	±	OL	OL	OL	±
F19	**10**	+++	-	+++	SCL	-	-	-	-	-	CL	CL	-	-	-	-	OL	OL	OL	<OL
F23	**10**	CL	-	OL	CL	-	-	<SCL	-	-	CL	CL	-	-	-	-	OL	OL	<OL	-
F24	**67**	SCL	-	SCL	SCL	-	-	-	-	-	SCL	SCL	-							
F25	**10**	++	-	<OL	<CL	-	±	2	-	-	CL	++	-							
F27	**10**	SCL	-	<CL	<CL	-	2	+	-	-	SCL	<CL	-	++	-	-	SCL	OL	SCL	-
F29	**10**	SCL	-	SCL	SCL	-	±	-	-	-	CL	CL	-	-	±	++	OL	OL	OL	-
F31	**67**	SCL	-	++	+	-	-	-	-	-	++	SCL	-	-	-	-	OL	OL	OL	-
F32	**10**	SCL	-	<SCL	<CL	-	1-5	-	-	-	<CL	SCL	-							
F35	**10**	+	-	SCL	SCL	-	+++	-	-	-	CL	CL	-							

Strain T12		Phage reactions at routine test dilution (*S.* Typhimurium)																
Lab code	Phage type	1	2	3	4	5	6	7	8	10	11	12	13	14	15	16	17	18	19
HPA	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F1	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F2	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F4	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F5	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F6	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F7	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F8	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F13	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F14	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F19	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F23	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F24	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F25	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F27	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F29	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F31	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F32	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F35	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Strain T12		Phage reactions at routine test dilution (*S.* Typhimurium)												Additional phages						
Lab code	Phage type	20	21	22	23	24	25	26	27	28	29	32	35	1	2	3	10	10VAR2	10VAR3	18
HPA	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OL	-
F1	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	CL	-
F2	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	<OL	-
F4	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OL	-
F5	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	SCL	-
F6	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	SCL	
F7	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OL	-
F8	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OL	-
F13	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OL	-
F14	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	2	OL	-
F19	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OL	-
F23	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	<OL	-
F24	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OL	-
F25	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OL	-
F27	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OL	-
F29	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OL	-
F31	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OL	-
F32	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	<OL	-
F35	U311	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	CL	-

Strain T13		Phage reactions at routine test dilution (*S.* Typhimurium)																	
Lab code	**Phage type**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**10**	**11**	**12**	**13**	**14**	**15**	**16**	**17**	**18**	**19**
HPA	**208**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F1	**208**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F2	**208**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F4	**208**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F5	**208**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F6	**U302**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F7	**208**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F8	**U302**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F13	**208**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F14	**208**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F19	**208**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F23	**208**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F24	**U302**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F25	**208**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F27	**208**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F29	**208**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F31	**U302**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F32	**208**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F35	**208**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Strain T13		Phage reactions at routine test dilution (*S.* Typhimurium)												Additional phages						
Lab code	**Phage type**	**20**	**21**	**22**	**23**	**24**	**25**	**26**	**27**	**28**	**29**	**32**	**35**	**1**	**2**	**3**	**10**	**10VAR2**	**10VAR3**	**18**
HPA	**208**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	SCL	SCL	SCL	SCL
F1	**208**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+++	CL	+++	+++
F2	**208**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	++	++	SCL
F4	**208**	-	-	-	-	-	-	-	-	-	-	-	-	1	±	+	OL	OL	OL	++
F5	**208**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+++	+++	++	++
F6	**U302**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+++	+++	+++	-
F7	**208**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OL	OL	OL	OL
F8	**U302**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OL	±	OL	++
F13	**208**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OL	OL	OL	OL
F14	**208**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OL	OL	OL	++
F19	**208**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OL	OL	OL	OL
F23	**208**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OL	<OL	SCL	<SCL
F24	**U302**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OL	OL	OL	-
F25	**208**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OL	<OL	<OL	<OL
F27	**208**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	SCL	OL	SCL	SCL
F29	**208**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OL	+++	+++	+
F31	**U302**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OL	SCL	SCL	-
F32	**208**	-	-	-	-	-	-	-	-	-	-	-	-	++	++	++	+++	OL	+++	+++
F35	**208**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	CL	CL	CL	SCL

Strain T14		Phage reactions at routine test dilution (*S.* Typhimurium)																	
Lab code	**Phage type**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**10**	**11**	**12**	**13**	**14**	**15**	**16**	**17**	**18**	**19**
HPA	**36**	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL
F1	**36**	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL
F2	**36**	SCL	CL	CL	OL	CL	CL	CL	CL	CL	CL	SCL	CL	CL	CL	CL	CL	CL	CL
F4	**36**	SCL	OL	OL	SCL	SCL	<CL	<CL	SCL	OL	OL	OL	SCL	<CL	<CL	<CL	<CL	<CL	<CL
F5	**36**	CL	<CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	<CL	CL	CL	CL	CL	CL	CL
F6	**36**	SCL	SCL	SCL	SCL	SCL	SCL	SCL	SCL	SCL	SCL	+++	SCL	SCL	SCL	SCL	SCL	+++	SCL
F7	**36**	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL
F8	**36**	SCL	SCL	CL	CL	CL	CL	CL	CL	SCL	CL	SCL	SCL	CL	CL	CL	CL	SCL	SCL
F13	**36**	SCL	SCL	SCL	SCL	SCL	SCL	SCL	SCL	SCL	SCL	<OL	SCL	SCL	SCL	SCL	SCL	+++	SCL
F14	**36**	CL	OL	CL	OL	CL	CL	CL	CL	CL	OL	OL	CL	CL	CL	CL	CL	CL	CL
F19	**36**	SCL	+++	CL	SCL	CL	CL	<CL	<CL	<CL	CL	CL	<CL	CL	CL	CL	CL	CL	CL
F23	**36**	<CL	SCL	CL	CL	CL	CL	CL	CL	CL	CL	<CL	<CL	CL	CL	CL	CL	CL	<CL
F24	**104c**	-	-	-	-	-	-	-	CL	-	-	SCL	SCL	-	-	-	-	SCL	-
F25	**36**	<SCL	<OL	<CL	OL	<CL	CL	<SCL	CL	<CL	SCL	<SCL	<CL	CL	CL	CL	<CL	SCL	SCL
F27	**36**	SCL	<CL	CL	OL	SCL	CL	<CL	<CL	<CL	<CL	<CL	<CL	CL	CL	CL	<CL	SCL	SCL
F29	**36**	CL	CL	CL	OL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL
F31	**36**	+++	++	SCL	CL	++	+++	+++	+++	++	++	+++	SCL	CL	CL	CL	CL	CL	+++
F32	**36**	SCL	SCL	SCL	SCL	SCL	<CL	SCL	<CL	<CL	<CL	<CL	<CL	SCL	SCL	SCL	SCL	<CL	SCL
F35	**36**	CL	CL	CL	OL	SCL	CL	CL	CL	CL	CL	SCL	SCL	CL	CL	CL	CL	CL	CL

Strain T14		Phage reactions at routine test dilution (*S.* Typhimurium)												Additional phages						
Lab code	**Phage type**	**20**	**21**	**22**	**23**	**24**	**25**	**26**	**27**	**28**	**29**	**32**	**35**	**1**	**2**	**3**	**10**	**10VAR2**	**10VAR3**	**18**
HPA	**36**	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	OL	+++	++	+++	OL	OL	OL	OL
F1	**36**	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	+++	++	+++	CL	CL	CL	CL
F2	**36**	SCL	CL	CL	<CL	<CL	CL	SCL	SCL	CL	CL	CL	CL	±	++	+	-	-	+	OL
F4	**36**	SCL	OL	SCL	SCL	SCL	<CL	<CL	<CL	<CL	<CL	SCL	OL							
F5	**36**	SCL	CL	CL	CL	CL	CL	CL	<CL	CL	CL	<CL	CL							
F6	**36**	SCL	SCL	SCL	SCL	SCL	SCL	+++	SCL	SCL	SCL	SCL	SCL	+	++	+++	SCL	SCL	SCL	SCL
F7	**36**	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL							
F8	**36**	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL	OL	<OL	OL	OL
F13	**36**	SCL	SCL	SCL	SCL	SCL	SCL	SCL	SCL	SCL	SCL	SCL	SCL	+	+	++	OL	OL	OL	SCL
F14	**36**	CL	CL	CL	CL	CL	CL	CL	CL	OL	CL	CL	OL	+	+++	+++	OL	OL	OL	CL
F19	**36**	+++	SCL	SCL	<CL	<CL	CL	+++	CL	CL	CL	CL	OL	+++	++	++	OL	OL	OL	CL
F23	**36**	CL	SCL	CL	CL	CL	SCL	CL	CL	CL	CL	CL	CL	+	+	+	OL	OL	<OL	CL
F24	**104c**	OL	-	-	-	-	-	-	-	OL	-	-	-							
F25	**36**	++	OL	<OL	<CL	<CL	<CL	<CL	<CL	OL	CL	<CL	OL							
F27	**36**	SCL	OL	<CL	OL	<CL	CL	CL	CL	CL	SCL	CL	CL	+++	++	-	SCL	OL	SCL	OL
F29	**36**	CL	OL	OL	CL	CL	CL	SCL	SCL	OL	CL	CL	OL	+	+	+++	OL	OL	OL	OL
F31	**36**	SCL	SCL	++	++	+++	++	+++	CL	2	++	CL	SCL	+++	++	+++	OL	OL	OL	SCL
F32	**36**	SCL	SCL	SCL	<CL	SCL	SCL	SCL	SCL	SCL	<CL	SCL	SCL							
F35	**36**	+++	CL	<CL	CL	CL	CL	CL	CL	CL	CL	CL	OL							

Strain T15		Phage reactions at routine test dilution (*S.* Typhimurium)																	
Lab code	Phage type	1	2	3	4	5	6	7	8	10	11	12	13	14	15	16	17	18	19
HPA	195	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F1	195	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F2	195	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F4	195	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F5	195	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F6	195	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F7	195	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F8	195	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F13	195	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F14	195	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	±
F19	Rough	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F23	195	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F24	99	-	-	-	-	-	-	-	-	-	<<	-	-	-	-	-	-	-	-
F25	195	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F27	NT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F29	195	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F31	195	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F32	195	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F35	195	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Strain T15		Phage reactions at routine test dilution (*S.* Typhimurium)												Additional phages						
Lab code	Phage type	20	21	22	23	24	25	26	27	28	29	32	35	1	2	3	10	10VAR2	10VAR3	18
HPA	195	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+++	-	-	-	-
F1	195	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+++	-	++	-	-
F2	195	-	-	-	-	-	-	-	-	-	-	-	-	-	-	++	-	-	-	-
F4	195	-	-	-	-	-	-	-	-	-	-	-	-	-	-	SCL	-	-	-	-
F5	195	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+++	-	+	-	-
F6	195	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+++	+	+	+	-
F7	195	-	-	-	-	-	-	-	-	-	-	-	-	-	+	SCL	OL	OL	OL	-
F8	195	-	-	-	-	-	-	-	-	-	-	-	-	-	-	++	-	-	OL	-
F13	195	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	<OL	+	+	-
F14	195	-	-	-	-	-	-	-	-	4	-	-	-	-	-	+++	3	++	4	-
F19	Rough	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+++	-	-	+	-
F23	195	-	-	-	-	-	-	-	-	-	-	-	-	-	-	++	+	+	-	-
F24	99	-	-	-	-	-	-	-	-	-	-	-	-							
F25	195	-	-	-	-	-	-	-	-	-	-	-	-	-	-	SCL	-	-	-	-
F27	NT	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	2	-	-
F29	195	-	-	-	-	-	-	-	-	1	-	-	-	-	-	SCL	1	4	-	-
F31	195	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+++	+	-	-	-
F32	195	-	-	-	-	-	-	-	-	-	-	-	-	-	-	<OL	-	-	-	-
F35	195	-	-	-	-	-	-	-	-	-	-	-	-	-	-	++	++	+	++	-

Strain T16		Phage reactions at routine test dilution (*S.* Typhimurium)																	
Lab code	**Phage type**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**10**	**11**	**12**	**13**	**14**	**15**	**16**	**17**	**18**	**19**
HPA	**104**	-	-	-	-	-	-	-	-	-	-	SCL	SCL	-	-	-	-	++	-
F1	**104**	-	-	-	-	-	-	-	-	-	-	CL	CL	-	-	-	-	CL	-
F2	**104**	-	-	-	-	-	-	-	-	-	-	SCL	<CL	-	-	-	-	SCL	-
F4	**104**	-	-	-	-	-	-	-	-	-	-	SCL	SCL	-	-	-	-	<SCL	-
F5	**104**	-	-	-	-	-	-	-	-	-	-	SCL	SCL	-	-	-	-	++	-
F6	**104**	-	-	-	-	-	-	-	-	-	-	+++	+++	-	-	-	-	+++	-
F7	**104**	-	-	-	-	-	-	-	-	-	-	CL	CL	-	-	-	-	CL	-
F8	**104**	-	-	-	-	-	-	-	-	-	-	SCL	SCL	-	-	-	-	++	-
F13	**110b**	-	-	-	-	-	-	-	-	-	-	-	+++	-	-	-	-	-	-
F14	**104**	-	-	-	-	-	-	-	-	-	-	<CL	CL	-	-	-	-	<CL	-
F19	**104**	-	-	-	-	-	-	-	-	-	-	<CL	<CL	-	-	-	-	+++	-
F23	**104**	-	-	-	-	-	-	-	-	-	-	<SCL	<SCL	-	-	-	-	+	-
F24	**12**	-	-	-	-	-	-	-	-	-	-	SCL	SCL	-	-	-	-	-	-
F25	**104**	-	-	-	-	-	-	-	-	-	-	<OL	OL	-	-	-	-	++	-
F27	**104**	-	-	-	-	-	-	-	-	-	-	SCL	SCL	-	-	-	-	<SCL	-
F29	**104**	-	-	-	-	-	-	-	-	-	-	++	+++	-	-	-	-	++	-
F31	**104**	-	-	-	-	-	-	-	-	-	-	+++	SCL	-	-	-	-	SCL	-
F32	**104**	-	-	-	-	-	-	-	-	-	-	SCL	SCL	-	-	-	-	±	-
F35	**104**	-	-	-	-	-	-	-	-	-	-	+	+++	-	-	-	-	++	-

Strain T16		Phage reactions at routine test dilution (*S.* Typhimurium)												Additional phages						
Lab code	**Phage type**	**20**	**21**	**22**	**23**	**24**	**25**	**26**	**27**	**28**	**29**	**32**	**35**	**1**	**2**	**3**	**10**	**10VAR2**	**10VAR3**	**18**
HPA	**104**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OL	OL	OL	-
F1	**104**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	CL	CL	CL	-
F2	**104**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F4	**104**	-	-	-	-	-	-	-	-	-	-	-	-							
F5	**104**	-	-	-	-	-	-	-	-	-	-	-	-							
F6	**104**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	SCL	SCL	SCL	-
F7	**104**	++	-	-	-	-	-	-	-	-	-	-	+							
F8	**104**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OL	<OL	OL	-
F13	**110b**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	SCL	SCL	SCL	-
F14	**104**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OL	OL	OL	-
F19	**104**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OL	OL	OL	-
F23	**104**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OL	OL	<OL	-
F24	**12**	OL	-	-	-	-	-	-	-	-	-	-	-							
F25	**104**	-	-	-	-	-	-	-	-	-	-	-	-							
F27	**104**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	SCL	OL	SCL	-
F29	**104**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OL	OL	OL	-
F31	**104**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OL	OL	OL	-
F32	**104**	-	-	-	-	-	-	-	-	-	-	-	-							
F35	**104**	-	-	-	-	-	-	-	-	-	-	-	-							

Strain T17		Phage reactions at routine test dilution (*S.* Typhimurium)																
Lab code	**Phage type**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**10**	**11**	**12**	**13**	**14**	**15**	**16**	**17**	**18**	**19**
HPA	**1**	CL	CL	CL	OL	CL	CL	CL	-	CL	OL	CL	CL	CL	CL	CL	CL	SCL	CL
F1	**1**	+++	+++	+++	CL	CL	CL	CL	-	+++	CL	CL	CL	CL	CL	CL	CL	CL	CL
F2	**1**	SCL	CL	CL	OL	<CL	OL	CL	-	SCL	CL	CL	CL	CL	CL	CL	CL	+++	<CL
F4	**1**	SCL	OL	OL	OL	OL	OL	OL	-	OL	OL	OL	OL	<CL	<CL	<CL	<CL	<CL	<CL
F5	**1**	<CL	<CL	CL	CL	CL	CL	CL	-	<CL	CL	CL	CL	CL	CL	CL	CL	CL	CL
F6	**1**	SCL	SCL	SCL	SCL	SCL	SCL	SCL	-	SCL	SCL	SCL	SCL	SCL	SCL	SCL	SCL	+++	SCL
F7	**1**	CL	CL	CL	CL	CL	+++	CL	-	CL	CL	CL	CL	CL	CL	CL	CL	CL	CL
F8	**1**	SCL	-	CL	CL	CL	CL	CL	-	SCL	CL	CL	CL	CL	CL	CL	+	SCL	+
F13	**U320**	SCL	SCL	SCL	SCL	SCL	SCL	SCL	-	SCL	SCL	+++	SCL	SCL	SCL	SCL	SCL	++	SCL
F14	**1**	CL	OL	CL	OL	CL	CL	CL	-	CL	CL	CL	CL	CL	CL	CL	OL	CL	CL
F19	**1**	+++	+++	CL	+++	CL	CL	<CL	-	+++	CL	CL	CL	CL	SCL	CL	CL	CL	CL
F23	**1**	CL	CL	CL	CL	CL	CL	CL	-	CL	CL	CL	CL	CL	CL	CL	CL	<CL	<CL
F24	**104**	-	-	-	-	-	-	-	-	-	-	<<	<<	-	-	-	-	<<	-
F25	**1**	<OL	<OL	OL	OL	OL	CL	<SCL	-	OL	<OL	<OL	OL	CL	OL	CL	<OL	SCL	SCL
F27	**1**	SCL	<CL	CL	OL	SCL	CL	<OL	-	CL	SCL	CL	CL	CL	CL	CL	CL	SCL	SCL
F29	**1**	<OL	OL	OL	OL	OL	OL	OL	1	OL	OL	SCL	SCL	OL	OL	OL	OL	CL	OL
F31	**1**	+++	++	+++	CL	++	+++	+++	-	+++	++	CL	CL	CL	CL	CL	CL	CL	SCL
F32	**1**	<CL	SCL	SCL	SCL	SCL	CL	SCL	1-5	<CL	SCL	<CL	<CL	SCL	<CL	<CL	<CL	<CL	SCL
F35	**1**	CL	SCL	++	OL	SCL	CL	CL	-	CL	CL	CL	CL	CL	CL	CL	CL	SCL	CL

Strain T17		Phage reactions at routine test dilution (*S.* Typhimurium)												Additional phages						
Lab code	**Phage type**	**20**	**21**	**22**	**23**	**24**	**25**	**26**	**27**	**28**	**29**	**32**	**35**	**1**	**2**	**3**	**10**	**10VAR2**	**10VAR3**	**18**
HPA	**1**	CL	CL	CL	CL	CL	CL	CL	CL	-	CL	CL	OL	+++	++	+++	OL	OL	OL	OL
F1	**1**	CL	CL	+++	+++	CL	CL	CL	CL	-	CL	++	CL	+	+++	CL	CL	CL	CL	CL
F2	**1**	++	CL	SCL	SCL	CL	+++	<CL	CL	±	CL	<CL	CL	++	+++	+++	-	-	-	<OL
F4	**1**	SCL	OL	SCL	SCL	+++	OL	OL	OL	-	OL	OL	OL							
F5	**1**	SCL	CL	<CL	CL	CL	CL	CL	CL	±	CL	CL	OL							
F6	**1**	+++	SCL	SCL	SCL	SCL	SCL	SCL	SCL	+	SCL	SCL	SCL	+	+	+++	SCL	SCL	SCL	SCL
F7	**1**	++	CL	CL	+++	CL	+++	CL	CL	+	CL	+++	CL							
F8	**1**	CL	CL	CL	CL	CL	CL	CL	CL	-	CL	CL	CL	+	+	+	OL	<OL	OL	CL
F13	**U320**	SCL	SCL	SCL	SCL	SCL	SCL	SCL	SCL	-	SCL	SCL	SCL	-	-	++	OL	OL	OL	OL
F14	**1**	<CL	OL	OL	CL	CL	OL	CL	CL	4	CL	OL	OL	++	+++	+++	OL	OL	OL	CL
F19	**1**	+++	SCL	SCL	SCL	+++	SCL	+++	CL	-	CL	CL	OL	+	+	+	OL	OL	OL	OL
F23	**1**	CL	<CL	CL	CL	CL	<CL	CL	CL	2	CL	CL	CL	++	++	++	OL	OL	<OL	CL
F24	**104**	-	-	-	-	-	-	-	-	-	-	-	-							
F25	**1**	++	OL	<OL	<OL	OL	<OL	SCL	OL	-	OL	SCL	OL							
F27	**1**	SCL	OL	<CL	CL	<OL	OL	<CL	OL	-	SCL	SCL	OL	+++	++	-	SCL	OL	SCL	OL
F29	**1**	SCL	OL	<OL	<OL	OL	OL	SCL	SCL	1	CL	OL	OL	+	+	+++	OL	OL	OL	OL
F31	**1**	SCL	SCL	++	+++	+++	++	+++	SCL	-	++	SCL	SCL	+++	+	+++	OL	OL	OL	OL
F32	**1**	SCL	<CL	SCL	<CL	SCL	<CL	SCL	<CL	-	CL	<CL	SCL							
F35	**1**	++	OL	<CL	CL	CL	OL	SCL	SCL	-	CL	CL	CL							

Strain T18		Phage reactions at routine test dilution (*S.* Typhimurium)																	
Lab code	Phage type	1	2	3	4	5	6	7	8	10	11	12	13	14	15	16	17	18	19
HPA	193	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F1	193	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F2	193	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F4	193	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F5	193	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F6	193	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F7	193	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F8	193	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F13	193	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F14	193	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F19	193	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F23	193	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F24	193	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F25	193	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F27	193	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F29	193	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F31	193	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F32	193	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F35	193	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Strain T18		Phage reactions at routine test dilution (*S.* Typhimurium)												Additional phages						
Lab code	Phage type	20	21	22	23	24	25	26	27	28	29	32	35	1	2	3	10	10VAR2	10VAR3	18
HPA	193	-	-	-	-	-	-	-	-	-	-	-	-	+++	+++	+++	-	-	-	-
F1	193	-	-	-	-	-	-	-	-	-	-	-	-	++	++	+++	-	-	-	-
F2	193	-	-	-	-	-	-	-	-	-	-	-	-	++	++	+++	-	-	-	-
F4	193	-	-	-	-	-	-	-	-	-	-	-	-	SCL	SCL	SCL	-	-	-	-
F5	193	-	-	-	-	-	-	-	-	-	-	-	-	++	++	SCL	-	-	-	-
F6	193	-	-	-	-	-	-	-	-	-	-	-	-	++	+++	+++	-	-	-	-
F7	193	-	-	-	-	-	-	-	-	-	-	-	-	SCL	SCL	SCL	-	-	+	-
F8	193	-	-	-	-	-	-	-	-	-	-	-	-	+	+	+	-	-	-	-
F13	193	-	-	-	-	-	-	-	-	-	-	-	-	++	++	++	-	-	-	-
F14	193	-	-	-	-	-	-	-	-	-	-	-	-	<SCL	<SCL	<SCL	1	±	5	-
F19	193	-	-	-	-	-	-	-	-	-	-	-	-	+++	+++	+++	-	-	-	-
F23	193	-	-	-	-	-	-	-	-	-	-	-	-	+++	+++	+++	-	-	-	-
F24	193	-	-	-	-	-	-	-	-	-	-	-	-	<SCL	<SCL	<SCL	-	-	-	-
F25	193	-	-	-	-	-	-	-	-	-	-	-	-	<SCL	SCL	<SCL	-	-	-	-
F27	193	-	-	-	-	-	-	-	-	-	-	-	-	+++	++	+	-	-	-	-
F29	193	-	-	-	-	-	-	-	-	-	-	-	-	+++	++	SCL	-	-	-	-
F31	193	-	-	-	-	-	-	-	-	-	-	-	-	+++	+	+++	-	-	-	-
F32	193	-	-	-	-	-	-	-	-	-	-	-	-	+++	+	<CL	-	-	-	-
F35	193	-	-	-	-	-	-	-	-	-	-	-	-	+++	+++	+++	-	-	-	-

Strain T19		Phage reactions at routine test dilution (*S.* Typhimurium)																	
Lab code	**Phage type**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**10**	**11**	**12**	**13**	**14**	**15**	**16**	**17**	**18**	**19**
HPA	**8**	-	-	-	-	-	-	-	+++	SCL	CL	-	-	-	-	+++	-	-	-
F1	**8**	-	-	-	-	-	-	-	CL	++	CL	-	-	-	-	++	-	-	-
F2	**8**	-	-	-	-	-	-	-	SCL	SCL	SCL	-	-	-	-	+++	-	-	-
F4	**8**	-	-	-	-	-	-	-	SCL	SCL	<SCL	-	-	-	-	++	-	-	-
F5	**8**	-	-	-	-	-	-	-	SCL	SCL	++	-	-	-	-	SCL	-	-	-
F6	**8**	-	-	-	-	-	-	-	+++	+++	++	-	-	-	-	+++	-	-	-
F7	**8**	-	-	-	-	-	-	-	+++	CL	SCL	-	-	-	-	SCL	-	-	-
F8	**66a**	-	-	-	-	-	-	-	OL	+	OL	-	-	-	-	OL	-	-	-
F13	**8**	-	-	-	-	-	-	-	SCL	SCL	SCL	-	-	-	-	+++	-	-	-
F14	**8**	-	-	-	-	-	-	-	SCL	<CL	<CL	-	-	-	-	SCL	-	-	-
F19	**8**	-	-	-	-	-	-	-	<SCL	+++	++	-	-	-	-	++	-	-	-
F23	**8**	-	-	-	-	-	-	-	SCL	SCL	SCL	-	-	-	-	+++	-	-	-
F24	**U302**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
F25	**8**	-	-	-	-	-	-	-	<CL	<CL	<OL	-	-	-	-	<SCL	-	-	-
F27	**8**	-	-	-	-	-	-	-	<OL	SCL	SCL	-	-	-	-	+++	-	-	-
F29	**8**	-	-	-	-	-	-	-	SCL	SCL	++	-	-	-	-	+++	±	-	-
F31	**8**	-	-	-	-	-	-	-	+++	++	-	-	-	-	-	++	-	-	-
F32	**8**	-	-	-	-	-	-	-	SCL	SCL	++	-	-	-	-	±	-	-	-
F35	**8**	-	-	-	-	-	-	-	+++	+++	+	-	-	-	-	++	-	-	-

Strain T19		Phage reactions at routine test dilution (*S.* Typhimurium)											Additional phages						
Lab code	**Phage type**	**20**	**21**	**22**	**23**	**24**	**25**	**26**	**27**	**28**	**29**	**32**	**35**	**1**	**2**	**3**	**10**	**10VAR2**	**10VAR3**	**18**
HPA	**8**	SCL	-	SCL	SCL	-	++	+	-	-	CL	SCL	-	+	+	+	<OL	OL	OL	-
F1	**8**	++	±	+	++	-	±	±	-	-	CL	+	-	+	++	CL	CL	CL	CL	-
F2	**8**	+++	-	SCL	SCL	-	±	±	-	-	CL	SCL	-	±	++	++	±	OL	OL	-
F4	**8**	SCL	-	<SCL	<SCL	-	+	+	-	-	SCL	SCL	-							
F5	**8**	++	±	SCL	SCL	-	++	++	-	-	<CL	SCL	-							
F6	**8**	+++	+	SCL	SCL	-	++	-	-	-	SCL	SCL	-	+	+	+++	SCL	SCL	SCL	-
F7	**8**	CL	-	SCL	CL	-	+	+	-	-	CL	SCL	-							
F8	**66a**	OL	-	OL	SCL	-	-	-	-	-	SCL	-	-	+	+	+	OL	<OL	OL	-
F13	**8**	+++	-	SCL	SCL	-	+++	++	-	-	CL	SCL	-	-	+	+	OL	OL	OL	-
F14	**8**	<SCL	2	<CL	<CL	-	±	2	-	-	CL	CL	-	1	++	++	OL	OL	OL	-
F19	**8**	++	-	+++	+++	-	-	-	-	-	SCL	SCL	-	-	-	-	OL	OL	OL	-
F23	**8**	SCL	-	SCL	SCL	-	-	++	-	-	CL	SCL	-	+	++	++	OL	OL	<OL	-
F24	**U302**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	OL	OL	OL	-
F25	**8**	++	-	<OL	SCL	-	1	2	-	-	CL	<SCL	-							
F27	**8**	SCL	-	SCL	<OL	-	-	+	-	-	SCL	OL	-	+++	++	-	SCL	OL	SCL	-
F29	**8**	+++	±	++	+++	-	±	±	-	-	CL	CL	1	4	3	++	OL	OL	OL	-
F31	**8**	SCL	-	+++	+	-	-	-	-	-	++	SCL	-	++	-	+++	OL	OL	OL	-
F32	**8**	+++	-	SCL	SCL	-	1-5	-	-	-	<CL	SCL	-							
F35	**8**	+	-	+++	+++	-	+	-	-	-	CL	SCL	-							

Strain T20		Phage reactions at routine test dilution (*S.*Typhimurium)																	
Lab code	**Phage type**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**10**	**11**	**12**	**13**	**14**	**15**	**16**	**17**	**18**	**19**
HPA	**40**	CL	CL	CL	CL	CL	CL	CL	-	CL	CL	-	CL	CL	CL	CL	CL	CL	CL
F1	**40**	CL	+++	CL	CL	CL	CL	CL	-	+++	CL	-	CL	CL	CL	CL	CL	CL	CL
F2	**40**	SCL	SCL	CL	<CL	CL	SCL	<CL	-	CL	CL	-	CL	CL	CL	CL	CL	SCL	CL
F4	**40**	SCL	<CL	<CL	OL	OL	OL	OL	-	SCL	CL	-	OL	OL	OL	OL	OL	OL	<CL
F5	**40**	CL	CL	CL	OL	CL	+++	CL	-	CL	CL	-	CL	CL	CL	CL	CL	CL	CL
F6	**40**	SCL	SCL	SCL	SCL	SCL	+++	SCL	-	SCL	SCL	-	SCL	SCL	SCL	SCL	SCL	+++	SCL
F7	**41**	CL	CL	CL	CL	CL	CL	CL	-	CL	CL	-	-	CL	CL	CL	CL	CL	CL
F8	**40**	OL	+	SCL	CL	OL	OL	CL	-	SCL	OL	-	CL	CL	CL	CL	SCL	SCL	++
F13	**40**	SCL	SCL	SCL	SCL	SCL	SCL	SCL	-	SCL	SCL	-	SCL	SCL	SCL	SCL	SCL	++	SCL
F14	**40**	OL	OL	OL	OL	OL	OL	OL	-	OL	OL	-	OL	OL	OL	OL	OL	CL	OL
F19	**40**	+++	+++	CL	+++	CL	SCL	SCL	-	+++	CL	-	CL	CL	SCL	CL	CL	CL	CL
F23	**40**	CL	CL	CL	CL	CL	CL	CL	-	CL	CL	-	CL	CL	CL	CL	CL	CL	<CL
F24	**40**	SCL	SCL	<CL	<CL	<CL	CL	CL	-	SCL	SCL	-	<CL	<CL	<CL	CL	CL	SCL	SCL
F25	**40**	SCL	<OL	<CL	OL	<CL	SCL	<SCL	-	<CL	SCL	-	<CL	<CL	<CL	<CL	++	SCL	SCL
F27	**40**	<CL	SCL	CL	OL	SCL	<CL	CL	-	CL	<CL	-	CL	CL	CL	CL	CL	SCL	SCL
F29	**40**	SCL	OL	CL	OL	CL	CL	CL	±	CL	CL	-	CL	CL	CL	CL	CL	CL	CL
F31	**40**	SCL	+++	SCL	<CL	++	+++	SCL	-	+++	++	-	OL	OL	OL	OL	OL	CL	SCL
F32	**40**	<CL	SCL	SCL	SCL	SCL	OL	SCL	1-5	<CL	<CL	1-5	<OL	SCL	<CL	<CL	<CL	SCL	SCL
F35	**40**	CL	SCL	CL	OL	SCL	CL	CL	-	CL	CL	-	CL	CL	CL	CL	CL	++	SCL

Strain T20		Phage reactions at routine test dilution (*S.* Typhimurium)											Additional phages						
Lab code	**Phage type**	**20**	**21**	**22**	**23**	**24**	**25**	**26**	**27**	**28**	**29**	**32**	**35**	**1**	**2**	**3**	**10**	**10VAR2**	**10VAR3**	**18**
HPA	**40**	CL	CL	CL	CL	CL	CL	CL	CL	-	CL	CL	OL	+	+	+	OL	OL	OL	OL
F1	**40**	+++	CL	+++	+++	CL	CL	CL	CL	-	CL	+++	CL	++	+	+	CL	CL	CL	CL
F2	**40**	SCL	CL	<CL	CL	SCL	CL	<CL	<CL	±	CL	CL	<CL	-	++	±	-	±	±	CL
F4	**40**	SCL	<CL	<CL	<CL	<CL	<CL	SCL	SCL	-	<CL	<CL	OL							
F5	**40**	SCL	CL	<CL	<CL	CL	CL	CL	<CL	-	CL	<CL	OL							
F6	**40**	+++	SCL	SCL	SCL	SCL	SCL	+++	SCL	+	SCL	SCL	SCL	+	++	+++	SCL	SCL	SCL	SCL
F7	**41**	CL	CL	CL	CL	CL	CL	CL	CL	+	CL	CL	CL							
F8	**40**	CL	CL	CL	CL	CL	CL	CL	CL	-	CL	CL	CL	-	+	+	OL	<OL	OL	CL
F13	**40**	SCL	SCL	SCL	SCL	SCL	SCL	SCL	SCL	-	SCL	SCL	SCL	-	+	+	OL	OL	OL	SCL
F14	**40**	<CL	OL	OL	OL	OL	OL	CL	CL	1	OL	OL	OL	±	+	+	OL	OL	OL	CL
F19	**40**	+++	SCL	+++	CL	SCL	CL	++	CL	-	CL	CL	CL	+++	+++	+++	OL	OL	OL	OL
F23	**40**	CL	<CL	CL	CL	CL	<CL	CL	CL	1	CL	CL	CL	++	+++	++	OL	OL	<OL	CL
F24	**40**	CL	CL	<CL	SCL	CL	SCL	CL	SCL	-	<CL	SCL	OL							
F25	**40**	<SCL	OL	<OL	SCL	<CL	<CL	<CL	<CL	-	CL	<CL	OL							
F27	**40**	SCL	OL	<OL	CL	CL	CL	CL	CL	-	<CL	CL	OL	+++	++	-	SCL	OL	SCL	OL
F29	**40**	CL	OL	<OL	CL	CL	CL	CL	CL	2	CL	CL	OL	-	±	++	OL	OL	OL	OL
F31	**40**	SCL	SCL	++	++	SCL	++	+++	SCL	-	+++	SCL	SCL	++	+	+++	OL	OL	OL	OL
F32	**40**	SCL	<CL	SCL	SCL	SCL	SCL	SCL	<CL	1-5	<CL	SCL	SCL							
F35	**40**	+++	CL	SCL	SCL	CL	CL	SCL	CL	-	CL	CL	CL							

Annex 6. Results of the antimicrobial susceptibility testing by antibiotic for all laboratories

AMPICILLIN (AMP)															
Lab code	Method	Criteria used	A-1	A-2	A-3	A-4	A-5	A-6	A-7	A-8	A-9	A-10	N	Mi-nor	Ma-jor
CVI	MIC	S ≤8,R ≥32	>32 (R)	1 (S)	1 (S)	>32 (R)	1 (S)	>32 (R)	2 (S)	>32 (R)	>32 (R)	>32 (R)			
F4	MIC	≥16/ 4-8 /≤2	>16 (R)	≤1 (S)	2 (S)	2 (S)	2 (S)	>16 (R)	8 (I)	>16 (R)	>16 (R)	>16 (R)	9	1	0
F5	MIC	<16/≥16	R	S	S	S	S	R	S	R	R	R	9	0	0
F9	MIC	R/I/S	>128 (R)	<8 (S)	<8 (S)	>128 (R)	<8 (S)	>128 (R)	<8 (S)	>128 (R)	>128 (R)	>128 (R)	9	0	0
F12	MIC	≥32: R/ ≤8: S	≥32 (R)	≤2 (S)	≤2 (S)	≤2 (S)	≤2 (S)	≥32 (R)	≤2 (S)	≥32 (R)	≥32 (R)	≥32 (R)	9	0	0
F24	MIC	8/16/32	>64, R	1, S	2, S	1, S	1, S	>64, R	1, S	>64, R	>64, R	>64, R	9	0	0
F25	MIC	CLSI	>32 (R)	≤1 (S)	≤ (S)	≤1 (S)	≤1 (S)	>32 (R)	2 (S)	>32 (R)	≤1 (S)	>32 (R)	9	0	1
F26	MIC	R: >4	>32 (R)	1 (S)	1 (S)	>32 (R)	1 (S)	>32 (R)	2 (S)	>32 (R)	>32 (R)	>32 (R)	9	0	0
F28	MIC	R:≥16/S:≤8	>32 (R)	≤1 (S)	≤1 (S)	≤1 (S)	≤1 (S)	>32 (R)	2 (S)	>32 (R)	>32 (R)	>32 (R)	9	0	0
F33	MIC	≤8 (S)/16 (I)/≥32 (R)	>256 (R)	0.75 (S)	0.75 (S)	0.5 (S)	0.38 (S)	>256 (R)	1.0 (S)	>256 (R)	>256 (R)	>256 (R)	9	0	0
F34	MIC	<8/16/≥32	256 (R)	1 (S)	1 (S)	1 (S)	0.5 (S)	256 (R)	2 (S)	256 (R)	256 (R)	256 (R)	9	0	0
F35	MIC	8 µg/ml	R	S	S	S	S	R	S	R	R	R	9	0	0
F1	Disk	≤13/14-16/17≥	6 (R)	26 (S)	26 (S)	30 (S)	26 (S)	6 (R)	22 (S)	6 (R)	6 (R)	6 (R)	9	0	0
F2	Disk	R ≤13; I 14-16; S ≥17	6 (R)	22 (S)	24 (S)	24 (S)	25 (S)	6 (R)	23 (S)	6 (R)	6 (R)	6 (R)	9	0	0
F3	Disk	13/14-16/17	6 (R)	28 (S)	27 (S)	30 (S)	30 (S)	6 (R)	25 (S)	6 (R)	6 (R)	6 (R)	9	0	0
F6	Disk	≤13/14-16/≥17	7 (R)	26 (S)	26 (S)	27 (S)	29 (S)	7 (R)	24 (S)	7 (R)	7 (R)	7 (R)	9	0	0
F8	Disk	13/17	6 (R)	21 (S)	21 (S)	6 (R)	21 (S)	6 (R)	19 (S)	6 (R)	6 (R)	6 (R)	9	0	0
F10	Disk	-													
F11	Disk	S	R	S	S	S	S	R	S	R	R	R	9	0	0
F13	Disk	<13/14-16/>17	6 (R)	24 (S)	24 (S)	25 (S)	25 (S)	6 (R)	20 (S)	6 (R)	6 (R)	6 (R)	9	0	0
F14	Disk	CLSI (2007)	0 (R)	25.37 (S)	26.83 (S)	27.58 (S)	26.84 (S)	0 (R)	22.25 (S)	0 (R)	0 (R)	0 (R)	9	0	0
F15	Disk	13/14-16/17	6 (R)	25 (S)	25 (S)	26 (S)	26 (S)	6 (R)	23 (S)	6 (R)	6 (R)	6 (R)	9	0	0
F16	Disk	≤13 14-16 ≥17	06 (R)	24 (S)	27 (S)	26 (S)	28 (S)	06 (R)	24 (S)	06 (R)	06 (R)	06 (R)	9	0	0
F17	Disk	≤13/14-16/≥17	≤6 R	25 S	24 S	23 S	27 S	≤6 R	21 S	≤6 R	≤6 R	≤6 R	9	0	0
F18	Disk	≤13/14-16/≥17	6 (R)	23 (S)	23 (S)	25 (S)	24 (S)	6 (R)	22 (S)	6 (R)	6 (R)	6 (R)	9	0	0
F19	Disk	14-16	6 (R)	24 (S)	24 (S)	6 (R)	25 (S)	6 (R)	22 (S)	6 (R)	6 (R)	6 (R)	9	0	0
F22	Disk	13-17	6 (R)	25 (S)	26 (S)	28 (S)	27 (S)	6 (R)	25 (S)	6 (R)	6 (R)	6 (R)	9	0	0
F23	Disk	≤13 14-16 ≥17	6 (R)	26 (S)	27 (S)	6 (R)	30 (S)	6 (R)	24 (S)	6 (R)	6 (R)	6 (R)	9	0	0
F29	Disk	≤13 14-30/≥31	6 (R)	25 (I)	26 (I)	25 (I)	28 (I)	6 (R)	25 (I)	6 (R)	6 (R)	6 (R)	9	4	0
F30	Disk	≤13 … ≥17	6 (R)	27 (S)	25 (S)	26 (S)	27 (S)	6 (R)	26 (S)	6 (R)	25 (S)	6 (R)	9	0	1
F31	Disk	13/14-16/17	0 (R)	23 (S)	25 (S)	25 (S)	25 (S)	0 (R)	20 (S)	0 (R)	0 (R)	0 (R)	9	0	0
F36	Disk	≤13/14-16/≥17	6 (R)	27 (S)	26 (S)	27 (S)	31 (S)	6 (R)	25 (S)	6 (R)	6 (R)	6 (R)	9	0	0
N			30	30	30		30	30	30	30	30	30	270		
Minor			0	1	1		1	0	2	0	0	0		5	
Major			0	0	0		0	0	0	0	2	0			2

Dark grey cells = resistant (R), light grey = intermediate (I), white = susceptible (S). Grey text: excluded from evaluation.

MIC: in mg/L; disk: in mm.

CEFOTAXIME (CTX)															
Lab code	Method	Criteria used	A-1	A-2	A-3	A-4	A-5	A-6	A-7	A-8	A-9	A-10	N	Mi-nor	Ma-jor
CVI	MIC	S ≤1, R ≥4	0.12 (S)	≤0.06 (S)	0.12 (S)	0.12 (S)	≤0.06 (S)	0.25 (S)	0.12 (S)	≤0.06 (S)	>4 (R)	≤0.06 (S)			
F4	MIC	≥16/ 4-8 /≤2	≤1 (S)	≤1 (S)	≤1 (S)	≤1 (S)	≤1 (S)	≤1 (S)	≤1 (S)	≤1 (S)	16 (R)	≤1 (S)	9	0	0
F5*	MIC	<1/≥1	S	S	S	S	S	S	S	S	R	S	9	0	0
F9	MIC	R/S	<1 (S)	<1 (S)	<1 (S)	<1 (S)	<1 (S)	<1 (S)	<1 (S)	<1 (S)	<1 (S)	<1 (S)	9	0	0
F12	MIC	≥64: R/≤8: S	≤1 (S)	≤1 (S)	≤1 (S)	≤1 (S)	≤1 (S)	≤1 (S)	≤1 (S)	≤1 (S)	=16 (R)	≤1 (S)	9	0	0
F24	MIC	0,5/-/1	≤0,25, S	≤0,25, S	≤0,25, S	≤0,25, S	≤0,25, S	≤0,25, S	≤0,25, S	≤0,25, S	8, R	≤0,25, S	9	0	0
F25*	MIC	-													
F26	MIC	R: >0.5	0.12 (S)	≤0.06 (S)	0.12 (S)	0.12 (S)	≤0.06 (S)	≤0.06 (S)	0.25 (S)	0.12 (S)	>4 (R)	0.12 (S)	9	0	0
F28	MIC	R:≥4/S:≤2	≤0.125 (S)	≤0.125 (S)	≤0.125 (S)	≤0.125 (S)	≤0.125 (S)	≤0.125 (S)	≤0.125 (S)	≤0.125 (S)	4 (R)	≤0.125 (S)	9	0	0
F33	MIC	≤8 (S)/16-32 (I)/≥64 (R)	0.25 (S)	0.125 (S)	0.25 (S)	0.125 (S)	0.064 (S)	0.125 (S)	0.38 (S)	0.125 (S)	16 (I)	0.25 (S)	9	0	0
F34*	MIC														
F35	MIC	1 µg/ml	S	S	S	S	S	S	S	S	R	S	9	0	0
F1	Disk	≤14/15-22/23≥	34 (S)	34 (S)	32 (S)	34 (S)	34 (S)	34 (S)	34 (S)	30 (S)	18 (R)	35 (S)	9	0	0
F2	Disk	R ≤14; I 15-22; S ≥23	29 (S)	29 (S)	28 (S)	28 (S)	31 (S)	28 (S)	30 (S)	31 (S)	16 (I)R	30 (S)	9	0	0
F3	Disk	14/15-22/23	33 (S)	34 (S)	33 (S)	33 (S)	36 (S)	34 (S)	31 (S)	36 (S)	19 (I)	36 (S)	9	0	0
F6	Disk	≤14/15-22/≥23	32 (S)	31 (S)	32 (S)	30 (S)	37 (S)	30 (S)	29 (S)	31 (S)	19 (I)	32 (S)	9	0	0
F8*	Disk	14/23	27 (S)	27 (S)	29 (S)	27 (S)	28 (S)	28 (S)	28 (S)	29 (S)	15 (I)	27 (S)	9	0	0
F10	Disk	-													
F11	Disk	S	S	S	S	S	S	S	S	S	I	S	9	0	0
F13	Disk	<14/15-22/>23	30 (S)	32 (S)	30 (S)	31 (S)	32 (S)	32 (S)	29 (S)	30 (S)	16 (I)	29 (S)	9	0	0
F14	Disk	CLSI (2007)	34.38 (S)	32.84 (S)	35.63 (S)	32.81 (S)	35.99 (S)	31.63 (S)	30.98 (S)	33.46 (S)	18.48 (I)	33.79 (S)	9	0	0
F15	Disk	13/14-20/21	33 (S)	35 (S)	35 (S)	35 (S)	37 (S)	36 (S)	35 (S)	35 (S)	17 (I)	35 (S)	9	0	0
F16	Disk	≤14 15-22 ≥23	32 (S)	32 (S)	33 (S)	31 (S)	34 (S)	32 (S)	31 (S)	30 (S)	16 (I)	32 (S)	9	0	0
F17	Disk	≤14/15-22/≥23	29 S	28 S	29 S	26 S	33 S	25 S	25 S	24 S	18 I	27 S	9	0	0
F18	Disk	≤14/15-22/≥23	32 (S)	33 (S)	33 (S)	33 (S)	35 (S)	34 (S)	34 (S)	34 (S)	17 (R)	33 (S)	9	0	0
F19	Disk	15-22	28 (S)	31 (S)	28 (S)	26 (S)	32 (S)	27 (S)	27 (S)	28 (S)	16 (I)	28 (S)	9	0	0
F22	Disk	14-23	34 (S)	37 (S)	35 (S)	34 (S)	37 (S)	35 (S)	32 (S)	37 (S)	18 (I)	35 (S)	9	0	0
F23	Disk	≤14 15-22 ≤23	34 (S)	32 (S)	31 (S)	32 (S)	36 (S)	32 (S)	30 (S)	33 (S)	17 (I)	31 (S)	9	0	0
F29	Disk	-													
F30*	Disk	≤14 ... ≤23	32 (S)	34 (S)	32 (S)	33 (S)	33 (S)	34 (S)	32 (S)	30 (S)	37 (S)	31 (S)	9	0	0
F31	Disk	14/15-22/23	30 (S)	34 (S)	32 (S)	32 (S)	35 (S)	32 (S)	29 (S)	32 (S)	20 (I)	32 (S)	9	0	0
F36*	Disk	≤14/15-22/≥23	32 (S)	37 (S)	32 (S)	33 (S)	38 (S)	32 (S)	32 (S)	34 (S)	17 (I)	33 (S)	9	0	0
N			27	27	27	27	27	27	27	27		27	243		
Mi-nor			0	0	0	0	0	0	0	0		0		0	
Ma-jor			0	0	0	0	0	0	0	0		0			0

Dark grey cells = resistant (R), light grey = intermediate (I), white = susceptible (S). Grey text: excluded from evaluation.

MIC: in mg/L; disk: in mm.

CHLORAMPHENICOL (CHL)															
Lab code	Method	Criteria used	A-1	A-2	A-3	A-4	A-5	A-6	A-7	A-8	A-9	A-10	N	Mi-nor	Ma-jor
CVI	MIC	S ≤8,R ≥32	8 (S)	4 (S)	8 (S)	8 (S)	4 (S)	8 (S)	8 (S)	>64 (R)	4 (S)	8 (S)			
F4	MIC	≥16/ /≤8	≤4 (S)	≤4 (S)	8 (S)	8 (S)	≤4 (S)	8 (S)	8 (S)	>32 (R)	≤4 (S)	8 (S)	10	0	0
F5	MIC	<16/≥16	S	S	S	S	S	S	S	R	S	S	10	0	0
F9	MIC	R/S	<8 (S)	<8 (S)	<8 (S)	<8 (S)	<8 (S)	<8 (S)	<8 (S)	>8 (R)	<8 (S)	<8 (S)	10	0	0
F12	MIC	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA			
F24	MIC	8/16/32	2, S	4, S	2, S	4, S	2, S	4, S	4, S	>32, R	2, S	4, S	10	0	0
F25	MIC	CLSI	4 (S)	≤2 (S)	8 (S)	4 (S)	≤2 (S)	4 (S)	8 (S)	>32 (R)	4 (S)	8 (S)	10	0	0
F26	MIC	R: >16	8 (S)	4 (S)	8 (S)	8 (S)	8 (S)	8 (S)	8 (S)	>64 (R)	8 (S)	8 (S)	10	0	0
F28	MIC	R:≥32/I: 16/S:≤8	8 (S)	4 (S)	8 (S)	8 (S)	4 (S)	8 (S)	8 (S)	>64 (R)	4 (S)	4 (S)	10	0	0
F33	MIC	≤8 (S)/16 (I)/≥32 (R)	2 (S)	3 (S)	3 (S)	3 (S)	2 (S)	3 (S)	3 (S)	>256 (R)	3 (S)	2 (S)	10	0	0
F34	MIC	<8/16/≥32	4 (S)	4 (S)	4 (S)	4 (S)	2 (S)	4 (S)	4 (S)	256 (R)	4 (S)	2 (S)	10	0	0
F35	MIC	8 µg/ml	S	S	S	S	S	S	S	R	S	S	10	0	0
F1	Disk	≤12/13-17/18≥	26 (S)	28 (S)	30 (S)	27 (S)	28 (S)	30 (S)	23 (S)	6 (R)	26 (S)	28 (S)	10	0	0
F2	Disk	R ≤12; I 13-17; S ≥18	22 (S)	26 (S)	23 (S)	23 (S)	24 - S	23 (S)	22 (S)	6 (R)	24 (S)	25 (S)	10	0	0
F3	Disk	12/13-17/18	29 (S)	28 (S)	25 (S)	27 (S)	30 (S)	27 (S)	24 (S)	6 (R)	28 (S)	27 (S)	10	0	0
F6	Disk	≤12/13-17/≥18	23 (S)	26 (S)	22 (S)	24 (S)	25 (S)	23 (S)	20 (S)	7 (R)	23 (S)	23 (S)	10	0	0
F8	Disk	12/18	21 (S)	24 (S)	21 (S)	22 (S)	24 (S)	24 (S)	21 (S)	6 (R)	23 (S)	23	10	0	0
F10	Disk	S≥23, R<23	24 (S)	26 (S)	25 (S)	24 (S)	26 (S)	24 (S)	23 (S)	6 (R)	25 (S)	25 (S)	10	0	0
F11	Disk	S	S	S	S	S	S	S	S	R	S	S	10	0	0
F13	Disk	<12/13-17/>18	24 (S)	24 (S)	21 (S)	23 (S)	24 (S)	22 (S)	20 (S)	6 (R)	24 (S)	22 (S)	10	0	0
F14	Disk	CLSI (2007)	26.57 (S)	26.17 (S)	28.7 (S)	25.49 (S)	28.64 (S)	24.51 (S)	22.12 (S)	0 (R)	24.44 (S)	27.07 (S)	10	0	0
F15	Disk	12/13-17/18	26 (S)	27 (S)	25 (S)	27 (S)	28 (S)	26 (S)	21 (S)	6 (R)	26 (S)	26 (S)	10	0	0
F16	Disk	≤12 13-17 ≥18	28 (S)	30 (S)	27 (S)	27 (S)	28 (S)	28 (S)	26 (S)	06 (R)	30 (S)	29 (S)	10	0	0
F17	Disk	≤12/13-17/≥18	21 S	25 S	20 S	21 S	25 S	19 S	19 S	≤6 R	22 S	25 S	10	0	0
F18	Disk	≤12/13-17/≥18	26 (S)	27 (S)	25 (S)	26 (S)	28 (S)	27 (S)	23 (S)	6 (R)	26 (S)	27 (S)	10	0	0
F19	Disk	13-17	25 (S)	29 (S)	25 (S)	25 (S)	29 (S)	24 (S)	23 (S)	6 (R)	27 (S)	26 (S)	10	0	0
F22	Disk	12-18	25 (S)	26 (S)	24 (S)	25 (S)	27 (S)	24 (S)	21 (S)	6 (R)	26 (S)	24 (S)	10	0	0
F23	Disk	≤12 13-17 ≤18	26 (S)	27 (S)	25 (S)	26 (S)	27 (S)	24 (S)	24 (S)	6 (R)	26 (S)	27 (S)	10	0	0
F29	Disk	≤20/≥21	24 (S)	27 (S)	23 (S)	25 (S)	28 (S)	24 (S)	24 (S)	6 (R)	24 (S)	26 (S)	10	0	0
F30	Disk	≤12 ... ≥18	25 (S)	28 (S)	27 (S)	26 (S)	30 (S)	35 (S)	25 (S)	6 (R)	26 (S)	27 (S)	10	0	0
F31	Disk	12/13-17/18	25 (S)	28 (S)	26 (S)	28 (S)	30 (S)	27 (S)	24 (S)	0 (R)	28 (S)	29 (S)	10	0	0
F36	Disk	≤12/13-17/≥18	28 (S)	30 (S)	30 (S)	29 (S)	30 (S)	27 (S)	25 (S)	6 (R)	29 (S)	27 (S)	10	0	0
N			30	30	30	30	30	30	30	30	30	30	300		
Minor			0	0	0	0	0	0	0	0	0	0		0	
Major			0	0	0	0	0	0	0	0	0	0			0

Dark grey cells = resistant (R), light grey = intermediate (I), white = susceptible (S). Grey text: excluded from evaluation.

MIC: in mg/L; disk: in mm.

CIPROFLOXACIN (CIP)															
Lab code	Method	Criteria used	A-1	A-2	A-3	A-4	A-5	A-6	A-7	A-8	A-9	A-10	N	Mi-nor	Ma-jor
CVI	MIC	S ≤1, R ≥4	0.015 (S)	0.5 (I)	0.03 (S)	8 (R)	0.015 (S)	0.03 (S)	0.25 (I)	0.015 (S)	0.015 (S)	0.25 (I)			
F4	MIC	≥4/ 2 /≤1	≤0,06 (S)	0,5 (S)	≤0,06 (S)	16 (R)	≤0,06 (S)	≤0,06 (S)	0,5 (S)	≤0,06 (S)	≤0,06 (S)	0,25 (S)	10		
F5	MIC	<0.06/≥0.06 <2/ ≥2	S	I	S	R	S	S	I	S	S	I	10		
F9	MIC	R/I/S	<0.125 (S)	<0.125 (S)	<0.125 (S)	>1 (R)	<0.125 (S)	<0.125 (S)	<0.125 (S)	>0.125<1 (I)	<0.125 (S)	>0.125/1 (I)	10		
F12	MIC	≥4: R/≤1: S	≤0.25 (S)	=0.5 (S)	≤0.25 (S)	≥4 (R)	≤0.25 (S)	≤0.25 (S)	≤0.25 (S)	≤0.25 (S)	≤0.25 (S)	≤0.25 (S)	10		
F24	MIC	0,125/-/0,25	≤0,03, S	0,5, R	≤0,03, S	>4, R	≤0,03, S	≤0,03, S	0,125, S	≤0,03, S	≤0,03, S	0,25, R	10		
F25	MIC	CLSI	≤0.015 (S)	0.5 (S)	≤0.015 (S)	4 (R)	0.03 (S)	≤0.015 (S)	4 (R)	≤0.015 (S)	≤0.015 (S)	0.12 (S)	10		
F26	MIC	R: >0.06	0.015 (S)	0.5 (R)	0.03 (S)	8 (R)	0.015 (S)	0.03 (S)	0.25 (R)	0.015 (S)	0.03 (S)	0.25 (R)	10		
F28	MIC	R:≥0.125/S: ≤0.06	≤0.015 (S)	0.5 (R)	0.03 (S)	>4 (R)	≤0.015 (S)	0.03 (S)	0.25 (R)	0.03 (S)	≤0.015 (S)	0.25 (R)	10		
F33	MIC	≤1 (S)/2 (I)/≥4 (R)	0.016 (S)	0.38 (S)	0.032 (S)	6 (R)	0.016 (S)	0.023 (S)	0.19 (S)	0.023 (S)	0.032 (S)	0.125 (S)	10		
F34	MIC	≤/2/≥4	0.008 (S)	0.50 (S)	0.031 (S)	8 (R)	0.008 (S)	0.015 (S)	0.125 (S)	0.015 (S)	0.015 (S)	0.125 (S)	10		
F35	MIC	0.125 µg/ml (L), 0.5 µg/ml (H)	S	S	S	R	S	S	S	S	S	S	10		
F1	Disk	≤15/16-20/21≥	40 (S)	26 (S)/0,19 mg/l	34 (S)	12 (R)/4 mg/l	34 (S)	34 (S)	27 (S)/0,125 mg/l	32 (S)	32 (S)	34 (S)/0,064 mg/l	10		
F2	Disk	R ≤15; I 16-20; S ≥21	30 (S)	24 (S)	30 (S)	12 (R)	31 (S)	30 (S)	25 (S)	32 (S)	29 (S)	28 (S)	10		
F3	Disk	15/16-20/21	36 (S)	26 (S)	33 (S)	12 (R)	33 (S)	36 (S)	28 (S)	37 (S)	30 (S)	28 (S)	10		
F6	Disk	≤15/16-20/≥21	32 (S)	23 (S)	32 (S)	10 (R)	33 (S)	31 (S)	25 (S)	32 (S)	31 (S)	26 (S)	10		
F8	Disk	15/21	31 (S)	21 (S)	29 (S)	10 (R)	30 (S)	27 (S)	22 (S)	30 (S)	29 (S)	25 (S)	10		
F10	Disk	S≥25, R<22	34 (S)	23 (I)	36 (S)	10 (R)	33 (S)	35 (S)	26 (S)	34 (S)	34 (S)	28 (S)	10		
F11	Disk	S	S	S	S	I	S	S	S	S	S	S	10		
F13	Disk	<15/16-20/>21	32 (S)	22/0.25 (R)	31 (S)	9/8 R)	32 (S)	32 (S)	23/0,125 (R)	33 (S)	31 (S)	25/0,25 (R)	10		
F14	Disk	CLSI (2007)	35.76 (S)	27.03 (S)	36.45 (S)	13.92 (R)	35.58 (S)	31.99 (S)	29.19 (S)	36.2 (S)	32.18 (S)	28.93 (S)	10		
F15	Disk	15/16-20/21	38 (S)	25 (R)	35 (S)	11 (R)	37 (S)	35 (S)	26 (R)	36 (S)	35 (S)	30 (R)	10		
F16	Disk	≤15 16-20 ≥21	35 (S)	24 (S)	31 (S)	09 (R)	30 (S)	33 (S)	25 (S)	35 (S)	34 (S)	29 (S)	10		
F17	Disk	≤15/16-20/≥21	34 S	26 S	32 S	10 R	34 S	25 S	23 S	32 S	30 S	29 S	10		
F18	Disk	≤15/16-20/≥21	37 (S)	24 (R)	33 (S)	13 (R)	35 (S)	36 (S)	29 (R)	34 (S)	36 (S)	30 (R)	10		
F19	Disk	16-20/≥4, 2, ≤1	37 (S)	25 (S)	34 (S)	13 (R)	36 (S)	34 (S)	28 (S)	35 (S)	36 (S)	28 (S)	10		
F22	Disk	15-21	31 (S)	0.38 (S)*	32 (S)	8 (R)*	34 (S)	33 (S)	0.25 (S)*	35 (S)	32 (S)	0.25 (S)*	10		
F23	Disk	≤15 16-20 ≤21	34 (S)	26 (S)	33 (S)	15 (R)	36 (S)	33 (S)	29 (S)	35 (S)	34 (S)	28 (S)	10		
F29	Disk	≤20/21-29/≥30	34 (S)	25 (I)	33 (S)	14 (R)	36 (S)	35 (S)	27 (I)	37 (S)	35 (S)	29 (I)	10		
F30	Disk	≤15 ... ≥21	36 (S)	27 (S)	34 (S)	15 (R)	34 (S)	34 (S)	26 (S)	36 (S)	34 (S)	28 (S)	10		
F31	Disk	15/16-20/21	36 (S)	26 (S) 0,38	34 (S)	11 (R) 6	33 (S)	30 (S)	24 (S) 0,19	33 (S)	32 (S)	27 (S) 0,19	10		
F36	Disk	≤15/16-20/≥21	35 (S)	26*	33 (S)	11 (R)	35 (S)	34 (S)	25*	33 (S)	31 (S)	30*	10		
N			31	31	31	31	31	31	31	31	31	31	310		
Mi-nor															
Ma-jor															

Dark grey cells = resistant (R), light grey = intermediate (I), white = susceptible (S). Grey text: excluded from evaluation.

MIC: in mg/L; disk: in mm.

GENTAMICIN (GEN)															
Lab code	Method	Criteria used	A-1	A-2	A-3	A-4	A-5	A-6	A-7	A-8	A-9	A-10	N	Minor	Major
CVI	MIC	S ≤4, R ≥16	0.5 (S)	1 (S)	≤0.25 (S)	1 (S)	0.5 (S)	0.5 (S)	16 (R)	0.5 (S)	0.5 (S)	0.5 (S)			
F4	MIC	≥8/ 2-4 /≤1	1 (S)	1 (S)	≤0,5 (S)	1 (S)	≤0,5 (S)	≤0,5 (S)	>8 (R)	1 (S)	≤0,5 (S)	≤0,5 (S)	10	0	0
F5	MIC	<8/≥8	S	S	S	S	S	S	S	S	S	S	10	0	1
F9	MIC	R/S	<4 (S)	<4 (S)	<4 (S)	<4 (S)	<4 (S)	<4 (S)	>4 (R)	<4 (S)	<4 (S)	<4 (S)	10	0	0
F12	MIC	≥8: R/≤4: S	≤1 (S)	≤1 (S)	≤1 (S)	≤1 (S)	≤1 (S)	≤1 (S)	≥16 (R)	≤1 (S)	≤1 (S)	≤1 (S)	10	0	0
F24	MIC	04/08/2016	0,25, S	0,5, S	0,5, S	1, S	0,5, S	0,25, S	16, R	0,5, S	0,5, S	0,5, S	10	0	0
F25	MIC	CLSI	0.5 (S)	0.5 (S)	0.5 (S)	0.5 (S)	0.5 (S)	0.5 (S)	>16 (R)	≤0.25 (S)	0.5 (S)	0.5 (S)	10	0	0
F26	MIC	R: >2	0.5 (S)	0.5 (S)	0.5 (S)	1 (S)	0.5 (S)	≤0.25 (S)	16 (R)	≤0.25 (S)	0.5 (S)	0.5 (S)	10	0	0
F28	MIC	R:≥8/S:≤4	≤0.5 (S)	≤0.5 (S)	≤0.5 (S)	≤0.5 (S)	≤0.5 (S)	≤0.5 (S)	8 (R)	≤0.5 (S)	≤0.5 (S)	≤0.5 (S)	10	0	0
F33	MIC	≤4 (S)/8 (I)/≥16 (R)	1.5 (S)	1.5 (S)	1.5 (S)	2 (S)	1.5 (S)	1.5 (S)	48 (R)	2 (S)	2 (S)	1.5 (S)	10	0	0
F34	MIC	n.d.													
F35	MIC	4 µg/ml	S	S	S	S	S	S	R	S	S	S	10	0	0
F1	Disk	≤12/13-14/≥15	22 (S)	22 (S)	23 (S)	18 (S)	23 (S)	20 (S)	10 (R)	21 (S)	20 (S)	22 (S)	10	0	0
F2	Disk	R ≤12; I 13-14; S ≥15	19 (S)	18 (S)	20 (S)	18 (S)	20 (S)	19 (S)	11 (R)*	19 (S)	18 (S)	20 (S)	10	0	0
F3	Disk	12/13-14/15	26 (S)	24 (S)	25 (S)	23 (S)	27 (S)	23 (S)	10 (R)	24 (S)	20 (S)	24 (S)	10	0	0
F6	Disk	≤12/13-14/≥15	21 (S)	21 (S)	21 (S)	20 (S)	23 (S)	21 (S)	9 (R)	20 (S)	20 (S)	21 (S)	10	0	0
F8	Disk	12/15	22 (S)	22 (S)	22 (S)	21 (S)	23 (S)	23 (S)	12 (R)	22 (S)	21 (S)	23 (S)	10	0	0
F10	Disk	S≥18, R<16	25 (S)	25 (S)	29 (S)	25 (S)	26 (S)	25 (S)	15 (R)	24 (S)	24 (S)	25 (S)	10	0	0
F11	Disk	S	S	S	S	S	S	S	R	S	S	S	10	0	0
F13	Disk	<12/13-14/>15	19 (S)	21 (S)	21 (S)	19 (S)	22 (S)	19 (S)	8 (R)	20 (S)	19 (S)	20 (S)	10	0	0
F14	Disk	CLSI (2007)	19.59 (S)	19.4 (S)	21.57 (S)	20.09 (S)	21.76 (S)	19.51 (S)	11.23 (R)	20.34 (S)	17.83 (S)	19.23 (S)	10	0	0
F15	Disk	12/13-14/15	22 (S)	22 (S)	21 (S)	21 (S)	24 (S)	22 (S)	10 (R)	20 (S)	21 (S)	24 (S)	10	0	0
F16	Disk	≤12 13-14 ≥15	20 (S)	20 (S)	20 (S)	19 (S)	22 (S)	20 (S)	10 (R)	17 (S)	20 (S)	20 (S)	10	0	0
F17	Disk	≤12/13-14/≥15	23 S	21 S	22 S	20 S	22 S	18 S	11 R	21 S	22 S	23 S	10	0	0
F18	Disk	≤12/13-14/≥15	24 (S)	24 (S)	25 (S)	24 (S)	26 (S)	24 (S)	11 (R)	23 (S)	24 (S)	26 (S)	10	0	0
F19	Disk	13-14	24 (S)	25 (S)	25 (S)	22 (S)	27 (S)	24 (S)	12 (R)	21 (S)	23 (S)	25 (S)	10	0	0
F22	Disk	12-15	21 (S)	21 (S)	20 (S)	19 (S)	23 (S)	20 (S)	6 (R)	21 (S)	20 (S)	21 (S)	10	0	0
F23	Disk	≤12 13-14 ≤15	20 (S)	20 (S)	20 (S)	20 (S)	23 (S)	20 (S)	12 (R)	20 (S)	20 (S)	20 (S)	10	0	0
F29	Disk	-													
F30	Disk	≤12 ... ≥15	21 (S)	22 (S)	22 (S)	20 (S)	23 (S)	23 (S)	9 (R)	21 (S)	22 (S)	22 (S)	10	0	0
F31	Disk	12/13-14/15	23 (S)	23 (S)	23 (S)	22 (S)	25 (S)	21 (S)	8 (R)	22 (S)	22 (S)	24 (S)	10	0	0
F36	Disk	≤12/13-14/≥15	20 (S)	20 (S)	21 (S)	19 (S)	24 (S)	20 (S)	10 (R)	19 (S)	20 (S)	20 (S)	10	0	0
N			29	29	29	29	29	29	29	29	29	29	290		
Minor			0	0	0	0	0	0	0	0	0	0		0	
Major			0	0	0	0	0	0	1	0	0	0			1

Dark grey cells = resistant (R), light grey = intermediate (I), white = susceptible (S). Grey text: excluded from evaluation.

MIC: in mg/L; disk: in mm.

NALIDIXIC ACID (NAL)															
Lab code	Method	Criteria used	A-1	A-2	A-3	A-4	A-5	A-6	A-7	A-8	A-9	A-10	N	Minor	Major
CVI	MIC	S ≤16, R ≥32	≤4 (S)	16 (S)	≤4 (S)	>64 (R)	≤4 (S)	≤4 (S)	>64 (R)	≤4 (S)	≤4 (S)	>64 (R)			
F4	MIC	≥32/ /≤16	8 (S)	32 (R)	8 (S)	>32 (R)	8 (S)	8 (S)	>32 (R)	8 (S)	8 (S)	>32 (R)	10	0	1
F5	MIC	<16/≥16	S	S	S	R	S	S	R	S	S	R	10	0	0
F9	MIC	R/S	<16 (S)	<16 (S)	<16 (S)	>16 (R)	<16 (S)	<16 (S)	>16 (R)	<16 (S)	<16 (S)	>16 (R)	10	0	0
F12	MIC	-	-	-	-	-	-	-	-	-	-	-			
F24	MIC	32/-/32	2, S	32, R	4, S	>128, R	2, S	4, S	>128, R	4, S	8, S	>128, R	10	0	1
F25	MIC	CLSI	2 (S)	8 (S)	2 (S)	>32 (R)	2 (S)	2 (S)	>32 (R)	2 (S)	2 (S)	>32 (R)	10	0	0
F26	MIC	R: >16	≤4 (S)	16 (S)	8 (S)	>64 (R)	≤4 (S)	≤4 (S)	>64 (R)	≤4 (S)	≤4 (S)	>64 (R)	10	0	0
F28	MIC	R: ≥32/S:≤16	≤4 (S)	16 (S)	≤4 (S)	>64 (R)	≤4 (S)	≤4 (S)	>64 (R)	≤4 (S)	≤4 (S)	>64 (R)	10	0	0
F33	MIC	≤16 (S)/≥32 (R)	2 (S)	16 (S)	3 (S)	>256 (R)	2 (S)	3 (S)	>256 (R)	2 (S)	2 (S)	>256 (R)	10	0	0
F34	MIC	≤16/≥32	4 (S)	32 (R)	4 (S)	256 (R)	4 (S)	4 (S)	256 (R)	4 (S)	4 (S)	4 (S)	10	0	2
F35	MIC	16 µg/ml	S	R	S	R	S	S	R	S	S	R	10	0	1
F1	Disk	≤13/14-18/≥19	23 (S)	16 (I)	22 (S)	6 (R)	25 (S)	24 (S)	6 (R)	26 (S)	23 (S)	6 (R)	10	1	0
F2	Disk	R ≤13; I 14-18; S ≥19	22-S	16 (R)*	18 (I)	6 (R)	24 (S)	23 (S)	6 (R)	25 (S)	23 (S)	6 (R)	10	1	1
F3	Disk	13/14-18/19	25 (S)	18 (I)	24 (S)	6 (R)	25 (S)	24 (S)	6 (R)	24 (S)	22 (S)	6 (R)	10	1	0
F6	Disk	≤13/14-18/≥19	17 (I)	12 (R)	17 (I)	7 (R)	19 (S)	19 (S)	7 (R)	20 (S)	18 (I)	7 (R)	10	3	1
F8	Disk	13/19	19 (S)	15 (I)	19 (S)	6 (R)	19 (S)	20 (S)	6 (R)	20 (S)	19 (S)	6 (R)	10	1	0
F10	Disk	S≥20, R<15	22 (S)	12 (R)	22 (S)	6 (R)	20 (S)	21 (S)	6 (R)	21 (S)	20 (S)	6 (R)	10	0	1
F11	Disk	-	-	-	-	-	-	-	-	-	-	-			
F13	Disk	<13/14-18/>19	21 (S)	14 (I)	20 (S)	6 (R)	23 (S)	23 (S)	6 (R)	25 (S)	22 (S)	6 (R)	10	1	0
F14	Disk	CLSI (2007)	24.32 (S)	16.64 (I)	24.72 (S)	0 (R)	22.93 (S)	24.04 (S)	0 (R)	24.28 (S)	21.48 (S)	0 (R)	10	1	0
F15	Disk	13/14-18/19	23 (S)	13 (R)	22 (S)	6 (R)	22 (S)	22 (S)	6 (R)	23 (S)	22 (S)	6 (R)	10	0	1
F16	Disk	≤13 14-18 ≥19	24 (S)	13 (R)	22 (S)	06 (R)	25 (S)	23 (S)	06 (R)	24 (S)	24 (S)	06 (R)	10	0	1
F17	Disk	≤13/14-18/≥19	21 S	12 R	21 S	≤6 R	23 S	20 S	≤6 R	22 S	23 S	≤6 R	10	0	1
F18	Disk	≤13/14-18/≥19	21 (S)	15 (I)	19 (S)	6 (R)	23 (S)	22 (S)	6 (R)	21 (S)	21 (S)	6 (R)	10	1	0
F19	Disk	14-18	21 (S)	14 (I)	21 (S)	6 (R)	21 (S)	21 (S)	6 (R)	23 (S)	20 (S)	6 (R)	10	1	0
F22	Disk	13-19	21 (S)	12 (R)	19 (S)	6 (R)	21 (S)	20 (S)	6 (R)	26 (S)	20 (S)	6 (R)	10	0	1
F23	Disk	≤13 14-18 ≤19	26 (S)	18 (I)	24 (S)	6 (R)	25 (S)	26 (S)	6 (R)	26 (S)	25 (S)	6 (R)	10	1	0
F29	Disk	≤18/≥19	24 (S)	18 (R)	25 (S)	6 (R)	26 (S)	24 (S)	6 (R)	28 (S)	26 (S)	6 (R)	10	0	1
F30	Disk	≤13 ... ≥19	23 (S)	17 (I)	22 (S)	6 (R)	23 (S)	25 (S)	6 (R)	24 (S)	24 (S)	6 (R)	10	1	0
F31	Disk	13/14-18/19	21 (S)	14 (I)	21 (S)	0 (R)	21 (S)	21 (S)	0 (R)	22 (S)	20 (S)	0 (R)	10	1	0
F36	Disk	≤13/14-18/≥19	23 (S)	18 (I)	23 (S)	6 (R)	24 (S)	24 (S)	6 (R)	24 (S)	23 (S)	6 (R)	10	1	0
N			29	29	29	29	29	29	29	29	29	29	290		
Minor			1	11	2	0	0	0	0	0	1	0		15	
Major			0	12	0	0	0	0	0	0	0	1			13

Dark grey cells = resistant (R), light grey = intermediate (I), white = susceptible (S). Grey text: excluded from evaluation.

MIC: in mg/L; disk: in mm.

STREPTOMYCIN (STR)															
Lab code	Method	Criteria used	A-1	A-2	A-3	A-4	A-5	A-6	A-7	A-8	A-9	A-10	N	Minor	Major
CVI	MIC	S ≤16, R ≥32	>128 (R)	4 (S)	128 (R)	16 (S)	16 (S)	16 (S)	128 (R)	128 (R)	16 (S)	4 (S)			
F4	MIC	≥32/ 16 /≤8	>64 (R)	8 (S)	>64 (R)	16 (I)	16 (I)	8 (S)	>64 (R)	>64 (R)	8 (S)	≤4 (S)	10	2	0
F5	MIC	<32/≥32	R	S	R	S	S	S	R	R	S	S	10	0	0
F9	MIC	R/I/S	>8/<128 (I)	<8 (S)	>8/<128 (I)	<8 (S)	<8 (S)	<8 (S)	>8/<128 (I)	>8/<128 (I)	<8 (S)	<8 (S)	10	4	0
F12	MIC	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA			
F24	MIC	8/16/32	>64, R	4, S	>64, R	8, S	4, S	4, S	>64, R	>64, R	8, S	4, S	10	0	0
F25	MIC	CLSI	>64 (R)	≤32 (S)	>64 (R)	≤32 (S)	≤32 (S)	≤32 (S)	64 (R)	≤32 (S)	≤32 (S)	≤32 (S)	10	0	1
F26	MIC	R: >32	>128 (R)	4 (S)	>128 (R)	8 (S)	8 (S)	8 (S)	64 (R)	64 (R)	16 (S)	4 (S)	10	0	0
F28	MIC	R: ≥32/I: 16/S:≤8	128 (R)	≤8 (S)	128 (R)	≤8 (S)	≤8 (S)	≤8 (S)	64 (R)	128 (R)	16 (I)	≤8 (S)	10	1	0
F33	MIC	n.d.													
F34	MIC	0/≥64	512 (R)	8 (S)	256 (R)	16 (S)	8 (S)	8 (S)	64 (R)	128 (R)	8 (S)	2 (S)	10	0	0
F35	MIC	64 µg/ml	R	S	R	S	S	S	R	R	S	S	10	0	0
F1	Disk	≤11/12-14/≥5	6 (R)	17 (S)	6 (R)	16 (S)	16 (S)	16 (S)	7 (R)	6 (R)	13 (I)	18 (S)	10	1	0
F2	Disk	R ≤11; I 12-14; S ≥15	6 (R)	15 (S)	6 (R)	13 (I)	15 (S)	15 (S)	6 (R)	6 (R)	15 (S)	17 (S)	10	1	0
F3	Disk	11/12-14/15	6 (R)	19 (S)	6 (R)	16 (S)	17 (S)	16 (S)	7 (R)	7 (R)	15 (S)	18 (S)	10	0	0
F6	Disk	≤11/12-14/≥15	7 (R)	16 (S)	7 (R)	15 (S)	15 (S)	15 (S)	7 (R)	7 (R)	14 (I)	17 (S)	10	1	0
F8	Disk	11/15	6 (R)	19 (S)	6 (R)	16 (S)	18 (S)	15 (S)	9 (R)	9 (R)	15 (S)	19 (S)	10	0	0
F10	Disk	No breakpoint	6	18	6	16	16	17	6	6	17	19	10	0	0
F11	Disk	-	-	-	-	-	-	-	-	-	-	-			
F13	Disk	<11/12-14/>15	6 (R)	17 (S)	6 (R)	16 (S)	16 (S)	16 (S)	6 (R)	6 (R)	15 (S)	17 (S)	10	0	0
F14	Disk	CLSI (2007)	0 (R)	17.96 (S)	0 (R)	15.11 (S)	15.55 (S)	15.77 (S)	0 (R)	0 (R)	14.6 (I)	18.48 (S)	10	1	0
F15	Disk	11/12-14/15	6 (R)	16 (S)	6 (R)	15 (S)	15 (S)	15 (S)	6 (R)	6 (R)	13 (I)	18 (S)	10	1	0
F16	Disk	≤11 12-14 ≥15	06 (R)	16 (S)	06 (R)	14 (I)	15 (S)	14 (I)	06 (R)	06 (R)	13 (I)	15 (S)	10	3	0
F17	Disk	≤11/12-14/≥15	≤6 R	16 S	≤6 R	15 S	17 S	15 S	10 R	9 R	15 S	16 S	10	0	0
F18	Disk	≤11/12-14/≥15	6 (R)	19 (S)	6 (R)	16 (S)	17 (S)	16 (S)	8 (R)	8 (R)	15 (S)	22 (S)	10	0	0
F19	Disk	11-12	6 (R)	18 (S)	6 (R)	14 (S)	16 (S)	15 (S)	6 (R)	6 (R)	15 (S)	18 (S)	10	0	0
F22	Disk	11-15	6 (R)	18 (S)	6 (R)	15 (S)	18 (S)	15 (S)	6 (R)	6 (R)	15 (S)	18 (S)	10	0	0
F23	Disk	≤11 12-14 ≤15	6 (R)	18 (S)	6 (R)	17 (S)	19 (S)	17 (S)	8 (R)	7 (R)	16 (S)	19 (S)	10	0	0
F29	Disk	≤13/≥14	6 (R)	20 (S)	6 (R)	17 (S)	18 (S)	18 (S)	8 (R)	6 (R)	17 (S)	22 (S)	10	0	0
F30	Disk	≤11 ... ≥15	6 (R)	17 (S)	6 (R)	15 (S)	10 (R)	14 (I)	9 (R)	6 (R)	16 (S)	16 (S)	10	1	1
F31	Disk	11/12-14/15	0 (R)	18 (S)	0 (R)	13 (I)	11 (R)	14 (I)	0 (R)	0 (R)	12 (I)	18 (S)	10	3	1
F36	Disk	≤11/12-14/≥15	6 (R)	17 (S)	6 (R)	15 (S)	18 (S)	15 (S)	6 (R)	6 (R)	13 (I)	18 (S)	10	1	0
N			28	28	28	28	28	28	28	28	28	28	280		
Minor			1	0	1	4	1	3	1	1	8	0		20	
Major			0	0	0	0	2	0	0	1	0	0			3

Dark grey cells = resistant (R), light grey = intermediate (I), white = susceptible (S). Grey text: excluded from evaluation.

MIC: in mg/L; disk: in mm.

SULFONAMIDES (SUL)															
Lab code	Method	Criteria used	A-1	A-2	A-3	A-4	A-5	A-6	A-7	A-8	A-9	A-10	N	Minor	Major
CVI	MIC	S ≤256, R ≥512	>1024 (R)	≤8 (S)	>1024 (R)	≤8 (S)	≤8 (S)	≤8 (S)	>1024 (R)	>1024 (R)	≤8 (S)	≤8 (S)			
F4	MIC	≥256/64-128/ ≤32	>512 (R)	256 (R)	>512 (R)	512 (R)	128 (I)	256 (R)	>512 (R)	>512 (R)	128 (I)	128 (I)	10	3	3
F5	MIC	<512/≥512	R	S	R	S	S	S	R	R	S	S	10	0	0
F9	MIC	R/S	>64 (R)	<64 (S)	>64 (R)	<64 (S)	<64 (S)	<64 (S)	>64 (R)	>64 (R)	<64 (S)	<64 (S)	10	0	0
F12	MIC	-	-	-	-	-	-	-	-	-	-	-			
F24	MIC	256/-/512	>512, R	64, S	>512, R	16, S	16, S	16, S	>512, R	>512, R	32, S	16, S	10	0	0
F25	MIC	CLSI	>256 (R)	≤16 (S)	>256 (R)	64 (S)	32 (S)	≤16 (S)	>256 (R)	>256 (R)	128 (S)	≤16 (S)	10	0	0
F26	MIC	R: >256	>1024 (R)	16 (S)	>1024 (R)	≤8 (S)	≤8 (S)	≤8 (S)	>1024 (R)	>1024 (R)	16 (S)	16 (S)	10	0	0
F28	MIC	R:≥512/S:≤256	>1024 (R)	≤64 (S)	>1024 (R)	≤64 (S)	≤64 (S)	≤64 (S)	>1024 (R)	>1024 (R)	≤64 (S)	≤64 (S)	10	0	0
F33	MIC	-	-	-	-	-	-	-	-	-	-	-			
F34	MIC		1024 (R)	1024 (R)	1024 (R)	1024 (R)	1024 (R)	32 (S)	1024 (R)	1024 (R)	1024 (R)	512 (R)	10	0	5
F35	MIC	64 µg/ml	R	R	R	S	R	S	R	R	S	S	10	0	2
F1	Disk	≤12/13-16/≥17	6 (R)	26 (S)	6 (R)	24 (S)	26 (S)	26 (S)	6 (R)	6 (R)	24 (S)	15 (I)	10	1	0
F2	Disk	R ≤12; I13-17; S ≥17	6 (R)	18 (S)	6 (R)	18-R(film)	20 (S)	21 (S)	6 (R)	6 (R)	20 (S)	20 (S)	10	0	1
F3	Disk	11/12-17/18	6 (R)	24 (S)	6 (R)	19 (S)	22 (S)	21 (S)	6 (R)	6 (R)	22 (S)	23 (S)	10	0	0
F6	Disk	≤12/13-16/≥17	7 (R)	22 (S)	7 (R)	20 (S)	27 (S)	22 (S)	7 (R)	7 (R)	21 (S)	23 (S)	10	0	0
F8	Disk	10/16	6 (R)	23 (S)	6 (R)	23 (S)	25 (S)	24 (S)	22 (S)	6 (R)	25 (S)	18 (S)	10	0	1
F10	Disk	S≥17, R<12	6 (R)	24 (S)	6 (R)	22 (S)	26 (S)	26 (S)	6 (R)	6 (R)	24 (S)	25 (S)	10	0	0
F11	Disk	-	-	-	-	-	-	-	-	-	-	-			
F13	Disk	<12/13-16/>17	6 (R)	12 (R)	6 (R)	17 (S)	23 (S)	19 (S)	6 (R)	6 (R)	18 (S)	17 (S)	10	0	1
F14	Disk	CLSI (2007)	0 (R)	19.94 (S)	0 (R)	21.58 (S)	26.09 (S)	24.23 (S)	0 (R)	0 (R)	22.19 (S)	27.26 (S)	10	0	0
F15	Disk	12/13-16/17	6 (R)	22 (S)	6 (R)	20 (S)	26 (S)	25 (S)	6 (R)	6 (R)	24 (S)	21 (S)	10	0	0
F16	Disk	-													
F17	Disk	≤12/13-16/≥17	≤6 R	16 I	≤6 R	≤6 R	16 I	13 I	≤6 R	≤6 R	18 S	16 I	10	4	1
F18	Disk	-	-	-	-	-	-	-	-	-	-	-			
F19	Disk	13-16	6 (R)	24 (S)	6 (R)	21 (S)	24 (S)	25 (S)	6 (R)	6 (R)	17 (S)	21 (S)	10	0	0
F22	Disk	-													
F23	Disk	≤12 13-16 ≤17	6 (R)	24 (S)	6 (R)	26 (S)	31 (S)	27 (S)	6 (R)	6 (R)	27 (S)	29 (S)	10	0	0
F29	Disk	≤13/14-18/≥19	6 (R)	24 (S)	6 (R)	18 (I)	28 (S)	24 (S)	6 (R)	6 (R)	23 (S)	26 (S)	10	1	0
F30	Disk	---	-	-	-	-	-	-	-	-	-	-			
F31	Disk	12/13-16/17	0 (R)	25 (S)	0 (R)	27 (S)	29 (S)	27 (S)	0 (R)	0 (R)	26 (S)	28 (S)	10	0	0
F36	Disk	≤12/13-16/≥17	6 (R)	26 (S)	6 (R)	21 (S)	30 (S)	26 (S)	6 (R)	6 (R)	25 (S)	26 (S)	10	0	0
N			24	24	24	24	24	24	24	24	24	24	240		
Minor			0	1	0	1	2	1	0	0	1	3		9	
Major			0	4	0	4	2	1	1	0	1	1			14

Dark grey cells = resistant (R), light grey = intermediate (I), white = susceptible (S). Grey text: excluded from evaluation.

MIC: in mg/L; disk: in mm.

TETRATCYCLINE (TET)															
Lab code	Method	Criteria used	A-1	A-2	A-3	A-4	A-5	A-6	A-7	A-8	A-9	A-10	N	Minor	Major
CVI	MIC	S ≤4, R ≥16	>64 (R)	≤1 (S)	>64 (R)	2 (S)	2 (S)	2 (S)	4 (S)	64 (R)	≤1 (S)	2 (S)			
F4	MIC	≥8/ 2-4 /≤1	>8 (R)	2 (I)	>8 (R)	2 (I)	≤1 (S)	2 (I)	4 (I)	>8 (R)	≤1 (S)	2 (I)	10	5	0
F5	MIC	<8/≥8	R	S	R	S	S	S	S	R	S	S	10	0	0
F9	MIC	R/I/S	>128 (R)	<8 (S)	>128 (R)	<8 (S)	<8 (S)	<8 (S)	<8 (S)	>8/<128 (I)	<8 (S)	<8 (S)	10	1	0
F12	MIC	≥16: R/≤4: S	≥16 (R)	≤1 (S)	≥16 (R)	≤1 (S)	≤1 (S)	≤1 (S)	≤1 (S)	≥16 (R)	≤1 (S)	≤1 (S)	10	0	0
F24	MIC	04/08/2016	>16, R	1, S	>16, R	1, S	1, S	2, S	4, S	>16, R	1, S	2, S	10	0	0
F25	MIC	CLSI	>32 (R)	≤4 (S)	>32 (R)	≤4 (S)	≤4 (S)	≤4 (S)	≤4 (S)	32 (R)	≤4 (S)	≤4 (S)	10	0	0
F26	MIC	R: >8	>64 (R)	≤1 (S)	>64 (R)	2 (S)	2 (S)	2 (S)	2 (S)	>64 (R)	2 (S)	2 (S)	10	0	0
F28	MIC	R:≥16/I: 8/S:≤4	>32 (R)	≤2 (S)	>32 (R)	≤2 (S)	≤2 (S)	≤2 (S)	≤2 (S)	>32 (R)	≤2 (S)	≤2 (S)	10	0	0
F33	MIC	≤4 (S)/8 (I)/≥16 (R)	64 (R)	0.5 (S)	128 (R)	1.0 (S)	0.75 (S)	1.5 (S)	1.5 (S)	12 (R)	1.0 (S)	0.75 (S)	10	0	0
F34	MIC	≤4/8/≥16	256 (R)	2 (S)	256 (R)	2 (S)	2 (S)	4 (S)	4 (S)	64 (R)	4 (S)	4 (S)	10	0	0
F35	MIC	8 µg/ml	R	S	R	S	S	S	S	R	S	S	10	0	0
F1	Disk	≤11/12-14/15≥	6 (R)	25 (S)	6 (R)	21 (S)	23 (S)	21 (S)	17 (S)	11 (R)	24 (S)	23 (S)	10	0	0
F2	Disk	R ≤11; I 12-14; S ≥15	6 (R)	23 (S)	6 (R)	19 (S)	21 (S)	20 (S)	20 (S)	12 (R)*	22 (S)	21 (S)	10	0	0
F3	Disk	11/12-14/15	6 (R)	27 (S)	6 (R)	25 (S)	25 (S)	23 (S)	24 (S)	13 (I)	25 (S)	26 (S)	10	1	0
F6	Disk	≤11/12-14/≥15	7 (R)	22 (S)	7 (R)	17 (S)	23 (S)	19 (S)	14 (I)	7 (R)	17 (S)	21 (S)	10	1	0
F8	Disk	14/19	6 (R)	19 (S)	6 (R)	18 (S)	19 (S)	19 (S)	18 (S)	10 (R)	19 (S)	19 (S)	10	0	0
F10	Disk	S≥19, R<17	6 (R)	22 (S)	6 (R)	19 (S)	20 (S)	19 (S)	19 (S)	6 (R)	19 (S)	21 (S)	10	0	0
F11	Disk	S	R	S	R	S	S	S	S	I	S	S	10	1	0
F13	Disk	<14/15-18/>19	6 (R)	22 (S)	6 (R)	19 (S)	21 (S)	19 (S)	18 (I)	7 (R)	19 (S)	19 (S)	10	1	0
F14	Disk	CLSI (2007)	0 (R)	25.34 (S)	0 (R)	23.69 (S)	22.97 (S)	22.66 (S)	20.51 (S)	10.4 (R)	22.77 (S)	22.41 (S)	10	0	0
F15	Disk	11/12-14/15	6 (R)	25 (S)	6 (R)	23 (S)	25 (S)	22 (S)	21 (S)	10 (R)	23 (S)	24 (S)	10	0	0
F16	Disk	≤11 12-14 ≥15	06 (R)	24 (S)	06 (R)	23 (S)	22 (S)	22 (S)	22 (S)	09 (R)	24 (S)	24 (S)	10	0	0
F17	Disk	≤11/12-14/≥15	≤6 R	25 S	≤6 R	18 S	19 S	18 S	17 S	9 R	21 S	20 S	10	0	0
F18	Disk	≤11/12-14/≥15	6 (R)	24 (S)	6 (R)	21 (S)	24 (S)	22 (S)	22 (S)	11 (R)	25 (S)	24 (S)	10	0	0
F19	Disk	15-18	6 (R)	24 (S)	6 (R)	21 (S)	24 (S)	21 (S)	20 (S)	10 (R)	24 (S)	22 (S)	10	0	0
F22	Disk	11-15	6 (R)	24 (S)	6 (R)	20 (S)	23 (S)	19 (S)	15 (S)	6 (R)	21 (S)	21 (S)	10	0	0
F23	Disk	≤11 12-14 ≤15	6 (R)	26 (S)	6 (R)	26 (S)	26 (S)	24 (S)	22 (S)	13 (I)	24 (S)	26 (S)	10	1	0
F29	Disk	≤14/15-18/≥19	7 (R)	26 (S)	6 (R)	26 (S)	26 (S)	24 (S)	24 (S)	11 (R)	24 (S)	24 (S)	10	0	0
F30	Disk	≤11 ... ≥15	6 (R)	23 (S)	6 (R)	17 (S)	22 (S)	17 (S)	14 (I)	9 (R)	18 (S)	17 (S)	10	1	0
F31	Disk	14/15-18/19	0 (R)	24 (S)	0 (R)	23 (S)	22 (S)	23 (S)	19 (S)	10 (R)	23 (S)	25 (S)	10	0	0
F36	Disk	≤11/12-14/≥15	6 (R)	21 (S)	6 (R)	17 (S)	22 (S)	20 (S)	17 (S)	7 (R)	18 (S)	18 (S)	10	0	0
N			31	31	31	31	31	31	31	31	31	31	310		
Minor			0	1	0	1	0	1	4	4	0	1		12	
Major			0	0	0	0	0	0	0	0	0	0			0

Dark grey cells = resistant (R), light grey = intermediate (I), white = susceptible (S). Grey text: excluded from evaluation.

MIC: in mg/L; disk: in mm.

TRIMETHOPRIM (TMP)															
Lab code	Method	Criteria used	A-1	A-2	A-3	A-4	A-5	A-6	A-7	A-8	A-9	A-10	N	Minor	Major
CVI	MIC	S ≤8,R ≥16	≤0.5 (S)	≤0.5 (S)	>32 (R)	≤0.5 (S)	≤0.5 (S)	≤0.5 (S)	>32 (R)	≤0.5 (S)	≤0.5 (S)	≤0.5 (S)			
F4	MIC	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.			
F5	MIC	<8/≥8	S	S	R	S	S	S	R	S	S	S	10	0	0
F9	MIC	R/S	<2 (S)	<2 (S)	>2 (R)	<2 (S)	<2 (S)	<2 (S)	>2 (R)	<2 (S)	<2 (S)	<2 (S)	10	0	0
F12	MIC	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA			
F24	MIC	8/-/16	≤0,5, S	≤0,5, S	>16, R	≤0,5, S	≤0,5, S	≤0,5, S	>16, R	≤0,5, S	≤0,5, S	≤0,5, S	10	0	0
F25	MIC	-													
F26	MIC	R: >2	≤0.5 (S)	≤0.5 (S)	>32 (R)	≤0.5 (S)	≤0.5 (S)	≤0.5 (S)	>32 (R)	≤0.5 (S)	≤0.5 (S)	≤0.5 (S)	10	0	0
F28	MIC	R:≥8/S:≤4	≤1 (S)	≤1 (S)	>32 (R)	≤1 (S)	≤1 (S)	≤1 (S)	>32 (R)	≤1 (S)	≤1 (S)	≤1 (S)	10	0	0
F33	MIC	n.d.													
F34	MIC	≤8/≥16	0.25 (R)	0.50 (S)	32 (R)	0.50 (S)	0.5 (S)	0.50 (S)	32 (R)	0.50 (S)	0.50 (S)	0.50 (S)	10	0	1
F35	MIC	2 µg/ml	S	S	R	S	S	S	R	S	S	S	10	0	0
F1	Disk	≤10/11-15/16≥	24 (S)	24 (S)	6 (R)	25 (S)	24 (S)	24 (S)	6 (R)	25 (S)	23 (S)	26 (S)	10	0	0
F2	Disk	R ≤10; I 11-15; S ≥16	27 (S)	27 (S)	6 (R)	24 (S)	25 (S)	27 (S)	6 (R)	30 (S)	26 (S)	26 (S)	10	0	0
F3	Disk	10/11-15/16	30 (S)	29 (S)	6 (R)	29 (S)	26 (S)	27 (S)	6 (R)	28 (S)	27 (S)	27 (S)	10	0	0
F6	Disk	≤10/11-15/≥16	28 (S)	26 (S)	7 (R)	24 (S)	27 (S)	25 (S)	7 (R)	27 (S)	27 (S)	26 (S)	10	0	0
F8	Disk	n.d.													
F10	Disk	S≥20, R<16	29 (S)	26 (S)	6 (R)	25 (S)	26 (S)	26 (S)	6 (R)	27 (S)	27 (S)	26 (S)	10	0	0
F11	Disk	-	-	-	-	-	-	-	-	-	-	-			
F13	Disk	<10/11-15/>16	27 (S)	30 (S)	6 (R)	27 (S)	26 (S)	27 (S)	6 (R)	29 (S)	27 (S)	26 (S)	10	0	0
F14	Disk	-	-	-	-	-	-	-	-	-	-	-			
F15	Disk	10/11-15/16	33 (S)	29 (S)	6 (R)	29 (S)	30 (S)	30 (S)	6 (R)	30 (S)	29 (S)	28 (S)	10	0	0
F16	Disk	≤10 11-15 ≥16	31 (S)	29 (S)	06 (R)	28 (S)	27 (S)	29 (S)	06 (R)	30 (S)	31 (S)	29 (S)	10	0	0
F17	Disk	≤10/11-15/≥16	21 S	24 S	≤6 R	20 S	23 S	21 S	≤6 R	23 S	24 S	23 S	10	0	0
F18	Disk	≤10/11-15/≥16	29 (S)	27 (S)	6 (R)	26 (S)	27 (S)	26 (S)	6 (R)	28 (S)	28 (S)	26 (S)	10	0	0
F19	Disk	11-15	27 (S)	28 (S)	6 (R)	25 (S)	26 (S)	27 (S)	6 (R)	27 (S)	27 (S)	24 (S)	10	0	0
F22	Disk	10-16	34 (S)	32 (S)	6 (R)	29 (S)	32 (S)	31 (S)	6 (R)	33 (S)	32 (S)	33 (S)	10	0	0
F23	Disk	≤10 11-15 ≤16	32 (S)	31 (S)	6 (R)	31 (S)	31 (S)	31 (S)	6 (R)	32 (S)	31 (S)	32 (S)	10	0	0
F29	Disk	-													
F30	Disk	---													
F31	Disk	10/11-15/16	31 (S)	28 (S)	0 (R)	30 (S)	29 (S)	29 (S)	0 (R)	29 (S)	28 (S)	29 (S)	10	0	0
F36	Disk	≤10/11-15/≥16	29 (S)	30 (S)	6 (R)	26 (S)	28 (S)	30 (S)	6 (R)	30 (S)	31 (S)	30 (S)	10	0	0
N			22	22	22	22	22	22	22	22	22	22	220		
Minor			0	0	0	0	0	0	0	0	0	0		0	
Major			1	0	0	0	0	0	0	0	0	0			1

Dark grey cells = resistant (R), light grey = intermediate (I), white = susceptible (S). Grey text: excluded from evaluation.

MIC: in mg/L; disk: in mm.

Annex 7. Protocol

PROTOCOL OF THE SECOND EQA SCHEME (DECEMBER 2009) ON SEROTYPING, PHAGE TYPING AND ANTIMICROBIAL SUSCEPTIBILITY TYPING OF *SALMONELLA* STRAINS, FOR THE FWD LABORATORIES

Introduction

This External Quality Assurance (EQA) scheme on the typing of *Salmonella* strains is organised for the laboratories belonging to the Food and Waterborne Diseases Network (FWD-Net) of the European Centre for Disease Control (ECDC). The study is organised by the Laboratory for Zoonoses and Environmental Microbiology (LZO) of the National Institute of Public Health and the Environment (RIVM, Bilthoven, The Netherlands), in close cooperation with the Health Protection Agency (HPA, London, United Kingdom), and the Central Veterinary Institute of Wageningen UR (CVI, Lelystad, the Netherlands).
The objective of this typing study is to test the performance of the participating laboratories for serotyping, phage typing and antimicrobial susceptibility testing of *Salmonella* spp.
The study will take place in week 49 (starting on 30 November 2009). The timetable can be found on the last page of this protocol.
All data have to be reported in the test report, send to RIVM-LZO and will be used for analysis.

Transportation of the *Salmonella* strains to the laboratories.

RIVM-LZO will transport the strains for each part of the study in a separate parcel. The strains will be send as Biological Substance Category B (UN 3373) with a door-to-door courier to your laboratory.

Serotyping

A total number of 20 *Salmonella* strains (indicated S-1 till S-20) have to be serotyped. The method routinely performed in your laboratory can be used in this study. Each laboratory is allowed to send strains for serotyping to another reference laboratory in their country, if this is part of the normal routine procedure.

IN THE TEST REPORT OF THIS STUDY, TWO EXTRA TABLES ARE ADDED. PLEASE INDICATE THE REACTIONS FOR EVERY STRAIN-ANTISERUM COMBINATION USED. THIS SUPPLIES RIVM WITH MORE INFORMATION IN CASE OF ANY DEVIATING RESULTS.

The results for each strain have to be reported with the full formula for the O-antigens and H-antigens and the serovar names according to the White-Kauffman-le Minor scheme of 2007 (http://www.pasteur.fr/sante/clre/cadrecnr/salmoms/WKLM_2007.pdf).
Definite conclusions can only be based on agglutination with mono-specific antisera. Otherwise it is better to identify the strains by giving the antigenic formula as far as detected. The evaluation of the serotyping results will be performed by the Laboratory for Zoonoses and Environmental Microbiology (LZO) and the Laboratory for Infectious Diseases and Perinatal Screening (LIS) of the RIVM according to Table 1.

Table 1. Evaluation of serotyping results

Results	Evaluation	Abbreviation
Auto-agglutination or Incomplete set of antisera (outside range of antisera)	Not typable	NT
Partly typable due to incomplete set of antisera or Part of the formula (for the name of the serovar) or No name serovar	Partly correct	+/-
Wrong serovar or mixed sera formula	Incorrect	-

Phage typing

The laboratories will receive a parcel containing 20 *Salmonella* cultures for phage typing:

- □ 10 strains of *S*. Enteritidis numbered E1-E10
- □ 10 strains of *S*. Typhimurium numbered T11-T20

The evaluation of the phage typing results will be done in collaboration with the *Salmonella* Reference Unit of the HPA.

Antimicrobial susceptibility testing

The laboratories will receive 10 *Salmonella* strains (different from the ones used for sero- and phage typing) and one control strain (*E. coli* ATCC 25922) for antimicrobial susceptibility testing. The 10 test strains are numbered A-1 - A-10. These strains are to be tested for susceptibility to a list of antibiotics with the method routinely used in your laboratory.

The control strain LMG 8223 (= *E. coli* ATCC 25922) is provided for this second EQA scheme, but will probably also be needed in subsequent EQA schemes. The strain will only be provided once, therefore take care to store this strain in an appropriate way, e.g. in cryotubes at -70 °C.

For the list of antibiotics to be tested, the advices are followed as described in the EFSA Report of the Task Force on Zoonoses Data Collection which was published in 2007 (The EFSA Journal (2007), 96, 1-46). This report includes a proposal for a harmonized monitoring scheme of antimicrobial resistance in *Salmonella* in fowl (*Gallus gallus*), turkeys, and pigs and *Campylobacter jejuni* and *C. coli* in broilers This EFSA report indicates a list of 10 antibiotics that should be included in the antimicrobial resistance monitoring for *Salmonella*. In the previous EQA scheme 14 antibiotics were prescribed for testing. However, as the interpretation of the results of some antibiotics is complicated, it was decided to prescribe in this study only the 10 antibiotics as given in the EFSA report.

All strains should be tested against the following antibiotics:

1. Ampicillin (10 µg),
2. Cefotaxime (30 µg),
3. Chloramphenicol (30 µg),
4. Ciprofloxacin (5 µg),
5. Gentamicin (10 µg),
6. Nalidixic Acid (30 µg),
7. Streptomycin (10 µg),
8. Sulphonamides (eg Sulphamethoxazole, 240 µg),
9. Tetracycline (30 µg),
10. Trimethoprim (5 µg).

If the method routinely used in your laboratory is a disk diffusion method, please use disks with concentrations of the antibiotics as indicated between brackets. If you do not have disks with the specified amount please omit this antibiotic from your list. If dilution methods or E-tests are used to determine the Minimum Inhibitory Concentration (MIC) the same antibiotics as indicated above should be tested.
The evaluation of the antimicrobial susceptibility testing results will be done in collaboration with the Dutch National Reference Laboratory on Antimicrobial Resistance at CVI.

If you have questions or remarks about this EQA scheme, please contact:

Wilma Jacobs
P.O. Box 1
3720 BA Bilthoven
tel. number: +31-30-2744290
fax number: +31-30-2744434
e-mail: wilma.jacobs@rivm

Annex 8. Test report form

TEST REPORT

SECOND EQA SCHEME (DECEMBER 2009) ON SEROTYPING, PHAGE TYPING AND ANTIMICROBIAL SUSCEPTIBILITY TESTING OF *SALMONELLA* STRAINS FOR THE FWD LABORATORIES

Laboratory code	
Name contact person	
Email address contact person	
Name of laboratory	
Name department and/or institute	
Address	
Country	

Please write your remarks and comments at the end of the test report.

GENERAL QUESTIONS

Shipment of the strains	
Was your parcel damaged at arrival?	□ NO □ YES
Date of receipt at your laboratory	

Sub-culturing	
Medium used for sub-culturing the strains	Name…….. Manufacturer……..

REMARKS CONCERNING THE TABLES FOR SEROTYPING
Two extra tables are added to this test report, to give the RIVM more information about the antisera used. The tables on pages 4 and 5 concern reactions obtained with O-antisera and the tables on pages 6 and 7 with H-antisera. At the bottom of the table space is left to fill in other antisera than mentioned in the table. Please mention the manufacturer of the antisera used in the column next to the antisera. Indicate for each combination of strain and antisera if there was agglutination (+) or not (-). If the cell remains empty this indicates that the agglutination was not determined for the specific combination of antisera and strain.

QUESTIONS SEROTYPING	
What was the frequency of serotyping of *Salmonella* at your laboratory in 2008?	□ Daily □ Once a week □ Twice a week □ Thrice a week □ Weekly □ Monthly Other: ……
How many *Salmonella* strains did your laboratory (approximately) serotype in 2008?	Number of strains: ……..
What kind of sera do you use?	□ Prepared in own laboratory □ Commercial sera Manufacturer(s): …… …… …… ……

The strains in this EQA scheme were serotyped by:	□ Own laboratory □ Other laboratory, namely…….....…… Strains: ……

		Strains									
O-antisera	Manufacturer	1	2	3	4	5	6	7	8	9	10
Group B											
1, 4, 12, 27											
1, 4, 5, 12											
4, 5, 12											
4, 5, 27											
4, 5											
4											
5											
Group C											
7, 8											
6, 7, 8											
6, 7											
6_1, 6_2, 7											
6, 8											
8, 20											
6_1											
6											
7											
8											
Group D											
9											
9, 12											
1, 9, 12											
12											
9, 46											
9, (46)											
46											
Group E											
1, 3, 10, 15, 19, 34											
3, 10, 15, 19, 34											
(3), (15), 34											
3, 10, 15											
3, 10											
3, 15											
10											
15											
1, 3, 19											
19											
Group G											
13											

13, 22, 23											
22											
23											
Other O-antisera											

		Strains									
O-antisera	Manufacturer	11	12	13	14	15	16	17	18	19	20
Group B											
1, 4, 12, 27											
1, 4, 5, 12											
4, 5, 12											
4, 5, 27											
4, 5											
4											
5											
Group C											
7, 8											
6, 7, 8											
6, 7											
6_1, 6_2, 7											
6, 8											
8, 20											
6_1											
6											
7											
8											
Group D											
9											
9, 12											
1, 9, 12											
12											
9, 46											
9, (46)											
46											
Group E											
1, 3, 10, 15, 19, 34											
3, 10, 15, 19, 34											
(3), (15), 34											
3, 10, 15											
3, 10											
3, 15											
10											
15											
1, 3, 19											
19											
Group G											
13											

13, 22, 23											
22											
23											
Other O-antisera											

		Strains									
H-antisera	Manufacturer	1	2	3	4	5	6	7	8	9	10
b											
d											
E (complex)											
e, h											
e, n											
e, n, x											
e, n, z_{15}											
h											
x											
x (z_{16})											
z_{15}											
G (complex)											
g, p											
g, m											
f											
m											
s											
q											
t											
q, s, t, p, u											
i											
k											
L (complex)											
l, v											
l, w											
v											
w											
r											
y											
z											
z_{10}											
1 (complex)											
2											
5											

6											
7											
Other H-antisera											

		Strains									
H-antisera	Manufacturer	11	12	13	14	15	16	17	18	19	20
b											
d											
E (complex)											
e, h											
e, n											
e, n, x											
e, n, z_{15}											
h											
x											
x (z_{16})											
z_{15}											
G (complex)											
g, p											
g, m											
f											
m											
s											
q											
t											
q, s, t, p, u											
i											
k											
L (complex)											
l, v											
l, w											
v											
w											
r											
y											
z											
z_{10}											
1 (complex)											
2											
5											

6											
7											
Other H-antisera											

TEST RESULTS SEROTYPING

Laboratory code	
Starting date of serotyping	
Finishing date of serotyping	

Strain no.	O-antigens detected	H-antigens detected	Serovar name
S-1			
S-2			
S-3			
S-4			
S-5			
S-6			
S-7			
S-8			
S-9			
S-10			
S-11			
S-12			
S-13			
S-14			
S-15			
S-16			
S-17			
S-18			
S-19			
S-20			

QUESTIONS PHAGE TYPING

Does your laboratory perform phage typing?	□ Yes □ No
If yes, which *Salmonella* strains do you phage type?	□ *Salmonella* Typhimurium □ *Salmonella* Enteritidis □ Other(s): ……
Which typing system is used for:	□ *Salmonella* Typhimurium ……. □ *Salmonella* Enteritidis …….
How many strains did your laboratory (approximately) phage type in 2008?	Number of strains……...

TEST RESULTS PHAGE TYPING

Laboratory code	
Starting date of phage typing	
Finishing date of phage typing	

		Phage reactions at Routine Test Dilution (*S.*Enteritidis)																
Strain number	Phage type	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
E1																		
E2																		
E3																		
E4																		
E5																		
E6																		
E7																		
E8																		
E9																		
E10																		

TEST RESULTS PHAGE TYPING

Laboratory code	
Starting date of phage typing	
Finishing date of phage typing	

		Phage reactions at Routine Test Dilution (*S.* Typhimurium)																	
Strain number	Phage type	1	2	3	4	5	6	7	8	10	11	12	13	14	15	16	17	18	19
T11																			
T12																			
T13																			
T14																			
T15																			
T16																			
T17																			
T18																			
T19																			
T20																			

		Phage reactions at Routine Test Dilution (*S.* Typhimurium)												Additional phages						
Strain number	Phage type	20	21	22	23	24	25	26	27	28	29	32	35	1	2	3	10	10 var 2	10 var 3	18
T11																				
T12																				
T13																				
T14																				
T15																				
T16																				
T17																				
T18																				
T19																				
T20																				

Notations:

- :	no reaction	O*: O pooled	
+ :	5-20 plaques	(<)CL: clear lysis	
+ :	21-40 plaques	(<)OL: opaque lysis	
++ :	41-80 plaques	SCL: semi confluent lysis	
+++	81-100 plaques	<< : Merging plaques towards semi-confluent lysis	

QUESTIONS ANTIMICROBIAL SUSCEPTIBILITY TESTING (AST)

What method do you use for antimicrobial susceptibility testing?	Disk:
	MIC:
Which control strain(s) do you use with routine analysis?	Disk:
	MIC:
Which agar/broth medium do you use?	Disk:

	MIC:
What is the concentration of the inoculum in bacteria per ml?	Disk:
	MIC:
How many strains were (approximately) tested for antimicrobial susceptibility in your lab in 2008?	Number of strains: ……

Which antibiotics did you use in this EQA scheme?

Antibiotic	Abbreviation	Disk load (µg)	Manufacturer	Breakpoints/ interpretive criteria used (R/I/S)	Range used in MIC determination
Ampicillin	AMP				
Cefotaxime	CEF				
Chloramphenicol	CHL				
Ciprofloxacin	CIP				
Gentamicin	GEN				
Nalidixic Acid	NAL				
Streptomycin	STR				
Sulphonamides	SUL				
Tetracycline	TET				
Trimethoprim	TMP				

RESULTS ANTIMICROBIAL SUSCEPTIBILITY TESTING (AST)

Laboratory code	
Starting date of AST	
Finishing date of AST	

Please fill in the diameter of the inhibition zones in mm if your method is disk diffusion and the MIC-value in µg/ml if your method of choice is the Minimal Inhibition Concentration and include your interpretation according to your criteria between brackets (R, I, or S)

Strain number	Antibiotic									
	AMP	CEF	CHL	CIP	GEN	NAL	STR	SUL	TET	TMP
A-1										
A-2										
A-3										
A-4										
A-5										
A-6										
A-7										
A-8										
A-9										
A-10										
ATCC 25922										

REMARKS AND COMMENTS

Name of person(s) carrying out the typing	
Date (and signature)	

Name of person in charge	
Date (and signature)	