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Tenth CRL-*Salmonella* interlaboratory comparison study (2005) on typing of *Salmonella* spp.

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Abstract

Tenth CRL-*Salmonella* interlaboratory comparison study (2005) on typing of *Salmonella* spp.

The tenth interlaboratory comparison study on the typing of *Salmonella* was organised by the Community Reference Laboratory for *Salmonella* (CRL-*Salmonella*, Bilthoven, The Netherlands) in collaboration with the Health Protection Agency (HPA, London, United Kingdom) and the Central Institute for Animal Disease Control (CIDC, Lelystad, The Netherlands) in March 2005. Twenty-six National Reference Laboratories for *Salmonella* (NRLs-*Salmonella*), including Norway and 14 Enter-Net Laboratories (ENLs), participated in the study. In total, 20 strains of the species *Salmonella enterica* subspecies *enterica* were selected for serotyping. Ten strains of *Salmonella* Enteritidis (SE) and 10 strains of *Salmonella* Typhimurium (STM) were selected for phage typing. Ten strains of *Salmonella* spp. were selected for antimicrobial susceptibility testing. In general, no problems were encountered with the typing of the O antigens. Ninety-nine per cent of the NRLs and 100 % of the ENLs were able to correctly type the O antigens. A few laboratories had problems typing the H antigens. The H antigens were typed correctly by 97 % of the NRLs and by 99 % of the ENLs. Ninety-four per cent of the NRLs and 99 % of the ENLs indicated correct serovar names for the 20 serotyping strains. The phage typing results of the majority of the laboratories were found to be good. This was also valid for the quality of the antimicrobial susceptibility testing of both the NRLs and the ENLs.

Key words: CRL-*Salmonella*, *Salmonella* spp., serotyping, phage typing, antimicrobial susceptibility.

Rapport in het kort

Tiende CRL-*Salmonella* ringonderzoek (2005) voor de typering van *Salmonella* spp.

Het tiende ringonderzoek voor de typering van *Salmonella* werd in maart 2005 georganiseerd door het Communautair Referentie Laboratorium voor *Salmonella* (CRL-Salmonella, Bilthoven, Nederland) in samenwerking met de Health Protection Agency (HPA, Londen, Verenigd Koninkrijk) en het Centraal Instituut voor Dierziekte Controle (CIDC, Lelystad, Nederland). Zesentwintig Nationale Referentie Laboratoria voor *Salmonella* (NRLs-*Salmonella*) inclusief Noorwegen en 14 Enter-Net Laboratoria (ENLs) namen deel aan de studie. Twintig stammen van species *Salmonella enterica* subspecies *enterica* werden geselecteerd voor de serotypering. Tien stammen van *Salmonella* Enteritidis (SE) en 10 stammen van *Salmonella* Typhimurium (STM) werden geselecteerd voor faagtypering. Tien stammen van *Salmonella* spp. werden geselecteerd voor antimicrobiële gevoeligheidsbepalingen. In het algemeen werden geen problemen gevonden met de typering van de O-antigenen. Negenennegentig procent van de NRLs en 100 % van de ENLs typeerden de O-antigenen correct. Slechts enkele laboratoria hadden problemen met het typeren van de H-antigenen. De H-antigenen werden correct getypeerd door 97 % van de NRLs en door 99 % van de ENLs. Vierennegentig procent van de NRLs en 99 % van de ENLs gaven de 20 serotyperingsstammen de goede serovar naam. De meeste laboratoria vonden goede resultaten met de faagtypering. Ook de kwaliteit van de antimicrobiële gevoeligheidsbepalingen uitgevoerd door zowel de NRLs als door de ENLs was goed.

Trefwoorden: CRL-*Salmonella*, *Salmonella*, serotypering, faagtypering, antimicrobiële gevoeligheids bepalingen.

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Summary

In 2005 the tenth interlaboratory comparison study on typing of *Salmonella* was organised by the EU Community Reference Laboratory for *Salmonella* (CRL-*Salmonella*, Bilthoven, the Netherlands) in collaboration with the Health Protection Agency (HPA, Colindale) in London and the Central Institute for Animal Disease Control (CIDC) – Department of Bacteriology and TSEs (Lelystad, the Netherlands). Laboratories that were interested were able to perform phage typing and antimicrobial susceptibility testing as well. The main objective of the study was to evaluate whether examination of samples by the National Reference Laboratories (NRLs-*Salmonella*) as well as by the EnterNet Laboratories (ENLs) was carried out uniformly and whether comparable results were obtained.

Twenty-five NRLs-*Salmonella* of the Member States of the European Union participated, as well as NRL-Norway. Furthermore, 14 EnterNet laboratories participated.

Seven of the participating NRLs-*Salmonella* and ten of the ENLs also performed phage typing. A total of 20 strains of the species *Salmonella enterica* subspecies *enterica* were selected for serotyping by the CRL-*Salmonella*. The strains had to be typed with the method routinely used in each laboratory. The laboratories were allowed to send strains for serotyping to another specialised laboratory in their country. No, or very few problems were encountered with the typing of the O-antigens. Some problems existed with the H-antigens, although the group of laboratories facing these problems seem to diminish. Ninety-nine percent of the NRLs and 100 % of the ENLs were able to correctly type the O-antigens. The H-antigens were typed correctly by 97 % of the NRLs and by 99 % of the ENLs. Ninety-four percent of the NRLs and 99 % of the ENLs indicated correct serovar names for the 20 serotyping strains. The HPA selected 20 strains for phage typing, 10 were of the serovar *Salmonella* Enteritidis (SE) and 10 of the serovar *Salmonella* Typhimurium (STM). The phage typing results of the majority of the laboratories were good. For antimicrobial susceptibility testing (AST), ten strains of various *Salmonella* serovars had to be tested with a panel of fourteen antibiotics. Three different kinds of tests were used in this study, namely, minimal inhibition concentration (MIC) determinations with broth dilution tests, Etest and the disc diffusion test. Based on the results of the study, the value of the inclusion of streptomycin, amoxicillin/clavulanate in monitoring programs is questionable, as the interpretation of the results obtained with these antibiotics caused much problems. This study demonstrated that based on the AST strains distributed and antibiotics tested, less deviating results were produced by MIC determinations than by disc diffusion. If a quality limit of 95 % accuracy would have been used, all laboratories that determined MICs would have been approved, while four laboratories using disc diffusion would not have complied.

List of abbreviations

AMC	Amoxicillin+clavanulate
AMP	Ampicillin
AST	Antimicrobial Susceptibility Testing
BGA	Brilliant Green Agar
CEF	Cefotaxime
CHL	Chloramphenicol
CIDC	Central Institute for Animal Disease Control
CIP	Ciprofloxacin
CLSI	Clinical and Laboratory Standards Insitute
CRL- <i>Salmonella</i>	Community Reference Laboratory – <i>Salmonella</i>
ENL	EnterNet Laboratory
ENRO	Enrofloxacin
ESBL	Extended Spectrum Beta-Lactamases
EU	European Union
FLO	Florfenicol
GEN	Gentamicin
HPA	Health Protection Agency
I	Intermediate
KAN	Kanamycin
LEP	Laboratory of Enteric Pathogens
MIC	Minimal Inhibition Concentration
NAL	Nalidixic acid
NEO	Neomycin
NRL- <i>Salmonella</i>	National Reference Laboratory – <i>Salmonella</i>
Nt	not typable
PFGE	Pulse Field Gel Electrophorese
PT	Phage Type
R	Resistant
RIVM	National Institute for Public Health and the Environment
S	Susceptible
SD	Standard Deviation
SE	<i>Salmonella</i> Enteritidis
STM	<i>Salmonella</i> Typhimurium
STR	Streptomycin
SXT	Sulfamethoxazole + Trimethoprim
SUL	Sulfonamides
TET	Tetracycline
TMP	Trimethoprim
TSI	Triple Sugar Iron agar
XLT	Xylose Lysine Tergitol

1. Introduction

This report describes the 10th interlaboratory comparison study on the typing of *Salmonella* strains. The study was organised by the Community Reference Laboratory for *Salmonella* (CRL-*Salmonella*, Bilthoven, the Netherlands). According to the Council Directive 2003/99/EC and the Commission Decision 2004/564/EC it is one of the tasks of the CRL-*Salmonella* to organise interlaboratory comparison studies for the National Reference Laboratories for *Salmonella* (NRLs-*Salmonella*). The main objective is that the examination of samples in the Member States will be carried out uniformly and comparable results will be obtained. The history of the various typing studies starting in 1995 is shown in Table 1.

Table 1 History of interlaboratory comparison studies on typing of *Salmonella* spp

Study NRLs	Study ENLs	Year	Type and number of serotyping strains of <i>Salmonella</i> spp	Number and type of phage typing strains	Antibiotic resistance testing	Reference
I		1995	spp. <i>enterica</i> 18 spp. <i>salamae</i> 1 spp. <i>houtenae</i> 1			Voogt et al., 1996 (RIVM report 284500004)
II		1996/ 1997	spp. <i>enterica</i> 20			Voogt et al., 1997 (RIVM report 284500008)
III		1998	spp. <i>enterica</i> 20	SE 4 STM 5		Voogt et al., 1998 (RIVM report 284500010)
IV	I	1999	spp. <i>enterica</i> 16	SE 10 STM 10		Raes et al., 2000 (RIVM report 284500013)
V	II	2000	spp. <i>enterica</i> 18 spp. <i>salamae</i> 1 spp. <i>houtenae</i> 1	SE 10 STM 10	YES	Raes et al., 2001 (RIVM report 284500016)
VI	III	2001	spp. <i>enterica</i> 19 spp. <i>arizonae</i> 1	SE 10 STM 10	YES	Korver et al., 2002 (RIVM report 284500020)
VII	IV	2002	spp. <i>enterica</i> 20	SE 10 STM 10		Korver et al., 2002 (RIVM report 284500022)
VIII	V	2003	spp. <i>enterica</i> 20	SE 10 STM 10	YES	Korver et al., 2003 (RIVM report 330300002)
IX	VI	2004	spp. <i>enterica</i> 20	SE 10 STM 10	YES	Korver et al., 2005 (RIVM report 330300006)
X	VII	2005	spp. <i>enterica</i> 20	SE 10 STM 10	YES	This report

Twenty-six NRLs-*Salmonella* (three of them are also EnterNet Laboratory) and eighteen EnterNet Laboratories (ENLs) participated in this tenth study. However, four EnterNet Laboratories sent in their results very late, therefore their results could not be used in this report and thus results of only fourteen ENLs are given. The main objective of this study was to compare the results of typing of *Salmonella* spp. among the NRLs-*Salmonella* and among the ENLs. All participants performed serotyping of the strains.

Seven of the NRLs-*Salmonella* and 10 ENLs performed phage typing on 10 *Salmonella* Enteritidis and 10 *Salmonella* Typhimurium strains. The selection of these strains and interpretation of the results of the phagotyping was performed in close cooperation with the Health Protection Agency, London, UK.

With the help of the Central Institute for Animal Disease Control (CIDC, Department of Bacteriology and TSEs, Lelystad, the Netherlands) ten strains of various *Salmonella* serotypes and one control strain were selected for antimicrobial susceptibility testing. The *Salmonella*'s were selected on the resistance phenotype and the MIC-values were confirmed by repeated testing at CIDC by broth microdilution or *Etest*. These eleven strains were tested by the participants with a panel of fourteen antibiotics. Twenty-five NRLs and twelve ENLs participated with either the Minimal Inhibition Concentration method, *Etest* or disc diffusion test.

2. Participants

Country	Institute/City	National Reference Laboratory for <i>Salmonella</i> (NRL) or EnterNet Laboratory (ENL)	
Austria	Institut für Medizinische Mikrobiologie und Hygiene, Graz	NRL	ENL
Belgium	Veterinary and Agrochemical Research Center (VAR) Brussels	NRL	
Belgium	Institute Scientifique de Santé Publique – Louis Pasteur Brussels		ENL
Cyprus	Laboratory for the Control of Foods of Animal Origin (LCFAO) Nicosia	NRL	
Czech Republic	National Reference Laboratory for Salmonellosis, State Veterinary Institute Prague	NRL	
Czech Republic	National Reference Laboratory for Salmonella National Institute of Public Health Prague		ENL
Denmark	Danish Veterinary Laboratory Copenhagen	NRL	
Denmark	Statens Serum Institut Department of Gastrointestinal Infections Copenhagen		ENL
Estonia	Estonian Veterinary and Food Laboratory Diagnostic Department, Bacteriology Laboratory Tartu	NRL	
Finland	National Veterinary and Food Research Institute Kuopio Department Kuopio	NRL	
Finland	National Public Health Institute (KTL) Laboratory of Enteric Pathogens, Helsinki		ENL
France	Agence française de sécurité sanitaire des aliments (AFSSA), Laboratoire d'études et de recherches avicoles et porcines (LERAP), Ploufragan	NRL	

Country	Institute/City	National Reference Laboratory for <i>Salmonella</i> (NRL) or EnterNet Laboratory (ENL)	
France	Unité Biodiversité des Bactéries Institute Pasteur Paris		ENL
Germany	Federal Institute for Risk Assessment (BfR) National Veterinary Salmonella Reference Lab. Berlin	NRL	
Germany	Robert-Koch Institut Bereich Wernigerode Harz		ENL
Greece	Veterinary Laboratory of Halkis Halkis	NRL	
Greece	National School of Public Health, Department of Public & Administrative Health (Serotyping) and Department of Microbiology, Medical School, University of Athens (Phage typing) Athens		ENL
Hungary	National Food Investigation Institute of Hungary Department Food Microbiology Budapest	NRL	
Ireland	Department of Agriculture and Food Central Veterinary Research Laboratory Dublin	NRL	
Ireland	National Salmonella Reference Laboratory University College Hospital Galway		ENL
Italy	Istituto Zooprofilattico Sperimentale delle Venezie Centro Nazionale di Riferenza per le Salmonellosi - Legnaro	NRL	
Italy	Istituto Superiore di Sanità Lab. of Medical Bacteriology & Mycology Rome		ENL
Latvia	State Veterinary Medicine Diagnostic Centre (SVMDC) Riga	NRL	
Lithuania	National Veterinary Laboratory Vilnius	NRL	
Luxembourg	Laboratoire de Médecine Vétérinaire de l'Etat Animal Zoonosis Luxembourg	NRL	
Luxembourg	Laboratoire National de Santé Luxembourg		ENL

Country	Institute/City	National Reference Laboratory for <i>Salmonella</i> (NRL) or EnterNet Laboratory (ENL)	
The Netherlands	National Institute for Public Health and the Environment (RIVM) Bilthoven	NRL	ENL
Northern Ireland (UK)	Department of Agriculture for Northern Ireland Veterinary Sciences Division, Bact. Department Belfast	NRL	
Norway	National Institute of Public Health Oslo	NRL	ENL
Poland	National Veterinary Research Institute Microbiological Department Pulawy	NRL	
Portugal	Laboratório Nacional de Investigaçã Veterinária Lisbon	NRL	
Scotland (UK)	Scottish Salmonella Reference Laboratory Department of Bacteriology Glasgow		ENL
Slovak Republic	State Veterinary and Food Institute Reference laboratory for Salmonella Bratislava	NRL	
Slovenia	National Veterinary Institute Veterinary Faculty Ljubljana	NRL	
Spain	Laboratorio de Sanidad Y Produccion Animal de Algete Madrid	NRL	
Spain	Laboratorio de Enterobacterias, CNM Instituto de Salud Carlos III Madrid		ENL
Sweden	National Veterinary Institute Department of Bacteriology Uppsala	NRL	
Sweden	Swedish Institute of Infectious Disease Control Department of Bacteriology Solna		ENL
Switzerland	University of Berne Institute of Veterinary Bacteriology Bern		ENL
United Kingdom	Veterinary Laboratories Agency Weybridge Department of Bacterial Diseases New Haw, Addlestone	NRL	

3. Materials and Methods

3.1 *Salmonella* strains for serotyping

Twenty strains for serotyping were sent to the participants. The *Salmonella* strains used for the interlaboratory comparison study on serotyping originated from the collection of the National *Salmonella* Centre in the Netherlands. The strains were typed once again by this Centre before mailing. The complete antigenic formula according to the most recent Kauffmann-White scheme (Popoff, 2001) of the 20 serovars are shown in Table 2.

Table 2 *Antigenic formulas of the 20 Salmonella strains according to the Kauffmann-White scheme determined by CRL-Salmonella*

No	Serovar	O antigens	H antigens	Origin of strains
S1	<i>S. Mbandaka</i>	6, 7, <u>14</u>	$z_{10} : e, n, z_{15}$	Chicken
S2	<i>S. Oranienburg</i>	6, 7, <u>14</u>	$m, t : [z_{57}]$	Seed
S3	<i>S. Poona</i>	<u>1</u> , 13, 22	$z : 1, 6 : [z_{44}]$	Human
S4	<i>S. Derby</i>	<u>1</u> , 4, [5], 12	$f, g : [1, 2]$	Pig
S5	<i>S. Banana</i>	<u>1</u> , 4, [5], 12	$m, t : [1, 5]$	Ref.strain
S6	<i>S. Hadar</i>	6, 8	$z_{10} : e, n, x$	Chicken
S7	<i>S. Gloucester</i>	<u>1</u> , 4, 12, <u>27</u>	$i : l, w$	Turkey
S8	<i>S. Heidelberg</i>	<u>1</u> , 4, [5], 12	$r : 1, 2$	Human
S9	<i>S. Infantis</i>	6, 7, <u>14</u>	$r : 1, 5$	Meat product
S10	<i>S. Dublin</i>	<u>1</u> , 9, 12, [Vi]	$g, p : -$	Cattle
S11	<i>S. Paratyphi B var Java</i>	<u>1</u> , 4, [5], 12	$b : 1, 2$	Human
S12	<i>S. Matadi</i>	17	$k : e, n, x$	Human
S13	<i>S. Newport</i>	6, 8, <u>20</u>	$e, h : 1, 2 : [z_{67}]$	Human
S14	<i>S. Livingstone</i>	6, 7, <u>14</u>	$d : l, w$	Pig
S15	<i>S. Kedougou</i>	<u>1</u> , 13, 23	$i : l, w$	Human
S16	<i>S. Mikawasima</i>	6, 7, <u>14</u>	$y : e, n, z_{15}$	Human
S17	<i>S. Typhimurium</i>	<u>1</u> , 4, [5], 12	$i : 1, 2$	Human
S18	<i>S. Enteritidis</i>	<u>1</u> , 9, 12	$g, m : -$	Human
S19	<i>S. Virchow</i>	6, 7, <u>14</u>	$r : 1, 2$	Cattle
S20	<i>S. Typhimurium</i>	<u>1</u> , 4, [5], 12	$i : 1, 2$	Human

3.2 *Salmonella* strains for phage typing

The strains of *Salmonella* for the comparison study on phage typing were from the collection of the Salmonella Reference Unit of the Health Protection Agency (HPA), Laboratory of Enteric Pathogens (LEP), National *Salmonella* Reference Laboratory for England and Wales, London, UK. Ten strains of *Salmonella* Enteritidis and 10 strains of *Salmonella* Typhimurium were selected.

The explanation of the various notations in Tables 3 and 4 and the Tables in Annex 3 are as follows:

-	=	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 3 Phage reactions of the *Salmonella* Enteritidis strains, determined by HPA

QA No.	Phage type	Phages at Routine Test Dilution															
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
E1	8	-	-	scl	scl	cl	scl	scl	ol	cl	ol	scl	cl	-	-	-	-
E2	1b	ol	scl	cl	scl	cl	scl	cl	scl	ol	ol	cl	cl	cl	cl	scl	cl
E3	4	-	scl	cl	scl	cl	scl	cl	scl	ol	ol	cl	cl	cl	-	-	-
E4	13a	-	-	-	scl	-	scl	-	scl	scl	ol	-	-	-	-	-	-
E5	1	ol	scl	cl	scl	cl	scl	cl	scl	scl	ol	cl	cl	cl	cl	-	-
E6	22	ol	-	-	scl	-	scl	-	ol	ol	ol	-	-	-	cl	-	-
E7	5a	-	scl	±	scl	ol	scl	±	-	ol	-	-	ol	-	-	-	-
E8	14b	-	-	-	-	-	scl	-	-	±	-	-	-	-	-	-	-
E9	44	ol	scl	cl	-	cl	scl	cl	ol	-	ol	cl	cl	cl	cl	-	-
E10	6	-	scl	-	scl	-	scl	-	scl	ol	ol	-	-	-	-	-	-

Table 4 *Phage reactions of the Salmonella Typhimurium strains, determined by HPA*

QA No.	Phage type	Phages at Routine Test Dilution																	
		1	2	3	4	5	6	7	8	10	11	12	13	14	15	16	17	18	19
M11	15	-	-	-	-	-	-	-	-	-	ol	scl	scl	-	ol	-	ol	scl	ol
M12	36	ol	ol	ol	ol	ol	ol	ol	scl	ol	ol	ol	ol	ol	ol	ol	ol	cl	ol
M13	U291	-	-	-	ol	cl	scl	-	-	-	cl	-	-	cl	cl	cl	-	scl	cl
M14	U310	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
M15	12	-	-	-	-	-	-	-	-	-	-	scl	cl	-	-	-	-	-	-
M16	193	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
M17	104	-	-	-	-	-	-	-	-	-	-	++	scl	-	-	-	-	++	-
M18	10	-	-	-	-	-	-	-	-	cl	ol	cl	cl	-	-	cl	-	-	-
M19	15a	-	-	-	-	-	-	-	-	-	ol	ol	ol	-	ol	-	ol	-	ol
M20	110	-	-	-	-	-	-	-	-	-	-	-	cl	-	-	-	-	cl	-

QA No.	Phage type	Phages at Routine Test Dilution												Additional phages					
		20	21	22	23	24	25	26	27	28	29	32	35	1	2	3	10	10 var	18
M11	15	scl	-	-	-	-	-	-	±	-	-	ol	-	±	±	±	ol	ol	-
M12	36	ol	ol	ol	ol	ol	ol	ol	ol	ol	ol	ol	ol	+	+	+	ol	ol	ol
M13	U291	+	-	-	-	-	scl	cl	cl	-	-	-	-	±	±	-	ol	ol	±
M14	U310	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ol	-
M15	12	-	-	-	-	-	-	-	-	-	-	-	-	+	+	+	ol	ol	-
M16	193	-	-	-	-	-	-	-	-	-	-	-	-	++	++	++	++	±	-
M17	104	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ol	ol	-
M18	10	cl	-	cl	cl	-	-	scl	-	-	cl	cl	-	±	±	-	ol	ol	-
M19	15a	ol	-	-	-	-	-	-	±	-	-	ol	-	±	±	±	ol	ol	-
M20	110	-	-	-	-	-	-	-	±	-	-	-	±	±	±	±	ol	ol	-

3.3 Strains and antibiotics for antimicrobial susceptibility testing (AST)

The *Salmonella* strains used for the antimicrobial susceptibility testing originated from the collection of the Central Institute for Animal Disease Control (CIDC), Department of Bacteriology and TSEs (Lelystad, the Netherlands). The ten strains were numbered AST-1 to AST-10. The strains were selected on their resistance phenotype. All sero- and phage typing was performed by the CRL-*Salmonella*. *S. Corvallis* showed an atypical quinolone resistance phenotype (CIP reduced susceptible, NAL susceptible), which is occasionally observed in the CIDC's resistance monitoring programme. *S. Kentucky* was high level resistant to ciprofloxacin; this is a serovar that has been detected occasionally in the last years. These strains were always isolated from human patients and were related to travel to Egypt. A summary of the serotypes and sources of AST-1 – AST-10 are given in Table 5.

Table 5 Serotypes and sources of AST-strains

AST strains	Source	Serotype
AST-1	Human	<i>S. Enteritidis</i> Pt 36
AST-2	Beef	<i>S. Typhimurium</i>
AST-3	Human	<i>S. Typhimurium</i>
AST-4	Human	<i>S. Corvallis</i>
AST-5	Broiler	<i>S. Infantis</i>
AST-6	Human	<i>S. Enteritidis</i> Pt 1
AST-7	Layer	<i>S. Hadar</i>
AST-8	Human	<i>S. Typhimurium</i>
AST-9	Human	<i>S. Kentucky</i>
AST-10	Human	<i>S. Typhimurium</i> (DT104)

The strains were tested for their susceptibility by broth microdilution method using Sensititre plates produced by Trek Diagnostic systems in the United Kingdom in duplicate, or by *E-test*. *E. coli* ATCC 25922 was used as control strain. The MIC values determined for the prescribed panel of antibiotics and the categories (resistant (R), intermediate (I) and susceptible (S) based on CLSI breakpoints, are shown in Table 6. Strains AST1, 3, 7-10 were classified S for amoxicillin-clavulanic acid (AMC) because these strains were all producing an inhibitor susceptible β -lactamase enzyme. The elevated MICs were methodologically derived. In the test systems used the clavulanic acid competes with the β -lactamase. Once it was all used, the small amount of enzyme that was left resulted in increased MICs.

Table 6 MIC results (in µg/ml) of AST-strains and of control strain *Escherichia coli* ATCC 25922 determined with the prescribed panel of antibiotics by CIDC. Of *E. coli* ATCC 25922 also the inhibition zones of the disc diffusion test are given

	Antibiotics						
	AMC	AMP/AM OX	CEF	CHL	CIP	ENRO	FLO
Strains							
AST 1	16/8 ¹	> 64	≤ 0.12	8	≤ 0.06	0.125	4
AST 2	8/4	> 64	0.25	16	≤ 0.06	0.19	8
AST 3	16/8 ¹	> 64	≤ 0.12	8	≤ 0.06	0.125	4
AST 4	1/0.5	≤ 0.5	≤ 0.12	8	0.5	1.5	4
AST 5	> 16/8	> 64	> 16	8	≤ 0.06	0.125	4
AST 6	1/0.5	1	≤ 0.12	8	0.25	1	4
AST 7	16/8 ¹	> 64	≤ 0.12	8	0.25	1	4
AST 8	16/8 ¹	> 64	0.5	8	1	1	4
AST 9	16/8 ¹	> 64	0.25	8	> 8	> 32	4
AST 10	16/8 ¹	> 64	≤ 0.12	> 128	≤ 0.06	0.094	128
<i>E. coli</i> (MIC)	2/1-8/4	2-8	0.03- 0.125	2-8	0.004- 0.015	0.08-0.03	2-8
<i>E. coli</i> (disc) ⁴	(20/10) 18-24	(10) 16-22	(30) 29-35	(30) 21-27	(5) 30-40	(5) 32-40	(30) 22-28

	Antibiotics								
	GEN	KAN	NAL	NEO	STR ²	SXT	TET	TMP	SUL ³
Strains									
AST 1	0.5	4	4	≤ 1	1/4	≤ 0.12/2.38	2	≤ 0.5	16
AST 2	0.5	> 16	8	64	6/16	> 16/304	> 64	> 64	> 1024
AST 3	0.5	16	4	≤ 1	128/> 64	0.25/4.75	> 64	≤ 0.5	> 1024
AST 4	1	8	16	≤ 1	192/> 64	0.25/4.75	> 64	≤ 0.5	> 1024
AST 5	0.5	4	4	≤ 1	4/16	0.25/4.75	2	≤ 0.5	16
AST 6	≤ 0.25	2	> 128	≤ 1	1/4	≤ 0.12/2.38	2	≤ 0.5	16
AST 7	> 32	> 16	> 128	≤ 1	32/> 64	≤ 0.12/2.38	64	≤ 0.5	> 1024
AST 8	> 32	> 16	> 128	> 128	12/32	0.5/9.5	> 64	≤ 0.5	> 1024
AST 9	16	> 16	> 128	> 128	384/> 64	> 16/304	> 64	> 64	> 1024
AST 10	1	4	4	≤ 1	48/> 64	0.25/4.75	32	≤ 0.5	> 1024
<i>E. coli</i> (MIC)	0.25-1	1-4	1-4	NA	NA	≤ 0.5/9.5	0.5-2	0.5-2	8-32
<i>E. coli</i> (disc) ⁴	(10) 19-26	(30) 17-25	(30) 22-28	NA	NA	(1.25/23.75) 23-29	(30) 18-25	(5) 21-28	(250 or 300) 15-23

Light grey cells = Resistant (R); dark grey cells = Intermediate (I); White cells = Susceptible (S);
 1: Classified as S, see text for an explanation; 2: For STR Etest and broth micro dilution results displayed; 3: Sulfamethoxazole results displayed; 4: Disc load in µg between brackets, zone diameter in mm. NA = not applicable

This ring trial was organised to standardise methods used for susceptibility testing and to harmonise the susceptibility test results, with the specific purpose of resistance monitoring. This is not necessarily identical to reporting an advice for therapy. Resistance monitoring should aim at the detection of acquired resistance. Therefore for amoxicillin and clavulanate (AMC) the intermediate category was classified S.

For streptomycin in previous year a large variation in results occurred for the AST-strains with MICs below the R break point (categorized S or I). Because validated CLSI criteria are lacking for MIC-determinations of streptomycin, and the major purpose of the inclusion of this antibiotic in monitoring panels is the early detection of DT104 (STR R), in this ring trial only one breakpoint is used ($R \geq 32 \mu\text{g/ml}$).

The participating laboratories were asked to use their standard method for susceptibility testing. The methods used varied between Minimal Inhibition Concentration (MIC) test, or breakpoint-MIC determination with a broth micro dilution test, MICs obtained with *Etest* or inhibition zone diameters obtained with the disc diffusion test.

The requested discs in the diffusion tests were: amoxicillin + clavulanate (30 μg), ampicillin (10 μg), cefotaxime (30 μg), chloramphenicol (30 μg), ciprofloxacin (5 μg), florfenicol (30 μg), gentamicin (10 μg), kanamycin (30 μg), nalidixic acid (30 μg), neomycin (30 μg), streptomycin (10 μg), sulfamethoxazole + trimethoprim (25 μg), sulfonamides (250 or 300 μg) and trimethoprim (5 μg). Laboratories that did not have the discs with the required amount of antibiotics were asked to omit that antibiotic from their list. For the MIC determinations, the participants were asked to test the same antibiotics as required for the diffusion tests.

Those participants that used a quantitative method were asked to record the MIC values determined. Moreover, all participants were asked to categorise their results as susceptible (S), intermediate (I) or resistant (R) according to the breakpoints used in the NRLs and ENLs. The deviations from the categories determined by CIDC were classified as minor or major deviations. A R–I or a S–I deviation was called a minor deviation and a S–R deviation, a major deviation. R–S deviations are considered very major deviations. The CLSI breakpoints for MICs according to NCCLS guideline M100-S15 and interpretive criteria for disc diffusion according to guideline M100-S15/M31-A2 are shown in Table 7.

Table 7 CLSI breakpoints in µg/mL for MIC and in mm for disc diffusion

Antibiotics	MIC (M100-S15) (µg/ml)		Disc diffusion (M100-S15/M31-A2) (mm)	
	Susceptible	Resistant	Susceptible	Resistant
Amoxicillin + Clavanulate	≤ 8/4	≥ 32/16	≥ 18	≤ 13
Ampicillin	≤ 8	≥ 32	≥ 17	≤ 13
Cefotaxime	≤ 8	≥ 64	≥ 23	≤ 14
Cefotaxime (ESBL)	-	≥ 2	-	≤ 27
Chloramphenicol	≤ 8	≥ 32	≥ 18	≤ 12
Ciprofloxacin	≤ 1	≥ 4	≥ 21	≤ 15
Enrofloxacin	≤ 0.25	≥ 2	≥ 23	≤ 16
Florfenicol*	≤ 8	≥ 32	-	-
Gentamicin	≤ 4	≥ 16	≥ 15	≤ 12
Kanamycin	≤ 16	≥ 64	≥ 18	≤ 13
Nalidixic Acid	≤ 16	≥ 32	≥ 19	≤ 13
Neomycin*	≤ 16	≥ 32	-	-
Streptomycin	≤ 16	≥ 32 [#]	≥ 15	≤ 11
Trimethoprim + Sulphamethoxazole (1:19)	≤ 2 / 38	≥ 4 / 76	≥ 16	≤ 10
Sulfonamides**	≤ 256	≥ 512	≥ 17	≤ 12
Trimethoprim	≤ 8	≥ 16	≥ 16	≤ 10

* No CLSI breakpoint, MARAN 2003 breakpoints used; [#] Streptomycin R-breakpoint provided by Sensititre manufacturer; **CLSI breakpoints for sulfisoxazole used.

3.4 Laboratory codes

The NRLs were assigned a laboratory code (labcode) from one to twenty-six (1-26) by CRL-*Salmonella*, which differed from the previous typing studies. The alphabetical labcodes for the ENLs were given by HPA, London, UK.

3.5 Transport

All samples were packed and transported as dangerous goods. The parcels containing strains for serotyping and antimicrobial susceptibility testing for the NRLs were sent by CRL-*Salmonella* in week 9, 2004. The parcels containing strains for phage typing for the NRLs were sent by HPA, London, UK. The ENLs received all their parcels from HPA.

3.6 Guidelines for evaluation of serotyping results

The evaluation of the various serotyping results as mentioned in this report are described in Table 8.

Table 8 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

4. Questionnaire

A questionnaire was incorporated in the testreport of the interlaboratory comparison study. In this part of the report the questions and answers of this questionnaire are summarised.

4.1 General questions

Question 1: Was your parcel containing the strains for serotyping damaged at arrival?

All packages were received in a perfect state and no damage occurred during transport.

Question 2: What was the date of receipt at the laboratory (strains for serotyping)?

Nineteen NRLs received their parcel within the same week as the samples were sent (week 9, 2005). The laboratories with labcode 4, 12, 15, 18, 20 and 24 received the parcel after 7-8 days of transport. The NRL with labcode 6 received the parcel only after 10 days. The average transport time for the NRLs was 3.7 days. The shipment of the parcels to the EnterNet Laboratories was organised by HPA, London, UK.

Question 3: Was your parcel containing the strains for phage typing damaged at arrival?

All packages were received in good condition and no damage occurred during transport.

Question 4: What was the date of receipt at the laboratory (strains for phage typing)?

Seven NRLs (labcodes 5, 6, 9, 12, 17, 19, 22 and 26) received their parcels in week 10 (2005). Two packages (labcodes G and P) were received by the ENLs in week 10 and the other eight (labcodes A, B, C, D, E, H, L and M) in week 11.

Question 5: What kind of medium did you use for subculturing the strains ?

The NRLs as well as the ENLs used a variety of media from various manufacturers for the subculturing of the *Salmonella* strains. This varied from non-selective nutrient agar to selective media like XLD.

4.2 Questions regarding serotyping

Question 6: What was the frequency of serotyping at your laboratory in 2004 ?

Question 7: How many strains did your laboratory serotype in 2004 ?

Table 9 Frequency and number of strains serotyped in 2004

Labcode NRLs	Typing frequency	Number of strains serotyped in 2004	Labcode ENL	Typing frequency	Number 2004
1	Daily	506	A	Daily	11318
2	Daily	1800	B	Daily	700
3	Monthly	13	C	Daily	2000
4	Twice a week	147	D	Daily	7000
5	Daily	2,327	E	Daily	5539
6	Daily	2888	F	Thrice a week	1536
7	Thrice a week	157	G	Daily	1100
8	Daily	732	H	Monthly	100
9	Daily	8516	J	Daily	487
10	Weekly	2000	L	Daily	8690
11	Daily	269	M	Thrice a week	4020
12	Weekly	795	P	Daily	2012
13	Weekly	122	Q	Daily	1838
14	Thrice a week	280	R	Daily	1102
15	Twice a week	321			
16	Daily	400-600			
17	Daily	10275			
18	Daily	6456			
19	Weekly	5000			
20	Daily	600			
21	Thrice a week	162			
22	Daily	6180			
23	Daily	800-1000			
24	Daily	911			
25	Daily	1067			
26	Daily	3899			

Question 8: What kind of sera do you use (commercially available or prepared in own laboratory) ?

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

Number of manufacturers	Number of NRLs	Number of ENLs
From 1 manufacturer	5	5
From 2 manufacturers	9	2
From 3 manufacturers	9	1
From 4 manufacturers	1	4
From 5 manufacturers	1	1
Preparation in own laboratory	6	3
No information	1	--

Table 11 Number of laboratories using sera from the following manufacturers

Name manufacturer	Number of NRLs (n=26)	Number of ENLs (n=14)
Biorad (=Sanofi)	8	7
Biostat	1	0
Biotrading	0	1
Dade Behring	3	2
Denka Seiken	1	2
Difco	4	0
Eurobio	1	1
Immunolab	1	0
Imuna (Slovak Republic)	0	1
Mast	0	1
Murex-Abbott	3	1
Prolab	4	1
Reagensia AB	2	2
Sevapharma (Czech Republic)	0	1
Sifin (Germany)	10	4
SSIC (Statens Serum Institute, Copenhagen)	21	9

Question 9: Were the strains in the collaborative study typed in your own laboratory?
One NRL-Salmonella (labcode 16) sent some strains to another laboratory for serotyping.

4.3 Questions regarding phage typing

Question 11: Does your laboratory perform phage typing of *Salmonella* Enteritidis, *S. Typhimurium* and/or of other strains ?

Seven NRLs and ten ENLs performed phage typing of *S. Typhimurium* and/or *S. Enteritidis* strains. For routine purposes four NRLs and five ENLs also phage typed other strains like, *S. Agona*, *S. Bovismorbificans*, *S. Hadar*, *S. Paratyphi B*, *S. Typhi*, *S. Virchow*.

Question 12: How many strains did your laboratory phage type in 2004 ?

Table 12 Number of phage typings and their relationship to the serotyping in 2004

Laboratory codes	Number of strains serotyped in 2004	Number of strains phage typed in 2004
5	2327	396
6	2888	1770
9	8516	1227
17	10275	8745
19	5000	2000
22	6180	3946
26	3899	1646
A	11318	1160
B	700	389
C	2000	1250
D	7000	687
E	5539	4100
G	1100	457
H	100	500
L	8690	6395
M	4020	2162
P	2012	1147

4.4 Questions regarding antimicrobial susceptibility testing

Twenty-five NRLs and twelve ENLs performed the antimicrobial susceptibility testing

Question 13: What is/are the name(s) of your control strain(s) ?

Twenty-four NRLs and twelve ENLs used *E. coli* as their control strain. In all laboratories, except for laboratory 9, *Escherichia coli* ATCC 25922 was used. Laboratory 9 used *E. coli* NCTC 10418. Several laboratories used more than one control strain, like *Pseudomonas aeruginosa* (ATCC 27853), *Escherichia coli* (ATCC 35218), *Staphylococcus aureus* (ATCC 25923 and ATCC 29213), *Enterococcus faecalis* (ATCC 29212) and *Klebsiella pneumoniae* (ATCC 13883 and ATCC 70603).

Question 14: What is the concentration of the AST inoculum in bacteria per ml ?*Table 13 Concentration of the inoculum of NRLs and ENLs using the disc diffusion method*

Labcode	Inoculum	Labcode	Inoculum
1	0.5 McFarland	A	0.5 McFarland
2	0.5 McFarland	C	0.5 McFarland
3	0.5 McFarland	D	1×10^6 cfu/ml
4	0.5 McFarland	F	0.5 McFarland
5	ca 1×10^5 cfu/ml	G	0.5 McFarland
6	0.5 McFarland	H	0.5 McFarland
7	0.5 McFarland	J	0.5 McFarland
9	0.5 McFarland	L	1×10^6 cfu/ml
11	0.5 McFarland		
12	1×10^8 cfu/ml		
13	0.5 McFarland		
14	0.5 McFarland		
15	0.5 McFarland		
16	1×10^8 cfu/ml		
17	1×10^6 cfu/ml		
18	0.5 McFarland		
21	0.5 McFarland		
25	1×10^8 cfu/ml		

Table 14 Concentration of inoculum in bacteria per ml for NRLs and ENLs using MIC

NRLs	ENLs	Density
11, 20	B, Q	0.5 McFarland
22	--	1×10^5 cfu/ml
8, 26	--	$1 - 5 \times 10^5$ cfu/ml
19, 23, 24	R	5×10^5 cfu/ml
--	E	1×10^6 cfu/ml

Question 15: For how many strains was the antimicrobial susceptibility tested in you lab in 2004 ?

Table 15 Number of strains tested for AST in 2004 and relevant method used by the NRLs and the ENLs

Labcode NRL	Number of strains tested for AST in 2004	Method	Labcode ENL	Number of strains	Method
1	18	Disc Diffusion	A	771	Disc Diffusion
2	1400	Disc Diffusion	B	200	MIC
3	30-40	Disc Diffusion	C	2000	Disc Diffusion
4	674	Disc Diffusion	D	1000	Disc Diffusion
5	2272	Disc Diffusion	E	5938	MIC
6	2800	Disc Diffusion	F	1000	Disc Diffusion
7	178	Disc Diffusion	G	1100	Disc Diffusion
8	1000	MIC	H	350	Disc Diffusion
9	4300	Disc Diffusion	J	2635	Disc Diffusion
11	450 + 200	Disc Diffusion + MIC	L	3113	Disc Diffusion
12	166	Disc Diffusion	Q	751	MIC
13	146	Disc Diffusion	R	1035	MIC
14	> 1000	Disc Diffusion			
15	342	Disc Diffusion			
16	193	Disc Diffusion			
17	10275	Disc Diffusion			
18	1746	Disc Diffusion			
19	2500	MIC			
20	250	MIC			
21	150	Disc Diffusion			
22	10000	MIC			
23	1500	MIC			
24	200	MIC			
25	481	Disc Diffusion			
26	3806	MIC			

MIC = Minimal Inhibition Concentration

Question 16: Which antibiotics did you use in this collaborative study ?*Table 16 Antibiotics and manufacturers tested by NRLs and ENLs*

Lab	Company	AMC	AMP	CEF	CHL	CIP	FLO	GEN	KAN	NAL	NEO	STR	SXT	SUL	TMP
1	Biomerieux	+	+	+	+	+	+	+	+	+	+	+	+	-	-
2	Oxoid	+	+	-	+	+	-	+	+	+	-	+	+	+	-
3	BD	+	+	+	+	+	-	+	+	+	-	+	+	+	+
4	Biorad	+	+	+	+	+	-	+	+	+	+	⁺ BD	+	-	+
5	BD	-	+	+	+	+	-	-	-	+	-	+	+	+	-
6	BBL	-	+	+	+	+	-	+	+	+	+	+	+	+	+
7	Bioanalyse	-	+	-	+	+	-	+	+	+	+	+	⁺ BBL	-	⁺ BBL
8	No info	-	+	-	+	-	-	+	-	+	+	+	-	+	+
9	Oxoid	+	+	-	-	-	-	+	-	+	-	-	+	+	-
11	Oxoid (DD)	+	+	+	+	+	⁺ Krka	+	+	+	+	+	+	+	+
11	Trios (MIC)	-	+	+	+	+	-	+	-	-	-	-	+	-	+
12	Biorad	+	+	+	+	+	-	+	+	+	-	+	+	⁺ O	+
13	Oxoid	+	+	+	+	+	-	+	+	+	+	+	⁺ BBL	+	+
14	Oxoid	+	+	+	+	+	+	+	+	+	+	+	+	+	+
15	BBL, BD	+	+	+	+	+	⁺ HM	+	+	+	+	+	+	+	⁺ O
16	Biorad	+	+	+	+	+	⁺ BD	+	+	+	-	+	+	-	+
17	Oxoid	+	+	+	+	+	-	+	+	+	-	+	-	+	+
18	BD	+	+	+	+	+	+	+	+	+	+	+	+	-	-
19	Sensititre	-	+	+	+	+	+	+	-	+	+	-	-	+	+
20	No info	+	+	+	+	+	+	+	-	+	+	+	+	+	+
21	BD	+	+	+	+	+	-	+	-	+	+	+	+	+	+
22	Trek	+	+	-	+	+	+	+	-	+	+	+	-	+	+
23	VetMic	-	+	+	+	+	+	+	-	+	+	+	-	+	+
24	Trek	+	+	+	+	+	+	+	-	+	+	+	+	-	+
25	Oxoid	+	+	+	+	+	-	+	+	+	-	+	-	+	+
26	Trek	+	+	-	+	+	+	+	+	+	+	+	+	+	+
A	Biorad	+	+	+	+	+	⁺ M	+	+	+	+	+	+	+	+
B	Home-made	+	+	+	+	+	-	+	+	+	-	+	+	-	+
C	Oxoid	-	+	+	+	+	-	+	-	+	-	+	-	+	+
D	Biorad	+	-	-	+	+	-	+	+	+	-	+	+	+	+
E	Various	-	⁺ B	⁺ H	⁺ C	⁺ B	-	⁺ RA	⁺ U	⁺ S	-	⁺ G	⁺ BE	-	-
F	Biorad	+	+	+	+	+	-	+	+	+	+	+	+	+	+
G	Oxoid	-	+	+	+	+	-	+	+	+	-	+	-	+	+
H	BD	-	+	+	+	+	-	+	+	+	-	+	+	+	+
J	BD	+	+	+	+	+	-	+	+	+	-	+	+	+	+
L	Oxoid	+	+	+	+	+	-	+	+	+	-	+	+	+	-
Q	Biomerieux	+	+	+	+	+	-	+	+	-	-	+	+	+	-
R	Trek	+	+	-	+	+	+	+	-	+	+	+	-	-	+

B = Bayer AG ; BD = Becton-Dickinson; BE = Berlin ; C = Cephasaar ; DD = Disc Diffusion;

G = Grunenthal ; H = Hoechst ; HM = home made ; M = Mast ; MIC = Minimal Inhibition Concentration; O = Oxoid ;

RA = Ratiopharm ; S = Sigma ; U = Ursapharm; + = Antibiotic tested; - = Antibiotic not tested.

5. Results

5.1 Serotyping by the NRLs-*Salmonella*

5.1.1 Evaluation per laboratory

The evaluation of the detection of O- and H-antigens and identification of the strains per laboratory are shown in Figures 1, 2 and 3 and the percentages which were correct in Figure 4.

Twenty-two laboratories (labcode 1, 2, 4, 5, 6, 8, 9, 11, 12, 13, 14, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25 and 26) typed all O-antigens accurately. Fifteen laboratories (labcodes 2, 4, 5, 6, 8, 9, 11, 16, 17, 18, 19, 22, 23, 25 and 26) typed all H-antigens correctly and thirteen laboratories (labcodes 2, 5, 6, 9, 11, 16, 17, 18, 19, 22, 23, 25 and 26) identified all serovar names correctly.

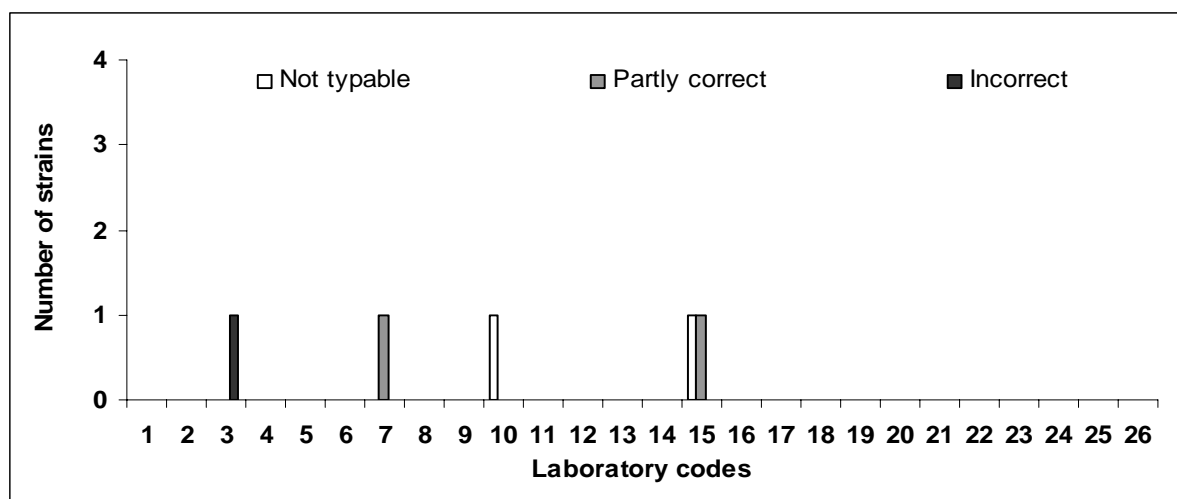


Figure 1 Evaluation of serotyping of O-antigens per NRL

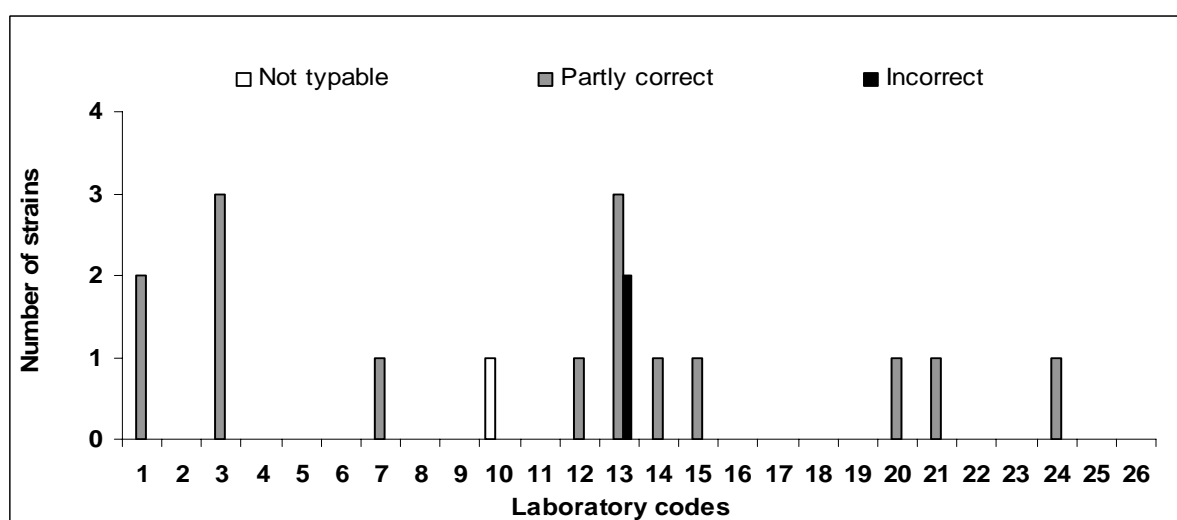


Figure 2 Evaluation of serotyping of H-antigens per NRL

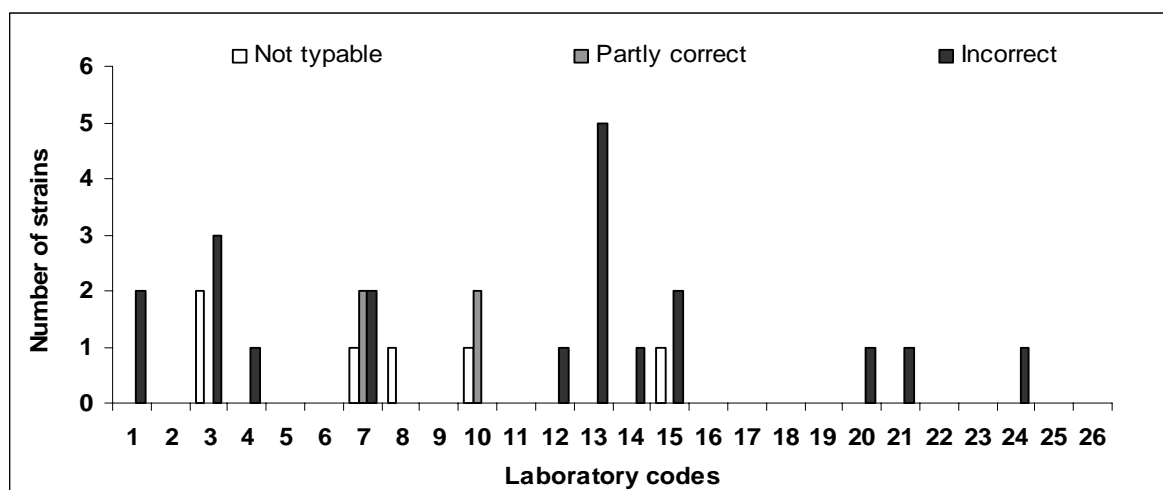


Figure 3 Evaluation of the correct serovar names per NRL

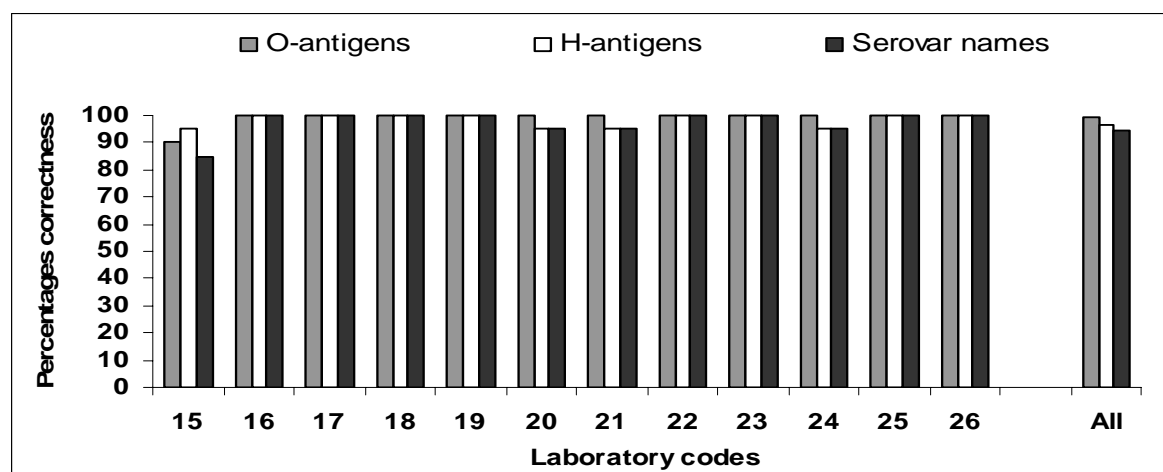
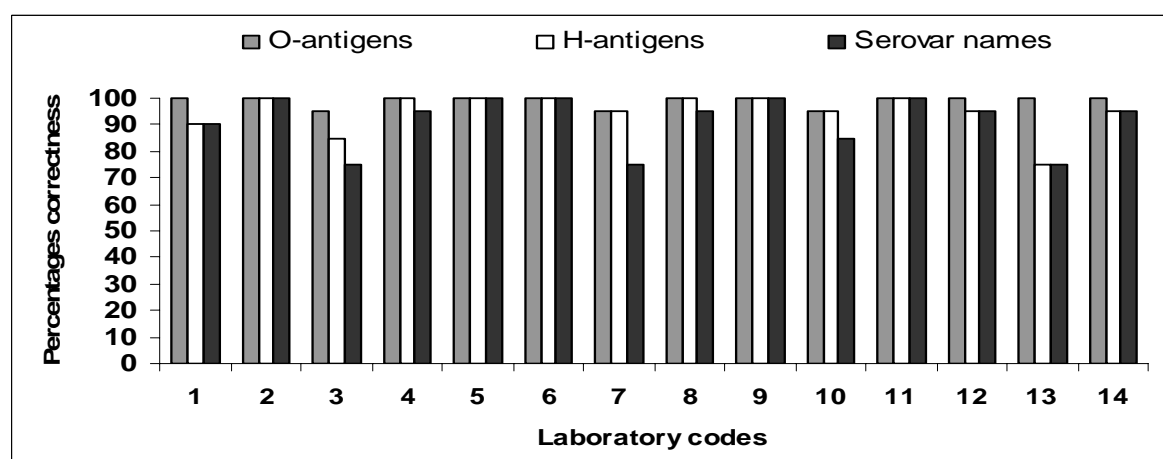


Figure 4 Achievements in percentages that were correct by NRLs

Ninety-nine percent of the NRLs were able to correctly type the O-antigens. The H-antigens were typed correctly by 97 % and the serovar names by 94 % of the NRLs.

5.1.2 Evaluation per strain

The evaluation of the detection of O- and H-antigens and identification of the serovar names per strain are shown in Table 17. The O-antigens of 17 strains were typed correctly by all participants. The H-antigens were typed correctly for 8 strains by all participating laboratories. Problems arose with strains *S. Oranienburg* (strain 2), *S. Banana* (strain 5) and *S. Matadi* (strain 12). A total correct identification by all participants was obtained for eight strains [*S. Gloucester*, *S. Heidelberg*, *S. Dublin*, *S. Paratyphi B var. Java*, *S. Kedougou*, *S. Enteritidis*, *S. Virchow* and *S. Typhimurium* (strain 20)].

Table 17 Evaluation of the typing of strains by the NRLs

Strain		O antigen detected*				H antigen detected*				Name serovar*			
No.	Serotype	+	nt	+/-	-	+	nt	+/-	-	+	nt	+/-	-
1	<i>S. Mbandaka</i>	26	0	0	0	25	0	1	0	25	1	0	0
2	<i>S. Oranienburg</i>	26	0	0	0	22	0	4	0	17	1	2	6
3	<i>S. Poona</i>	25	0	1	0	25	0	0	1	24	1	0	1
4	<i>S. Derby</i>	26	0	0	0	25	0	1	0	25	0	0	1
5	<i>S. Banana</i>	26	0	0	0	23	0	3	0	21	0	2	3
6	<i>S. Hadar</i>	25	0	1	0	25	0	1	0	24	0	0	2
7	<i>S. Gloucester</i>	26	0	0	0	26	0	0	0	26	0	0	0
8	<i>S. Heidelberg</i>	26	0	0	0	26	0	0	0	26	0	0	0
9	<i>S. Infantis</i>	26	0	0	0	25	0	1	0	25	0	0	1
10	<i>S. Dublin</i>	26	0	0	0	26	0	0	0	26	0	0	0
11	<i>S. Paratyphi B var Java</i>	26	0	0	0	26	0	0	0	26	0	0	0
12	<i>S. Matadi</i>	23	2	0	1	25	1	0	0	23	2	0	1
13	<i>S. Newport</i>	26	0	0	0	25	0	1	0	24	0	0	2
14	<i>S. Livingstone</i>	26	0	0	0	25	0	0	1	25	0	0	1
15	<i>S. Kedougou</i>	26	0	0	0	26	0	0	0	26	0	0	0
16	<i>S. Mikawasima</i>	26	0	0	0	24	0	2	0	24	1	0	1
17	<i>S. Typhimurium</i>	26	0	0	0	25	0	1	0	25	0	0	1
18	<i>S. Enteritidis</i>	26	0	0	0	26	0	0	0	26	0	0	0
19	<i>S. Virchow</i>	26	0	0	0	26	0	0	0	26	0	0	0
20	<i>S. Typhimurium</i>	26	0	0	0	26	0	0	0	26	0	0	0

+ = correct; nt = not typable; +/- = partly correct; - = incorrect

* = The figures indicate the number of laboratories finding the relevant results (total number of labs = 26)

The characterisations that caused major problems in serotyping by the NRLs are shown in Table 18. The empty cells in the table indicate that strains were typed correctly by the laboratories mentioned.

Table 18 Identifications per strain that caused major problems in serotyping by NRLs

Labcodes	Strain 2	Strain 5	Strain 12
	<i>S. Oranienburg</i> 6, 7, 14 ; m, t : [z ₅₇]	<i>S. Banana</i> 1, 4, [5], 12 ; m, t : [1, 5]	<i>S. Matadi</i> 17 ; k : e, n, x
Labcode 1	<i>S. Othmarchen</i> 6, 7, 14 : g, m, t : -	<i>S. California</i> 4, 12 : g, m, t : -	
Labcode 3	<i>S. Oakey</i> 6, 7 : m, t : -		<i>S. Nuatja</i> 16 : k : e, n, x
Labcode 4	<i>S. Oakey</i> 6, 7 : m, t : -		
Labcode 7	<i>S. Group C 1</i> 7 : m, t : -	<i>S. Group B</i> 4 : m, t	
Labcode 8	<i>S. ???</i> 6, 7 : m, t : -		
Labcode 10	<i>S. O 6, 7 : m, t</i> 6, 7 : m, t : -	<i>S. O 4, 5 : m, t : -</i> 4, 5 : m, t : -	OMC OMC : -
Labcode 13	<i>S. Oakey</i> 6, 7 ; m, t : z ₆₄		
Labcode 14		<i>S. California</i> 4, 12 : g, m, t	
Labcode 15		<i>S. California</i> 4, 12 : g, m, t : [z ₆₇]	<i>S. ???</i> ??? : k : e, n, x
Labcode 21	<i>S. Winston</i> 6, 7 : m, t : 1, 6		
Labcode 24	<i>S. Oakey</i> 6, 7 : m, t : z ₆₄		

OMC = mix of antisera

5.2 Serotyping by the ENLs

5.2.1 Evaluation per laboratory

The evaluation of the detection of H-antigens and the correctness of the serovar names are shown in Figures 5 and 6 and the percentages correctness in Figure 7.

All fourteen ENLs (labcodes A, B, C, D, E, F, G, H, J, L, M, P, Q and R) typed all O-antigens correct.

Four ENLs (labcodes B, C, E and Q) typed all H-antigens correctly. Two laboratories (labcodes H and R) typed the H-antigens for one or two strains partly correct. However, the problems with the typing of the H-antigens was in almost all cases caused by strains S19 (*S. Virchow*). Several laboratories seemed to have received (unintentionally) a non-motile variant of S19. This was reported by ENLs A, D, F, J, M and P. In Figures 5 and 6 these results are indicated as non-typable.

Three laboratories namely G, H and R used an incorrect serovar name for one or more serovars. For two laboratories (G and H) this concerned again strain S19.

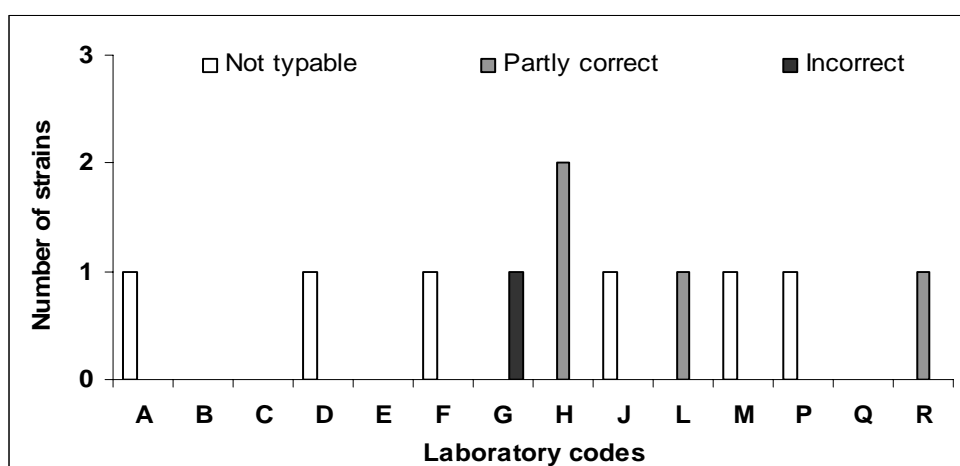


Figure 5 Evaluation of serotyping of H-antigens per ENL

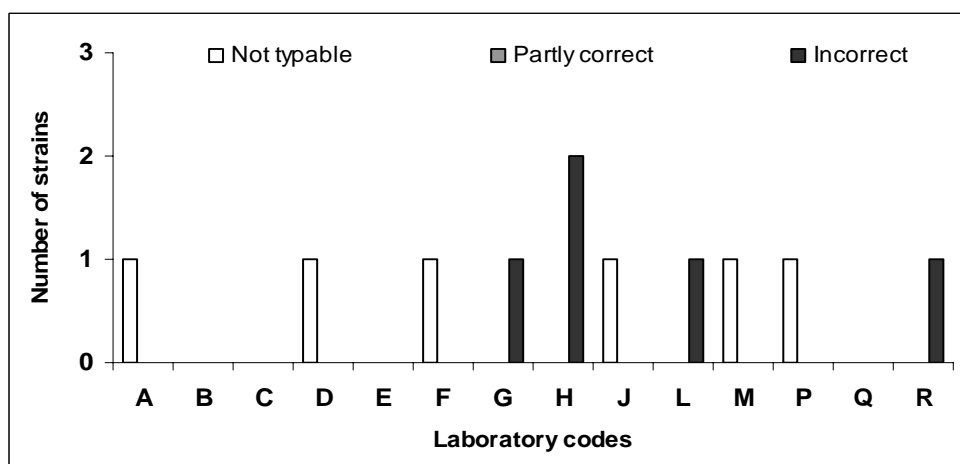


Figure 6 Evaluation of the correct serovar names per ENL

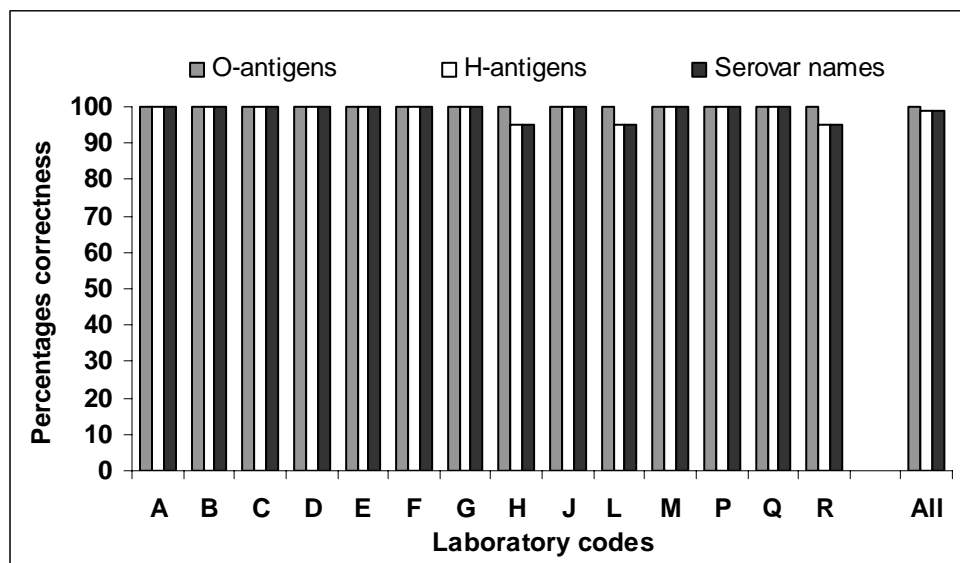


Figure 7 Achievements in percentages that were correct by ENLs

For the calculations of the percentages correctness the results of strain S19 was not taken into account (for all laboratories). Resulting in 100 % of the ENLs being able to correctly type the O-antigens. The H-antigens were then typed correctly by 99 % of the ENLs and the serovar names also by 99 % of the ENLs.

5.2.2 Evaluation per strain

The evaluation of the detection of O- and H-antigens and identification of serovar names per strain are shown in Table 19. As mentioned earlier, *S. Virchow* (strain 19) caused the main problems for typing of the H-antigens. Six laboratories indicated non-motility of the strain and thus not typable. Two laboratories did not type the H-antigens correctly and gave a different serovar name. Details of the problems of strain 19 found by the different ENLs are summarised in Table 20. In addition to strain 19, the H-antigens for three further strains (strains 2, 7 and 16) were only partly correct (see Table 19). For the remaining strains the H-antigens were typed correctly.

Table 19 Evaluation of the typing of strains by the ENLs

Strain		O antigen detected*				H antigen detected*				Name serovar*			
No.	Serotype	+	nt	+/-	-	+	nt	+/-	-	+	nt	+/-	-
1	<i>S. Mbandaka</i>	14	0	0	0	14	0	0	0	14	0	0	0
2	<i>S. Oranienburg</i>	14	0	0	0	13	0	1	0	13	0	0	1
3	<i>S. Poona</i>	14	0	0	0	14	0	0	0	14	0	0	0
4	<i>S. Derby</i>	14	0	0	0	14	0	0	0	14	0	0	0
5	<i>S. Banana</i>	14	0	0	0	14	0	0	0	14	0	0	0
6	<i>S. Hadar</i>	14	0	0	0	14	0	0	0	14	0	0	0
7	<i>S. Gloucester</i>	14	0	0	0	13	0	1	0	13	0	0	1
8	<i>S. Heidelberg</i>	14	0	0	0	14	0	0	0	14	0	0	0
9	<i>S. Infantis</i>	14	0	0	0	14	0	0	0	14	0	0	0
10	<i>S. Dublin</i>	14	0	0	0	14	0	0	0	14	0	0	0
11	<i>S. Paratyphi B var Java</i>	14	0	0	0	14	0	0	0	14	0	0	0
12	<i>S. Matadi</i>	14	0	0	0	14	0	0	0	14	0	0	0
13	<i>S. Newport</i>	14	0	0	0	14	0	0	0	14	0	0	0
14	<i>S. Livingstone</i>	14	0	0	0	14	0	0	0	14	0	0	0
15	<i>S. Kedougou</i>	14	0	0	0	14	0	0	0	14	0	0	0
16	<i>S. Mikawasima</i>	14	0	0	0	13	0	1	0	13	0	0	1
17	<i>S. Typhimurium</i>	14	0	0	0	14	0	0	0	14	0	0	0
18	<i>S. Enteritidis</i>	14	0	0	0	14	0	0	0	14	0	0	0
19	<i>S. Virchow</i>	14	0	0	0	6	6	1	1	6	6	0	2
20	<i>S. Typhimurium</i>	14	0	0	0	14	0	0	0	14	0	0	0

+ = correct; nt = not typable ; +/- = partly correct ; - = incorrect

* = The figures indicate the number of laboratories finding the relevant results (total number of labs = 14)

Table 20 *Identifications per strain that caused major problems in serotyping by ENLs*

Labcodes	Strain 19
	<i>S. Virchow</i> 6, 7, 14 ; r : 1, 2
Labcode A	<i>S. 6, 7 : - : -</i> 6, 7 : - : -
Labcode D	Subspecies <i>enterica</i> (non-motile) 6, 7 : - : -
Labcode F	<i>S. ??</i> 6, 7 : - : -
Labcode G	<i>S. Bulovka</i> 6, 7 : z ₄₄
Labcode H	<i>S. Galiema</i> 6, 7 : k : 1, 2
Labcode J	Subspecies <i>enterica</i> 6, 7 : - : -
Labcode M	Subspecies I 6, 7 : - : -
Labcode P	<i>S. Group C 1</i> 6, 7 : - : -

5.3 Serotyping of strain *S. Banana*

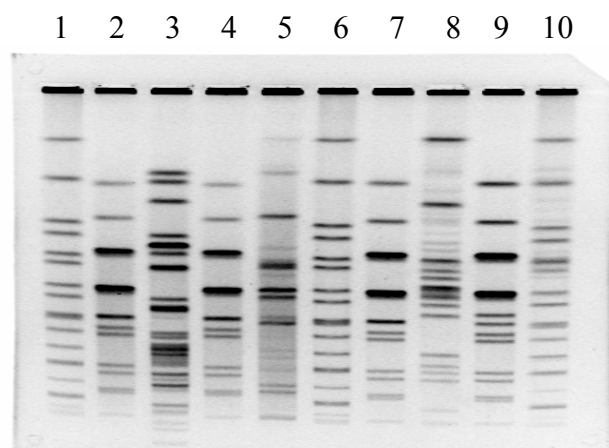
During the interlaboratory comparison study on typing of 2004, *S. Banana* (S1-2004) was included which caused major problems in correctly typing of the H-antigens. In total 14 of the 25 NRLs and 7 of the 18 ENLs found (partly) different results for the H-antigens of this strain. Of this group of laboratories, 9 NRLs and 6 ENLs reported serovar name *S. California* for S1-2004. As this strain caused so many problems additional research was carried out by two EnterNet laboratories (France and Canada) and by the CRL-*Salmonella*. ENL-France as well as CRL-*Salmonella* serotyped the S1 of 2004 as *S. Banana* 1, 4, [5], 12 ; m, t : [1,5]. ENL-Canada identified the strain as *S. California* 4, 12 ; g, m, t : -.

ENL-Canada performed several tests to distinguish between *S. Banana* and *S. California*:

- This ENL used a G-complex to screen isolates. With a known *S. Banana* strains the G-complex was negative, whereas four *S. California* strains were positive as well as S1-2004.
- A *S. Banana* strains of the ENL was inositol negative after 14 days, while all tested *S. California* strains as well as S1-2004 were inositol positive.
- A molecular profile (Pulsed Field Gel Electrophoresis (PFGE)) was made of *S. Banana* and *S. California* strains as well as of S1-2004. These profiles showed more similarity between S1-2004 and *S. California* than between S1-2004 and other *S. Banana* strains (Figure 8).

PFGE profiles of S1-2004 and of a *S. California* strain were made by CRL-*Salmonella* together with the PFGE profile of another *S. Banana* strain (obtained from Institute Pasteur in France). Results are given in Figure 9. These profiles also showed more similarity between S1-2004 and *S. California* than between S1-2004 and *S. Banana*. This latter strain was used in the typing study of 2005 (S5-2005).

In the 2005 study, the *S. Banana* strain (S5-2005) caused less problems. Still 5 NRLs (of the 26) had problems with correctly typing the H-antigens and/or giving the correct serovar name. Three of these NRLs typed this strain (again) as *S. California*. None of the ENLs had problems with the typing of *S. Banana*.



1. Standard
2. *S. California* (S-645 : Canada)
3. *S. Banana* (S-764 : CDC)
4. *S. California* (S-908 : CDC)
5. *S. California* (S-1415 : ATCC 23201)
6. Standard
7. *S. California* (S-1416 : Institut Pasteur)
8. *S. Istanbul* (S-1628)
9. S1-2004
10. Standard

Figure 8 *Pulsed Field Gel Electrophoresis profiles of several *S. California* and *S. Banana* strains, as well as of strain S1 from typing study 2004 (S1-2004), performed by ENL-Canada*

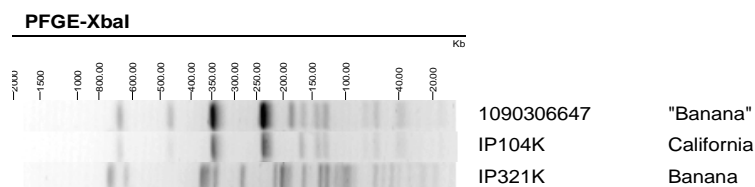


Figure 9 *PFGE profiles of S1-2004 ("Banana"), *S. California* and *S. Banana* (S5-2005), performed by CRL-Salmonella*

From the study of 2004 it became clear that many problems could be attributed to unfamiliarity with the separate parts of polyvalent antisera, non-specific reactions of monovalent antisera (e.g. g-antisera) and the discriminating capacity of mixed antisera (e.g. H: g,m antiserum versus H: g,p antiserum). Some NRLs used a polyvalent H: G-serum, but this antiserum is not always discriminative between g,m and m,t (or g,m,t) strains. Examples of serovars which can not be distinguished if polyvalent antisera for the detection of H-antigens are used can be found in Table 21. Another important aspect with the use of antisera is the fact that the prescriptions of the manufacturer should be followed strictly. For instance, if a laboratory uses antisera of different manufacturers, the prescriptions can easily become mixed-up. This may (for instance) result in the fact that for a certain antiserum a shaking time of one minute is used, while a maximum of 10 seconds is prescribed. This may affect the results. Examples of differences in prescriptions of 4 manufacturers are given in Table 22.

Table 21 Serotypes which can not be distinguished if polyvalent antisera for detecting the H-antigens are used

Serovar	O - antigens	H - antigens
<i>S. Banana</i>	<u>1</u> , 4, 5, <u>12</u>	m, t : [1, 5]
<i>S. California</i>	4, 12	g, m, t : -
<i>S. Othmarschen</i>	6, 7, <u>14</u>	g, m, [t] : -
<i>S. Oranienburg</i>	6, 7, <u>14</u>	m, t : [z ₅₇]
<i>S. Cannstatt</i>	1, 3, 19	m, t : -
<i>S. Kouka</i>	1, 3, 19	g, m, [t] : -

Table 22 Prescriptions of 4 different manufacturers for handling their antisera

	Manufacturer of antisera			
	SIFIN	SSI	Bio-rad	Prolab
Suspension of antiserum and bacteria	One drop of antiserum with some bacterial mass	Apply a small drop (20 µl) with bacterial mass	Deposit one drop of antiserum and take one loop of culture	Loopfull normal saline solution, suspend small part of colony and one loopfull of antiserum
Time of shaking	1-20 shakes > 20 shakes : negative reaction	5 – 10 seconds	Maximum of one minute	Maximum of one minute
Reading of the reaction	Naked eye against indirect illumination	Naked eye against indirect illumination	Naked eye over a dark surface or over a concave mirror	Normal lighting conditions, preferably using a low power objective

In 2005, the CRL-*Salmonella* performed some extra tests with antisera of four different manufacturers to test whether these antisera could make distinctions between *Salmonella* strains containing H-antigens m,t or g,m,t. The results are summarised in Table 23. The results in this table show unexpected (a-typical) results with the antisera of Prolab for both *S. Banana* strains and for *S. Cannstatt*. The results found with the antisera of the other 3 manufacturers showed no serological differences between both *S. Banana* strains (S1-2004 and S5-2005). Unfortunately, no distinction could be made between the *S. Banana* strains and the *S. California* isolate because of the weak g factor in the *S. California*. However, CRL-*Salmonella* did not have the availability of another *S. California* strain at that time.

Summarising the results: *S. Banana* S1-2004 and *S. Banana* S5-2005 are serological alike, but genotypical different.

Table 23 *Testing of g,p-antisera and G-antisera of different manufacturers*

<i>Salmonella</i> strains	Results with antisera			
	SIFIN H-G antiserum Art.nr: TR 1406 Lot: 1681103	SSI H-g,p antiserum Art.nr: 40302 Lot: 732A	Bio-rad H-g,p antiserum Art.nr: 61122 Lot: 4G2021	Prolab H-g,p antiserum Art.nr: PL 6123 Lot: 687
<i>S. Dublin</i> (KH 29)	++++	++++	++++	++++
<i>S. Montevideo</i> (S 1090501902) field isolate	++++	++++	++++	++++
<i>S. Enteritidis</i> (S 1090300295) field isolate	++++	++++	++++	++++
<i>S. Banana</i> (S 1090306647) S1-2004	0	0	0	++
<i>S. Banana</i> (IP 321 K) S5-2005	0	0	0	++++
<i>S. California</i> (IP 104 K) 4,5,12:(g),m,t:-	0	0	0	++
<i>S. Oranienburg</i> (S 1090404839) Study 2005	0	0	0	0
<i>S. Cannstatt</i> (S 1090200464) Study 2003	0	0	0	+

More +: stronger reaction; 0: no reaction

5.4 Results phage typing

5.4.1 Results phage typing by the NRLs-*Salmonella*

The phage typing results of the NRLs were evaluated per strain and by laboratory and are shown in Tables 24 and 25. Seven laboratories performed phage typing for *Salmonella* Enteritidis. Five laboratories (labcode 6, 9, 17, 22 and 26) assigned the correct phage type for all ten of the *S. Enteritidis* (SE) strains (PT 8, 1b, 4, 13a, 1, 22, 5a, 14b, 44 and 6) and two laboratories (labcode 5 and 19) had only one incorrect result. Labcode 5 incorrectly identified strain E10, (PT6) and lab code 19 misidentified strain E1 (PT8). Six NRLs performed *Salmonella* Typhimurium phage typing and four laboratories (labcode 5, 9, 17 and 22) correctly phage typed all ten strains. (PT 15, 36, U291, U310, 12, 193, 104, 10, 15a and 110). Two laboratories (labcode 6 and 26) assigned correct phage types to nine of the strains but both incorrectly identified strain M1 (PT15). Three laboratories (labcode 9, 17, and 22) correctly identified the ten SE strains and the ten STM strains. Separate notations per phage and per laboratory are given in Annex 3. The achievements in percentage correctness are presented in Figure 10.

Table 24 Results of *Salmonella* Enteritidis phage typing by the NRLs

Strain	PT	Phage type of each laboratory						
		5	6	9	17	19	22	26
E1	8	8	8	8	8	28	8	8
E2	1b	1b	1b	1b	1b	1b	1b	1b
E3	4	4	4	4	4	4	4	4
E4	13a	13a	13a	13a	13a	13a	13a	13a
E5	1	1	1	1	1	1	1	1
E6	22	22	22	22	22	22	22	22
E7	5a	5a	5a	5a	5a	5a	5a	5a
E8	14b	14b	14b	14b	14b	14b	14b	14b
E9	44	44	44	44	44	44	44	44
E10	6	5c	6	6	6	6	6	6

PT = Phage type; RDNC = Strains reacting with the typing phages but not conform to any of the current recognised patterns; grey cells = deviating results

Table 25 Results of *Salmonella Typhimurium* phage typing by the NRLs

Strain	PT	Phage type of each laboratory						
		5	6	9	17	19	22	26
M11	15	15	18	15	15	Nt	15	104H
M12	36	36	36	36	36	Nt	36	36
M13	U291	U291	U291	U291	U291	Nt	U291	U291
M14	U310	U310	U310	U310	U310	Nt	U310	U310
M15	12	12	12	12	12	Nt	12	12
M16	193	193	193	193	193	Nt	193	193
M17	104	104	104	104	104	Nt	104	104
M18	10	10	10	10	10	Nt	10	10
M19	15a	15a	15a	15a	15a	Nt	15a	15a
M20	110	110	110	110	110	Nt	110	110

PT = Phage Type; NT = Not Tested

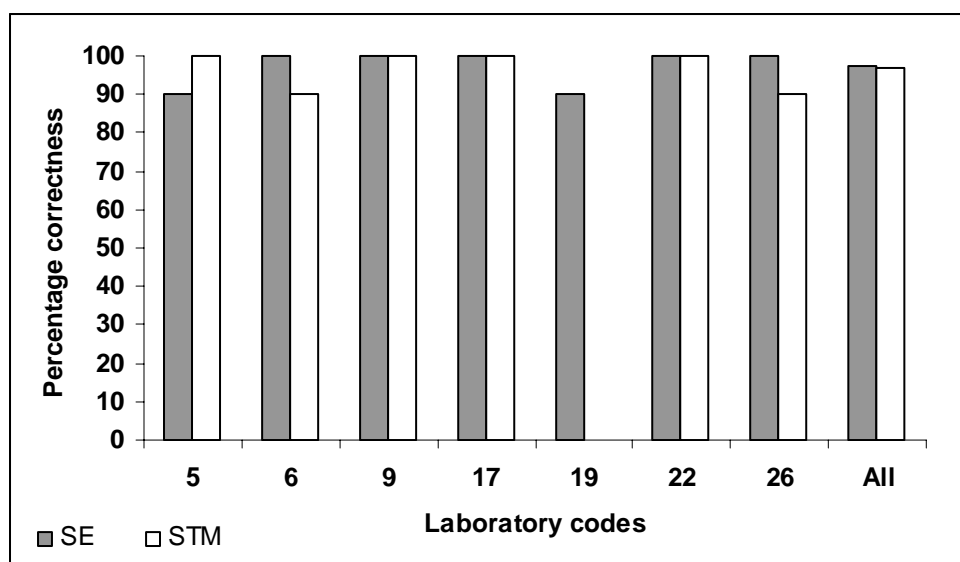


Figure 10 Achievements in percentages that were correct for the NRLs

5.4.2 Results phage typing by the ENLs

The phage-typing results of the ENLs are summarised in Tables 26 and 27. Ten laboratories performed *S. Enteritidis* phage typing. Four laboratories (labcode A, C, E and G) correctly phage typed all ten *S. Enteritidis* strains. Five laboratories (labcode B, D, L, M and P) had one incorrect result and one laboratory (labcode H) misidentified two of the SE strains. Nine ENLs performed *S. Typhimurium* phage typing. Four ENLs (labcode E, G, M and P) assigned correct phage types to all ten STM strains (PT 15, 36, U291, U310, 12, 193, 104 10 15a and 110). Three laboratories correctly phage typed nine of the STM strains and incorrectly identified strain M14, PTU310. One laboratory (labcode A) incorrectly identified two strains (M18 and M19) and one laboratory (labcode B) incorrectly identified three strains (M13, M15 and M16). Two laboratories (labcode E and G) identified all ten SE strains and all ten STM strains correctly. Separate notations per phage and per laboratory are given in Annex 3. The achievements in percentage correctness are presented in Figure 11.

Table 26 Results of *Salmonella Enteritidis* phage typing by the ENLs

Strain	PT	Phage type of each laboratory									
		A	B	C	D	E	G	H	L	M	P
E1	8	8	8	8	8	8	8	8	8	8	8
E2	1b	1b	1b	1b	1b	1b	1b	1b	1b	1b	1b
E3	4	4	4b	4	4	4	4	4	4	4	4
E4	13a	13a	13a	13a	13a	13a	13a	13a	28	13a	13a
E5	1	1	1	1	1	1	1	1	1	1	1
E6	22	22	22	22	22	22	22	22	22	22	22
E7	5a	5a	5a	5a	6b	5a	5a	6b	5a	6b	5a
E8	14b	14b	14b	14b	14b	14b	14b	14b	14b	14b	14b
E9	44	44	44	44	44	44	44	37	44	44	37
E10	6	6	6	6	6	6	6	6	6	6	6

PT = Phage type; RDNC = Strains reacting with the typing phages but not conform to any of the current recognised patterns; grey cells = deviating results

Table 27 Results of Salmonella Typhimurium phage typing by the ENLs

Strain	PT	Phage type of each laboratory									
		A	B	C	D	E	G	H	L	M	P
M11	15	15	15	15	Nt	15	15	15	15	15	15
M12	36	36	36	36	Nt	36	36	36	36	36	36
M13	U291	291	142	291	Nt	291	291	291	291	291	291
M14	U310	310	310	302	Nt	310	310	302	302	310	310
M15	12	12	109	12	Nt	12	12	12	12	12	12
M16	193	193	195	193	Nt	193	193	193	193	193	193
M17	104	104	104	104	Nt	104	104	104	104	104	104
M18	10	67	10	10	Nt	10	10	10	10	10	10
M19	15a	289	15a	15a	Nt	15a	15a	15a	15a	15a	15a
M20	110	110	110	110	Nt	110	110	110	110	110	110

*** = Untypable; PT = Phage type; grey cells = deviating results

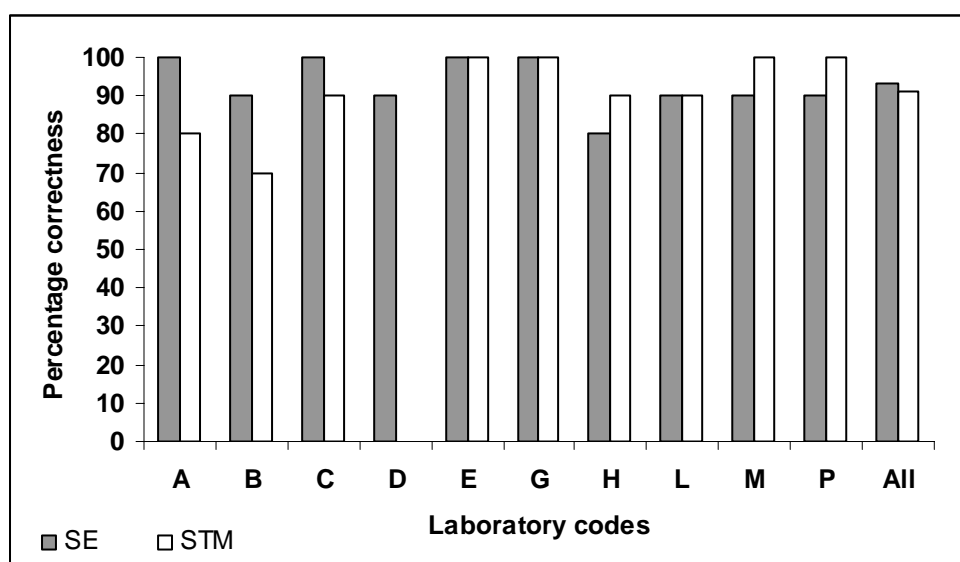


Figure 11 Achievements in percentages that were correct for the ENLs

5.5 Antimicrobial susceptibility testing

5.5.1 Results per antibiotic by NRLs and ENLs

Twenty-five NRLs and twelve ENLs tested the AST strains for susceptibility. The number of ENLs and NRLs that determined MICs with broth microdilution, Etest or disc diffusion, varied for each antibiotic and the results of all laboratories are shown in the tables of Annex 4. For those laboratories that determined MICs, the concentration is given in µg/ml. For the laboratories that used disc diffusion, the zone diameters are given in mm's. In this Annex 4, for each AST strain the mean zone diameter, the standard deviation (SD) and 2SD level in mm's are also given. Because for disc diffusion the same method is used by all participants it is possible to analyse the data quantitatively for systematic differences. If for a specific AST strain/antibiotic combination the zone diameter of a laboratory is within the 2SD range ($\text{mean} \pm 2\text{SD} \approx 95\%$ confidence interval), the result is with 95 % certainty not different from the results of the other laboratories. Optimally all results should vary around the mean within the 2SD ranges. If one laboratory systematically scores higher or lower than the mean or scores outside the 2SD ranges, it indicates as systematic difference in the method used.

For the MIC results this type of analysis is much more difficult because more variation in methods used and concentration ranges tested exist.

In Annex 5 and 6, the number of errors is displayed for each AST strain.

Amoxicillin/clavulanic acid

As stated in chapter 3.3, for the interpretation of the results, the strains AST1, 3, 7-10 were classified S (susceptible) for amoxicillin/clavulanic acid (AMC). Therefore all results produced by the participants for these strains that were classified I, were also interpreted as S. The direct reason is that these strains produced a β -lactamase that is susceptible to clavulanic acid, but because of the limitations of the *in vitro* methodologies to test this combination, the MICs are slightly increased or the inhibition zone diameters slightly decreased. Because it is the goal of the CRL to harmonise susceptibility test results for resistance monitoring or surveillance purposes, the CRL advises not to use the S breakpoint or interpretive criterium for AMC and solely use the R breakpoint.

If the results are analysed in this way, still 16 major errors were made and 1 minor error. All major errors were the result of the above mentioned analytical problem and were produced both with quantitative or qualitative test methods. This means that using AMC for surveillance purposes would lead to an overestimation of AMC resistant strains. Real AMC resistant strains (like AST-5) produce β -lactamases resistant to clavulanate. These β -lactamases are typical of *AmpC* (e.g. *CMY-2*), but can incidentally also be observed in other Extended Spectrum Beta Lactamases. These β -lactamases are often plasmid mediated and are considered a public health threat. This phenotype can also be the result of derepression of the promoter of the

chromosomally present *AmpC*-gene by mutation in the promoter. AST-5 harbours the *CMY-2* gene on a plasmid, which explains the typical phenotype.

Finally, the zone diameters of NRL 1 were systematically smaller than the mean, indicating systematic differences.

Ampicillin/amoxicillin

Because of 100 % cross-resistance, the results of this ring trial predict the accuracy of both ampicillin and amoxicillin. Only 1 major and 5 minor deviating results were produced for this antibiotic. NRL 24 accidentally classified AST-4 as R (MIC > 64 µg/ml) in stead of S. NRL 5 classified AST-4 and 6 I in stead of S, although based on CLSI criteria they should have been classified S. NRL 15 classified ASTs 7, 8 and 9 I in stead of R.

The zone diameters of NRL 5 were systematically larger than the mean, indicating systematic differences, resulting in two minor errors.

Cefotaxime

For this ring trial only one cefotaxime resistant strain was included in the panel: *CMY-2* positive *S. Infantis* (AST-5). No deviating results were produced on the susceptible strains. AST-5 was classified I in stead of R by four NRLs. These NRLs accurately used the standard CLSI criteria for cefotaxime, except NRL 24 that classified AST-5 I based on MIC 32 µg/ml, which should have been R. However, for ESBL detection, CLSI advises the use of a low breakpoint ($R \geq 2 \mu\text{g/ml}$ or $R \leq 27 \text{ mm}$). Cefotaxime is included in the panel as indicator of presence of ESBLs; therefore the low breakpoints should preferably be used for the interpretation of the MICs. If these breakpoints would have been used, no deviating results would have been produced.

The 95 % interval of the zone diameters was quite wide (*circa* 12 mm), indicating a wide variation in the results of the participating laboratories. The zone diameters of NRL 5, 6, 17 and ENL C were systematically larger than the mean, indicating systematic differences. Incidentally results were outside the 95 % confidence interval. The zone diameters of NRLs 11, 13, 16 and 18 were systematically smaller than the mean.

Chloramphenicol

For chloramphenicol for all AST-strains except AST-2 no deviating results were produced. AST-2 repeatedly showed slightly reduced susceptibility in the broth microdilution test and consequently the strain was classified by CIDC as I using the CLSI breakpoints.

The MIC distribution of all *Salmonella* strains tested in the Netherlands for susceptibility with broth micro dilution to chloramphenicol from 1999 – 2003 (n = 7954) was as shown in Figure 12.

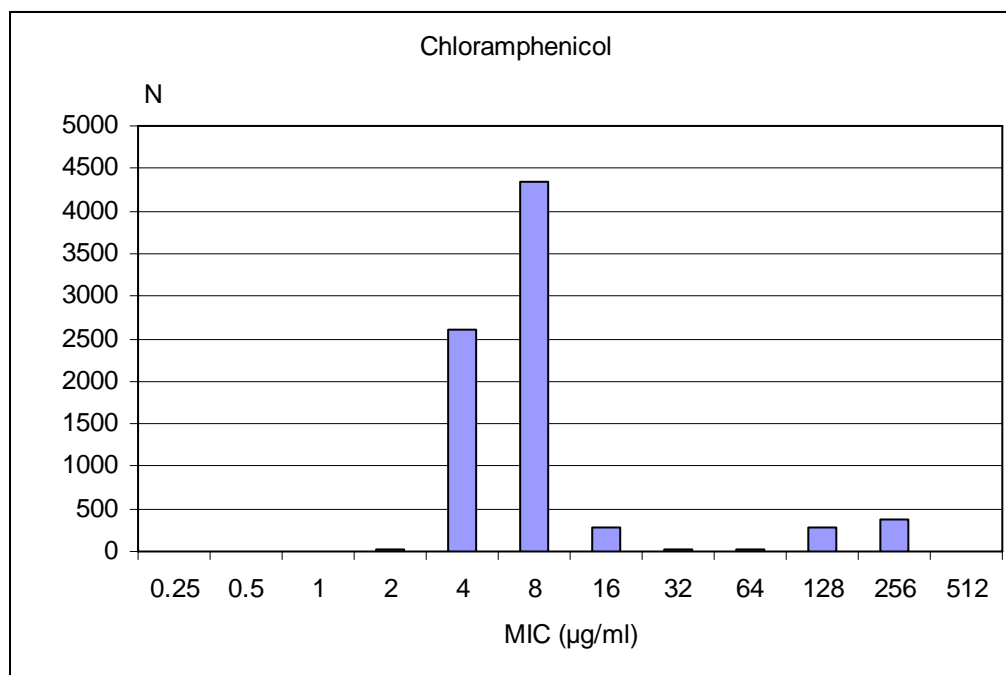


Figure 12 The MIC distribution of all Salmonella strains tested in the Netherlands for susceptibility with broth micro dilution to chloramphenicol from 1999 – 2003 (n = 7945)

Figure 12 demonstrates that strains with MIC 16 µg/ml are part of the wild type population and do not harbour any acquired resistance gene. It can be concluded that the CLSI S breakpoint for chloramphenicol ≤ 8 µg/ml is not 100 % adequate to distinguish the susceptible population. The raw data indicate that all participating laboratories adequately performed the susceptibility test of AST-2 and the deviations that were recorded based on the CLSI criteria will not be included in the summary of the results.

The zone diameters of ENLs D and L were systematically larger than the mean, indicating systematic differences. Incidentally results were outside the 95 % confidence interval. The zone diameters of NRL 1 and ENL H were systematically smaller than the mean.

Ciprofloxacin

No deviating results were produced for the susceptible, wild type strains AST-1, 2, 3, 5 and 10. One minor error was made on the highly resistant *S. Kentucky* (AST-9) by NRL 7 and one by NRL 1 on AST-8. The deviating results produced by NRL 23 and ENL J on the reduced susceptible strains AST-4, 6, 7, and 8 were obviously caused by the use of a lower R breakpoint ($R \geq 0.25$ µg/ml) and were therefore not due to errors made.

The zone diameters of NRLs 5, 15 and ENLs C, D and L were systematically larger than the mean indicating systematic differences. Incidentally results were outside the 95% confidence interval. The zone diameters of NRLs 1, 3, 4, 11 and ENL F were systematically smaller than the mean. For NRL-1 this resulted in a deviating result for AST-8.

Florfenicol

For florfenicol no deviating results were produced.

The zone diameters of NRLs 16 were systematically smaller than the mean.

Gentamicin

For gentamicin NRL-7 produced deviating results for the susceptible strains. Obviously NRL-7 did not use CLSI interpretive criteria. AST-9 demonstrated a different resistance phenotype than strains AST-7 and 8. Its MIC 16 µg/ml is just above the MIC breakpoint, therefore it was expected that a number of minor errors were made.

The zone diameters of NRLs 6, 15 and ENL C were systematically larger than the mean, indicating systematic differences. Incidentally results were outside the 95 % confidence interval. The zone diameters of NRLs 7, 25 and ENL F were systematically smaller than the mean. Incidentally results were outside the 95 % confidence interval.

Kanamycin

Kanamycin is a somewhat difficult antibiotic to include in ring trials because the CLSI criteria are very wide. The CLSI R breakpoint for MICs is ≥ 64 µg/ml and the R criterium for disc diffusion ≤ 13 mm (equals ≤ 25 µg/ml), which may lead to differences in interpretation between laboratories that determine MICs and those that use disc diffusion.

The wild type population's susceptibility is ≤ 4 µg/ml for *Salmonella* (not yet publically available information at the EUCAST website), although the wild type distribution is not defined yet. This means that the CLSI breakpoints are truly clinical breakpoints and not related to the susceptibility distribution of *Salmonella*'s.

Still for the highly resistant strains AST-2, 8 and 9 and all susceptible AST strains, only 3 minor errors were produced by one NRL (21). For AST-7 many deviating results were produced by disc diffusion. Obviously disc diffusion resulted in more variation in the zone diameters and the classification than MIC determinations for this strain.

The zone diameters of NRLs 15, 17 and 21 were systematically larger than the mean, indicating systematic differences. Results of NRL 21 were systematically outside the 95 % confidence interval, resulting in three minor errors. The zone diameters of ENL F were systematically smaller than the mean.

Nalidixic acid

For nalidixic acid the highly resistant strains AST 6 – 9, and the highly susceptible AST 1, 3, 5 (1 minor error) and 10 caused no problems for the participants. Strains AST 2 and 4 repeatedly showed a slightly reduced susceptibility but still below the breakpoint, caused more variation in the results. Disc diffusion and its interpretive criteria did not adequately distinguish between the categories S, I and R. AST-4 is a *S. Corvallis* with an atypical phenotype. Reduced susceptible to ciprofloxacin (MIC 0.5 µg/ml) and susceptible to nalidixic acid (MIC 16 µg/ml), a phenotype occasionally observed for *S. Corvallis* and other serovars by CIDC. The genetic background is still unknown. All laboratories that determined MICs classified this AST strain correctly, while with disc diffusion 15 minor and 4 major deviating

results were produced. Similarly 10 minor deviations were produced for AST-2 with disc diffusion.

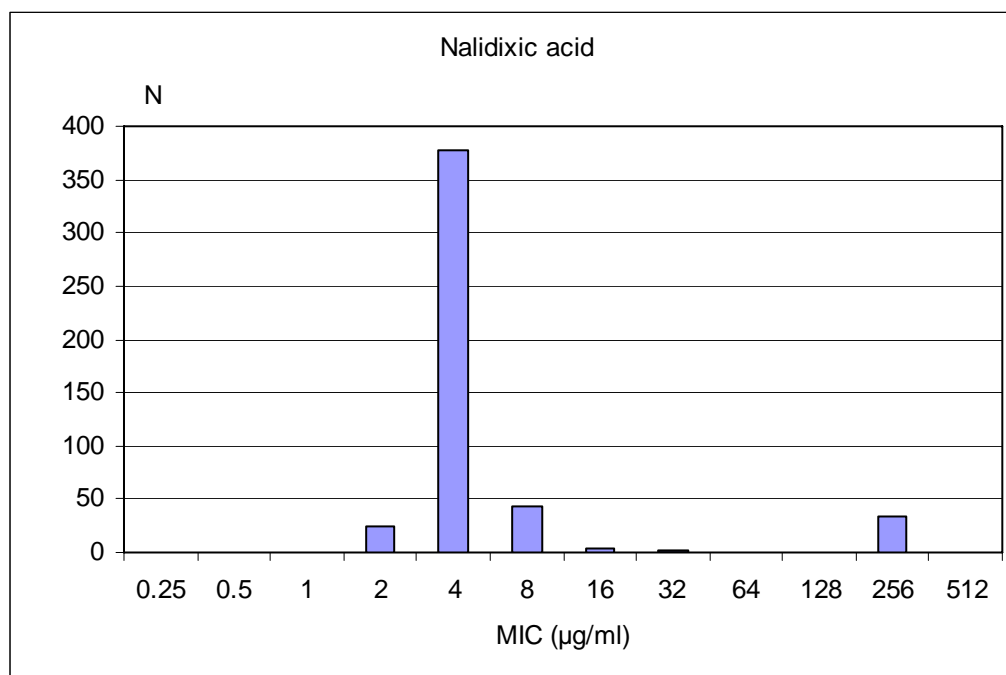


Figure 13 Susceptibility of *Salmonella* strains for nalidixic acid

For nalidixic acid no intermediate population exists. Strains are either wild type (MIC 2 – 16 µg/ml) or highly resistant (MIC ≥ 256 µg/ml, see Figure 13). This means that the interpretive criteria for disc diffusion are not adequate.

The zone diameters of NRLs 5, 12, 15, 17 and 21 were systematically larger than the mean, indicating systematic differences. The zone diameters of NRLs 3, 6, 16 and ENL F were systematically smaller than the mean. Incidentally results were outside the 95 % confidence interval.

Neomycin

Neomycin is also a problematic antibiotic in ring trials because no CLSI criteria exist.

However, the AST strains were all classified similar as done by CIDC. Except NRL 7 that produced 4 minor deviations. The results show that different interpretive criteria for disc diffusion were used.

The zone diameters of NRLs 6 and ENL A were systematically larger than the mean, indicating systematic differences. The zone diameters of NRLs 7, 11, 14 and ENL F were systematically smaller than the mean. Incidentally results were outside the 95 % confidence interval.

Streptomycin

In previous ring trials for streptomycin a lot of variation in results was seen, specifically for the 'susceptible' isolates. It was advised that only an R breakpoint of ≥ 32 µg/ml should be

used. CIDC determined the reference MICs with broth microdilution. Three borderline strains (AST-2, 5 and 8) were difficult to classify. For confirmation an Etest was performed; the results were 6 µg/ml for AST-2, 4 µg/ml for AST-5 and 12 µg/ml for AST-8. Therefore all three strains were classified S by CIDC. Again a wide variation in results was observed for these three strains. The highly resistant strains were all classified correct by all laboratories. Like what was done in previous years, streptomycin will not be included in the overall analysis of the accuracy of the laboratories.

The zone diameters of NRLs 2, 5, 21 and ENL L were systematically larger than the mean, indicating systematic differences. The zone diameters of NRLs 11 and ENL F were systematically smaller than the mean.

Sulphamethoxazole + trimethoprim

In spite of the fact that sulphonamides and trimethoprim are difficult antibiotics in susceptibility tests because of the presence of antagonists in the broth or agar, for all three antibiotics very little deviating results were produced. The results show the importance for resistance surveillance purposes of testing the individual substances. Strains will only be resistant to the combination if they are resistant to both individual substances.

ENL B correctly classified AST 10 S, although based on CLSI breakpoints they should have classified this strain R. ENL E produced an MIC slightly outside the QC range for *E. coli* 25922. On AST-4 two minor errors were made with disc diffusion.

The zone diameters of NRLs 5 and 15 were systematically larger than the mean, indicating systematic differences. Incidentally results were outside the 95 % confidence interval. The zone diameters of NRL 16 and ENLs F and H were systematically smaller than the mean.

Sulphonamides

This is the only antibiotic for which the disc loads and the specific sulphonamide to be tested is not fully standardised. CLSI prescribes criteria for sulfisoxazole, but includes that other sulphonamides may be used as well. A disc load 250 – 300 µg is advised. Also by the participating laboratories a variation in disc loads were used, the results, however, were very good. Only a few errors were made, none by MIC determinations. NRL 3 systematically produced smaller inhibition zones and classified AST 1 and 6 as R. NRL 11 produced a major error on AST-7 and NRL 13 a minor error on AST-5.

Since the disc loads were not identical it is not possible to compare the diameters of the zones of inhibition between the participants.

Trimethoprim

Traditionally, trimethoprim causes little or no confusion when *Salmonella*'s are tested for susceptibility. Not deviating results were produced.

The zone diameters of NRLs 15 and 17 and ENLs A and D were systematically larger than the mean, indicating systematic differences. Incidentally results were outside the 95 % confidence interval. The zone diameters of NRLs 11 and 16 and ENLs F and H were systematically smaller than the mean.

5.5.2 Results MIC testing by NRLs

The quality of the categorisation results of the NRLs based on MICs was very good. Three truly deviating results were produced by one NRL. The results are summarised in Table 28.

A summary can also be found in Figure 14.

Table 28 Totals, minor and major errors and percentages based on MIC testing by NRLs for all strains and all antibiotics except streptomycin, chloramphenicol (AST-2) and amox/clavulanic acid (intermediate category)

Lab code	Total tests per lab	Minor error	Major error
8	90	0	0
11	70	0	0
19	100	0	0
20	120	0	0
22	120	0	0
23	110	0	3* (2.7 %)
24	120	1 (0.8 %)	2 (1.6 %)
26	130	0	0
For all NRLs	860	1 (0.1 %)	5 (0.6)

* Low R breakpoint used.

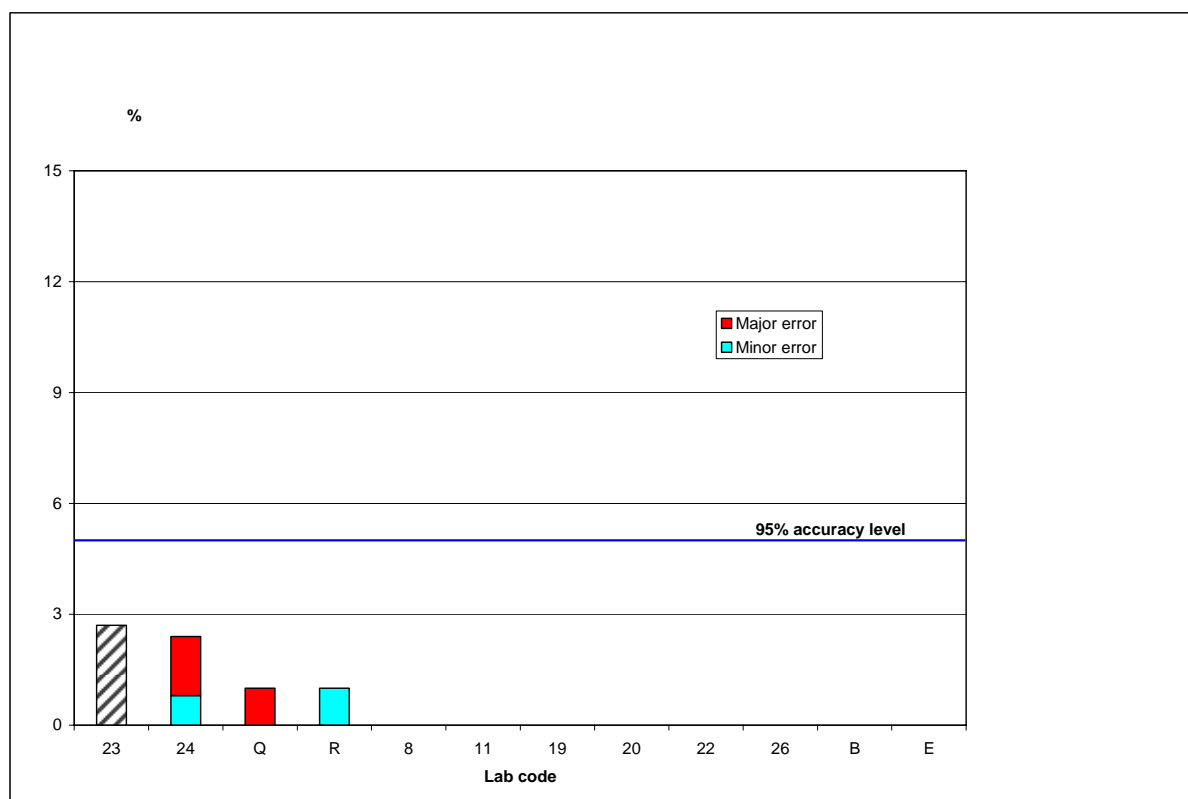
5.5.3 Results MIC testing by ENLs

The quality of the categorisation results of the ENLs based on MICs was also very good.

Results are summarised in Table 29 and Figure 14.

Table 29 Totals, minor and major errors and percentages of results of MIC Testing by ENLs for all strains and all antibiotics except streptomycin, chloramphenicol (AST-2) and amox/clavulanic acid (intermediate category)

Lab code	Total tests per lab	Minor error	Major error
B	110	0	2 (1.8 %)
E	90	0	0
Q	100	0	1 (1 %)
R	100	1 (1 %)	0
For all ENLs	400	1 (0.25 %)	3 (0.75 %)



* NRL 23 used a low breakpoint for ciprofloxacin

Figure 14 Percentages of minor and major errors made by NRLs and ENLs that determined MICs, except streptomycin, chloramphenicol (AST-2) and amox/clavulanic acid (intermediate category).

5.5.4 Results disc diffusion tests by NRLs

As was observed in 2003 and 2004 the number of deviations in the results of the NRLs that used the disc diffusion test is larger than those obtained with MIC-determinations. The interpretive criteria used to discriminate between S, I and R are derived from breakpoint MICs by regression analysis. The predictive value of these criteria varies from antibiotic to antibiotic and from bacterial species to bacterial species. Keeping that in mind, the results are of high quality. The majority of the errors were made with kanamycin and nalidixic acid on strains with 'borderline' susceptibility. For these strains the NCCLS criteria are not adequate. The percentage of minor errors varied from 0 – 11 %, the percentage of major errors varied from 0 – 3.8 %. Results are summarised in Table 30 and Figure 15

Table 30 Totals, minor and major errors and percentages of results of disc diffusion testing by NRLs for all strains and all antibiotics except streptomycin, chloramphenicol (AST-2) and amox/clavulanic acid (intermediate category)

Lab code	Total tests per lab	Minor error	Major error
1	110	3 (2.7 %)	3 (2.7 %)
2	100	4 (4 %)	0
3	130	3 (2.3 %)	5 (3.8 %)
4	120	1 (0.8 %)	0
5	90	2 (2.2 %)	0
6	130	2 (1.5 %)	2 (1.5 %)
7	100	11 (11 %)	2 (2 %)
9	60	0	0
11	140	1 (0.7 %)	2 (1.4 %)
12	120	0	1 (0.8 %)
13	130	4 (3.1 %)	0
14	140	1 (0.7 %)	1 (0.7 %)
15	140	4 (2.8 %)	1 (0.7 %)
16	120	3 (2.4 %)	0
17	110	3 (2.7 %)	0
18	120	2 (1.6 %)	1 (0.8 %)
21	130	3 (2.3 %)	1 (0.8 %)
25	110	0	1 (0.9 %)
ALL NRLs	2100	47 (2.2 %)	20 (0.9 %)

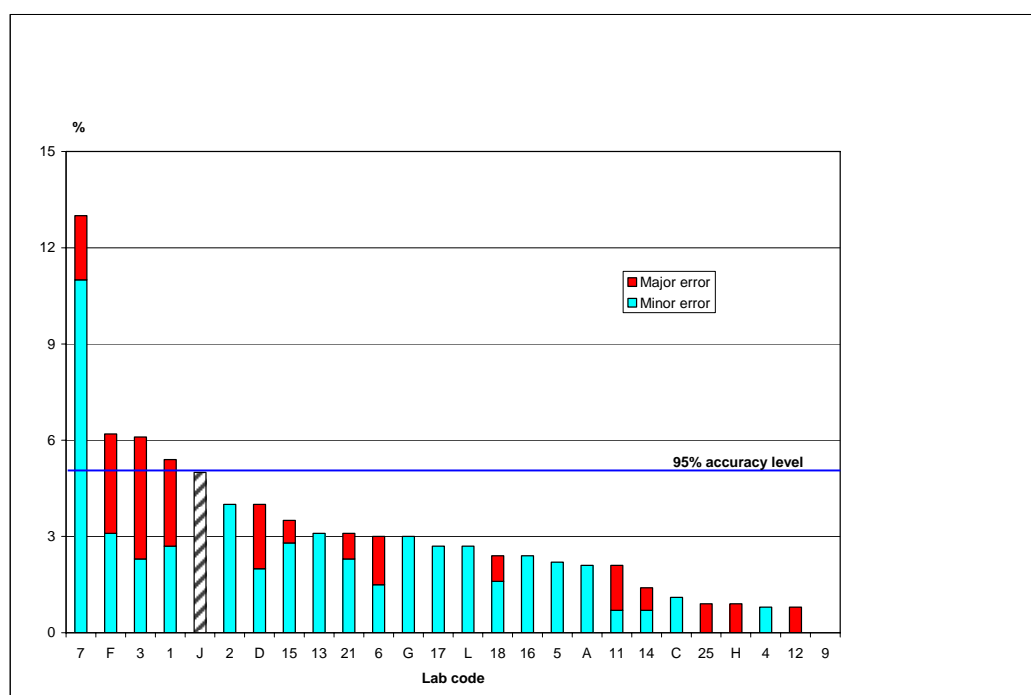
5.5.5 Results disc diffusion tests by ENLs

For the ENLs, the percentage of minor errors varied from 0 – 3.1 %, the percentage of major errors varied from 0 – 5 % (see Table 31 and Figure 15).

Table 31 Totals, minor and major errors and percentages of results of disc diffusion testing by ENLs for all strains and all antibiotics except streptomycin, chloramphenicol (AST-2) and amox/clavulanic acid (intermediate category)

Lab code	Total tests per lab	Minor error	Major error
A	140	3 (2.1 %)	0
C	90	1 (1.1 %)	0
D	100	2 (2 %)	2 (2 %)
F	130	4 (3.1 %)	4 (3.1 %)
G	100	3 (3 %)	0
H	110	0	1 (0.9 %)
J	120	0	6* (5 %)
L	110	3 (2.7 %)	0
For all ENLs	900	16 (1.8 %)	13 (1.4 %)

* 4 major deviations were the result of the use of a low R breakpoint



*ENL J used a low breakpoint for ciprofloxacin

Figure 15 Percentages of minor and major errors made by NRLs and ENLs that determined zone diameters (except streptomycin, chloramphenicol (AST-2) and amox/clavulanic acid (intermediate category))

6. Discussion

Serotyping

Like in the earlier typing studies, the serotyping of the O-antigens did not cause much problems. The problems that existed, were mainly caused by the detection of the H-antigens. In the 2004 study strain S1, known at CRL-*Salmonella* as *S. Banana* caused a number of problems. Almost half of the number of NRLs and ENLs serotyped the strain differently. In many cases the strain was typed as *S. California*. It was therefore decided to include again an *S. Banana* strain in the 2005 study (S5). This *S. Banana* strain was obtained from the culture collection in France and was not the same isolate as the one used in the study of 2004. The *S. Banana* strain of 2005 still caused some problems in 5 NRLs, although less pronounced than with the *S. Banana* isolate of 2004. None of the ENL laboratories had problems with serotyping this strain.

Another strain in this study which caused problems was strain S2, which was typed by CRL-*Salmonella* as *S. Oranienburg*. Nine NRLs (but none of the ENLs) faced problems with this strain. Four of those NRLs typed S2 as *S. Oakey*. The majority of the problems with typings S-2 were caused by the fact that these NRLs were not able to (correctly) identify the second phase of the H-antigens.

Three of the NRLs also faced problems with strain S12 (*S. Matadi*). This might have been due to the fact that the NRLs did not possess O:17 antisera or possess discriminative polyvalent antisera.

Finally 8 ENLs had problems with S19 (*S. Virchow*). In the process of culturing, some subcultures of this strain may have become, non-motile, causing the main problems in these ENLs.

For the calculations of the percentages correctness, the results of strain S19 were excluded for all ENLs. This resulted in the fact that 100 % of the ENLs and 99 % of the NRLs were able to correctly type the O-antigens. The H-antigens were typed correctly by 97 % of the NRLs and by 99 % of the ENLs. Correct serovar names were given by 94 % of the NRLs and by 99 % of the ENLs. These results show an improvement to the results of 2004. Although the ENLs still score somewhat better than the NRLs, the differences are becoming smaller.

Phage typing

The strains of *S. Enteritidis* and *S. Typhimurium* for this study were selected from the culture collection of the National Salmonella Reference Laboratory in England and Wales. Strains were chosen based on their occurrence in outbreaks and incidents in the European Union and from worldwide travel in 2004. The *S. Enteritidis* strain that gave most problems was SE PT5a where three ENLs incorrectly identified it as PT6b. However two of the laboratories

had the correct phage readings for PT5a only gave the wrong phagetype. All of the NRLs correctly identified the strain of PT5a. Two ENLs had a problem with SE PT44 identifying it as PT37. Both laboratories had a negative reading with phage type 2 and it is possible that the phage titre was low as all the NRLs and remaining ENLs correctly identified this strain as PT44.

S. Enteritidis PT44 has been linked to travel to the Canary Islands since it was first recognised. *S. Enteritidis* PT22 was included for the first time in this study following an increase in human isolates of this type in England and Wales during 2004, compared with one isolate of PT22 in 2003, from a patient who had travelled to Spain.

The phage typing of *S. Typhimurium* continues to be encouraging with four NRLs and four ENLs identifying all the strains correctly. *S. Typhimurium* PT U310 was misidentified by three ENLs where an extra phage reading was obtained. It is possible that the titre of this phage may have been too strong. All the NRLs identified this strain correctly.

S. Typhimurium PT U310 has an association with pigs and pig products in the UK.

Overall the results were good with all the NRLs and the majority of ENLs obtaining at least 90 % correct results. The NRL results were excellent with 97 % correct typing for both *S. Enteritidis* and *S. Typhimurium*, compared to 83 % for *S. Enteritidis* and 91 % for *S. Typhimurium* achieved by the ENLs.

Antimicrobial susceptibility testing

In this study the susceptibility of 10 AST strains was tested to a panel of fourteen antibiotics. Laboratories were free to choose their method: the determination of MICs by dilution methods or Etest or zone diameters by disc diffusion. Therefore the results in this report are classified according to these methods. The results of the Etest are included with those obtained with dilution methods.

The overall number of deviating results was substantially less than in 2004. The majority of the deviating results were produced on amoxicillin/clavulanic acid, this despite of the fact that all I classifications for AST-1, 3, 7 – 9 were disregarded in the results, kanamycin (AST-7 by disc diffusion) and nalidixic acid (AST-2 and 4 by disc diffusion). Streptomycin again proved to be a difficult antibiotic to test correctly. Although for this antibiotic highly resistant strains were all classified without deviations, susceptible strains showed a wide variation in level of susceptibility and were often wrongly classified as R. For correct classification of cefotaxime, a very important antibiotic used as indicator for presence of ESBLs, low CLSI breakpoints should be used.

Amoxicillin/clavulanic acid should not be included in test panels for resistance surveillance purposes. It will lead to an overestimation of the presence inhibitor-resistant β -lactamases. The presence of ESBLs should preferably be tested by two cephalosporins (cefotaxime and ceftazidime), using low CLSI breakpoints. For an attempt to further characterize the ESBL-phenotype, all ESBL-suspected isolates should subsequently be tested for synergy with

clavulanic acid by Etest or double-disc test. Moreover susceptibility testing to cefoxitin will provide information on the *AmpC*-phenotype, a.o. typical of *CMY-2* gene in the virulent *S. Newport* in the US.

Trimethoprim-sulphamethoxazole was tested accurately in 2004, as was the sulphonamide group.

Overall, the laboratories that determined MICs produced more accurate results than those that used disc diffusion, for which the interpretive criteria are derived from breakpoint MICs by regression analysis of a large population of strains tested by several laboratories. This method is intrinsically less accurate than quantitative MIC-testing. Interestingly ENL Q used MIC-test qualitatively, but still only produced only one deviating result.

Disc diffusion results were analyzed quantitatively. Several laboratories systematically produced zone diameters larger than the mean values (NRL-5, 15 and 17), and others produced zone diameters smaller than the mean values (NRL-16 and ENL-F). This does not necessarily lead to a large number of incorrect classifications but is indicative of systematic differences in methodologies. Next to disc load the most important sources of variation for disc diffusion are the final inoculum, the quality and thickness of the agar plates used, and the incubation conditions.

The majority of the NRLs and ENLs regularly use *E. coli* (ATCC 25922) and other strains as their control strain. In this study the results of this strain were included and deviating results were reported. Relatively often results outside the QC-ranges provided by CLSI were reported. If laboratories are accredited according to ISO17025, these outlying results should have lead to correcting measures in the laboratories.

If similar as in 2004 a quality limit of 90 % accuracy have been used, all but one laboratory would have been approved. If 95 % accuracy would be used, which seems more realistic as the criterium, four laboratories using disc diffusion would not have complied.

7. Conclusions

Serotyping

In general, the results of the serotyping were very good. Problems with the typing of the O-antigens were of minor importance. Some problems existed with the typing of the H-antigens, although the group of laboratories (NRLs as well as ENLs) facing these problems seems to diminish. Although most of the O-antigens and a majority of the H-antigens were typed correctly, 6 % of the NRLs were still unable to give the correct serovar names. For the ENLs this problem was of minor importance.

Phage typing

The phage-typing results of the majority of the laboratories were good. The problems encountered were minor and the fact that all the laboratories use identical phage preparations enables a direct comparison between the individual results and help can be given to the small number of laboratories that had problems. It is essential that the laboratories continue to use the standardised methods and typing reagents.

Antimicrobial susceptibility testing

The quality of susceptibility testing of NRLs and ENLs participating in this ring trial is very good. Errors were mainly made on a number of strains with borderline susceptibility and on two antibiotics that proved to be very problematic in this respect.

Based on the results of this interlaboratory comparison study, the value of the inclusion of streptomycin, amoxicillin/clavulanate in monitoring programs is questionable, or the methods should be validated first.

If a quality limit of 95 % accuracy would have been used, all laboratories that determined MICs would have been approved however four laboratories using disc diffusion would not have complied.

References

- Korver H, Raes M, Maas HME, Ward LR, Wannet WJB and Henken AM, 2002.
Test results of *Salmonella* typing by the NRLs-*Salmonella* in the Member States of the EU and the EnterNet Laboratories. Collaborative study VI (2001) on typing of *Salmonella* [RIVM, Bilthoven], RIVM report 284500020.
- Korver H, Maas HME, Ward LR, Wannet WJB and Henken AM, 2002.
Test results of *Salmonella* typing by the NRLs-*Salmonella* in the Member States of the EU and the EnterNet Laboratories. Collaborative study VII (2002) on typing of *Salmonella* [RIVM, Bilthoven], RIVM report 284500022.
- Korver H, Maas HME, Mooijman KA, Ward LR, Mevius DJ, Wannet WJB and Henken AM, 2003. Test results of *Salmonella* typing by the NRLs-*Salmonella* in the Member States of the EU and the EnterNet Laboratories. Collaborative study VIII (2003) on typing of *Salmonella* [RIVM, Bilthoven], RIVM report 330300002.
- Korver H, Maas HME, Mooijman KA, Ward LR, Mevius DJ, Wannet WJB and Mooijman KA, 2005. Ninth CRL-*Salmonella* interlaboratory comparison study (2004) on typing of *Salmonella* spp. [RIVM, Bilthoven], RIVM report 330300006.
- Popoff MY and Le Minor L, 1997.
Guidelines for the preparation of *Salmonella* antisera, WHO Collaborating Centre for Reference and Research on *Salmonella*. Institut Pasteur, Paris.
- Popoff MY, 2001.
Antigenic formulas of the *Salmonella* serovars (8th edition). WHO Collaborating Centre for Reference and Research on *Salmonella*. Institut Pasteur, Paris.
- Raes M, Ward LR, Maas HME, Leeuwen WJ van and Henken AM, 2000.
Test results of *Salmonella* sero- and phage typing by the National Reference Laboratories and the EnterNet Laboratories in the Member States of the European Union. Collaborative study IV on sero- and phage typing [RIVM, Bilthoven], RIVM report 284500013.
- Raes M, Ward LR, Maas HME, Wannet WJB and Henken AM, 2001.
Test results of *Salmonella* sero-, phage and antibiotic resistance pattern typing by the National Reference Laboratories for *Salmonella* and the EnterNet Laboratories in the Member States of the European Union. Collaborative study V on sero-, phage and antibiotic resistance pattern typing [RIVM, Bilthoven], RIVM report 284500016.

Voogt N, Maas HME, Leeuwen WJ van and Henken AM, 1996.

A collaborative study on serotyping of *Salmonella* amongst the National Reference Laboratories for *Salmonella* [RIVM, Bilthoven], RIVM report 284500004.

Voogt N, Maas HME, Leeuwen WJ van and Henken AM, September 1997.

Test results of *Salmonella* serotyping in the Member States of the European Union. A collaborative study amongst the National Reference Laboratories for *Salmonella* [RIVM, Bilthoven], RIVM report 284500008.

Voogt N, Maas HME, Leeuwen WJ van and Henken AM, September 1999.

Test results of *Salmonella* serotyping in the Member States of the European Union. Collaborative study III amongst the National Reference Laboratories for *Salmonella* [RIVM, Bilthoven], RIVM report 284500010.

Annex 1 Protocol

PROTOCOL OF THE TENTH INTERLABORATORY COMPARISON STUDY (X, 2005) ON SERO- AND PHAGE TYPING OF *SALMONELLA* STRAINS AND TESTING OF ANTIMICROBIAL SUSCEPTIBILITY ORGANISED BY CRL-*SALMONELLA*

Introduction

The Community Reference Laboratory (CRL) - *Salmonella* organises the tenth interlaboratory comparison study on the typing of *Salmonella* strains amongst the National Reference Laboratories for *Salmonella* (NRLs-*Salmonella*) and EnterNet laboratories (ENLs).

The main objective of this typing study is to compare the test results of sero- and phage typing and antimicrobial susceptibility testing of the participating laboratories with the results obtained by the CRL-*Salmonella*.

For the NRLs-*Salmonella* the performance of the study will take place in week 10 (starting on 7 March 2005) or one week earlier or later. For the ENLs the study will be performed a few weeks later.

All data will be reported in the study report, send to the CRL-*Salmonella* and will be used for analysis. **The data on phage typing will be sent to CRL-*Salmonella* and to Linda Ward, Health Protection Agency (HPA), London, UK.**

Transportation of the *Salmonella* strains to the NRLs, - and ENLs-*Salmonella*.

CRL-*Salmonella* will mail to the NRLs the parcels with the strains for serotyping and antimicrobial susceptibility testing from Schiphol Airport (the Netherlands) to the airport of destination. The participants have to collect the parcels at their airport. To be able to collect the parcel from the airport you need the airway bill number. This number and other important information will be mentioned in an e-mail which will be send to the NRLs one week (= week 8) before mailing the parcels. The transport costs from the airport of destination to the laboratory cannot be paid by the CRL-*Salmonella*, so this will be at the expense of the participant. The shipment of the strains for phage typing to the NRLs and the shipment of all strains to the ENLs will be arranged by Linda Ward, HPA, London, UK.

Serotyping

A total number of 20 *Salmonella* strains (numbered S-1 till S-20), supplied by the CRL-*Salmonella*, 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.

The results will be evaluated by the CRL-*Salmonella*. 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 according to Table 1.

Table 1 Guidelines for evaluation

Results	Evaluation	Abbreviation
Autoagglutination 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	-

Phagetyping

The laboratories will receive a parcel containing 20 *Salmonella* cultures (supplied by HPA, London) for phage typing:

- ❑ 10 strains of *S. Enteritidis* numbered E1-E10
- ❑ 10 strains of *S. Typhimurium* numbered M11-M20

The evaluation of the phage typing results will be done in collaboration with Linda Ward, HPA, London, UK.

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 strains are numbered from AST-1 till AST-10 and are to be tested according to **NCCLS guidelines** with one of the following methods: Minimal Inhibition Concentration (MIC) or disc diffusion method.

The strains should be tested against the following antibiotics:

1. Amoxicillin + clavulanic acid (30 µg)
2. Ampicillin (10 µg),
3. Cefotaxime (30 µg),
4. Chloramphenicol (30 µg),
5. Ciprofloxacin (5 µg),
6. Florfenicol (30 µg),
7. Gentamicin (10 µg),
8. Kanamycin (30 µg),
9. Nalidixic Acid (30 µg),
10. Neomycin (30 µg),
11. Streptomycin (10 µg),
12. Sulphamethoxazole + Trimethoprim (23,75 + 1,25 µg),
13. Sulphonamide (eg sulfoxazole),
14. Trimethoprim (5 µg).

The numbers between brackets are the concentrations of antibiotics in the discs. The same antibiotics may be tested with the MIC if this method is your method of choice. If you do not have discs with the specified amount please omit this antibiotic from your list.

The evaluation of the antimicrobial susceptibility testing will be done in collaboration with Dik Mevius of Central Institute for Animal Disease Control, Lelystad, the Netherlands.

If you have questions or remarks about the interlaboratory comparison study please contact:

Hans Korver (research assistant CRL-*Salmonella*)

P.O. Box 1

3720 BA Bilthoven

tel. number: ..-31-30-2744263

fax. number: ..-31-30-2744434

e-mail: Hans.Korver@rivm.nl

If you have questions or remarks on the phage typing please contact:

Linda R. Ward

Public Health Laboratory Service, Laboratory of Enteric Pathogens

61 Colindale Avenue, London NW9 5HT

tel. Number: ..- 44-20-8200 4400

fax number: ..- 44-20-8905 9929

e-mail: Linda.Ward@HPA.org.uk

Timetable of the tenth interlaboratory comparison study (2005) on sero- and phage typing and antimicrobial susceptibility testing.

Week	Date	Topic
5	31 January- 4 February	Mailing of the protocol and test report 2005 (to NRLs and ENLs)
8	21-25 February	The airway bill number and other important information will be mentioned in an e-mail which will be send to you in this week (only NRLs)
9	28 February- 4 March	Mailing the strains to the participants (NRLs) After arrival at the laboratory the strains need to be subcultured and stored until the performance of the typing. If the parcel has not arrived at the airport on 4 March, please do contact the CRL immediately.
10	7-11 March	Starting with the identification of the strains.
12	21-25 March	Completion of the test report. Sending of the complete report to the CRL by e-mail. The original test report will be send to the CRL by mail. Send the results of the phage typing <u>also</u> to HPA, London (<i>only printed versions of the test report will be accepted</i>). Deadline for NRLs: End of March 2004 Deadline for ENLs: End of April 2004
13	28 March- 1 April and onwards	A printed version of the individual results will be send to all NRLs and ENLs by CRL. Checking of the results on this printed version will be done by the NRLs and ENLs. NRLs and ENLs will inform CRL whether their results are correct. If CRL does not receive a reaction within one week after receipt of the printed version the CRL will consider the results as correct.

N.B. For the ENLs the data in the time table may be one or two weeks later.

Annex 2. Testreport

TEST REPORT

INTERLABORATORY COMPARISON STUDY ON TYPING OF *SALMONELLA* STRAINS AND ANTIMICROBIAL SUSCEPTIBILITY TESTING 2005

TENTH STUDY FOR THE NATIONAL REFERENCE LABORATORIES AND SEVENTH FOR THE INTERNET LABORATORIES

Laboratory code	
Name contact person	
Name of laboratory	
Name department and/or institute	
Address	
Country	
Is your laboratory accredited/certified and according to which system ?	Serotyping: Yes/No System:..... Phagotyping: Yes/No System:..... Antimicrobial susceptibility testing: Yes/No System:.....
If you are not yet accredited/certified are you planning to do so in the near future ?	Yes/No System:.....

Please write your remarks and comments on page 9 of the test report !!

GENERAL QUESTIONS**Shipment of serotyping strains**

Was your parcel damaged at arrival ?	<input type="checkbox"/> NO <input type="checkbox"/> YES
Date of receipt at your laboratory	

Shipment of phagotyping strains

Was your parcel damaged at arrival ?	<input type="checkbox"/> NO <input type="checkbox"/> YES
Date of receipt at your laboratory	

Subculturing

Medium used for subculturing the strains	Name..... Manufacturer.....
--	--------------------------------

QUESTIONS SEROTYPING

What was the frequency of serotyping of <i>Salmonella</i> at your laboratory in 2004 ?	<input type="checkbox"/> Daily <input type="checkbox"/> Once a week <input type="checkbox"/> Twice a week <input type="checkbox"/> Thrice a week <input type="checkbox"/> Weekly <input type="checkbox"/> Monthly
How many <i>Salmonella</i> strains did your laboratory serotype in 2004 ?	Number of strains:.....
What kind of sera do you use ?	<input type="checkbox"/> Prepared in own laboratory <input type="checkbox"/> Commercial sera Manufacturer(s):
The strains in this collaborative study were serotyped by:	<input type="checkbox"/> Own laboratory, Strain..... <input type="checkbox"/> Other laboratory, namely..... Strains:.....

TEST RESULTS SEROTYPING

Labcode	
Starting date of serotyping	
Finishing date of serotyping	

Strain no.	O-antigens detected	H-antigens detected	Serovar
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			

Does your laboratory perform phage typing of the following strains ?	<input type="checkbox"/> <i>Salmonella</i> Typhimurium <input type="checkbox"/> <i>Salmonella</i> Enteritidis <input type="checkbox"/> Other(s):
Which typing system is used for:	<input type="checkbox"/> <i>Salmonella</i> Typhimurium <input type="checkbox"/> <i>Salmonella</i> Enteritidis
How many strains did your laboratory phage type in 2004 ?	Number of strains.....

Labcode
Starting date of typing	
Finishing date of typing	

[illegible]

TEST RESULTS PHAGETYPING

Labcode	
Starting date of phagotyping	
Finishing date of phagotyping	

		Phages at Routine Test Dilution (<i>S. Typhimurium</i>)																		
QA number	Phage type	1	2	3	4	5	6	7	8	10	11	12	13	14	15	16	17	18	19	
M11																				
M12																				
M13																				
M14																				
M15																				
M16																				
M17																				
M18																				
M19																				
M20																				

		Phages at Routine Test Dilution (<i>S. Typhimurium</i>)												Additional phages					
QA number	Phage type	20	21	22	23	24	25	26	27	28	29	32	35	1	2	3	10	10 var	18
M11																			
M12																			
M13																			
M14																			
M15																			
M16																			
M17																			
M18																			
M19																			
M20																			

O*: O pooled

(<)CL: clear lysis

(<)OL: opaque lysis

SCL: semi confluent lysis

<< : Merging plaques towards semi-confluent lysis

QUESTIONS ANTIMICROBIAL SUSCEPTIBILITY TESTING (AST)

Which standard method for antimicrobial susceptibility testing do you use ?	Disc:
	MIC:
Which control strain(s) do you use ?	Disc:
	MIC:
What is the concentration of the inoculum in bacteria per ml ?	Disc:
	MIC:
How many strains were tested for susceptibility in your lab in 2004 ?	

Please fill in the table below which antibiotics you used in this comparison study ?
--

Antibiotic	Abbreviat.	Disc load (µg)	Manufacturer	Breakpoints/interpretive criteria used (R/I/S)	Range used in MIC determination
Amox/clavalunate	AMC				
Ampicillin	AMP				
Cefotaxime	CEF				
Chloramphenicol	CHL				
Ciprofloxacin	CIP				
Florfenicol	FLO				
Gentamicin	GEN				
Kanamycin	KAN				
Nalidixic Acid	NAL				
Neomycin	NEO				
Streptomycin	STR				
Sulphamethoxazole +Trimethoprim	SXT				
Sulphonamide	SUL				
Trimethoprim	TMP				

RESULTS ANTIMICROBIAL SUSCEPTIBILITY TESTING (AST)

Labcode	
Starting date of AST	
Finishing date of AST	

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

[illegible]

REMARKS AND COMMENTS

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

Name of person in charge	
Date and signature	

Annex 3. Test results of phage typing per strain

Strain E 1

Lab code	Phage type	Phages reactions at Routine Test Dilution (<i>S. Enteritidis</i>)															
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
HPA	8	-	-	scl	scl	cl	scl	scl	ol	cl	ol	scl	cl	-	-	-	-
5	8	-	-	++ +	++ m	cl	++ +	±± ±	ol	±± ±	cl	±± ±	cl	-	- l	-	-
6	8	±	-	scl	+	cl	+	++ +	+L	(<) ol	(<) ol	scl	cl	-	-	-	-
9	8	-	-	scl	++ n	cl	±± n	scl	ol	++ n	cl	scl	cl	-	-	-	-
17	8	-	-	scl	++ s	cl	scl	scl	sol	sol	ol	scl	cl	-	-	-	-
19	28	-	-	++	scl	scl	scl	++	ol	ol	ol	+	scl	-	-	-	-
22	8	±	-	sol	sol	cl	++	++	ol	<ol	ol	scl	cl	-	-	-	-
26	8	- 2	-	scl	±±	cl	+	< cl	ol	scl	ol	cl	cl	-	-	-	-
A	8	-	-	++ +	++ +	scl	++	++ +	ol	scl	ol	++ +	cl	-	+	-	-
B	8	-	-	cl	scl	cl	++ +	scl	scl	scl	scl	cl	cl	-	-	-	-
C	8	±	-	scl	++ +	cl	++	++ +	scl	++ +	cl	scl	cl	±	±	+	-
D	8	-	-	cl	RT D	cl	RT D	RT D	cl	RT D	cl	cl	cl	-	-	-	-
E	8	-	-	olo	< scl	ol	< scl	scl	ol	++ n	ol	++ l	< cl	-	-	-	-
G	8	-	-	cl	< ol	cl	±± ±	++	ol	< ol	ol	< cl	cl	-	-	-	-
H	8	-	-	scl	scl	cl	scl	scl	ol	scl	ol	scl	cl	-	-	-	-
L	8	2l	-	< cl	++ < scl	cl	< scl	<cl	++ <ol	++ + scl	ol	++ <cl	cl	-	-	-	-
M	8	-	-	cl -	scl	++ scl	scl	++ scl	ol	scl	ol	++ scl	cl	-	-	-	-
P	8	-	-	< cl	scl	cl	scl	cl	ol	< ol	ol	< cl	cl	-	-	-	-

O*: O pooled

(<)CL: clear lysis

(<)OL: opaque lysis

SCL: semi confluent lysis

<< : Merging plaques towards semi-confluent lysis

Strain E 2

Lab code	Phage type	Phages reactions at Routine Test Dilution (<i>S. Enteritidis</i>)															
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
HPA	1b	ol	scl	cl	scl	cl	scl	cl	scl	ol	ol	cl	cl	cl	cl	scl	cl
5	1b	ol	++	cl	++ m	cl	scl	cl	scl	++ +	++ +	cl	cl	cl	cl	scl	scl
6	1b	ol	++ +	cl	+	(<) cl	+	scl <<	±	ol	±± ±	scl	cl	cl	cl	ol	ol
9	1b	scl	scl	cl	±± n	cl	+n	cl	ol	±± n	scl	cl	cl	cl	cl	scl	scl
17	1b	ol .	++ ns	cl	++ ns	cl	sol	ol	sol	sol	ol .	ol	cl	cl	cl	++/ << ss	sol
19	1b	scl	scl	cl	< ol	cl	cl	cl	ol	ol	ol	cl	cl	cl	cl	cl	cl
22	1b	<ol	<ol	<cl	sol	cl	++	<cl	<ol	<ol	<ol	<cl	cl	cl	cl	scl	<cl
26	1b	ol	scl	cl	++	cl	+	cl	scl	< ol	scl	cl	cl	cl	cl	< scl	< cl
A	1b	scl	scl	cl	++ +	cl	++	scl	scl	scl	scl	scl	cl	scl	cl	++	++
B	1b	scl	scl	cl	++ +	cl	++ +	scl	scl	scl	scl	ol	cl	cl	scl	< ol	ol
C	1b	scl	++ +	cl	++ +	cl	++ +	++ +	++ +	++ +	scl	scl	cl	cl	scl	++ +	scl
D	1b	RT D	RT D	cl	RT D	cl	RT D	cl	RT D	++ +	++ +	cl	cl	cl	cl	++ +	++ +
E	1b	< scl	++ +sc	< cl	< scl	< cl	< scl	ol	+++ nc	++ n	++ +n	scl	< cl	scl	scl	++ lc	scl
G	1b	ol	scl	cl	ol	cl	< scl	scl	ol	ol	scl	< cl	cl	cl	cl	<< scl	scl
H	1b	ol	scl	cl	++ +	scl	scl	cl	ol	ol	ol	cl	cl	scl	cl	ol	ol
L	1b	cl	++ + scl	cl	++ +	cl	++ + scl	cl	+	++ +	ol	< cl	cl	cl	cl	< cl	< cl
M	1b	ol	cl	cl	scl	cl -	scl	cl	ol	scl	ol	cl	cl	cl	cl	scl	scl
P	1b	ol	scl	cl	scl	cl	scl	cl	ol	< ol	ol	cl	cl	cl	cl	cl	cl

O*: O pooled

(<)CL: clear lysis

(<)OL: opaque lysis

SCL: semi confluent lysis

<< : Merging plaques towards semi-confluent lysis

Strain E 3

Lab code	Phage type	Phages reactions at Routine Test Dilution (<i>S. Enteritidis</i>)															
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
HPA	4	-	scl	cl	scl	cl	scl	cl	scl	ol	ol	cl	cl	cl	-	-	-
5	4	- 2	++ +	cl	scl	cl	cl	cl	ol	ol	++ +	cl	cl	cl	-	-	-
6	4	-	++ +	(<)cl	+	(<)cl	+	scl	+	ol	(<)ol	scl	cl	cl	-	-	-
9	4	-	scl	cl	++ n	cl	+n	cl	ol	++ n	cl	cl	cl	cl	-	-	-
17	4	-	< scl	cl	< scl	cl	sol	cl	ol	ol .	ol	cl	cl	cl	-	-	-
19	4	-	scl	scl	scl	cl	scl	cl	ol	ol	ol	cl	cl	cl	-	-	-
22	4	-	<ol	<cl	sol	cl	++	<cl	ol	ol	ol	cl	cl	cl	-	-	-
26	4	-	scl	cl	scl	cl	+	cl	ol	< ol	ol	cl	cl	cl	-	-	-
A	4	-	scl	scl	scl	cl	++ +	cl	scl	ol	ol	cl	cl	scl	-	-	-
B	4b	-	scl	cl	scl	cl	++ +	scl	scl	< ol	scl	scl	cl	cl	-	-	++ +
C	4	-	++ +	cl	++ +	cl	++ +	scl	++ +	++ +	ol	cl	cl	cl	+	±	-
D	4	-	cl	cl	RT D	cl	RT D	cl	cl	RT D	RT D	cl	cl	cl	-	-	-
E	4	-	scl	ol	++ +n	ol	< scl	ol	scl	< scl	ol	ol	< cl	< cl	-	-	-
G	4	-	scl	cl	< ol	cl	< scl	cl	cl	ol	cl	cl	cl	cl	-	-	-
H	4	-	scl	cl	scl	scl	scl	cl	ol	ol	ol	cl	cl	cl	-	-	-
L	4	4n	< cl	cl	scl	cl	++ < scl	cl	+n	cl	ol	cl	cl	cl	3n	-	-
M	4	-	cl	cl	ol	cl	scl	cl	ol	ol	ol	cl	cl	cl	-	-	-
P	4	-	scl	cl	< ol	cl	scl	cl	ol	ol	ol	cl	cl	cl	-	-	-

O*: O pooled

(<)CL: clear lysis

(<)OL: opaque lysis

SCL: semi confluent lysis

<<: Merging plaques towards semi-confluent lysis

Strain E 4

Lab code	Phage type	Phages reactions at Routine Test Dilution (<i>S. Enteritidis</i>)															
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
HPA	13a	-	-	-	scl	-	scl	-	scl	scl	ol	-	-	-	-	-	-
5	13a	-	-	-	++ m	-	scl	-	ol	±± ±	±± ±	-	-	-	-	-	-
6	13a	-	-	-	+μ	-	+ MS	-	±μ	(<) ol	(<) ol	-	-	-	-	-	-
9	13a	-	-	-	++ n	-	+n	-	ol	++ n	scl	-	-	-	-	-	-
17	13a	-	-	-	++ +ns	-	scl	-	sol	ol .	<ol	-	-	-	-	-	-
19	13a	-	-	-	scl	-	scl	-	ol	ol	ol	-	-	-	-	-	-
22	13a	-	-	-	sol	-	++	-	<ol	<ol	<ol	-	-	-	-	-	-
26	13a	-	-	-	±±	-	±	-	< 4	< ol	< ol	±m	-	-	-	-	-
A	13a	-	-	-	++	-	++	-	ol	scl	ol	-	-	-	-	-	-
B	13a	-	-	-	++ +	-	++ +	-	scl	scl	scl	-	-	-	-	-	-
C	13a	-	-	-	++ +	-	++ +	-	++ +	++ +	scl	+	-	-	-	-	-
D	13a	-	-	+	RT D	RT D	RT D	++ +	cl	scl	scl	+	RT D	-	-	-	-
E	13a	-	-	-	< scl	-	< scl	-	scl	++ n	scl	-	-	-	-	-	-
G	13a	-	-	-	< ol	-	++ +	-	ol	ol	< ol	-	-	-	-	-	-
H	13a	-	-	-	scl	-	scl	-	ol	ol	ol	-	-	-	-	-	-
L	28	3n	-	-	++ + scl	++ -N	++ << scl	±s	+ << scl	scl	ol	±s	scl	-	-	-	-
M	13a	-	-	-	scl	-	scl	-	ol	ol	ol	-	-	-	-	-	-
P	13a	-	-	-	scl	-	scl	-	ol	< ol	ol	-	-	-	-	-	-

O*: O pooled

(<)CL: clear lysis

(<)OL: opaque lysis

SCL: semi confluent lysis

<< : Merging plaques towards semi-confluent lysis

Strain E 5

Lab code	Phage type	Phages reactions at Routine Test Dilution (<i>S. Enteritidis</i>)															
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
HPA	1	ol	scl	cl	scl	cl	scl	cl	scl	scl	ol	cl	cl	cl	cl	-	-
5	1	ol	±± ±	cl	±± ±m	cl	++ +	cl	ol	++ +	scl	cl	cl	cl	cl	-	-
6	1	ol	++ +	cl	±	cl	+µ	scl	+	(<) ol	(<) ol	scl	cl	cl	scl	-	-
9	1	ol	++ n	cl	++ n	cl	+n	cl	ol	++ n	ol	cl	cl	cl	cl	-	-
17	1	ol	< scl	cl	< scl	cl	sol	cl	ol	sol	ol	cl	cl	cl	cl	-	-
19	1	ol	scl	cl	ol	cl	scl	cl	ol	ol	ol	cl	cl	cl	cl	-	-
22	1	ol	<ol	cl	sol	cl	++	<cl	<ol	<ol	ol	<cl	cl	cl	ol	-	-
26	1	ol	scl	cl	±±	cl	+	cl	ol	< ol	ol	cl	cl	cl	< cl	-	-
A	1	ol	scl	cl	++ +	cl	++	cl	scl	ol	ol	cl	cl	cl	cl	-	-
B	1	ol	scl	scl	++ +	cl	++ +	scl	scl	scl	scl	cl	cl	cl	cl	-	-
C	1	ol	++ +	cl	++ +	cl	++ +	ol	scl	++ +	ol	scl	cl	cl	scl	10 L (ol)	-
D	1	cl	RT D	scl	RT D	cl	++ +	cl	cl	RT D	cl	cl	cl	cl	cl	-	-
E	1	< scl	< scl	< cl	< scl	< cl	< scl	ol	scl	+n ++s	+++ nc	scl	< cl	scl	scl	-	-
G	1	ol	++ +	cl	ol	cl	++ +	cl	cl	ol	ol	cl	cl	cl	cl	-	-
H	1	ol	scl	cl	ol	cl	scl	scl	ol	ol	ol	scl	cl	cl	cl	-	-
L	1	ol	++ +	cl	++ +	cl	++ < scl	cl	+n	++ + scl	ol	cl	cl	cl	cl	-	-
M	1	ol	cl	cl	ol	++ scl	ol	cl	ol	ol	ol	cl -	cl	cl	cl	+	+
P	1	ol	scl	cl	scl	cl	scl	cl	ol	< ol	ol	cl	cl	cl	cl	-	-

O*: O pooled

(<)CL: clear lysis

(<)OL: opaque lysis

SCL: semi confluent lysis

<< : Merging plaques towards semi-confluent lysis

Strain E 6

Lab code	Phage type	Phages reactions at Routine Test Dilution (<i>S. Enteritidis</i>)															
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
HPA	22	ol	-	-	scl	-	scl	-	ol	ol	ol	-	-	-	cl	-	-
5	22	ol	-	-	++ +	-	scl	-	ol	++ +	ol	-	-	-	cl	-	-
6	22	ol	-	-	+μ	-	±± ML	-	±L	(<) ol	ol	-	-	-	cl	-	-
9	22	cl	-	-	++ n	-	+n	-	ol	±± n	ol	-	-	-	cl	-	-
17	22	ol	-	-	< scl	-	sol	-	ol	sol	ol	-	-	-	cl	-	-
19	22	ol	-	-	scl	-	scl	-	ol	ol	ol	-	-	-	cl	-	-
22	22	ol	-	-	sol	-	++	-	<ol	<ol	ol	-	-	-	<cl	-	-
26	22	ol	-	-	±±	-	+	-	ol	< ol	ol	-	-	-	< cl	-	-
A	22	ol	-	-	++ +	-	++ +	-	ol	scl	ol	-	-	-	cl	-	-
B	22	ol	-	-	++ +	-	++ +	-	scl	scl	ol	-	-	-	cl	-	-
C	22	ol	-	-	++ +	-	++ +	-	cl	++ +	cl	-	-	-	scl	±	-
D	22	cl	-	-	RT D	-	RT D	-	cl	RT D	scl	-	-	-	cl	-	-
E	22	++ +n	-	-	< scl	-	< scl	-	scl	+n ++s	scl	-	-	-	scl	-	-
G	22	ol	-	-	scl	-	++ +	-	ol	< ol	ol	-	-	-	cl	-	-
H	22	ol	-	-	scl	-	scl	-	ol	ol	ol	-	-	-	-	-	-
L	22	ol	-	-	++ + scl	-	++ s	-	+n	++ + scl	ol	-	-	-	cl	-	-
M	22	ol	-	-	scl	-	scl	-	ol	scl	ol	-	-	-	cl	-	-
P	22	ol	-	-	scl	-	scl	-	ol	scl	ol	-	-	-	cl	-	-

O*: O pooled

(<)CL: clear lysis

(<)OL: opaque lysis

SCL: semi confluent lysis

<< : Merging plaques towards semi-confluent lysis

Strain E 7

Lab code	Phage type	Phages reactions at Routine Test Dilution (<i>S. Enteritidis</i>)															
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
HPA	5a	-	scl	±	scl	ol	scl	±	-	ol	-	-	ol	-	-	-	-
5	5a	-	++	±	±± ±	cl	++ +	+	-	++ +	-	±	cl	-	-	-	-
6	5a	-	++ +	-	+	ol	+L	-	-	(<)ol	-	-	cl	-	-	-	-
9	5a	-	++ n	-	++ n	ol	+n	-	-	++ n	-	±n	cl	-	-	-	-
17	5a	-	< scl	±s	< sol	cl	sol	±s	-	< ol	-	±s	cl	-	-	-	-
19	5a	-	scl	±	scl	scl	scl	+	-	ol	-	-	scl	-	-	-	-
22	5a	-	<ol	-	sol	<ol	++	-	-	<ol	-	-	<ol	-	-	-	-
26	5a	-	±±	-	+	scl	+	-	-	< ol	-	-	< cl	-	-	-	-
A	5a	-	scl	-	++	scl	++	+	-	scl	-	+	cl	-	-	-	-
B	5a	-	scl	++	++ +	cl	scl	+	-	scl	-	+	cl	-	-	-	-
C	5a	-	++ +	±	++ +	ol	++ +	-	-	++ +	-	+	ol	-	-	-	-
D	6b	-	++ +	-	++ +	++ +	++ +	-	1p	++ +	-	-	++ +	-	-	-	-
E	5a	-	scl	+s	< scl	< cl	< scl	-	-	++ n	-	-	ol	-	-	-	-
G	5a	-	scl	-	< ol	cl	++ +	-	-	ol	-	-	cl	-	-	-	-
H	6b	-	scl	-	scl	++ +	scl	-	-	ol	-	-	scl	-	-	-	-
L	5a	-	++ + scl	++ +	++ + scl	cl	+ << scl	++ + scl	-	++ + scl	++	++ +	cl	++ +	-	-	-
M	6b	-	cl	-	ol	-	scl	-	-	ol	-	-	cl	-	-	-	-
P	5a	-	scl	-	< ol	cl	scl	-	-	< ol	-	-	cl	-	-	-	-

O*: O pooled

(<)CL: clear lysis

(<)OL: opaque lysis

SCL: semi confluent lysis

<< : Merging plaques towards semi-confluent lysis

Strain E 8

Lab code	Phage type	Phages reactions at Routine Test Dilution (<i>S. Enteritidis</i>)															
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
HPA	14b	-	-	-	-	-	scl	-	-	±	-	-	-	-	-	-	-
5	14b	-	-	-	- ₃	-	scl	-	-	±	-	-	-	-	-	-	-
6	14b	-	-	-	-	-	±±	-	-	±	-	-	-	-	-	-	-
9	14b	-	-	-	±n	-	+n	-	-	-	-	-	-	-	-	-	-
17	14b	-	-	-	-	-	scl	-	-	-	-	-	-	-	-	-	-
19	14b	-	-	-	+	-	scl	-	-	+	-	-	-	-	-	-	-
22	14b	-	-	-	-	-	++	-	-	-	-	-	-	-	-	-	-
26	14b	-	-	-	- ₁	-	+	-	-	- ₂	-	-	-	-	-	-	-
A	14b	-	-	-	-	-	++ +	-	-	+	-	-	-	-	-	-	-
B	14b	-	-	-	-	-	++ +	-	-	+	-	-	-	-	-	-	-
C	14b	-	-	-	-	-	++ +	-	-	-	-	-	-	-	-	-	-
D	14b	-	-	-	-	-	++ +	-	-	2p	-	-	-	-	-	-	-
E	14b	-	-	-	2n	-	< scl	-	-	-	-	-	-	-	-	-	-
G	14b	-	-	-	-	-	++ +	-	-	-	-	-	-	-	-	-	-
H	14b	-	-	-	-	-	scl	-	-	-	-	-	-	-	-	-	-
L	14b	-	-	-	1s	-	+ << scl	-	-	6s	-	-	-	-	-	-	-
M	14b	-	-	-	-	-	scl	-	-	-	-	-	-	-	-	-	-
P	14b	-	-	-	-	-	scl	-	-	-	-	-	-	-	-	-	-

O*: O pooled

(<)CL: clear lysis

(<)OL: opaque lysis

SCL: semi confluent lysis

<< : Merging plaques towards semi-confluent lysis

Strain E 9

Lab code	Phage type	Phages reactions at Routine Test Dilution (<i>S. Enteritidis</i>)															
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
HPA	44	ol	scl	cl	-	cl	scl	cl	ol	-	ol	cl	cl	cl	cl	-	-
5	44	ol	±± ±	cl	-	cl	scl	cl	ol	-	scl	cl	cl	cl	cl	-	-
6	44	ol	++ +	cl	-	cl	+μ	scl	±L	-	(<) ol	scl	cl	cl	cl	-	-
9	44	ol	scl	ol	-	cl	+n	cl	ol	-	ol	cl	cl	cl	cl	-	-
17	44	ol	++ ns	cl	-	cl	sol	cl	< ol	-	ol	< cl	cl	cl	cl	-	-
19	44	ol	scl	cl	-	cl	ol	scl	ol	-	ol	scl	cl	cl	cl	-	-
22	44	ol	<ol	cl	-	cl	++	<cl	ol	-	<ol	<cl	cl	cl	cl	-	-
26	44	ol	< scl	cl	-	cl	+	cl	ol	-	ol	cl	cl	cl	< cl	-	-
A	44	ol	scl	cl	-	cl	++	scl	ol	-	ol	scl	cl	cl	cl	-	-
B	44	ol	scl	cl	-	cl	scl	scl	++ +	-	scl	++ +	cl	cl	scl	-	-
C	44	++ +	++	cl	-	cl	++ +	scl	++ +	-	ol	++ +	cl	cl	scl	6-	-
D	44	cl	RT D	cl	-	cl	RT D	cl	cl	-	RT D	RT D	cl	cl	RT D	-	-
E	44	++ +n	< scl	< cl	-	scl	< scl	ol	scl	-	scl	scl	< cl	< cl	scl	-	-
G	44	ol	scl	cl	-	cl	< scl	scl	cl	-	ol	scl	cl	cl	cl	-	-
H	37	ol	-	cl	-	ol	scl	ol	ol	-	ol	scl	scl	scl	cl	-	-
L	44	ol	scl	cl	-	cl	++ < scl	cl	++ N	-	ol	< cl	cl	cl	cl	-	-
M	44	ol	cl	cl	-	cl	scl	cl	ol	-	ol	cl	cl	cl	cl	-	-
P	37	ol	-	cl	-	cl	scl	cl	ol	-	ol	cl	cl	cl	cl	-	-

O*: O pooled

(<)CL: clear lysis

(<)OL: opaque lysis

SCL: semi confluent lysis

<< : Merging plaques towards semi-confluent lysis

Strain E 10

Lab code	Phage type	Phages reactions at Routine Test Dilution (<i>S. Enteritidis</i>)															
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
HPA	6	-	scl	-	scl	-	scl	-	scl	ol	ol	-	-	-	-	-	-
5	5c	-	±± ±	+	++ +	scl	scl	+	ol	scl	++ +	+	ol	++ +	-	-	-
6	6	-	±±	-	±	-	+	-	±	(<) ol	(<) ol	-	-	-	-	-	-
9	6	-	++ n	-	+n	-	+n	-	ol	±± n	ol	-	-	-	-	-	-
17	6	-	< scl	-	< scl	-	scl	-	ol	< ol	ol	-	-	-	-	-	-
19	6	-	scl	-	scl	-	scl	-	ol	ol	ol	-	-	-	-	-	-
22	6	-	++ +	-	< sol	-	++	-	ol	<ol	ol	-	-	-	2	-	-
26	6	-	scl	-	±±	-	±	-	< ol	< ol	< ol	-	-	-	-	-	-
A	6	-	scl	-	++ +	-	++ +	-	scl	scl	ol	-	-	-	-	-	-
B	6	-	scl	-	scl	-	++ +	-	++ +	scl	++ +	-	-	-	-	-	-
C	6	-	++ +	-	scl	-	++ +	-	++ +	++ +	scl	-	-	-	-	-	-
D	6	-	RT D	-	RT D	-	RT D	-	cl	scl	cl	-	-	-	-	-	-
E	6	-	< scl	-	< scl	-	< scl	-	scl	< scl	scl	-	-	-	-	-	-
G	6	-	scl	-	< ol	-	++ +	-	ol	< ol	ol	-	-	-	-	-	-
H	6	-	scl	-	scl	-	scl	-	ol	ol	ol	-	-	-	-	-	-
L	6	8n	++ + scl	-	++ + scl	-	++ << scl	-	++ N	++ + scl	ol	-	?	-	-	-	-
M	6	-	cl	-	ol	-	scl	-	ol	ol	ol	-	-	-	-	-	-
P	6	-	scl	-	scl	-	scl	-	ol	< ol	ol	-	-	-	-	-	-

O*: O pooled

(<)CL: clear lysis

(<)OL: opaque lysis

SCL: semi confluent lysis

<< : Merging plaques towards semi-confluent lysis

Strain M 11 (A)

Labcode	Phage type	Phages at Routine Test Dilution (<i>S.Typhimurium</i>)																	
		1	2	3	4	5	6	7	8	10	11	12	13	14	15	16	17	18	19
HPA	15	-	-	-	-	-	-	-	-	-	ol	scl	scl	-	ol	-	ol	scl	ol
5	15	-	-	-	-	-	-	-	±	-	scl	scl	++ +	-	±± ±	-	++	cl	++
6	18	-	-	-	-	-	-	-	-	-	scl	-	-	-	cl	-	scl	+	±
9	15	-	-	-	-	-	-	-	-	-	ol	±± L <<	+L <<	-	ol	-	ol	scl	±n
17	15	-	-	-	-	-	-	-	-	-	sol	scl	scl	-	sol	-	±n	scl	++ s
22	15	-	-	-	-	-	-	-	-	-	< ol	++	++ +	-	ol	-	< ol	< cl	++
26	104H	-	-	-	-	-	-	-	-	-	-	< scl	< cl	-	-	-	-	< scl	-
A	15	-	-	-	-	-	-	-	-	-	+	++ +	++ +	-	scl	-	+	+	++ +
B	15	-	-	-	-	-	-	-	-	-	++ +	scl	scl	-	++ +	-	scl	scl	++ +
C	15	-	-	-	-	-	-	-	±	-	scl	++ +	scl	-	ol	-	scl	scl	scl
E	15	-	-	-	-	-	-	-	-	-	scl	++ n	++ nc	-	++ s	-	++ s	scl	++ +s
G	15	-	-	-	-	-	-	-	-	-	++ +	++ +	scl	-	ol	-	++ +	< cl	++
H	15	-	-	-	-	-	-	-	-	-	ol	scl	scl	-	ol	scl	scl	scl	scl
L	15	-	-	-	-	-	-	-	-	-	< ol	++ l < cl	scl	-	scl	-	< cl	cl	++ + < scl
M	15	-	-	-	-	-	-	-	-	-	ol	ol	ol	-	ol	-	scl	cl	ol
P	15	-	-	-	-	-	-	-	-	-	ol	< cl	cl	-	ol	-	ol	cl	scl

O*: O pooled

(<)CL: clear lysis

(<)OL: opaque lysis

SCL: semi confluent lysis

<< : Merging plaques towards semi-confluent lysis

Strain M 11 (B)

Labcode	Phage type	Phages at Routine Test Dilution (<i>S.Typhimurium</i>)												Additional phages					
		20	21	22	23	24	25	26	27	28	29	32	35	1	2	3	10	10 var	18
HPA	15	scl	-	-	-	-	-	-	±	-	-	ol	-	±	±	±	ol	ol	-
5	15	±± ±	-	-	-	-	-	-	-	- 1	-	++	±	-	±	±	ol	ol	- 3
6	18	scl	-	-	-	-	-	-	(<) scl	1	-	+L	+ L						
9	15	scl	-	-	-	-	-	-	±L	-	-	scl	+ L	+ n	+ n	+ n	ol	ol	-
17	15	sol	-	-	-	-	-	-	±n	2n	-	< ol	+ n	+ ns	++ ns	++ ns	< ol	< ol	3s
22	15	sol	-	-	-	-	-	-	±	-	-	< ol	-	±	+	±	ol	< ol	-
26	104H	-	-	-	-	-	-	-	-	-	-	-	-						
A	15	++	-	-	-	-	-	-	+	-	-	scl	+	++	++	++	++ +	scl	+
B	15	scl	-	-	-	-	-	-	++	-	-	scl	sc l						
C	15	scl	-	-	-	-	-	-	+	-	-	scl	-	±	++	++	ol	ol	-
E	15	< scl	-	-	-	-	-	-	3n	1s	-	< scl	4 n						
G	15	++ +	-	-	-	-	-	-	-	-	-	++ +	-						
H	15	scl	-	-	-	-	-	-	+	-	-	++ +	+ +	-	±	-	ol	ol	-
L	15	< cl	-	-	-	-	-	-	±	-	-	< cl	3l						
M	15	ol	-	-	-	-	-	-	++ L scl	-	-	++ L scl	+ + L sc l	+	++	+	ol	ol	+ L
P	15	ol	-	-	-	-	-	-	+	-	-	< ol	+ -						

O*: O pooled

(<)CL: clear lysis

(<)OL: opaque lysis

SCL: semi confluent lysis

<< : Merging plaques towards semi-confluent lysis

Strain M 12 (A)

Labcode	Phage type	Phages at Routine Test Dilution (<i>S.Typhimurium</i>)																	
		1	2	3	4	5	6	7	8	10	11	12	13	14	15	16	17	18	19
HPA	36	ol	ol	ol	ol	ol	ol	ol	scl	ol	ol	ol	ol	ol	ol	ol	ol	cl	ol
5	36	cl	ol	cl	ol	scl	cl	cl	cl	cl	cl	cl	cl	cl	cl	cl	scl	cl	cl
6	36	scl <<	scl <<	scl	scl	scl	ol	scl	scl	scl	cl	scl	scl	(<) cl	cl	cl	scl	++ +	scl <<
9	36	cl	cl	cl	cl	cl	cl	cl	cl	cl	cl	cl	cl	cl	cl	cl	cl	scl	cl
17	36	< cl	< scl	scl	cl	< cl	< cl	cl	< cl	cl	cl	< cl	cl	cl	cl	cl	< scl	cl	< cl
22	36	< cl	< cl	< cl	ol	< cl	cl	cl	< cl	cl	cl	cl	cl	cl	cl	cl	cl	< cl	cl
26	36	cl	< cl	cl	ol	< cl	cl	cl	cl	cl	cl	< cl	cl	cl	cl	cl	cl	< cl	< cl
A	36	scl	scl	scl	scl	scl	++ +	scl	scl	scl	scl	scl	scl	cl	cl	cl	scl	scl	scl
B	36	cl	cl	cl	cl	cl	cl	cl	cl	cl	cl	cl	cl	cl	cl	cl	cl	scl	cl
C	36	scl	ol	scl	scl	scl	cl	ol	cl	scl	ol	scl	ol	scl	cl	ol	scl	scl	ol
E	36	scl	scl	ol	ol	ol	ol	ol	ol	ol	ol	scl	ol	ol	ol	ol	ol	scl	ol
G	36	cl	< cl	cl	cl	cl	cl	cl	cl	scl	cl	cl	cl	cl	cl	cl	scl	cl	cl
H	36	scl	scl	scl	scl	scl	scl	scl	scl	scl	scl	scl	scl	scl	scl	scl	scl	scl	scl
L	36	cl	< cl	cl	ol	< cl	cl	cl	cl	cl	cl	< cl	cl	cl	cl	cl	cl	cl	cl
M	36	<u>cl</u>	+L scl	cl	cl	cl	cl	cl	cl	cl	cl	<u>cl</u>	cl	cl	cl	cl	cl	cl	cl
P	36	cl	cl	cl	cl	cl	cl	cl	cl	cl	cl	cl	cl	cl	cl	cl	cl	cl	cl

O*: O pooled

(<)CL: clear lysis

(<)OL: opaque lysis

SCL: semi confluent lysis

<< : Merging plaques towards semi-confluent lysis

Strain M 12 (B)

Labcode	Phage type	Phages at Routine Test Dilution (<i>S.Typhimurium</i>)												Additional phages					
		20	21	22	23	24	25	26	27	28	29	32	35	1	2	3	10	10 var	18
HPA	36	ol	ol	ol	ol	ol	ol	ol	ol	ol	ol	ol	ol	+	+	+	ol	ol	ol
5	36	scl	ol	ol	cl	cl	++ +	cl	ol	ol	cl	scl	ol	-	+	+	ol	ol	ol
6	36	scl	±	ol	scl	scl <<	+ L	scl	cl	cl	scl	±	ol						
9	36	cl	cl	cl	cl	cl	scl	cl	cl	cl	cl	cl	ol	+ n	+ n	++ n	ol	ol	ol
17	36	cl	< cl	cl	< cl	cl	< cl	cl	cl	ol	cl	cl	ol	++ ns	++ ns	++ ns	ol	ol .	cl
22	36	< cl	cl	< ol	cl	cl	scl	cl	cl	ol	ol	cl	ol	±	±	±	ol	< ol	cl
26	36	< cl	cl	ol	< cl	cl	< cl	cl	cl	ol	cl	< cl	ol						
A	36	++	scl	scl	scl	scl	scl	scl	cl	ol	cl	scl	scl	++	++ +	++ +	scl	scl	scl
B	36	cl	cl	cl	cl	cl	scl	scl	cl	cl	cl	cl	cl						
C	36	scl	ol	ol	scl	ol	ol	ol	ol	ol	scl	scl	scl	++ +	++ +	++ +	ol	cl	ol
E	36	ol	ol	scl	scl	scl	scl	scl	ol	ol	ol	scl	ol						
G	36	cl	cl	cl	cl	scl	< cl	< cl	cl	cl	cl	++ +	ol						
H	36	scl	scl	scl	scl	scl	scl	scl	scl	ol	scl	scl	ol	+	+	+	ol	ol	scl
L	36	cl	++ l < cl	< cl	cl	cl	< cl	cl	cl	< cl	cl	< cl	ol						
M	36	cl	cl	cl	++ L scl	cl	++ L scl	scl	cl	cl	cl	++ L scl	ol	+	++	++	ol	ol	ol
P	36	cl	cl	cl	cl	< cl	< cl	< cl	cl	ol	cl	cl	ol						

O*: O pooled

(<)CL: clear lysis

(<)OL: opaque lysis

SCL: semi confluent lysis

<< : Merging plaques towards semi-confluent lysis

Strain M 13 (A)

		Phages at Routine Test Dilution (<i>S.Typhimurium</i>)																	
Labcode	Phage type	1	2	3	4	5	6	7	8	10	11	12	13	14	15	16	17	18	19
HPA	U291	-	-	-	ol	cl	scl	-	-	-	cl	-	-	cl	cl	cl	-	scl	cl
5	U291	-	-	-	ol	scl	scl	-	- 2	-	cl	-	-	cl	cl	cl	-	scl	scl
6	U291	-	-	-	scl	(cl	ol	-	-	-	cl	-	-	cl	cl	cl	-	++ +	scl <<
9	U291	-	-	-	cl	cl	ol	-	-	-	cl	-	-	cl	cl	cl	-	scl	scl
17	U291	-	-	-	<cl	<cl	ol	-	-	-	cl	-	-	cl	cl	cl	-	scl	scl
22	U291	-	-	-	ol	<cl	scl	-	-	-	cl	-	-	cl	cl	cl	-	++ +	<ol
26	U291	-	-	-	ol	+	++ m	-	-	-	cl	-	-	cl	cl	cl	-	<< scl	< scl
A	U291	-	-	-	scl	scl	+	-	-	-	++ +	-	-	ol	ol	ol	-	scl	scl
B	142	-	-	-	scl	scl	++ +	-	-	-	++ +	-	-	scl	scl	scl	-	-	++ +
C	U291	-	-	-	scl	scl	scl	-	7-	-	scl	-	-	scl	cl	cl	-	++ +	scl
E	U291	-	-	-	ol	ol	scl	-	-	-	ol	-	-	ol	ol	ol	-	scl	ol
G	U291	-	-	-	cl	cl	ol	-	-	-	cl	-	-	cl	cl	ol	-	<cl	++ +
H	U291	-	-	-	scl	scl	ol	-	-	-	scl	-	-	cl	cl	cl	-	++ +	scl
L	U291	-	-	-	ol	<cl	scl	-	-	-	cl	-	-	cl	cl	cl	-	++ + scl	cl
M	U291	-	-	-	ol	cl	scl	-	-	-	cl	-	-	cl	cl	cl	-	cl	cl
P	U291	-	-	-	cl	cl	<cl	-	-	-	cl	-	-	cl	cl	cl	-	cl	<cl

O*: O pooled

(<)CL: clear lysis

(<)OL: opaque lysis

SCL: semi confluent lysis

<< : Merging plaques towards semi-confluent lysis

Strain M 13 (B)

Labcode	Phage type	Phages at Routine Test Dilution (<i>S.Typhimurium</i>)												Additional phages					
		20	21	22	23	24	25	26	27	28	29	32	35	1	2	3	10	10 var	18
HPA	U291	+	-	-	-	-	scl	cl	cl	-	-	-	-	±	±	-	ol	ol	±
5	U291	+	-	-	-	-	scl	ol	scl	-	-	-	-	-	±	-	ol	ol	++
6	U291	+L	-	-	-	-	+L	scl	scl	-	-	-	-						
9	U291	±n	-	-	-	-	± L	cl	cl	-	-	-	-	± n	±n	±n	ol	ol	± L
17	U291	+s	-	-	-	-	scl	cl	< ol	-	-	-	-	±s	+n s	± ns	ol	ol	±l ns
22	U291	+	-	-	-	-	++	cl	< cl	-	-	-	-	±	±	±	ol	< ol	±
26	U291	- 2	-	-	-	-	+	cl	< cl	-	-	-	-						
A	U291	+	-	-	-	-	scl	scl	scl	-	-	-	+	+	+	+	scl	scl	++
B	142	++	-	++ +	++ +	-	++	++	-	-	scl	-	-						
C	U291	-	-	-	-	-	scl	cl	cl	-	-	-	-	1-	2-	++	ol	ol	5-
E	U 291	< scl	-	-	-	-	scl	scl	scl	-	-	-	-						
G	U291	-	-	-	-	-	++ +	cl	cl	-	-	-	-						
H	U291	±	-	-	-	-	scl	scl	scl	-	-	-	-	-	-	-	ol	ol	scl
L	U291	10 1	-	-	-	-	< cl	cl	< cl	-	-	-	-						
M	U291	+	-	-	-	-	+ L scl	++ L scl	cl	-	-	-	-	-	+	-	ol	ol	++ L scl
P	U291	++	-	-	-	-	< cl	cl	cl	-	-	-	-						

O*: O pooled

(<)CL: clear lysis

(<)OL: opaque lysis

SCL: semi confluent lysis

<< : Merging plaques towards semi-confluent lysis

Strain M 14 (A)

Labcode	Phage type	Phages at Routine Test Dilution (<i>S.Typhimurium</i>)																	
		1	2	3	4	5	6	7	8	10	11	12	13	14	15	16	17	18	19
HPA	U310	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
5	U310	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
6	U310	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
9	U310	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
17	U310	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
22	U310	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
26	U310	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
A	U310	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
B	U310	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
C	U302	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
E	U310	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
G	U310	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
H	U302	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
L	U302	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
M	U310	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
P	U310	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

O*: O pooled

(<)CL: clear lysis

(<)OL: opaque lysis

SCL: semi confluent lysis

<< : Merging plaques towards semi-confluent lysis

Strain M 14 (B)

Labcode	Phage type	Phages at Routine Test Dilution (<i>S.Typhimurium</i>)												Additional phages					
		20	21	22	23	24	25	26	27	28	29	32	35	1	2	3	10	10 var	18
HPA	U310	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ol	-
5	U310	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2 ol	-
6	U310	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	± L	(<)ol	-
9	U310	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ol	-
17	U310	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	± ns	sol	-
22	U310	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	±	sol	-
26	U310	-	-	-	-	-	-	-	-	-	-	-	-	-	2	-	4	3 ol	-
A	U310	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	scl	-
B	U310	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ol	-
C	U302	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ol	ol	-
E	U310	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	++ n	ol	-
G	U310	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ol	-
H	U302	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ol	ol	-
L	U302	-	-	-	-	-	-	-	-	-	-	-	-	-	2s	6s	++ l < scl	scl	-
M	U310	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ol	-
P	U310	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ol	-

O*: O pooled

(<)CL: clear lysis

(<)OL: opaque lysis

SCL: semi confluent lysis

<< : Merging plaques towards semi-confluent lysis

Strain M 15 (A)

Labcode	Phage type	Phages at Routine Test Dilution (<i>S.Typhimurium</i>)																	
		1	2	3	4	5	6	7	8	10	11	12	13	14	15	16	17	18	19
HPA	12	-	-	-	-	-	-	-	-	-	-	scl	cl	-	-	-	-	-	-
5	12	-	-	-	-	-	-	-	-	-	-	++ +	++ +	-	-	-	-	-	-
6	12	-	-	-	-	-	-	-	-	-	-	scl	scl	-	-	-	-	-	-
9	12	-	-	-	-	-	-	-	-	-	-	scl	scl	-	-	-	-	-	-
17	12	-	-	-	-	-	-	-	-	-	-	< scl	scl	-	-	-	-	-	-
22	12	-	-	-	-	-	-	-	-	-	-	scl	scl	-	-	-	-	-	-
26	12	-	-	-	-	-	-	-	-	-	-	± L	< cl	-	-	-	-	-	-
A	12	-	-	-	-	-	-	-	-	-	-	scl	scl	-	-	-	-	-	-
B	109	-	-	-	-	-	-	-	-	-	-	scl	scl	-	-	-	++	-	-
C	12	-	-	-	-	-	-	-	-	-	-	scl	ol	-	-	-	-	-	-
E	12	-	-	-	-	-	-	-	-	-	-	++ lc	scl	-	-	-	-	-	-
G	12	-	-	-	-	-	-	-	-	-	-	++ +	cl	-	-	-	-	-	-
H	12	-	-	-	-	-	-	-	-	-	-	scl	scl	-	-	-	-	-	-
L	12	-	-	-	-	-	-	-	-	-	-	++ l> scl	scl	-	-	-	-	-	-
M	12	-	-	-	-	-	-	-	-	-	-	++ L scl	scl	-	-	-	-	-	-
P	12	-	-	-	-	-	-	-	-	-	-	cl	cl	-	-	-	-	-	-

O*: O pooled

(<)CL: clear lysis

(<)OL: opaque lysis

SCL: semi confluent lysis

<< : Merging plaques towards semi-confluent lysis

Strain M 15 (B)

Labcode	Phage type	Phages at Routine Test Dilution (<i>S.Typhimurium</i>)												Additional phages					
		20	21	22	23	24	25	26	27	28	29	32	35	1	2	3	10	10 var	18
HPA	12	-	-	-	-	-	-	-	-	-	-	-	-	+	+	+	ol	ol	-
5	12	-	-	-	-	-	-	-	-	-	-	-	-	-	+	+	ol	ol	-
6	12	-	-	-	-	-	-	-	-	-	-	-	-						
9	12	-	-	-	-	-	-	-	-	-	-	-	-	± ±n	+ n	++ n	ol	ol	-
17	12	-	-	-	-	-	-	-	-	-	-	-	-	+ +s m	++ ns	++ +ns	< ol	so l	-
22	12	-	-	-	-	-	-	-	-	-	-	-	-	+	++	±	ol	< ol	-
26	12	-	-	-	-	-	-	-	-	-	-	-	-						
A	12	-	-	-	-	-	-	-	-	-	-	-	-	+ +	++ +	++ +	scl	scl	-
B	109	+	-	-	-	-	-	-	-	-	-	-	-						
C	12	-	-	-	-	-	-	-	-	-	-	-	-	+ +	++ +	++ +	ol	ol	-
E	12	-	-	-	-	-	-	-	-	-	-	-	-						
G	12	-	-	-	-	-	-	-	-	-	-	-	-	++ +	++ +	++ +	ol	ol	-
H	12	-	-	-	-	-	-	-	-	-	-	-	-	+	+	+	ol	ol	-
L	12	-	-	-	-	-	-	-	-	-	-	-	-						
M	12	-	-	-	-	-	-	-	-	-	-	-	-	+	++ +	+	ol	ol	-
P	12	-	-	-	-	-	-	-	-	-	-	-	-						

O*: O pooled

(<)CL: clear lysis

(<)OL: opaque lysis

SCL: semi confluent lysis

<< : Merging plaques towards semi-confluent lysis

Strain M 16 (A)

Labcode	Phage type	Phages at Routine Test Dilution (<i>S.Typhimurium</i>)																	
		1	2	3	4	5	6	7	8	10	11	12	13	14	15	16	17	18	19
HPA	193	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
5	193	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
6	193	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
9	193	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
17	193	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
22	193	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
26	193	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
A	193	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
B	195	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
C	193	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
E	193	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
G	193	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
H	193	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
L	193	-	-	-	-	-	-	-	-	-	-	2s	1s	-	-	-	-	-	-
M	193	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
P	193	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

O*: O pooled

(<)CL: clear lysis

(<)OL: opaque lysis

SCL: semi confluent lysis

<< : Merging plaques towards semi-confluent lysis

Strain M 16 (B)

Labcode	Phage type	Phages at Routine Test Dilution (<i>S.Typhimurium</i>)												Additional phages					
		20	21	22	23	24	25	26	27	28	29	32	35	1	2	3	10	10 var	18
HPA	193	-	-	-	-	-	-	-	-	-	-	-	-	++ +	++ +	++ +	++ +	±	-
5	193	-	-	-	-	-	-	-	-	-	-	-	-	-	++	++	++ /ol	++ /ol	-
6	193	-	-	-	-	-	-	-	-	-	-	-	-	scl	scl	scl	-	-	-
9	193	-	-	-	-	-	-	-	-	-	-	-	-	scl	scl	scl	+ n	+ n	-
17	193	-	-	-	-	-	-	-	-	-	-	-	-	++ ns m	++ ns	++ ns m	+ m μ	+ μ	-
22	193	-	-	-	-	-	-	-	-	-	-	-	-	++	++ +	+	< ol	-	-
26	193	-	-	-	-	-	-	-	-	-	-	-	-	++	+	scl	scl	scl	-
A	193	-	-	-	-	-	-	-	-	-	-	-	-	++	++	++	++ +*	++ +*	-
B	195	-	-	-	-	-	-	-	-	-	-	-	-	-	+	++ +	++ +	scl	-
C	193	-	-	-	-	-	-	-	-	-	-	-	-	++ +	++ +	++ +	-	-	-
E	193	-	-	-	-	-	-	-	-	-	-	-	-	scl	scl	++ +n	-	-	-
G	193	-	-	-	-	-	-	-	-	-	-	-	-	++ +	++ +	++ +	-	-	-
H	193	-	-	-	-	-	-	-	-	-	-	-	-	+	++	++	ol	ol	-
L	193	-	-	-	-	-	-	-	-	-	-	-	-	++ + scl	++ + scl	++ + scl	scl	scl	-
M	193	-	-	-	-	-	-	-	-	-	-	-	-	++	++	++	ol	ol	-
P	193	-	-	-	-	-	-	-	-	-	-	-	-	< cl	< cl	< cl	-	< ol	-

O*: O pooled

(<)CL: clear lysis

(<)OL: opaque lysis

SCL: semi confluent lysis

<< : Merging plaques towards semi-confluent lysis

Strain M 17 (A)

Labcode	Phage type	Phages at Routine Test Dilution (<i>S.Typhimurium</i>)																	
		1	2	3	4	5	6	7	8	10	11	12	13	14	15	16	17	18	19
HPA	104	-	-	-	-	-	-	-	-	-	-	++	scl	-	-	-	-	++	-
5	104	-	-	-	-	-	-	-	± 11	-	-	++ +	++ +	-	-	-	-	++ +	-
6	104	-	-	-	-	-	-	-	-	-	-	scl	scl	-	-	-	-	±	-
9	104L	-	-	-	-	-	-	-	-	-	-	±L <<	±L <<	-	-	-	-	+n	-
17	104L	-	-	-	-	-	-	-	-	-	-	+/ n< <ss	++ n< <ss	-	-	-	-	++ ns	-
22	104	-	-	-	-	-	-	-	-	-	-	++	scl	-	-	-	-	++	-
26	104L	-	-	-	-	-	-	-	-	-	-	± L	scl	-	-	-	-	±	-
A	104L	-	-	-	-	-	-	-	-	-	-	++	++ +	-	-	-	-	++ +	-
B	104	-	-	-	-	-	-	-	-	-	-	scl	scl	-	-	-	-	++ +	-
C	104	-	-	-	-	-	-	-	-	-	-	++ +	scl	-	-	-	-	++	-
E	104L	-	-	-	-	-	-	-	-	-	-	++ n	++ +l	-	-	-	-	< scl	-
G	104	-	-	-	-	-	-	-	-	-	-	++ +	< cl	-	-	-	-	++ +	-
H	104L	-	-	-	-	-	-	-	-	-	-	scl	scl	-	-	-	-	+	-
L	104L	-	-	-	-	-	-	-	-	-	-	scl	scl	-	-	-	-	++ + < scl	-
M	104	-	-	-	-	-	-	-	-	-	-	++ L scl	scl	-	-	-	-	++ +	-
P	104	-	-	-	-	-	-	-	3s	-	-	scl	< cl	-	-	-	-	++ + su	-

O*: O pooled

(<)CL: clear lysis

(<)OL: opaque lysis

SCL: semi confluent lysis

<< : Merging plaques towards semi-confluent lysis

Strain M 17 (B)

		Phages at Routine Test Dilution (<i>S.Typhimurium</i>)												Additional phages					
Labcode	Phage type	20	21	22	23	24	25	26	27	28	29	32	35	1	2	3	10	10 var	18
HPA	104	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ol	ol	-
5	104	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ol	ol	-
6	104	-	-	-	-	-	-	-	-	-	-	-	-						
9	104L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ol	ol	-
17	104L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ol	sol	-
22	104	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ol	< ol	-
26	104L	-	-	-	-	-	-	-	-	-	-	-	-						
A	104L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	scl	scl	-
B	104	-	-	-	-	-	-	-	-	-	-	-	-						
C	104	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ol	ol	-
E	104L	-	-	-	-	-	-	-	-	-	-	-	-						
G	104	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ol	ol	-
H	104L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ol	ol	-
L	104L	-	-	-	-	-	-	-	-	-	-	-	-						
M	104	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	ol	ol	-
P	104	-	-	-	-	-	-	-	-	-	-	-	-						

O*: O pooled

(<)CL: clear lysis

(<)OL: opaque lysis

SCL: semi confluent lysis

<< : Merging plaques towards semi-confluent lysis

Strain M 18 (A)

		Phages at Routine Test Dilution (<i>S.Typhimurium</i>)																	
Labcode	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	-	-	-
5	10	-	-	-	-	-	-	-	-	cl	ol	cl	cl	-	-	scl	-	-	-
6	10	-	-	-	-	-	-	-	-	scl	scl	scl	scl	-	-	++ +	-	-	-
9	10	-	-	-	-	-	-	-	-	cl	cl	cl	cl	-	-	cl	-	-	-
17	10	-	-	-	-	-	-	-	-	< cl	< cl	< cl	cl	-	-	cl .	-	-	-
22	10	-	-	-	-	-	-	-	-	< cl	ol	< cl	ol	-	-	scl	-	-	-
26	10	-	-	-	-	-	-	-	-	cl	ol	< cl	cl	-	-	+	-	-	-
A	67	-	-	-	-	-	-	-	-	scl	+	scl	scl	-	-	scl	-	-	-
B	10	-	-	-	-	-	-	-	-	cl	scl	cl	cl	-	-	scl	-	-	-
C	10	-	-	-	-	-	-	-	-	scl	scl	cl	cl	-	-	scl	-	-	-
E	10	-	-	-	-	-	-	-	-	< cl	scl	scl	< cl	-	-	scl	-	-	-
G	10	-	-	-	-	-	-	-	-	scl	cl	cl	cl	-	-	scl	-	-	-
H	10	-	-	-	-	-	-	-	-	scl	scl	scl	-	-	-	scl	-	-	-
L	10	-	-	-	-	-	-	-	-	cl	++ l > cl	cl	cl	-	-	< cl	-	-	±n
M	10	-	-	-	-	-	-	-	-	cl	scl	cl	cl	-	-	scl	-	-	-
P	10	-	-	-	-	-	-	-	-	< cl	ol	cl	cl	-	-	< cl	-	-	-

O*: O pooled

(<)CL: clear lysis

(<)OL: opaque lysis

SCL: semi confluent lysis

<< : Merging plaques towards semi-confluent lysis

Strain M 18 (B)

Labcode	Phage type	Phages at Routine Test Dilution (<i>S.Typhimurium</i>)												Additional phages					
		20	21	22	23	24	25	26	27	28	29	32	35	1	2	3	10	10 var	18
HPA	10	cl	-	cl	cl	-	-	scl	-	-	cl	cl	-	±	±	-	ol	ol	-
5	10	scl	-	ol	scl	-	-1	±	-	-	scl	scl	-	-	±	±	ol	ol	-
6	10	scl	-	ol	scl	-	-	±	-	-	scl	± L	-						
9	10	scl	-	cl	scl	-	±n	±n	-	-	cl	cl	-	+n	+n	+n	ol	ol	-
17	10	< cl	-	cl .	< cl	-	3n	±n	-	-	cl	cl	-	2s	±s m	±s m	ol	ol .	-
22	10	< cl	±	< cl	< cl	-	2	++	-	-	cl	cl	-	-	2	-	ol	< ol	-
26	10	< cl	-	ol	< cl	-	-	+	-	-	cl	scl	-						
A	67	++	-	scl	scl	-	+	+	-	-	scl	cl	-	+	+	++	scl	scl	-
B	10	cl	-	cl	cl	-	-	++	-	-	cl	scl	-						
C	10	scl	-	scl	scl	-	-	+	-	-	scl	scl	-	-	±	±	ol	ol	-
E	10	< cl	-	scl	scl	-	4n	1s 4n	-	-	ol	scl	-						
G	10	scl	-	cl	< cl	-	-	-	-	-	cl	++ +	-						
H	10	scl	-	scl	++ +	-	-	+	-	-	cl	scl	-	-	-	-	ol	ol	-
L	10	< cl	-	< cl	cl	-	-	++ -n	-	-	cl	< cl	-						
M	10	cl	-	cl	++ L scl	-	-	+	-	-	cl	cl	-	+	+	+	ol	ol	-
P	10	cl	-	cl	cl	-	+-	+-	-	-	cl	cl	-						

O*: O pooled

(<)CL: clear lysis

(<)OL: opaque lysis

SCL: semi confluent lysis

<< : Merging plaques towards semi-confluent lysis

Strain M 19 (A)

Labcode	Phage type	Phages at Routine Test Dilution (<i>S.Typhimurium</i>)																	
		1	2	3	4	5	6	7	8	10	11	12	13	14	15	16	17	18	19
HPA	15a	-	-	-	-	-	-	-	-	-	ol	ol	ol	-	ol	-	ol	-	ol
5	15a	-	-	-	-	-	-	-	-	-	ol	cl	cl	-	ol	-	++ +	-	++ +
6	15a	-	-	-	-	-	-	-	-	-	ol	scl	cl	-	ol	-	scl	-	±
9	15a	-	-	-	-	-	-	-	-	-	ol	cl	cl	-	ol	-	ol	-	±L
17	15a	-	-	-	-	-	-	-	-	-	ol	< cl	cl	-	ol	-	±/ n	-	+++ n< <ss
22	15a	-	-	-	-	-	-	-	-	-	ol	< cl	ol	-	ol	-	ol	-	++
26	15a	-	-	-	-	-	-	-	-	-	ol	< cl	cl	-	< ol	-	< ol	2	±
A	U289	-	-	-	-	-	-	-	-	-	scl	scl	scl	-	ol	-	++	-	++
B	15a	-	-	-	-	-	-	-	-	-	scl	cl	cl	-	ol	-	ol	-	scl
C	15a	-	-	-	-	-	-	-	-	-	scl	cl	cl	-	scl	-	scl	-	scl
E	15a	-	-	-	-	-	-	-	-	-	ol	< cl	< cl	-	scl	-	ol	-	ol
G	15a	-	-	-	-	-	-	-	-	-	scl	cl	cl	-	< ol	-	++ +	-	++ +
H	15a	-	-	-	-	-	-	-	-	-	ol	scl	scl	-	ol	-	ol	-	scl
L	15a	-	-	-	-	-	-	-	-	-	ol	cl	cl	-	scl	-	ol	-	scl
M	15a	-	-	-	-	-	-	-	-	-	ol	scl	cl	-	ol	-	ol	-	scl
P	15a	-	-	-	-	-	-	-	-	-	ol	cl	cl	-	ol	-	ol	-	scl

O*: O pooled

(<)CL: clear lysis

(<)OL: opaque lysis

SCL: semi confluent lysis

<< : Merging plaques towards semi-confluent lysis

Strain M 19 (B)

Labcode	Phage type	Phages at Routine Test Dilution (<i>S.Typhimurium</i>)												Additional phages					
		20	21	22	23	24	25	26	27	28	29	32	35	1	2	3	10	10 var	18
HPA	15a	ol	-	-	-	-	-	-	±	-	-	ol	-	±	±	±	ol	ol	-
5	15a	ol	-	-	-	-	-	-	-	-	-	++ +	±	-	+	+	ol	ol	-
6	15a	(<)ol	-	-	-	-	-	-	+ L	±	-	± L	+ L						
9	15a	ol	-	-	-	-	-	-	± L	-	-	ol	3L	± n	± n	+ n	ol	ol	-
17	15a	< ol	-	-	-	-	-	-	+ ln	3 ln	-	ol	+l << ss	++ ns	++ ns	++ ns	sol	sol	± ln
22	15a	< ol	-	-	-	-	-	-	±	-	-	< ol	1	±	±	±	ol	< ol	3
26	15a	ol	-	-	-	-	-	-	-	-	-	scl	- 1						
A	U289	++	-	-	-	-	-	-	+	-	-	ol	+	+	+	+	scl	scl	+
B	15a	ol	-	-	-	-	-	-	++	-	-	scl	++ +						
C	15a	scl	-	-	-	-	-	-	+	-	-	scl	-	±	+	++	ol	ol	-
E	15a	ol	-	-	-	-	-	-	-	-	-	ol	+l						
G	15a	ol	-	-	-	-	-	-	-	-	-	++ +	-						
H	15a	-	-	-	-	-	-	-	+	-	-	scl	-	-	-	-	ol	ol	+
L	15a	scl	-	-	-	-	-	-	8l	-	-	ol	6l						
M	15a	scl	-	-	-	-	-	-	++ L scl	-	-	scl	++ L	++	++	++	ol	ol	-
P	15a	ol	-	-	-	-	-	-	+	-	-	ol	+-						

O*: O pooled

(<)CL: clear lysis

(<)OL: opaque lysis

SCL: semi confluent lysis

<< : Merging plaques towards semi-confluent lysis

Strain M 20 (A)

Labcode	Phage type	Phages at Routine Test Dilution (<i>S.Typhimurium</i>)																	
		1	2	3	4	5	6	7	8	10	11	12	13	14	15	16	17	18	19
HPA	110	-	-	-	-	-	-	-	-	-	-	-	cl	-	-	-	-	cl	-
5	110	-	-	-	-	-	-	-	\pm 10	-	-	-	cl	-	-	-	-	cl	-
6	110	-	-	-	-	-	-	-	-	-	-	-	scl	-	-	-	-	++ +L	-
9	110	-	-	-	-	-	-	-	-	-	-	-	cl	-	-	-	-	cl	-
17	110	-	-	-	-	-	-	-	-	-	-	-	< cl	-	-	-	-	cl	-
22	110	-	-	-	-	-	-	-	-	-	-	-	< cl	-	-	-	-	< cl	-
26	110	-	-	-	-	-	-	-	-	-	-	-	cl	-	-	-	-	scl	-
A	110	-	-	-	-	-	-	-	-	-	-	-	scl	-	-	-	-	scl	-
B	110	-	-	-	-	-	-	-	-	-	-	-	cl	-	-	-	-	++ +	-
C	110	-	-	-	-	-	-	-	5-	-	-	-	cl	-	-	-	-	scl	-
E	110	-	-	-	-	-	-	-	-	-	-	-	< cl	-	-	-	-	ol	-
G	110	-	-	-	-	-	-	-	-	-	-	-	cl	-	-	-	-	cl	-
H	110	-	-	-	-	-	-	-	-	-	-	-	scl	-	-	-	-	scl	-
L	110	-	-	-	-	-	-	-	-	-	-	-	cl	-	-	-	-	cl	-
M	110	-	-	-	-	-	-	-	-	-	-	-	cl	-	-	-	-	cl	-
P	110	-	-	-	-	-	-	-	-	-	-	-	cl	-	-	-	-	cl	-

O*: O pooled

(<)CL: clear lysis

(<)OL: opaque lysis

SCL: semi confluent lysis

<< : Merging plaques towards semi-confluent lysis

Strain M 20 (B)

Labcode	Phage type	Phages at Routine Test Dilution (<i>S.Typhimurium</i>)												Additional phages					
		20	21	22	23	24	25	26	27	28	29	32	35	1	2	3	10	10	18
HPA	110	-	-	-	-	-	-	-	±	-	-	-	±	±	±	±	ol	ol	-
5	110	-	-	-	-	-	-	-	-	-1	-	-	±	-	±	±	ol	ol	-
6	110	-	-	-	-	-	-	-	-	-	-	-	-						
9	110	-	-	-	-	-	-	-	± L	-	-	-	-	+n	+n	++ n	ol	ol	-
17	110	-	-	-	-	-	-	-	± ns	-	-	-	+ ns	± ns m	++ ns m	++ ns m	ol .	sol	-
22	110	-	-	-	-	-	-	2	-	-	-	-	-	±	+	±	ol	< ol	-
26	110	-	-	-	-	-	-	-	-	-	-	-	-						
A	110	-	-	-	-	-	-	-	-	-	-	-	-	+	+	++	scl	scl	-
B	110	-	-	-	-	-	-	-	+	-	-	-	+						
C	110	-	-	-	-	-	-	-	3-	-	-	-	-	+	++	++ +	ol	ol	-
E	110	-	-	-	-	-	-	-	3n	-	-	-	3n						
G	110	-	-	-	-	-	-	-	-	-	-	-	-						
H	110	-	-	-	-	-	-	-	±	-	-	-	-	-	+	+	ol	ol	-
L	110	-	-	-	-	-	-	-	2n	-	-	-	-						
M	110	-	-	-	-	-	-	-	-	-	-	-	-	+	++	++	ol	ol	-
P	110	-	-	-	-	-	-	-	+-	-	-	-	+-						

O*: O pooled

(<)CL: clear lysis

(<)OL: opaque lysis

SCL: semi confluent lysis

<< : Merging plaques towards semi-confluent lysis

Annex 4. Results antimicrobial susceptibility testing per antibiotic

AMOXICILLIN + CLAVALUNATE (AMC)												
Lab code	Method ¹	AST 1	AST 2	AST 3	AST 4	AST 5	AST 6	AST 7	AST 8	AST 9	AST 10	ATCC 25922
CRL	MIC	16/8	8/4	16/8	1/0.5	> 16/8	1/0.5	16/8	16/8	16/8	16/8	2/1 – 8/4
20	MIC	16	8	8	≤ 2	> 32	≤ 2	16	16	16	16	4
22	MIC	8	8	8	≤ 2	> 32	≤ 2	16	16	16	16	8
24	MIC	16/8	8/4	16/8	8/4	64/32	≤ 2/1	16/8	32/16	16/8	16/8	8/4
26	MIC	16/8	8/4	16/8	≤ 2/1	> 32/16	≤ 2/1	16/8	16/8	16/8	16/8	4/2
B	MIC	8/4	4/2	8/4	1/0.5	32/8	1/0.5	64/32	8/4	64/32	8/4	2/1
Q	MIC	S	S	S	S	R	S	I	I	S	I	S
R	MIC	16/8	8/4	16/8	≤ 2/1	> 32/16	≤ 2/1	16/8	16/8	16/8	16/8	4/2
	Disc load in µg											ATCC 25922 18-24
1	30	13	18	15	25	6	24	15	6	14	13	21
2	30	16	21	16	25	8	26	14	14	15	15	19
3	30	16	20	17	25	8	25	8	14	13	15	21
4	30	21	22	21	29	11	28	17	15	17	16	23
6	30	20	20	22	28	6	25	16	13	17	15	22
9	30	22	21	18	28	9	30	15	16	15	16	23
11	30	21	20	20	25	14	25	18	18	18	18	23
12	30	19	22	19	29	11	29	17	14	16	18	24
13	30	16	20	18	27	6	25	14	14	14	14	22
14	30	21	21	22	27	6	26	18	18	18	18	21
15	30	21	21	19	28	9	29	16	16	16	16	22
16	30	21	20	21	24	9	24	18	14	17	15	20
17	30	23	23	22	29	11	27	18	15	15	15	22
18	30	16	19	20	26	6	20	14	12	14	14	22
21	30	21	21	19	29	11	27	17	17	18	19	22
25	30	19	20	18	26	6	26	14	14	14	14	20
A	30	21	22	17	28	7	28	17	16	16	15	23
D	30	18	20	19	29	6	32	14	12	14	15	22
F	30	19	18	16	24	6	22	11	11	13	12	20
J	30	16	20	13	27	6	28	14	14	14	15	22
L	30	22	25	20	29	6	28	18	21	15	17	23
Mean		19.1	20.7	18.7	27.0	8.0	26.4	15.4	14.5	15.4	15.5	21.8
SD		2.7	1.6	2.4	1.8	2.4	2.7	2.6	3.0	1.6	1.7	1.3
2SD		5.4	3.2	4.8	3.6	4.8	5.5	5.1	6.0	3.3	3.5	2.5

¹ For MIC the concentration is given in µg/ml. For Disc diffusion the zone diameter is given in mm.
mean: mean zone diameter (in mm); SD: standard deviation in mm;

AMPICILLIN (AMP)												
Lab code	Method ¹	AST 1	AST 2	AST 3	AST 4	AST 5	AST 6	AST 7	AST 8	AST 9	AST 10	ATCC 25922
CRL	MIC	> 64	> 64	> 64	≤ 0.5	> 64	1	> 64	> 64	> 64	> 64	2 – 8
8	MIC	> 32	> 32	> 32	1	> 32	1	> 32	> 32	32	> 32	8
11	MIC	> 64	> 64	> 64	1	> 64	2	> 64	> 64	> 64	> 64	4
19	MIC	> 64	> 64	> 64	1	> 64	1	> 64	> 64	> 64	> 64	4
20	MIC	> 32	> 32	> 32	≤ 1	> 32	2	> 32	> 32	> 32	> 32	8
22	MIC	> 32	> 32	> 32	≤ 1	> 32	2	> 32	> 32	> 32	> 32	4
23	MIC	> 32	> 32	> 32	1	> 32	1	> 32	> 32	> 32	> 32	4
24	MIC	> 64	> 64	> 64	> 64	> 64	≤ 2	64	> 64	> 64	> 64	8
26	MIC	> 32	> 32	> 32	≤ 1	> 32	≤ 1	> 32	> 32	> 32	> 32	2
B	MIC	> 64	> 64	> 64	1	> 64	1	> 64	> 64	> 64	> 64	4
E	MIC	> 16	> 16	> 16	1	> 16	2	> 16	> 16	> 16	> 16	2
Q	MIC	R	R	R	S	R	S	R	R	R	R	S
R	MIC	> 32	> 32	> 32	≤ 1	> 32	2	> 32	> 32	> 32	> 32	2
	Disk load in ug											ATCC 25922
												16 -22
1	10	6	6	6	22	6	21	6	6	6	6	19
2	10	8	8	8	24	8	22	8	8	8	8	18
3	10	6	6	6	26	6	25	6	6	6	6	18
4	10	6	6	6	26	6	23	6	6	6	6	17
5	10	6	6	6	29	6	27	6	6	6	6	22
6	10	6	6	6	26	6	23	6	6	6	6	20
7	10	6	6	6	23	6	22	6	6	6	6	16
9	10	8	7	8	28	8	29	7	8	7	8	19
11	10	6	6	6	24	6	24	6	6	6	6	19
12	10	6	6	6	26	6	27	6	6	6	6	18
13	10	6	6	6	22	6	22	6	6	6	6	19
14	10	6	6	6	25	6	25	6	6	6	6	18
15	10	6	6	6	26	6	25	16	16	17	6	17
16	10	6	6	6	24	6	24	6	6	6	6	21
17	10	6	6	6	26	6	25	6	6	6	6	19
18	10	6	6	6	22	6	21	6	6	6	6	21
21	10	6	6	6	23	6	22	6	6	6	6	18
25	10	6	6	6	24	6	24	6	6	6	6	18
A	10	7	7	7	27	7	27	7	7	7	7	17
C	10	6	6	6	27	6	25	6	6	6	6	20
F	10	6	6	6	24	6	19	6	6	6	6	16
G	10	6	6	6	26	6	24	6	6	6	6	19
H	10	6	6	6	20	6	22	6	6	6	6	18
J	10	6	6	6	26	6	24	6	6	6	6	20
L	10	6	6	6	27	6	26	6	6	6	6	20
Mean		6.2	6.2	6.2	24.9	6.2	23.9	6.6	6.6	6.6	6.2	18.7
SD		0.6	0.5	0.6	2.1	0.6	2.3	2.0	2.0	2.2	0.6	1.5
2SD		1.2	0.9	1.2	4.3	1.2	4.6	4.0	4.1	4.4	1.2	3.0

¹ For MIC the concentration is given in µg/ml. For Disc diffusion the zone diameter is given in mm.
mean: mean zone diameter (in mm); SD: standard deviation in mm;

CEFOTAXIME (CEF)												
Lab code	Method ¹	AST 1	AST 2	AST 3	AST 4	AST 5	AST 6	AST 7	AST 8	AST 9	AST 10	ATCC 25922
CRL	MIC	≤ 0.12	0.25	≤ 0.12	≤ 0.12	> 16	≤ 0.12	≤ 0.12	0.5	0.25	≤ 0.12	0.03-0.125
11	MIC	≤ 0.125	≤ 0.125	≤ 0.125	≤ 0.125	16	≤ 0.125	≤ 0.125	≤ 0.125	≤ 0.125	≤ 0.125	0.125
19	MIC	≤ 0.125	0.25	≤ 0.125	≤ 0.125	> 16	≤ 0.125	≤ 0.125	0.5	0.5	≤ 0.125	≤ 0.125
20	MIC	1	1	≤ 0.5	≤ 0.5	> 8	1	≤ 0.5	1	1	1	< 0.5
23	MIC	0.12	0.12	0.06	0.06	32	0.06	0.12	0.25	0.12	0.06	0.06
24	MIC	≤ 4	≤ 4	≤ 4	≤ 4	32	≤ 4	≤ 4	≤ 4	≤ 4	≤ 4	≤ 4
B	MIC	≤ 0.25	≤ 0.25	≤ 0.25	≤ 0.25	> 32	≤ 0.25	≤ 0.25	0.5	≤ 0.25	≤ 0.25	≤ 0.25
E	MIC	1	1	1	1	> 16	1	1	1	1	1	1
Q	MIC	S	S	S	S	R	S	S	S	S	S	S
	Disk load in µg											ATCC 25922
												29-35
1	30	31	27	30	30	11	29	30	27	27	29	32
3	30	32	33	35	34	13	31	30	33	30	33	35
4	30	31	29	31	33	12	32	32	31	32	33	32
5	30	37	36	38	39	18	38	37	36	37	39	37
6	30	35	32	35	35	15	35	32	33	33	34	34
11	30	29	28	29	29	16	29	28	27	29	28	30
12	30	32	31	32	34	12	34	33	32	32	32	34
13	30	28	26	27	28	11	28	27	26	26	28	30
14	30	31	33	33	33	10	30	32	30	30	30	31
15	30	35	33	36	35	16	36	35	35	36	34	36
16	30	30	29	29	28	12	30	28	27	28	30	29
17	30	34	34	34	34	15	34	32	32	32	33	32
18	30	29	28	29	31	12	27	27	25	30	30	29
21	30	31	25	32	31	10	30	29	26	29	23	31
25	30	30	30	30	30	11	30	30	30	28	28	31
A	30	33	33	34	34	10	33	33	32	33	31	34
C	30	38	36	38	34	13	35	37	33	35	38	36
F	30	28	28	30	30	9	28	28	28	28	29	30
G	30	29	30	30	31	12	31	32	29	30	30	31
H	30	32	30	32	29	10	33	28	28	32	29	32
J	30	33	32	36	36	12	32	36	32	36	31	36
L	30	34	32	32	34	13	34	33	31	34	31	36
Mean		31.9	30.7	32.4	32.4	12.4	31.8	31.3	30.1	31.2	31.0	32.6
SD		2.8	3.0	3.1	2.9	2.3	2.9	3.1	3.1	3.1	3.5	2.5
2SD		5.5	6.0	6.1	5.7	4.6	5.8	6.2	6.2	6.2	6.9	5.1

¹ For MIC the concentration is given in µg/ml. For Disc diffusion the zone diameter is given in mm.
 mean: mean zone diameter (in mm); SD: standard deviation in mm;

CHLORAMPHENICOL (CHL)												
Lab code	Method ¹	AST 1	AST 2	AST 3	AST 4	AST 5	AST 6	AST 7	AST 8	AST 9	AST 10	ATCC 25922
CRL	MIC	8	16	8	8	8	8	8	8	8	> 128	2-8
8	MIC	4	8	4	4	4	4	4	4	4	> 128	4
11	MIC	2	4	2	2	2	2	1	1	2	64	2
19	MIC	8	16	8	8	8	8	8	8	8	> 128	4
20	MIC	4	8	8	4	8	8	4	8	8	> 64	4
22	MIC	4	8	4	4	8	4	4	4	4	> 64	4
23	MIC	4	8	4	4	4	4	4	4	4	> 128	4
24	MIC	4	8	8	4	8	8	4	8	4	> 64	4
26	MIC	4	16	8	4	4	4	4	4	4	> 64	4
B	MIC	4	8	4	4	8	4	4	4	4	> 32	4
E	MIC	4	8	8	8	8	8	8	4	4	> 32	8
Q	MIC	S	S	S	S	S	S	S	S	S	R	S
R	MIC	4	8	8	4	8	4	4	8	4	> 64	4
	Disk load in ug											ATCC 25922
												21-27
1	30	25	18	21	23	22	21	25	22	21	6	22
2	30	27	21	23	25	23	26	26	25	26	8	25
3	30	25	19	24	24	22	25	24	25	24	6	22
4	30	26	22	25	29	25	25	29	27	28	6	24
5	30	27	22	26	29	26	27	29	28	28	6	24
6	30	25	22	24	26	23	24	26	25	25	6	24
7	30	25	22	24	28	22	23	28	25	25	6	26
11	30	27	23	26	26	24	25	25	26	27	6	27
12	30	27	24	25	27	24	28	26	27	26	6	26
13	30	25	22	24	25	23	25	28	23	24	6	25
14	30	27	23	28	27	26	26	28	27	26	6	25
15	30	26	22	25	27	25	27	28	26	26	6	24
16	30	26	24	26	26	25	25	27	26	24	6	27
17	30	27	25	27	27	25	27	27	26	26	6	26
18	30	21	22	26	26	25	26	24	25	24	6	26
21	30	26	20	26	26	21	23	26	25	25	6	23
25	30	26	24	23	25	23	25	25	25	26	6	25
A	30	27	23	27	30	25	27	30	29	30	7	25
C	30	26	22	26	28	28	28	29	28	27	6	27
D	30	28	26	29	30	26	30	32	32	32	6	30
F	30	23	20	23	25	23	23	25	24	25	6	24
G	30	26	22	25	25	25	25	25	26	24	6	25
H	30	24	19	20	22	18	22	23	22	22	6	23
J	30	27	25	28	29	24	26	30	28	25	6	25
L	30	29	26	29	29	27	29	32	29	29	6	30
Mean		25.9	22.3	25.2	26.6	24.0	25.5	27.1	26.0	25.8	6.1	25.2
SD		1.6	2.1	2.2	2.1	2.1	2.1	2.4	2.2	2.4	0.4	2.0
2SD		3.3	4.2	4.5	4.2	4.2	4.3	4.9	4.5	4.8	0.9	4.0

¹ For MIC the concentration is given in µg/ml. For Disc diffusion the zone diameter is given in mm.
mean: mean zone diameter (in mm); SD: standard deviation in mm;

CIPROFLOXACIN (CIP)												
Lab code	Method ¹	AST 1	AST 2	AST 3	AST 4	AST 5	AST 6	AST 7	AST 8	AST 9	AST 10	ATCC 25922
CRL	MIC	≤ 0.06	≤ 0.06	≤ 0.06	0.5	≤ 0.06	0.25	0.25	1	> 8	≤ 0.06	0.004-0.016
11	MIC	≤ 0.063	≤ 0.063	≤ 0.063	0.5	≤ 0.063	0.25	0.25	0.25	> 8	≤ 0.063	≤ 0.063
19	MIC	≤ 0.06	≤ 0.06	≤ 0.06	0.25	≤ 0.06	0.25	0.25	0.5	8	≤ 0.06	≤ 0.06
20	MIC	≤ 0.03	≤ 0.03	≤ 0.03	0.5	≤ 0.03	0.5	0.25	0.5	> 4	≤ 0.03	< 0.03
22	MIC	≤ 0.03	0.06	≤ 0.03	0.5	≤ 0.03	0.25	0.25	0.5	> 4	≤ 0.03	≤ 0.03
23	MIC	0.03	0.06	0.03	0.5	0.03	0.25	0.25	0.5	8	0.03	0.015
24	MIC	≤ 0.06	≤ 0.06	≤ 0.06	0.5	≤ 0.06	0.12	0.25	0.5	> 8	0.06	≤ 0.06
26	MIC	≤ 0.03	≤ 0.03	≤ 0.03	0.25	≤ 0.03	0.25	0.25	0.25	> 4	≤ 0.03	≤ 0.03
B	MIC	≤ 0.032	≤ 0.064	≤ 0.032	0.5	≤ 0.032	0.25	0.25	0.5	> 4	0.125	≤ 0.032
C	MIC				0.25		0.19	0.125	0.25			
E	MIC	0.06	0.06	0.06	0.5	0.06	0.25	0.5	1	16	0.06	0.06
Q	MIC	S	S	S	S	S	S	S	S	R	S	S
R	MIC	≤ 0.03	≤ 0.03	≤ 0.03	0.25	≤ 0.03	0.12	0.25	0.5	> 4	≤ 0.03	≤ 0.03
	Disk load in µg											ATCC 25922 30-40
1	5	31	28	33	22	32	25	22	20	7	29	33
2	5	34	31	35	25	36	29	28	25	13	37	33
3	5	32	30	33	23	32	25	25	22	10	32	34
4	5	30	27	32	24	34	25	24	23	9	32	31
5	5	38	36	40	29	43	31	30	27	14	39	37
6	5	33	32	35	24	35	28	27	23	11	34	36
7	5	30	31	32	24	30	22	30	24	16	38	33
11	5	30	28	31	23	32	24	25	21	9	31	33
12	5	33	31	36	28	36	29	29	26	14	35	37
13	5	32	30	34	27	36	25	27	24	11	35	34
14	5	37	32	37	25	38	30	28	24	10	34	38
15	5	36	33	38	28	40	30	28	27	12	36	35
16	5	33	29	34	23	34	27	27	22	12	32	35
17	5	36	33	35	28	37	29	30	27	13	34	35
18	5	31	29	36	26	38	27	27	26	11	33	35
21	5	32	28	33	23	35	26	26	24	12	34	31
25	5	31	30	35	26	37	26	28	25	12	34	32
A	5	32	31	33	25	33	27	27	24	10	33	33
C	5	34	37	39		42				6	38	39
D	5	37	35	38	26	42	30	30	25	9	36	33
F	5	26	28	34	22	32	21	23	22	9	32	29
G	5	32	30	33	25	35	27	29	25	11	35	34
H	5	32	28	33	23	33	27	27	25	12	33	34
J	5	36	33	36	24	36	27	28	26	10	33	36
L	5	36	32	39	29	42	32	33	30	15	39	40
Mean		33.0	30.9	35.0	25.1	36.0	27.0	27.4	24.5	11.1	34.3	34.4
SD		2.8	2.6	2.4	2.2	3.6	2.7	2.5	2.2	2.4	2.5	2.5
2SD		5.6	5.2	4.9	4.3	7.2	5.4	4.9	4.5	4.7	5.1	5.1

¹ For MIC the concentration is given in µg/ml. For Disc diffusion the zone diameter is given in mm.
mean: mean zone diameter (in mm); SD: standard deviation in mm;

FLORFENICOL (FLO)												
Lab code	Method ¹	AST 1	AST 2	AST 3	AST 4	AST 5	AST 6	AST 7	AST 8	AST 9	AST 10	ATCC 25922
CRL	MIC	4	8	4	4	4	4	4	4	4	128	2-8
8	MIC	≤ 4	8	8	≤ 4	8	≤ 4	≤ 4	8	≤ 4	> 32	≤ 4
19	MIC	4	8	4	4	4	4	4	8	4	128	4
20	MIC	4	8	4	4	4	4	4	4	4	> 64	4
22	MIC	4	8	4	4	4	4	4	4	4	> 64	4
23	MIC	≤ 4	8	≤ 4	≤ 4	≤ 4	≤ 4	≤ 4	8	≤ 4	> 32	≤ 4
24	MIC	4	8	4	4	4	4	≤ 2	8	4	> 64	4
26	MIC	4	8	4	4	4	4	≤ 2	4	4	> 64	4
R	MIC	4	4	4	≤ 2	4	4	≤ 2	4	4	64	≤ 2
	Disk load in µg											ATCC 25922
												22-28
11	30	26	22	24	25	24	25	25	25	25	6	26
14	30	28	22	25	27	24	26	29	27	27	6	27
15	30	29	23	29	28	28	31	30	25	30	6	27
16	30	25	22	24	25	22	24	27	24	24	6	25
18	30	28	25	22	30	27	22	29	29	29	6	26
A	30	28	25	29	27	27	27	31	28	27	7	28
Mean		27.3	23.2	25.5	27.0	25.3	25.8	28.5	26.3	27.0	6.2	26.5
SD		1.5	1.5	2.9	1.9	2.3	3.1	2.2	2.0	2.3	0.4	1.0
2SD		3.0	2.9	5.8	3.8	4.7	6.1	4.3	3.9	4.6	0.8	2.1

¹ For MIC the concentration is given in µg/ml. For Disc diffusion the zone diameter is given in mm.
 mean: mean zone diameter (in mm); SD: standard deviation in mm;

GENTAMICIN (GEN)												
Lab code	Method ¹	AST 1	AST 2	AST 3	AST 4	AST 5	AST 6	AST 7	AST 8	AST 9	AST 10	ATCC 25922
CRL	MIC	0.5	0.5	0.5	1	0.5	≤ 0.25	> 32	> 32	16	1	0.25-1
8	MIC	1	1	≤ 0.5	1	2	1	64	> 64	32	1	1
11	MIC	0.5	0.5	0.5	0.5	0.5	0.5	> 32	> 32	32	0.5	0.5
19	MIC	0.5	0.5	≤ 0.25	0.5	≤ 0.25	0.5	> 32	> 32	16	0.5	0.5
20	MIC	≤ 1	≤ 1	≤ 1	≤ 1	≤ 1	≤ 1	> 32	> 32	16	≤ 1	< 1
22	MIC	≤ 1	≤ 1	≤ 1	≤ 1	≤ 1	≤ 1	> 32	> 32	16	≤ 1	≤ 1
23	MIC	≤ 0.05	1	1	≤ 0.05	≤ 0.05	1	> 64	> 64	32	2	1
24	MIC	≤ 1	≤ 1	≤ 1	≤ 1	≤ 1	≤ 1	> 32	> 32	16	≤ 1	≤ 1
26	MIC	≤ 1	≤ 1	≤ 1	≤ 1	≤ 1	≤ 1	> 32	> 32	16	≤ 1	≤ 1
B	MIC	0.5	0.5	0.5	1	0.5	0.5	> 32	> 32	16	0.5	0.5
E	MIC	1	1	1	0.5	0.5	0.5	> 8	> 8	> 8	1	0.5
Q	MIC	S	S	S	S	S	S	R	R	R	R	S
R	MIC	≤ 1	≤ 1	≤ 1	≤ 1	≤ 1	≤ 1	> 32	> 32	8	≤ 1	≤ 1
	Disk load in µg											ATCC 25922
												19-26
1	10	22	20	21	22	22	21	6	6	12	22	20
2	10	24	23	22	22	25	23	9	8	13	22	24
3	10	24	23	24	22	23	23	8	6	11	22	23
4	10	21	20	22	22	23	22	8	6	10	22	22
6	10	24	24	25	23	25	25	7	6	12	24	24
7	10	18	18	21	17	19	18	7	6	10	18	18
9	10	21	19	20	21	22	22	10	8	11	20	21
11	10	22	20	20	21	21	21	7	6	10	22	22
12	10	21	20	20	21	21	22	10	6	11	20	22
13	10	21	22	21	22	22	23	10	6	12	21	22
14	10	20	20	21	20	22	21	6	6	10	20	20
15	10	27	24	25	25	27	24	6	6	11	23	24
16	10	23	22	22	21	22	23	6	6	9	21	24
17	10	24	23	23	22	24	23	9	6	13	22	22
18	10	23	22	22	22	24	22	6	6	11	22	23
21	10	22	20	22	20	20	20	10	6	13	20	20
25	10	19	19	18	18	19	19	8	6	9	17	19
A	10	22	23	24	24	24	24	8	7	10	22	21
C	10	24	24	24	23	28	26	9	6	12	25	25
D	10	23	22	23	22	25	23	6	6	8	22	21
F	10	18	18	19	19	20	18	7	6	9	18	18
G	10	21	19	21	21	22	22	6	6	10	22	20
H	10	22	21	19	21	21	21	6	6	6	20	22
J	10	24	21	22	20	23	23	6	6	10	21	24
L	10	22	22	22	22	23	22	11	6	14	22	24
Mean		22.1	21.2	21.7	21.3	22.7	22.0	7.7	6.2	10.7	21.2	21.8
SD		2.1	1.9	1.8	1.7	2.2	1.9	1.7	0.6	1.8	1.8	2.0
2SD		4.1	3.7	3.7	3.5	4.5	3.9	3.3	1.2	3.5	3.6	4.0

¹ For MIC the concentration is given in µg/ml. For Disc diffusion the zone diameter is given in mm.
 mean: mean zone diameter (in mm); SD: standard deviation in mm;

KANAMYCIN (KAN)												
Lab code	Method ¹	AST 1	AST 2	AST 3	AST 4	AST 5	AST 6	AST 7	AST 8	AST 9	AST 10	ATCC 25922
CRL	MIC	4	> 16	16	8	4	2	> 16	> 16	> 16	4	1-4
26	MIC	≤ 4	> 64	≤ 4	≤ 4	≤ 4	≤ 4	16	> 64	> 64	≤ 4	≤ 4
B	MIC	2	> 32	4	2	2	2	16	> 32	> 32	4	4
E	MIC	2	> 32	4	2	2	2	> 32	> 32	> 32	4	4
Q	MIC	S	R	S	S	S	S	R	R	R	S	S
	Disk load in µg											ATCC 25922
												17 -25
1	30	23	6	21	21	22	23	10	6	6	22	20
2	30	23	8	22	22	23	23	17	8	8	22	23
3	30	22	6	22	22	22	22	15	6	6	20	21
4	30	21	6	22	20	22	21	13	6	6	21	20
6	30	23	6	23	23	24	24	12	6	6	22	23
7	30	18	6	18	19	19	20	18	6	6	22	20
11	30	22	6	21	20	21	22	21	6	6	20	21
12	30	21	6	22	21	21	22	18	6	6	20	22
13	30	21	6	20	19	21	21	17	6	6	20	20
14	30	22	6	22	21	23	22	18	6	6	21	21
15	30	25	6	24	23	26	25	19	6	6	23	22
16	30	22	6	22	20	22	21	16	6	6	20	22
17	30	24	6	24	23	25	24	19	6	6	22	22
18	30	21	6	20	20	21	20	17	6	6	20	23
21	30	32	15	33	30	29	31	30	14	15	31	30
25	30	20	6	20	19	21	22	18	6	6	19	19
A	30	23	7	24	23	23	23	20	7	7	22	20
D	30	23	6	22	22	25	24	19	6	6	22	20
F	30	19	6	20	20	20	19	14	6	6	18	18
G	30	22	6	23	21	23	23	15	6	6	24	22
H	30	21	6	21	20	21	21	10	6	6	20	21
J	30	22	6	22	20	23	21	11	6	6	20	23
L	30	22	6	22	22	23	23	17	6	6	20	21
Mean		22.3	6.5	22.2	21.3	22.6	22.5	16.7	6.5	6.5	21.3	21.5
SD		2.6	1.9	2.8	2.3	2.2	2.4	4.3	1.7	1.9	2.5	2.3
2SD		5.2	3.8	5.5	4.6	4.3	4.7	8.5	3.4	3.8	5.0	4.6

¹ For MIC the concentration is given in µg/ml. For Disk diffusion the zone diameter is given in mm.
mean: mean zone diameter (in mm); SD: standard deviation in mm;

NALIDIXIC ACID (NAL)												
Lab code	Method ¹	AST 1	AST 2	AST 3	AST 4	AST 5	AST 6	AST 7	AST 8	AST 9	AST 10	ATCC 25922
CRL	MIC	4	8	4	16	4	> 128	> 128	> 128	> 128	4	1-4
8	MIC	4	8	4	16	4	> 128	> 128	> 128	> 128	4	2
19	MIC	4	8	4	16	4	> 128	> 128	> 128	> 128	4	≤ 2
20	MIC	≤ 8	≤ 8	≤ 8	16	≤ 8	> 128	> 128	> 128	> 128	≤ 8	< 8
22	MIC	≤ 8	≤ 8	≤ 8	≤ 8	≤ 8	> 128	> 128	> 128	> 128	≤ 8	≤ 8
23	MIC	4	8	4	16	4	> 128	> 128	> 128	> 128	4	4
24	MIC	≤ 4	8	≤ 4	16	≤ 4	> 128	> 128	> 128	> 128	≤ 4	≤ 4
26	MIC	≤ 4	8	≤ 4	8	≤ 4	> 128	> 128	> 128	> 128	≤ 4	≤ 4
B	MIC	2	4	2	8	2	> 64	> 64	> 64	> 64	4	2
E	MIC	8	16	8	16	8	> 32	> 32	> 32	> 32	8	4
R	MIC	≤ 8	≤ 8	≤ 8	≤ 8	≤ 8	> 128	> 128	> 128	> 128	≤ 8	≤ 8
	Disk load in µg											ATCC 25922
												22-28
1	30	25	15	24	15	23	6	6	6	6	22	25
2	30	21	17	21	16	23	8	8	8	8	22	24
3	30	21	17	21	14	20	6	6	6	6	22	26
4	30	22	19	24	17	25	6	6	6	6	23	26
5	30	24	23	26	19	26	6	6	6	6	26	29
6	30	20	17	20	13	20	6	6	6	6	20	25
7	30	20	18	23	13	25	6	6	6	6	23	25
9	30	25	19	23	20	26	9	8	9	7	24	27
11	30	23	19	22	19	23	6	6	6	6	22	25
12	30	27	22	25	18	27	6	6	6	6	27	30
13	30	22	18	24	15	22	6	6	6	6	24	27
14	30	23	20	24	18	24	6	6	6	6	23	25
15	30	25	21	24	20	27	6	6	6	6	25	23
16	30	20	18	20	15	21	6	6	6	6	20	24
17	30	26	24	27	21	28	6	6	6	6	27	22
18	30	22	20	22	17	25	6	6	6	6	22	24
21	30	26	21	26	19	24	6	6	6	6	24	28
25	30	23	20	23	19	24	6	6	6	6	23	24
A	30	23	18	23	16	26	7	7	7	7	22	25
C	30	21	20	23	16	24	6	6	6	6	23	27
D	30	25	20	25	17	30	6	6	6	6	23	28
F	30	20	17	21	15	18	6	6	6	6	19	22
G	30	25	18	24	17	24	6	6	6	6	24	26
H	30	23	19	21	11	23	6	6	6	6	23	25
J	30	23	20	25	12	28	6	6	6	6	23	28
L	30	26	23	26	17	27	6	6	6	6	26	30
Mean		23.1	19.3	23.3	16.5	24.3	6.2	6.2	6.2	6.2	23.2	25.8
SD		2.1	2.1	1.9	2.6	2.8	0.7	0.6	0.7	0.5	2.0	2.2
2SD		4.3	4.3	3.9	5.2	5.5	1.4	1.1	1.4	0.9	3.9	4.4

¹ For MIC the concentration is given in µg/ml. For Disc diffusion the zone diameter is given in mm.

mean: mean zone diameter (in mm); SD: standard deviation in mm;

NEOMYCIN (NEO)												
Lab code	Method ¹	AST 1	AST 2	AST 3	AST 4	AST 5	AST 6	AST 7	AST 8	AST 9	AST 10	ATCC 25922
CRL	MIC	≤ 1	64	≤ 1	≤ 1	≤ 1	≤ 1	≤ 1	128	128	≤ 1	≤ 1 – 2
8	MIC	≤ 2	> 16	4	≤ 2	≤ 2	≤ 2	≤ 2	> 16	> 16	≤ 2	≤ 2
19	MIC	≤ 1	64	≤ 1	≤ 1	≤ 1	≤ 1	≤ 1	128	128	2	≤ 1
20	MIC	≤ 2	32	≤ 2	≤ 2	≤ 2	≤ 2	≤ 2	> 32	> 32	≤ 2	< 2
22	MIC	≤ 2	> 32	≤ 2	≤ 2	≤ 2	≤ 2	≤ 2	> 32	> 32	≤ 2	4
23	MIC	≤ 2	> 16	≤ 2	≤ 2	≤ 2	≤ 2	≤ 2	> 16	> 16	≤ 2	≤ 2
24	MIC	≤ 2	> 64	≤ 2	≤ 2	≤ 2	≤ 2	≤ 2	> 64	> 64	≤ 2	≤ 2
26	MIC	≤ 2	32	≤ 2	≤ 2	≤ 2	≤ 2	≤ 2	> 32	> 32	≤ 2	≤ 2
R	MIC	≤ 2	32	≤ 2	≤ 2	≤ 2	≤ 2	≤ 2	> 32	> 32	≤ 2	≤ 2
	Disk load in µg											ATCC 25922
												NA
1	30	20	7	20	19	20	19	20	7	6	19	20
3	30	21	11	21	20	20	20	20	11	6	20	20
4	30	20	11	23	21	22	20	20	10	10	20	21
6	30	22	12	23	22	24	21	23	11	10	22	20
7	30	17	11	16	15	17	16	16	10	9	17	17
11	30	18	9	17	17	17	17	16	10	8	16	17
13	30	21	13	20	19	20	20	20	10	11	20	21
14	30	17	10	18	18	18	18	17	10	6	18	17
15	30	20	10	20	20	19	21	20	6	6	19	20
18	30	21	10	20	20	22	20	19	10	6	20	21
21	30	18	12	19	18	18	18	17	11	10	18	18
A	30	23	13	22	23	24	23	22	12	11	20	22
F	30	18	10	18	16	17	15	18	9	9	16	17
Mean		19.7	10.7	19.8	19.1	19.8	19.1	19.1	9.8	8.3	19.8	19.3
SD		1.9	1.7	2.2	2.3	2.5	2.2	2.2	1.6	2.1	1.8	1.8
2SD		3.9	3.3	4.3	4.6	5.0	4.4	4.4	3.3	4.1	3.5	3.7

¹ For MIC the concentration is given in µg/ml. For Disc diffusion the zone diameter is given in mm.
mean: mean zone diameter (in mm); SD: standard deviation in mm;

STREPTOMYCIN (STR)												
Lab code	Method ¹	AST 1	AST 2	AST 3	AST 4	AST 5	AST 6	AST 7	AST 8	AST 9	AST 10	ATCC 25922
CRL	MIC	4	16	>64	> 64	16	4	> 64	32	> 64	> 64	
8	MIC	4	32	> 256	> 256	16	4	256	32	> 256	128	16
20	MIC	≤ 4	16	> 64	> 64	8	≤ 4	> 64	> 64	> 64	64	8
22	MIC	≤ 4	16	> 64	> 64	8	≤ 4	> 64	64	> 64	64	≤ 4
23	MIC	4	16	> 256	> 256	8	4	128	64	> 256	> 256	8
24	MIC	≤ 4	16	> 64	> 64	16	≤ 4	> 64	64	> 64	> 64	≤ 4
26	MIC	≤ 4	8	> 64	> 64	≤ 4	≤ 4	> 64	16	> 64	64	≤ 4
B	MIC	4	16	> 64	> 64	8	4	> 64	32	> 64	64	4
E	MIC	4	16	> 64	> 64	16	4	> 64	32	> 64	> 64	4
Q	MIC	S	S	R	R	S	S	R	R	R	R	S
R	MIC	≤ 4	8	> 64	> 64	≤ 4	≤ 4	> 64	16	> 64	64	≤ 4
	Disk load in µg											ATCC 25922
												NA
1	10	19	14	6	6	16	16	6	11	6	6	15
2	10	21	17	8	8	18	19	8	13	8	8	19
3	10	18	15	6	6	17	18	6	13	6	6	16
4	10	17	14	6	6	16	17	6	12	6	6	16
5	10	22	17	6	6	18	21	8	13	6	6	19
6	10	21	15	6	6	17	22	8	14	6	8	16
7	10	17	16	6	6	18	17	10	14	6	10	17
11	10	17	13	6	6	16	17	6	10	6	6	15
12	10	18	16	6	6	18	19	10	12	6	7	18
13	10	19	19	6	6	17	18	9	13	6	8	17
14	10	16	15	6	6	16	17	6	10	6	6	16
15	10	20	14	6	6	19	20	6	9	6	6	17
16	10	21	13	6	6	15	21	6	11	6	6	17
17	10	18	17	6	6	18	19	7	13	6	7	17
18	10	18	13	6	6	15	17	6	10	6	6	15
21	10	20	16	6	6	18	18	10	15	6	8	17
25	10	16	14	6	6	15	16	8	12	6	6	15
A	10	18	15	7	7	17	20	7	12	7	7	15
C	10	19	13	6	6	18	21	6	11	6	6	17
D	10	20	15	6	6	18	20	6	12	6	6	16
F	10	16	12	6	6	14	16	6	11	6	6	14
G	10	18	16	6	6	17	18	7	13	6	7	18
H	10	17	6	6	6	15	17	7	6	6	6	16
J	10	18	13	6	6	16	18	6	10	6	6	17
L	10	19	17	6	6	19	20	11	12	6	10	19
Mean		18.5	14.6	6.1	6.1	16.8	18.5	7.3	11.7	6.1	6.8	16.6
SD		1.7	2.5	0.4	0.4	1.4	1.8	1.6	1.9	0.4	1.2	1.4
2SD		3.4	4.9	0.9	0.9	2.7	3.5	3.2	3.8	0.9	2.4	2.7

¹ For MIC the concentration is given in µg/ml. For Disc diffusion the zone diameter is given in mm.
mean: mean zone diameter (in mm); SD: standard deviation in mm;

SULFAMETHOXAZOLE + TRIMETHOPRIM (SXT)												
Lab code	Method ¹	AST 1	AST 2	AST 3	AST 4	AST 5	AST 6	AST 7	AST 8	AST 9	AST 10	ATCC 25922
CRL	MIC	≤0.12 / 2.38	> 16/ 304	0.25/ 4.76	0.25/ 4.76	0.25/ 4.76	≤0.12 / 2.38	≤0.12 / 2.38	0.5/ 9.5	> 16/ 304	0.25/ 4.76	≤ 0.5 – 2
11	MIC	≤ 1	> 128	≤ 1	≤ 1	≤ 1	≤ 1	≤ 1	≤ 1	> 128	≤ 1	≤ 1
22	MIC	S	R	S	S	S	S	S	S	R	S	--
24	MIC	≤ 9.5/ 0.5	> 152/8	≤ 9.5/ 0.5	≤ 9.5/ 0.5	≤ 9.5/ 0.5	≤ 9.5/ 0.5	≤ 9.5/ 0.5	≤ 9.5/ 0.5	> 152/8	≤ 9.5/ 0.5	≤ 9.5/ 0.5
26	MIC	≤ 19/1	> 152/8	≤ 19/1	≤ 19/1	≤ 19/1	≤ 19/1	≤ 19/1	≤ 19/1	> 152/8	≤ 19/1	≤ 19/1
B	MIC	≤ 1	> 128	4	4	≤ 1	2	2	2	> 128	8	2
E	MIC	4	> 128	4	4	4	4	4	4	> 128	4	4
Q	MIC	S	R	S	S	S	S	S	S	R	S	S
	Disk load in µg											ATCC 25922
												24-29
1	25	27	6	24	23	28	26	27	25	6	24	25
2	25	30	8	20	20	28	26	24	27	8	20	26
3	25	28	6	25	23	29	27	26	28	6	24	27
4	25	25	6	22	18	30	25	27	26	6	21	26
5	25	33	6	28	26	35	32	32	31	6	27	29
6	25	27	6	23	20	30	26	27	27	6	22	26
7	25	26	6	21	17	26	25	28	24	6	23	26
9	25	28	8	27	28	31	28	29	30	9	25	28
11	25	26	6	22	21	27	26	26	25	6	22	25
12	25	29	6	24	22	30	29	28	27	6	25	27
13	25	28	6	23	20	28	25	25	24	6	23	23
14	25	28	6	25	24	31	27	30	28	6	25	26
15	25	35	6	28	28	38	35	33	33	6	36	30
16	25	24	6	19	18	26	22	24	22	6	18	24
18	25	26	6	24	23	28	28	28	25	6	20	26
21	25	31	6	27	24	32	29	30	26	6	26	28
A	25	27	7	22	15	30	26	29	26	7	16	24
D	25	30	6	23	19	31	27	32	28	6	20	26
F	25	24	6	18	14	24	24	24	25	6	18	24
H	25	26	6	21	19	27	23	26	23	6	21	23
J	25	28	6	25	21	32	27	29	27	6	22	29
L	25	31	6	25	21	34	31	32	29	6	26	29
Mean		28.0	6.2	23.5	21.1	29.8	27.0	28.0	26.6	6.3	22.9	26.2
SD		2.8	0.6	2.7	3.7	3.2	2.9	2.7	2.6	0.8	4.1	2.0
2SD		5.5	1.2	5.5	7.4	6.4	5.9	5.5	5.2	1.5	8.2	4.0

¹ For MIC the concentration is given in µg/ml. For Disc diffusion the zone diameter is given in mm.
mean: mean zone diameter (in mm); SD: standard deviation in mm;

SULPHONAMIDE (SUL)												
Lab code	Method ¹	AST 1	AST 2	AST 3	AST 4	AST 5	AST 6	AST 7	AST 8	AST 9	AST 10	ATCC 25922
CRL	MIC	16	> 1024	> 1024	> 1024	16	16	> 1024	> 1024	> 1024	> 1024	8 – 32
8	MIC	≤ 16	> 2048	> 2048	> 2048	≤ 16	32	> 2048	> 2048	> 2048	> 2048	≤ 16
19	MIC	16	> 1024	> 1024	> 1024	≤ 8	16	> 1024	> 1024	> 1024	> 1024	≤ 8
20	MIC	≤ 64	> 1024	> 1024	> 1024	128	≤ 64	> 1024	> 1024	> 1024	> 1024	< 64
22	MIC	≤ 64	> 1024	> 1024	> 1024	≤ 64	≤ 64	> 1024	> 1024	> 1024	> 1024	≤ 64
23	MIC	64	> 2048	> 2048	> 2048	64	64	> 2048	> 2048	> 2048	> 2048	≤ 16
26	MIC	64	> 512	> 512	> 512	64	64	> 512	> 512	> 512	> 512	≤ 32
Q	MIC	S	R	R	R	S	S	R	R	R	R	S
	Disk load in µg											ATCC 25922
												15 -23
2	300	23	8	8	8	21	24	8	8	8	8	24
3	23.75	12	6	6	6	17	12	6	6	6	6	16
5	250	26	6	6	6	25	27	6	6	6	6	21
6	250	23	6	6	6	22	24	6	6	6	6	20
9	3.300	22	8	8	9	25	24	8	7	9	9	24
11	300	17	6	6	6	19	17	17	6	6	6	19
12	??	23	6	6	6	25	27	6	6	6	6	24
13	300	20	6	6	6	16	20	6	6	6	6	22
14	300	20	6	6	6	20	20	6	6	6	6	21
15	300	26	6	6	6	30	29	6	6	6	6	25
17	300	24	6	6	6	27	26	6	6	6	6	26
21	300	23	6	6	6	18	22	6	6	6	6	24
25	3.300	21	6	6	6	22	21	6	6	6	6	20
A	300	29	7	7	7	25	30	7	7	7	7	22
C	300	25	6	6	6	26	25	6	6	6	6	21
D	200	28	6	6	6	34	30	6	6	6	6	23
F	300	25	6	6	6	21	23	6	6	6	6	21
G	300	23	6	6	6	26	23	6	6	6	6	23
H	300	20	6	6	6	21	23	6	6	6	6	18
J	250	17	6	6	6	17	18	6	6	6	6	18
L	300	24	6	6	6	28	26	6	6	6	6	26
Mean		22.4	6.2	6.2	6.3	23.1	23.4	6.8	6.2	6.3	6.3	22.1
SD		3.9	0.6	0.6	0.8	4.6	4.4	2.4	0.5	0.8	0.8	2.4
2SD		7.8	1.2	1.2	1.6	9.3	8.9	4.9	1.0	1.6	1.6	4.9

¹ For MIC the concentration is given in µg/ml. For Disc diffusion the zone diameter is given in mm.
mean: mean zone diameter (in mm); SD: standard deviation in mm;

TRIMETHOPRIM (TMP)												
Lab code	Method ¹	AST 1	AST 2	AST 3	AST 4	AST 5	AST 6	AST 7	AST 8	AST 9	AST 10	ATCC 25922
CRL	MIC	≤ 0.5	> 64	≤ 0.5	≤ 0.5	≤ 0.5	≤ 0.5	≤ 0.5	≤ 0.5	> 64	≤ 0.5	0.5 - 2
8	MIC	≤ 0.25	> 32	0.5	≤ 0.25	≤ 0.25	0.5	≤ 0.25	≤ 0.25	> 32	≤ 0.25	1
11	MIC	≤ 0.25	> 32	≤ 0.25	≤ 0.25	≤ 0.25	≤ 0.25	≤ 0.25	≤ 0.25	> 32	≤ 0.25	0.5
19	MIC	≤ 0.5	> 64	≤ 0.5	≤ 0.5	≤ 0.5	≤ 0.5	≤ 0.5	≤ 0.5	> 64	1	≤ 0.5
20	MIC	≤ 4	> 32	≤ 4	≤ 4	≤ 4	≤ 4	≤ 4	≤ 4	> 32	≤ 4	< 4
22	MIC	≤ 4	> 32	≤ 4	≤ 4	≤ 4	≤ 4	≤ 4	≤ 4	> 32	≤ 4	≤ 4
23	MIC	0.5	> 32	0.5	≤ 0.25	0.5	1	0.5	0.5	> 32	0.5	1
24	MIC	≤ 4	> 32	≤ 4	≤ 4	≤ 4	≤ 4	≤ 4	≤ 4	> 32	≤ 4	≤ 4
26	MIC	≤ 4	> 32	≤ 4	≤ 4	≤ 4	≤ 4	≤ 4	≤ 4	> 32	≤ 4	≤ 4
B	MIC	≤ 0.25	> 32	≤ 0.25	≤ 0.25	≤ 0.25	0.5	≤ 0.25	≤ 0.25	> 32	0.5	0.5
R	MIC	≤ 4	> 32	≤ 4	≤ 4	≤ 4	≤ 4	≤ 4	≤ 4	> 32	≤ 4	≤ 4
	Disk load in µg											ATCC 25922
												21 -28
3	5	28	6	32	29	26	25	28	29	6	28	26
4	5	25	6	27	28	27	25	28	29	6	27	24
6	5	26	6	28	27	26	25	28	27	6	26	24
7	5	29	6	29	26	28	25	31	28	6	29	23
11	5	26	6	26	24	26	24	27	27	6	25	23
12	5	30	6	31	28	28	29	30	29	6	30	27
13	5	27	6	26	26	27	25	27	26	6	27	25
14	5	29	6	30	27	30	27	30	28	6	28	26
15	5	32	6	32	31	32	30	32	35	6	30	25
16	5	23	6	25	24	25	23	25	26	6	23	23
17	5	31	6	34	31	32	31	30	31	6	30	28
21	5	30	6	32	29	29	26	29	28	6	28	23
25	5	28	6	27	26	28	26	28	27	6	27	25
A	5	26	7	29	28	28	28	30	30	7	20	24
C	5	30	6	32	30	34	29	32	31	6	29	26
D	5	30	6	30	30	32	30	32	36	6	28	28
F	5	25	6	25	21	23	23	26	27	6	24	21
G	5	28	6	30	28	29	28	30	27	6	30	26
H	5	25	6	26	24	26	23	26	26	6	25	23
J	5	27	6	28	29	30	26	30	30	6	26	25
Mean		27.8	6.1	29.0	27.3	28.3	26.4	29.0	28.9	6.1	27.0	24.8
SD		2.4	0.2	2.7	2.6	2.8	2.5	2.1	2.8	0.2	2.6	1.8
2SD		4.8	0.4	5.4	5.2	5.5	5.0	4.2	5.5	0.4	5.3	3.7

¹ For MIC the concentration is given in µg/ml. For Disc diffusion the zone diameter is given in mm.
mean: mean zone diameter (in mm); SD: standard deviation in mm;

Annex 5. Results antimicrobial susceptibility testing per strain with MIC test

STRAIN AST - 1														
Labcode	AMC (S)	AMP (R)	CEF (S)	CHL (S)	CIP (S)	FLO (S)	GEN (S)	KAN (S)	NAL (S)	NEO (S)	STR (S)	SXT (S)	SUL (S)	TMP (S)
8	--	R	--	S	--	S	S	--	S	S	S	--	S	S
11	--	R	S	S	S	--	S	--	--	--	--	S	--	S
19	--	R	S	S	S	S	S	--	S	S	--	--	S	S
20	I	R	S	S	S	S	S	--	S	S	S	--	S	S
22	S	R	--	S	S	S	S	--	S	S	S	S	S	S
23	--	R	S	S	S	S	S	--	S	S	S	--	S	S
24	I	R	S	S	S	S	S	--	S	S	S	S	--	S
26	I	R	--	S	S	S	S	S	S	S	S	S	S	S
B	S	R	S	S	S	--	S	S	S	--	S	S	--	S
E	--	R	S	S	S	--	S	S	S	--	S	S	--	--
Q	S	R	S	S	S	--	S	S	--	--	S	S	S	--
R	I	R	--	S	S	S	S	--	S	S	S	--	--	S
Total	7	12	8	12	11	8	12	4	10	8	10	7	7	10
Number S	3	0	8	12	11	8	12	4	10	8	10	7	7	10
Number I	4*	0	0	0	0	0	0	0	0	0	0	0	0	0
Number R	0	12	0	0	0	0	0	0	0	0	0	0	0	0
Minor error														
Major error														

S = Susceptible; I = Intermediate; R = Resistant; * interpreted as S, for explanation see chapter 3.2

STRAIN AST - 2														
Labcode	AMC (S)	AMP (R)	CEF (S)	CHL (I)	CIP (S)	FLO (S)	GEN (S)	KAN (R)	NAL (S)	NEO (R)	STR (S)	SXT (R)	SUL (R)	TMP (R)
8	--	R	--	S	--	S	S	--	S	R	R	--	R	R
11	--	R	S	S	S	--	S	--	--	--	--	R	--	R
19	--	R	S	S	S	S	S	--	S	R	--	--	R	R
20	S	R	S	S	S	S	S	--	S	R	I	--	R	R
22	S	R	--	S	S	S	S	--	S	R	I	R	R	R
23	--	R	S	S	S	S	S	--	S	R	S	--	R	R
24	S	R	S	S	S	S	S	--	S	R	I	R	--	R
26	S	R	--	I	S	S	S	R	S	R	S	R	R	R
B	S	R	S	S	S	--	S	R	S	--	R	R	--	R
E	--	R	S	S	S	--	S	R	S	--	I	R	--	--
Q	S	R	S	S	S	--	S	R	--	--	S	R	R	--
R	S	R	--	S	S	S	S	--	S	R	S	--	--	R
Total	7	12	8	12	11	8	12	4	10	8	10	7	7	10
Number S	7	0	8	11*	11	8	12	0	10	0	4	0	0	0
Number I	0	0	0	1	0	0	0	0	0	0	4	0	0	0
Number R	0	12	0	0	0	0	0	4	0	8	2	7	7	10
Minor error											4			
Major error											2			

S = Susceptible; I = Intermediate; R = Resistant; * No classified as minor error. For clarification see text.

STRAIN AST - 3														
Labcode	AMC (S)	AMP (R)	CEF (S)	CHL (S)	CIP (S)	FLO (S)	GEN (S)	KAN (S)	NAL (S)	NEO (S)	STR (R)	SXT (S)	SUL (R)	TMP (S)
8	--	R	--	S	--	S	S	--	S	S	R	--	R	S
11	--	R	S	S	S	--	S	--	--	--	--	S	--	S
19	--	R	S	S	S	S	S	--	S	S	--	--	R	S
20	S	R	S	S	S	S	S	--	S	S	R	--	R	S
22	S	R	--	S	S	S	S	--	S	S	R	S	R	S
23	--	R	S	S	S	S	S	--	S	S	R	--	R	S
24	I	R	S	S	S	S	S	--	S	S	R	S	--	S
26	I	R	--	S	S	S	S	S	S	S	R	S	R	S
B	S	R	S	S	S	--	S	S	S	--	R	S	--	S
E	--	R	S	S	S	--	S	S	S	--	R	S	--	--
Q	S	R	S	S	S	--	S	S	--	--	R	S	R	--
R	I	R	--	S	S	S	S	--	S	S	R	--	--	S
Total	7	12	8	12	11	8	12	4	10	8	10	7	7	10
Number S	4	0	8	12	11	8	12	4	10	8	0	7	0	10
Number I	3*	0	0	0	0	0	0	0	0	0	0	0	0	0
Number R	0	12	0	0	0	0	0	0	0	0	10	0	7	0
Minor error														
Major error														

*S = Susceptible; I = Intermediate; R = Resistant; * interpreted as S, for explanation see chapter 3.2*

STRAIN AST - 4														
Labcode	AMC (S)	AMP (S)	CEF (S)	CHL (S)	CIP (S)	FLO (S)	GEN (S)	KAN (S)	NAL (S)	NEO (S)	STR (R)	SXT (S)	SUL (R)	TMP (S)
8	--	S	--	S	--	S	S	--	S	S	R	--	R	S
11	--	S	S	S	S	--	S	--	--	--	--	S	--	S
19	--	S	S	S	S	S	S	--	S	S	--	--	R	S
20	S	S	S	S	S	S	S	--	S	S	R	--	R	S
22	S	S	--	S	S	S	S	--	S	S	R	S	R	S
23	--	S	S	S	R	S	S	--	S	S	R	--	R	S
24	S	R	S	S	S	S	S	--	S	S	R	S	--	S
26	S	S	--	S	S	S	S	S	S	S	R	S	R	S
B	S	S	S	S	S	--	S	S	S	--	R	S	--	S
C	--	--	--	--	S	--	--	--	--	--	--	--	--	--
E	--	S	S	S	S	--	S	S	S	--	R	S	--	--
Q	S	S	S	S	S	--	S	S	--	--	R	S	R	--
R	S	S	--	S	S	S	S	--	S	S	R	--	--	S
Total	7	12	8	12	12	8	12	4	10	8	10	7	7	10
Number S	7	11	8	12	11	8	12	4	10	8	0	7	0	10
Number I	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Number R	0	1	0	0	1	0	0	0	0	0	10	0	7	0
Minor error														
Major error		1			1									

S = Susceptible; I = Intermediate; R = Resistant

STRAIN AST - 5														
Labcode	AMC (R)	AMP (R)	CEF (R)	CHL (S)	CIP (S)	FLO (S)	GEN (S)	KAN (S)	NAL (S)	NEO (S)	STR (S)	SXT (S)	SUL (S)	TMP (S)
8	--	R	--	S	--	S	S	--	S	S	I	--	S	S
11	--	R	R	S	S	--	S	--	--	--	--	S	--	S
19	--	R	R	S	S	S	S	--	S	S	--	--	S	S
20	R	R	R	S	S	S	S	--	S	S	S	--	S	S
22	R	R	--	S	S	S	S	--	S	S	S	S	S	S
23	--	R	R	S	S	S	S	--	S	S	S	--	S	S
24	R	R	I	S	S	S	S	--	S	S	I	S	--	S
26	R	R	--	S	S	S	S	S	S	S	S	S	S	S
B	R	R	R	S	S	--	S	S	S	--	S	S	--	S
E	--	R	R	S	S	--	S	S	S	--	I	S	--	--
Q	R	R	R	S	S	--	S	S	--	--	S	S	S	--
R	R	R	--	S	S	S	S	--	S	S	S	--	--	S
Total	7	12	8	12	11	8	12	4	10	8	10	7	7	10
Number S	0	0	0	12	11	8	12	4	10	8	7	7	7	10
Number I	0	0	1	0	0	0	0	0	0	0	3	0	0	0
Number R	7	12	7	0	0	0	0	0	0	0	0	0	0	0
Minor error			1								3			
Major error														

S = Susceptible; I = Intermediate; R = Resistant

STRAIN AST - 6														
Labcode	AMC (S)	AMP (S)	CEF (S)	CHL (S)	CIP (S)	FLO (S)	GEN (S)	KAN (S)	NAL (R)	NEO (S)	STR (S)	SXT (S)	SUL (S)	TMP (S)
8	--	S	--	S	--	S	S	--	R	S	S	--	S	S
11	--	S	S	S	S	--	S	--	--	--	--	S	--	S
19	--	S	S	S	S	S	S	--	R	S	--	--	S	S
20	S	S	S	S	S	S	S	--	R	S	S	--	S	S
22	S	S	--	S	S	S	S	--	R	S	S	S	S	S
23	--	S	S	S	R	S	S	--	R	S	S	--	S	S
24	S	S	S	S	S	S	S	--	R	S	S	S	--	S
26	S	S	--	S	S	S	S	S	R	S	S	S	S	S
B	S	S	S	S	S	--	S	S	R	--	S	S	--	S
C	--	--	--	--	S	--	--	--	--	--	--	--	--	--
E	--	S	S	S	S	--	S	S	R	--	S	S	--	--
Q	S	S	S	S	S	--	S	S	--	--	S	S	S	--
R	S	S	--	S	S	S	S	--	R	S	S	--	--	S
Total	7	12	8	12	12	8	12	4	10	8	10	7	7	10
Number S	7	12	8	12	11	8	12	4	0	8	10	7	7	10
Number I	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Number R	0	0	0	0	1	0	0	0	10	0	0	0	0	0
Minor error														
Major error					1									

S = Susceptible; I = Intermediate; R = Resistant

STRAIN AST - 7														
Labcode	AMC (S)	AMP (R)	CEF (S)	CHL (S)	CIP (S)	FLO (S)	GEN (R)	KAN (R)	NAL (R)	NEO (S)	STR (R)	SXT (S)	SUL (R)	TMP (S)
8	--	R	--	S	--	S	R	--	R	S	R	--	R	S
11	--	R	S	S	S	--	R	--	--	--	--	S	--	S
19	--	R	S	S	S	S	R	--	R	S	--	--	R	S
20	I	R	S	S	S	S	R	--	R	S	R	--	R	S
22	I	R	--	S	S	S	R	--	R	S	R	S	R	S
23	--	R	S	S	R	S	R	--	R	S	R	--	R	S
24	I	R	S	S	S	S	R	--	R	S	R	S	--	S
26	I	R	--	S	S	S	R	R	R	S	R	S	R	S
B	R	R	S	S	S	--	R	R	R	--	R	S	--	S
C	--	--	--	--	S	--	--	--	--	--	--	--	--	--
E	--	R	S	S	S	--	R	R	R	--	R	S	--	--
Q	I	R	S	S	S	--	R	R	--	--	R	S	R	--
R	I	R	--	S	S	S	R	--	R	S	R	--	--	S
Total	7	12	8	12	12	8	12	4	10	8	10	7	7	10
Number S	0	0	8	12	11	8	0	0	0	8	0	7	0	10
Number I	6*	0	0	0	0	0	0	0	0	0	0	0	0	0
Number R	1	12	0	0	1	0	12	4	10	0	10	0	7	0
Minor error														
Major error	1				1									

S = Susceptible; I = Intermediate; R = Resistant; * interpreted as S, for explanation see chapter 3.2

STRAIN AST - 8														
Labcode	AMC (S)	AMP (R)	CEF (S)	CHL (S)	CIP (S)	FLO (S)	GEN (R)	KAN (R)	NAL (R)	NEO (R)	STR (S)	SXT (S)	SUL (R)	TMP (S)
8	--	R	--	S	--	S	R	--	R	R	R	--	R	S
11	--	R	S	S	S	--	R	--	--	--	--	S	--	S
19	--	R	S	S	S	S	R	--	R	R	--	--	R	S
20	I	R	S	S	S	S	R	--	R	R	R	--	R	S
22	I	R	--	S	S	S	R	--	R	R	R	S	R	S
23	--	R	S	S	R	S	R	--	R	R	R	--	R	S
24	R	R	S	S	S	S	R	--	R	R	R	S	--	S
26	I	R	--	S	S	S	R	R	R	R	I	S	R	S
B	S	R	S	S	S	--	R	R	R	--	R	S	--	S
C	--	--	--	--	S	--	--	--	--	--	--	--	--	--
E	--	R	S	S	S	--	R	R	R	--	R	S	--	--
Q	I	R	S	S	S	--	R	R	--	--	R	S	R	--
R	I	R	--	S	S	S	R	--	R	R	I	--	--	S
Total	7	12	8	12	12	8	12	4	10	8	10	7	7	10
Number S	1	0	8	12	11	8	0	0	0	0	0	7	0	10
Number I	5*	0	0	0	0	0	0	0	0	0	2	0	0	0
Number R	1	12	0	0	1	0	12	4	10	8	8	0	7	0
Minor error											2			
Major error	1				1						8			

S = Susceptible; I = Intermediate; R = Resistant; * interpreted as S, for explanation see chapter 3.2

STRAIN AST - 9														
Labcode	AMC (S)	AMP (R)	CEF (S)	CHL (S)	CIP (R)	FLO (S)	GEN (R)	KAN (R)	NAL (R)	NEO (R)	STR (R)	SXT (R)	SUL (R)	TMP (R)
8	--	R	--	S	--	S	R	--	R	R	R	--	R	R
11	--	R	S	S	R	--	R	--	--	--	--	R	--	R
19	--	R	S	S	R	S	R	--	R	R	--	--	R	R
20	I	R	S	S	R	S	R	--	R	R	R	--	R	R
22	I	R	--	S	R	S	R	--	R	R	R	R	R	R
23	--	R	S	S	R	S	R	--	R	R	R	--	R	R
24	I	R	S	S	R	S	R	--	R	R	R	R	--	R
26	I	R	--	S	R	S	R	R	R	R	R	R	R	R
B	R	R	S	S	R	--	R	R	R	--	R	R	--	R
E	--	R	S	S	R	--	R	R	R	--	R	R	--	--
Q	S	R	S	S	R	--	R	R	--	--	R	R	R	--
R	I	R	--	S	R	S	I	--	R	R	R	--	--	R
Total	7	12	8	12	11	8	12	4	10	8	10	7	7	10
Number S	1	0	8	12	0	8	0	0	0	0	0	0	0	0
Number I	5*	0	0	0	0	0	1	0	0	0	0	0	0	0
Number R	1	12	0	0	11	0	11	4	10	8	10	7	7	10
Minor error							1							
Major error	1													

S = Susceptible; I = Intermediate; R = Resistant; * interpreted as S, for explanation see chapter 3.2

STRAIN AST - 10														
Labcode	AMC (S)	AMP (R)	CEF (S)	CHL (R)	CIP (S)	FLO (R)	GEN (S)	KAN (S)	NAL (S)	NEO (S)	STR (R)	SXT (S)	SUL (R)	TMP (S)
8	--	R	--	R	--	R	S	--	S	S	R	--	R	S
11	--	R	S	R	S	--	S	--	--	--	--	S	--	S
19	--	R	S	R	S	R	S	--	S	S	--	--	R	S
20	I	R	S	R	S	R	S	--	S	S	R	--	R	S
22	I	R	--	R	S	R	S	--	S	S	R	S	R	S
23	--	R	S	R	S	R	S	--	S	S	R	--	R	S
24	I	R	S	R	S	R	S	--	S	S	R	S	--	S
26	I	R	--	R	S	R	S	S	S	S	R	S	R	S
B	S	R	S	R	S	--	S	S	S	--	R	S	--	S
E	--	R	S	R	S	--	S	S	S	--	R	S	--	--
Q	I	R	S	R	S	--	R	S	--	--	R	S	R	--
R	I	R	--	R	S	R	S	--	S	S	R	--	--	S
Total	7	12	8	12	11	8	12	4	10	8	10	7	7	10
Number S	1	0	8	0	11	0	11	4	10	8	0	7	0	10
Number I	6*	0	0	0	0	0	0	0	0	0	0	0	0	0
Number R	0	12	0	12	0	8	1	0	0	0	10	0	7	0
Minor error														
Major error							1							

S = Susceptible; I = Intermediate; R = Resistant; * interpreted as S, for explanation see chapter 3.2

Annex 6. Results antimicrobial susceptibility testing per strain with disc diffusion test

STRAIN AST - 1

Labcode	AMC (S)	AMP (R)	CEF (S)	CHL (S)	CIP (S)	FLO (S)	GEN (S)	KAN (S)	NAL (S)	NEO (S)	STR (S)	SXT (S)	SUL (S)	TMP (S)
1	R	R	S	S	S	--	S	S	S	S	S	S	--	--
2	I	R	--	S	S	--	S	S	S	--	S	S	S	--
3	I	R	S	S	S	--	S	S	S	S	S	S	R	S
4	S	R	S	S	S	--	S	S	S	S	S	S	--	S
5	--	R	S	S	S	--	--	--	S	--	S	S	S	--
6	S	R	S	S	S	--	S	S	S	S	S	S	S	S
7	--	R	--	S	S	--	I	S	S	S	S	S	--	S
9	S	R	--	--	--	--	S	--	S	--	--	S	S	--
11	S	R	S	S	S	S	S	S	S	S	S	S	S	S
12	S	R	S	S	S	--	S	S	S	--	S	S	S	S
13	I	R	S	S	S	--	S	S	S	S	S	S	S	S
14	S	R	S	S	S	S	S	S	S	S	S	S	S	S
15	S	R	S	S	S	S	S	S	S	S	S	S	S	S
16	S	R	S	S	S	S	S	S	S	--	S	S	--	S
17	S	R	S	S	S	--	S	S	S	--	S	--	S	S
18	I	R	S	S	S	S	S	S	S	S	S	S	--	--
21	S	R	S	S	S	--	S	S	S	S	S	S	S	S
25	S	R	S	S	S	--	S	S	S	--	S	--	S	S
A	S	R	S	S	S	S	S	S	S	S	S	S	S	S
C	--	R	S	S	S	--	S	--	S	--	S	--	S	S
D	I	--	--	S	S	--	S	S	S	--	S	S	S	S
F	S	R	S	S	S	--	S	S	S	S	S	S	S	S
G	--	R	S	S	S	--	S	S	S	--	S	--	S	S
H	--	R	S	S	S	--	S	S	S	--	S	S	S	S
J	I	R	S	S	S	--	S	S	S	--	S	S	S	S
L	S	R	S	S	S	--	S	S	S	--	S	S	S	--
Total	21	25	22	25	25	6	25	23	26	13	25	22	21	20
Number S	14	0	22	25	25	6	24	23	26	13	25	22	20	20
Number I	6*	0	0	0	0	0	1	0	0	0	0	0	0	0
Number R	1	25	0	0	0	0	0	0	0	0	0	0	1	0
Minor error							1							
Major error	1												1	

S = Susceptible; I = Intermediate; R = Resistant; * interpreted as S, for explanation see chapter 3.2

STRAIN AST - 2

Labcode	AMC (S)	AMP (R)	CEF (S)	CHL (I)*	CIP (S)	FLO (S)	GEN (S)	KAN (R)	NAL (S)	NEO (R)	STR (S)	SXT (R)	SUL (R)	TMP (R)
1	S	R	S	S	S	--	S	R	I	R	I	R	--	--
2	S	R	--	S	S	--	S	R	I	--	S	R	R	--
3	S	R	S	S	S	--	S	R	I	R	S	R	R	R
4	S	R	S	S	S	--	S	R	S	R	I	R	--	R
5	--	R	S	S	S	--	--	--	S	--	S	R	R	--
6	S	R	S	S	S	--	S	R	I	R	S	R	R	R
7	--	R	--	S	S	--	I	R	I	R	S	R	--	R
9	S	R	--	--	--	--	S	--	S	--	--	R	R	--
11	S	R	S	S	S	S	S	R	S	R	I	R	R	R
12	S	R	S	S	S	--	S	R	S	--	S	R	R	R
13	S	R	S	S	S	--	S	R	I	R	S	R	R	R
14	S	R	S	S	S	S	S	R	S	R	S	R	R	R
15	S	R	S	S	S	S	S	R	S	R	I	R	R	R
16	S	R	S	S	S	S	S	R	I	--	I	R	--	R
17	S	R	S	S	S	--	S	R	S	--	S	--	R	R
18	S	R	S	S	S	S	S	R	S	R	I	R	--	--
21	S	R	S	S	S	--	S	I	S	R	S	R	R	R
25	S	R	S	S	S	--	S	R	S	--	I	--	R	R
A	S	R	S	S	S	S	S	R	I	R	S	R	R	R
C	--	R	S	S	S	--	S	--	S	--	I	--	R	R
D	I	--	--	S	S	--	S	R	S	--	S	R	R	R
F	S	R	S	S	S	--	S	R	I	R	I	R	R	R
G	--	R	S	S	S	--	S	R	I	--	S	--	R	R
H	--	R	S	S	S	--	S	R	S	--	R	R	R	R
J	S	R	S	S	S	--	S	R	S	--	I	R	R	R
L	S	R	S	S	S	--	S	R	S	--	S	R	R	--
Total	21	25	22	25	25	6	25	23	26	13	25	22	21	20
Number S	20	0	22	25*	25	6	24	0	16	0	14	0	0	0
Number I	1	0	0	0	0	0	1	1	10	0	10	0	0	0
Number R	0	25	0	0	0	0	0	22	0	13	1	22	21	20
Minor error	1						1	1	10		10			
Major error											1			

*S = Susceptible; I = Intermediate; R = Resistant; * not interpreted as deviating results, see text for explanation*

STRAIN AST - 3

Labcode	AMC (S)	AMP (R)	CEF (S)	CHL (S)	CIP (S)	FLO (S)	GEN (S)	KAN (S)	NAL (S)	NEO (S)	STR (R)	SXT (S)	SUL (R)	TMP (S)
1	I	R	S	S	S	--	S	S	S	S	R	S	--	--
2	I	R	--	S	S	--	S	S	S	--	R	S	R	--
3	I	R	S	S	S	--	S	S	S	S	R	S	R	S
4	S	R	S	S	S	--	S	S	S	S	R	S	--	S
5	--	R	S	S	S	--	--	--	S	--	R	S	R	--
6	S	R	S	S	S	--	S	S	S	S	R	S	R	S
7	--	R	--	S	S	--	S	S	S	I	R	S	--	S
9	S	R	--	--	--	--	S	--	S	--	--	S	R	--
11	S	R	S	S	S	S	S	S	S	S	R	S	R	S
12	S	R	S	S	S	--	S	S	S	--	R	S	R	S
13	S	R	S	S	S	--	S	S	S	S	R	S	R	S
14	S	R	S	S	S	S	S	S	S	S	R	S	R	S
15	S	R	S	S	S	S	S	S	S	S	R	S	R	S
16	S	R	S	S	S	S	S	S	S	--	R	S	--	S
17	S	R	S	S	S	--	S	S	S	--	R	--	R	S
18	S	R	S	S	S	S	S	S	S	S	R	S	--	--
21	S	R	S	S	S	--	S	S	S	S	R	S	R	S
25	S	R	S	S	S	--	S	S	S	--	R	--	R	S
A	I	R	S	S	S	S	S	S	S	S	R	S	R	S
C	--	R	S	S	S	--	S	--	S	--	R	--	R	S
D	I	--	--	S	S	--	S	S	S	--	R	S	R	S
F	I	R	S	S	S	--	S	S	S	S	R	S	R	S
G	--	R	S	S	S	--	S	S	S	--	R	--	R	S
H	--	R	S	S	S	--	S	S	S	--	R	S	R	S
J	R	R	S	S	S	--	S	S	S	--	R	S	R	S
L	S	R	S	S	S	--	S	S	S	--	R	S	R	--
Total	21	25	22	25	25	6	25	23	26	13	25	22	21	20
Number S	14	0	22	25	25	6	25	23	26	12	0	22	0	20
Number I	6*	0	0	0	0	0	0	0	0	1	0	0	0	0
Number R	1	25	0	0	0	0	0	0	0	0	25	0	21	0
Minor error										1				
Major error	1													

*S = Susceptible; I = Intermediate; R = Resistant; * interpreted as S, for explanation see chapter 3.2*

STRAIN AST - 4

Labcode	AMC (S)	AMP (S)	CEF (S)	CHL (S)	CIP (S)	FLO (S)	GEN (S)	KAN (S)	NAL (S)	NEO (S)	STR (R)	SXT (S)	SUL (R)	TMP (S)
1	S	S	S	S	S	--	S	S	I	S	R	S	--	--
2	S	S	--	S	S	--	S	S	I	--	R	S	R	--
3	S	S	S	S	S	--	S	S	I	S	R	S	R	S
4	S	S	S	S	S	--	S	S	I	S	R	S	--	S
5	--	I	S	S	S	--	--	--	S	--	R	S	R	--
6	S	S	S	S	S	--	S	S	R	S	R	S	R	S
7	--	S	--	S	S	--	I	S	R	I	R	S	--	S
9	S	S	--	--	--	--	S	--	S	--	--	S	R	--
11	S	S	S	S	S	S	S	S	S	S	R	S	R	S
12	S	S	S	S	S	--	S	S	S	--	R	S	R	S
13	S	S	S	S	S	--	S	S	I	S	R	S	R	S
14	S	S	S	S	S	S	S	S	I	S	R	S	R	S
15	S	S	S	S	S	S	S	S	S	S	R	S	R	S
16	S	S	S	S	S	S	S	S	I	--	R	S	--	S
17	S	S	S	S	S	--	S	S	S	--	R	--	R	S
18	S	S	S	S	S	S	S	S	I	S	R	S	--	--
21	S	S	S	S	S	--	S	S	S	S	R	S	R	S
25	S	S	S	S	S	--	S	S	S	--	R	--	R	S
A	S	S	S	S	S	S	S	S	I	S	R	I	R	S
C	--	S	S	S	--	--	S	--	I	--	R	--	R	S
D	S	--	--	S	S	--	S	S	I	--	R	S	R	S
F	S	S	S	S	S	--	S	S	I	S	R	I	R	S
G	--	S	S	S	S	--	S	S	I	--	R	--	R	S
H	--	S	S	S	S	--	S	S	R	--	R	S	R	S
J	S	S	S	S	R	--	S	S	R	--	R	S	R	S
L	S	S	S	S	S	--	S	S	I	--	R	S	R	--
Total	21	25	22	25	24	6	25	23	26	13	25	22	21	20
Number S	21	24	22	25	23	6	24	23	8	12	0	22	0	20
Number I	0	1	0	0	0	0	1	0	14	1	0	2	0	0
Number R	0	0	0	0	1	0	0	0	4	0	25	0	21	0
Minor error		1					1		14	1		2		
Major error					1				4					

S = Susceptible; I = Intermediate; R = Resistant

STRAIN AST - 5

Labcode	AMC (R)	AMP (R)	CEF (R)	CHL (S)	CIP (S)	FLO (S)	GEN (S)	KAN (S)	NAL (S)	NEO (S)	STR (S)	SXT (S)	SUL (S)	TMP (S)
1	R	R	R	S	S	--	S	S	S	S	S	S	--	--
2	R	R	--	S	S	--	S	S	S	--	S	S	S	--
3	R	R	R	S	S	--	S	S	S	S	S	S	S	S
4	R	R	R	S	S	--	S	S	S	S	S	S	--	S
5	--	R	R	S	S	--	--	--	S	--	S	S	S	--
6	R	R	I	S	S	--	S	S	S	S	S	S	S	S
7	--	R	--	S	S	--	I	S	S	S	S	S	--	S
9	R	R	--	--	--	--	S	--	S	--	--	S	S	--
11	I	R	R	S	S	S	S	S	S	S	S	S	S	S
12	R	R	R	S	S	--	S	S	S	--	S	S	S	S
13	R	R	R	S	S	--	S	S	S	S	S	S	I	S
14	R	R	R	S	S	S	S	S	S	S	S	S	S	S
15	R	R	I	S	S	S	S	S	S	S	S	S	S	S
16	R	R	R	S	S	S	S	S	S	--	S	S	--	S
17	R	R	I	S	S	--	S	S	S	--	S	--	S	S
18	R	R	R	S	S	S	S	S	S	S	S	S	--	--
21	R	R	R	S	S	--	S	S	S	S	S	S	S	S
25	R	R	R	S	S	--	S	S	S	--	S	--	S	S
A	R	R	R	S	S	S	S	S	S	S	S	S	S	S
C	--	R	R	S	S	--	S	--	S	--	S	--	S	S
D	R	--	--	S	S	--	S	S	S	--	S	S	S	S
F	R	R	R	S	S	--	S	S	I	S	I	S	S	S
G	--	R	R	S	S	--	S	S	S	--	S	--	S	S
H	--	R	R	S	S	--	S	S	S	--	S	S	S	S
J	R	R	R	S	S	--	S	S	S	--	S	S	S	S
L	R	R	R	S	S	--	S	S	S	--	S	S	S	--
Total	21	25	22	25	25	6	25	23	26	13	25	22	21	20
Number S	0	0	19	25	25	6	24	23	25	13	24	22	20	20
Number I	1	0	3	0	0	0	1	0	1	0	1	0	1	0
Number R	20	25	0	0	0	0	0	0	0	0	0	0	0	0
Minor error	1		3				1		1		1			
Major error													1	

S = Susceptible; I = Intermediate; R = Resistant

STRAIN AST - 6

Labcode	AMC (S)	AMP (S)	CEF (S)	CHL (S)	CIP (S)	FLO (S)	GEN (S)	KAN (S)	NAL (R)	NEO (S)	STR (S)	SXT (S)	SUL (S)	TMP (S)
1	S	S	S	S	S	--	S	S	R	S	S	S	--	--
2	S	S	--	S	S	--	S	S	R	--	S	S	S	--
3	S	S	S	S	S	--	S	S	R	S	S	S	R	S
4	S	S	S	S	S	--	S	S	R	S	S	S	--	S
5	--	I	S	S	S	--	--	--	R	--	S	S	S	--
6	S	S	S	S	S	--	S	S	R	S	S	S	S	S
7	--	S	--	S	S	--	I	S	R	I	S	S	--	S
9	S	S	--	--	--	--	S	--	R	--	--	S	S	--
11	S	S	S	S	S	S	S	S	R	S	S	S	S	S
12	S	S	S	S	S	--	S	S	R	--	S	S	S	S
13	S	S	S	S	S	--	S	S	R	S	S	S	S	S
14	S	S	S	S	S	S	S	S	R	S	S	S	S	S
15	S	S	S	S	S	S	S	S	R	S	S	S	S	S
16	S	S	S	S	S	S	S	S	R	--	S	S	--	S
17	S	S	S	S	S	--	S	S	R	--	S	--	S	S
18	S	S	S	S	S	S	S	S	R	S	S	S	--	--
21	S	S	S	S	S	--	S	S	R	S	S	S	S	S
25	S	S	S	S	S	--	S	S	R	--	S	--	S	S
A	S	S	S	S	S	S	S	S	R	S	S	S	S	S
C	--	S	S	S	--	--	S	--	R	--	S	--	S	S
D	S	--	--	S	S	--	S	S	R	--	S	S	S	S
F	S	S	S	S	S	--	S	S	R	S	S	S	S	S
G	--	S	S	S	S	--	S	S	R	--	S	--	S	S
H	--	S	S	S	S	--	S	S	R	--	S	S	S	S
J	S	S	S	S	R	--	S	S	R	--	S	S	S	S
L	S	S	S	S	S	--	S	S	R	--	S	S	S	--
Total	21	25	22	25	24	6	25	23	26	13	25	22	21	20
Number S	21	24	22	25	23	6	24	23	0	12	25	22	20	20
Number I	0	1	0	0	0	0	1	0	0	1	0	0	0	0
Number R	0	0	0	0	1	0	0	0	26	0	0	0	1	0
Minor error		1					1			1				
Major error					1								1	

S = Susceptible; I = Intermediate; R = Resistant

STRAIN AST - 7

Labcode	AMC (S)	AMP (R)	CEF (S)	CHL (S)	CIP (S)	FLO (S)	GEN (R)	KAN (R)	NAL (R)	NEO (S)	STR (R)	SXT (S)	SUL (R)	TMP (S)
1	I	R	S	S	S	--	R	R	R	S	R	S	--	--
2	I	R	--	S	S	--	R	I	R	--	R	S	R	--
3	R	R	S	S	S	--	R	I	R	S	R	S	R	S
4	I	R	S	S	S	--	R	R	R	S	R	S	--	S
5	--	R	S	S	S	--	--	--	R	--	R	S	R	--
6	I	R	S	S	S	--	R	R	R	S	R	S	R	S
7	--	R	--	S	S	--	R	S	R	I	R	S	--	S
9	S	R	--	--	--	--	R	--	R	--	--	S	R	--
11	S	R	S	S	S	S	R	S	R	S	R	S	S	S
12	I	R	S	S	S	--	R	S	R	--	R	S	R	S
13	I	R	S	S	S	--	R	I	R	S	R	S	R	S
14	S	R	S	S	S	S	R	S	R	S	R	S	R	S
15	I	I	S	S	S	S	R	S	R	S	R	S	R	S
16	S	R	S	S	S	S	R	I	R	--	R	S	--	S
17	S	R	S	S	S	--	R	S	R	--	R	--	R	S
18	I	R	S	S	S	S	R	I	R	S	R	S	--	--
21	I	R	S	S	S	--	R	S	R	S	R	S	R	S
25	I	R	S	S	S	--	R	S	R	--	R	--	R	S
A	I	R	S	S	S	S	R	S	R	S	R	S	R	S
C	--	R	S	S	--	--	R	--	R	--	R	--	R	S
D	I	--	--	S	S	--	R	S	R	--	R	S	R	S
F	R	R	S	S	S	--	R	I	R	S	R	S	R	S
G	--	R	S	S	S	--	R	I	R	--	R	--	R	S
H	--	R	S	S	S	--	R	R	R	--	R	S	R	S
J	I	R	S	S	R	--	R	R	R	--	R	S	R	S
L	S	R	S	S	S	--	R	I	R	--	R	S	R	--
Total	21	25	22	25	24	6	25	23	26	13	25	22	21	20
Number S	6	0	22	25	23	6	0	10	0	12	0	22	1	20
Number I	13*	1	0	0	0	0	0	8	0	1	0	0	0	0
Number R	2	24	0	0	1	0	24	5	26	0	25	0	20	0
Minor error		1						8		1				
Major error	2				1			10					1	

*S = Susceptible; I = Intermediate; R = Resistant; * interpreted as S, for explanation see chapter 3.2*

STRAIN AST - 8

Labcode	AMC (S)	AMP (R)	CEF (S)	CHL (S)	CIP (S)	FLO (S)	GEN (R)	KAN (R)	NAL (R)	NEO (R)	STR (S)	SXT (S)	SUL (R)	TMP (S)
1	R	R	S	S	I	--	R	R	R	R	R	S	--	--
2	I	R	--	S	S	--	R	R	R	--	I	S	R	--
3	I	R	S	S	S	--	R	R	R	R	I	S	R	S
4	I	R	S	S	S	--	R	R	R	R	I	S	--	S
5	--	R	S	S	S	--	--	--	R	--	R	S	R	--
6	R	R	S	S	S	--	R	R	R	R	I	S	R	S
7	--	R	--	S	S	--	R	R	R	R	I	S	--	S
9	S	R	--	--	--	--	R	--	R	--	--	S	R	--
11	S	R	S	S	S	S	R	R	R	R	R	S	R	S
12	I	R	S	S	S	--	R	R	R	--	I	S	R	S
13	I	R	S	S	S	--	R	R	R	R	I	S	R	S
14	S	R	S	S	S	S	R	R	R	R	R	S	R	S
15	I	I	S	S	S	S	R	R	R	R	r	S	R	S
16	I	R	S	S	S	S	R	R	R	--	R	S	--	S
17	I	R	S	S	S	--	R	R	R	--	I	--	R	S
18	R	R	S	S	S	S	R	R	R	R	R	S	--	--
21	I	R	S	S	S	--	R	I	R	R	S	S	R	S
25	I	R	S	S	S	--	R	R	R	--	I	--	R	S
A	I	R	S	S	S	S	R	R	R	R	I	S	R	S
C	--	R	S	S	--	--	R	--	R	--	R	--	R	S
D	R	--	--	S	S	--	R	R	R	--	R	S	R	S
F	R	R	S	S	S	--	R	R	R	R	R	S	R	S
G	--	R	S	S	S	--	R	R	R	--	I	--	R	S
H	--	R	S	S	S	--	R	R	R	--	R	S	R	S
J	I	R	S	S	R	--	R	R	R	--	R	S	R	S
L	S	R	S	S	S	--	R	R	R	--	I	S	R	--
Total	21	25	22	25	24	6	25	23	26	13	25	22	21	20
Number S	4	0	22	25	22	6	0	0	0	0	1	22	0	20
Number I	12*	1	0	0	1	0	0	1	0	0	12	0	0	0
Number R	5	24	0	0	1	0	24	22	26	13	12	0	21	0
Minor error		1			1			1			12			
Major error	5				1						12			

*S = Susceptible; I = Intermediate; R = Resistant; * interpreted as S, for explanation see chapter 3.2*

STRAIN AST - 9

Labcode	AMC (S)	AMP (R)	CEF (S)	CHL (S)	CIP (R)	FLO (S)	GEN (R)	KAN (R)	NAL (R)	NEO (R)	STR (R)	SXT (R)	SUL (R)	TMP (R)
1	I	R	S	S	R	--	R	R	R	R	R	R	--	--
2	I	R	--	S	R	--	I	R	R	--	R	R	R	--
3	R	R	S	S	R	--	R	R	R	R	R	R	R	R
4	I	R	S	S	R	--	R	R	R	R	R	R	--	R
5	--	R	S	S	R	--	--	--	R	--	R	R	R	--
6	I	R	S	S	R	--	R	R	R	R	R	R	R	R
7	--	R	--	S	I	--	R	R	R	R	R	R	--	R
9	S	R	--	--	--	--	R	--	R	--	--	R	R	--
11	S	R	S	S	R	S	R	R	R	R	R	R	R	R
12	I	R	S	S	R	--	R	R	R	--	R	R	R	R
13	I	R	S	S	R	--	R	R	R	R	R	R	R	R
14	S	R	S	S	R	S	R	R	R	R	R	R	R	R
15	I	I	S	S	R	S	R	R	R	R	R	R	R	R
16	I	R	S	S	R	S	R	R	R	--	R	R	--	R
17	I	R	S	S	R	--	I	R	R	--	R	--	R	R
18	I	R	S	S	R	S	R	R	R	R	R	R	--	--
21	S	R	S	S	R	--	I	I	R	R	R	R	R	R
25	I	R	S	S	R	--	R	R	R	--	R	--	R	R
A	I	R	S	S	R	S	R	R	R	R	R	R	R	R
C	--	R	S	S	R	--	R	--	R	--	R	--	R	R
D	I	--	--	S	R	--	R	R	R	--	R	R	R	R
F	R	R	S	S	R	--	R	R	R	R	R	R	R	R
G	--	R	S	S	R	--	R	R	R	--	R	--	R	R
H	--	R	S	S	R	--	R	R	R	--	R	R	R	R
J	I	R	S	S	R	--	R	R	R	--	R	R	R	R
L	I	R	S	S	R	--	I	R	R	--	R	R	R	--
Total	21	25	22	25	25	6	25	23	26	13	25	22	21	20
Number S	4	0	22	25	0	6	0	0	0	0	0	0	0	0
Number I	15*	1	0	0	1	0	4	1	0	0	0	0	0	0
Number R	2	24	0	0	24	0	21	22	26	13	25	22	21	20
Minor error		1			1		4	1						
Major error	2													

*S = Susceptible; I = Intermediate; R = Resistant; * interpreted as S, for explanation see chapter 3.2*

STRAIN AST - 10

Labcode	AMC (S)	AMP (R)	CEF (S)	CHL (R)	CIP (S)	FLO (R)	GEN (S)	KAN (S)	NAL (S)	NEO (S)	STR (R)	SXT (S)	SUL (R)	TMP (S)
1	R	R	S	R	S	--	S	S	S	S	R	S	--	--
2	I	R	--	R	S	--	S	S	S	--	R	S	R	--
3	I	R	S	R	S	--	S	S	S	S	R	S	R	S
4	I	R	S	R	S	--	S	S	S	S	R	S	--	S
5	--	R	S	R	S	--	--	--	S	--	R	S	R	--
6	I	R	S	R	S	--	S	S	S	S	R	S	R	S
7	--	R	--	R	S	--	I	S	S	S	R	S	--	S
9	S	R	--	--	--	--	S	--	S	--	--	S	R	--
11	S	R	S	R	S	R	S	S	S	S	R	S	R	S
12	S	R	S	R	S	--	S	S	S	--	R	S	R	S
13	I	R	S	R	S	--	S	S	S	S	R	S	R	S
14	S	R	S	R	S	R	S	S	S	S	R	S	R	S
15	I	R	S	R	S	R	S	S	S	S	R	S	R	S
16	I	R	S	R	S	R	S	S	S	--	R	S	--	S
17	I	R	S	R	S	--	S	S	S	--	R	--	R	S
18	I	R	S	R	S	R	S	S	S	S	R	S	--	--
21	S	R	S	R	S	--	S	S	S	S	R	S	R	S
25	I	R	S	R	S	--	S	S	S	--	R	--	R	S
A	I	R	S	R	S	R	S	S	S	S	R	S	R	S
C	--	R	S	R	S	--	S	--	S	--	R	--	R	S
D	I	--	--	R	S	--	S	S	S	--	R	S	R	S
F	R	R	S	R	S	--	S	S	S	S	R	S	R	S
G	--	R	S	R	S	--	S	S	S	--	R	--	R	S
H	--	R	S	R	S	--	S	S	S	--	R	S	R	S
J	I	R	S	R	S	--	S	S	S	--	R	S	R	S
L	I	R	S	R	S	--	S	S	S	--	R	S	R	--
Total	21	25	22	25	25	6	25	23	26	13	25	22	21	20
Number S	5	0	22	0	25	0	24	23	26	13	0	22	0	20
Number I	14*	0	0	0	0	0	1	0	0	0	0	0	0	0
Number R	2	25	0	25	0	6	0	0	0	0	25	0	21	0
Minor error							1							
Major error	2													

*S = Susceptible; I = Intermediate; R = Resistant; * interpreted as S, for explanation see chapter 3.2*