The External Quality Assurance System of the WHO Global Foodborne Infections Network, 2016

Public Health Agency of Canada
Agence de la santé publique du Canada

World Health Organization

CDC
Centers for Disease Control and Prevention

international network
Institut Pasteur

DTU Food
National Food Institute

THE EXTERNAL QUALITY ASSURANCE SYSTEM OF THE WHO GLOBAL FOODBORNE INFECTIONS NETWORK YEAR 2016

Susanne Karlsmose Pedersen, Jens-Ole Frimann, Frank M. Aarestrup, Rene Hendriksen

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The report is available at
www.food.dtu.dk
National Food Institute
Technical University of Denmark
Kemitorvet
Building 204
DK-2800 Kgs. Lyngby
Denmark
Tel: +45 35 88 70 00
Fax +45 35 88 70 01

Revision in January 2019 includes adjustments in the report to correctly reflect the data in the tables.

List of Abbreviations

AGISAR, WHO Advisory Group on Integrated Surveillance of Antimicrobial Resistance

AST, Antimicrobial Susceptibility Testing

ATCC, American Type Culture Collection

CAZ, Ceftazidime

CDC, Centers for Disease Control and Prevention

CRO, Ceftriaxone

CTX, Cefotaxime

DTU Food, Technical University of Denmark - National Food Institute

EQAS, External Quality Assurance System

ESBL, Extended Spectrum Beta-Lactamase

GEN, Gentamicin

IP, Institute Pasteur

MERO, Meropenem

MIC, Minimum Inhibitory Concentration

NSSC, National *Salmonella* and *Shigella* Center, Thailand

PHAC, Public Health Agency of Canada

QC, Quality Control

SMX, Sulfamethoxazole

TET, Tetracycline

WHO, World Health Organization

WHO GFN, WHO Global Foodborne Infections Network

1. Introduction

Since 2000, 15 WHO External Quality Assurance System (EQAS) reports have been issued with this report being the 16th. The WHO Global Foodborne Infections Network (WHO GFN) and the WHO Advisory Group on Integrated Surveillance of Antimicrobial Resistance (AGISAR) focus on enhancing World Health Organization (WHO) Member States' capacity to detect and respond to foodborne disease outbreaks and the emerging of antimicrobial resistance (AMR) bacterial pathogens by conducting laboratory-based surveillance of *Salmonella* and other important foodborne pathogens. Thus, the WHO EQAS align with the 2015 WHO global action plan to target AMR worldwide, objective 2: Strengthen knowledge through surveillance and research, action 2, laboratory capacity.

Since its inception, the scope of WHO EQAS has expanded to include additional foodborne pathogens like *Shigella* and *Campylobacter*. *Salmonella*, *Campylobacter* and *Shigella* are among the most important foodborne pathogens worldwide and account for millions of cases of diarrheal disease and thousands of deaths per year impacting both developing and industrialized countries. Furthermore, the increased number of *Salmonella*, *Campylobacter* and *Shigella* isolates which are resistant to antimicrobials is of major concern since these isolates are associated with infections characterized by increased morbidity and mortality.

The WHO EQAS is organized annually by DTU Food in collaboration with World Health Organization (WHO) in Geneva, Switzerland; Centers for Disease Control and Prevention (CDC) in Atlanta, USA; Public Health Agency of Canada (PHAC) in Canada; National *Salmonella* and *Shigella* Center (NSSC), National Institute of Health, Department of Medical Science in Thailand and Institute Pasteur (IP) in Paris, France.

Individual laboratory data are confidential and only known by the participating laboratory, the EQAS Organizer (DTU Food) and possibly the respective WHO GFN regional centre/WHO AGISAR country representative. All summary conclusions are public. The goal set by WHO GFN/AGISAR aims towards having all national reference laboratories perform *Salmonella* serotyping with a maximum of one deviation out of eight strains tested (error rate of 13%) and performing antimicrobial susceptibility testing (AST) of *Salmonella* with a maximum error rate of 10% (either <5% very major / major errors and <5% minor errors, or <10% minor errors). Minor deviations are defined as classification of an intermediate strain as susceptible, resistant or vice versa (*i.e.* I $\leftrightarrow$ S or I $\leftrightarrow$R). Major deviation is the classification of a susceptible strain as resistant (*i.e.* S $\rightarrow$ R). Very major deviation is the classification of a resistant strain as susceptible (*i.e.* R $\rightarrow$ S). In this report, the deviations of AST results are divided into two categories, *i.e.* critical deviations which include major and very major deviations, and total deviations which include also the minor deviations. In EQAS 2014, the regions were redefined for all countries worldwide for the analysis of data from the WHO GFN EQAS. This lead to some reorganization of countries into new regions compared to previous years, why interpretation of regional-based results from 2014 and onwards with results from before 2014 should be conducted with care. The countries belonging to each region is listed in Appendix 1.

Appendices 2-5 present additional background information in relation to the WHO EQAS 2016.

2. Summary

The summary report is divided into five sections; the *Salmonella* components, the *Shigella* components, reporting of ESBL *Salmonella* and *Shigella*, the *Campylobacter* components, and identification of the unknown strain. All results reported in the summary can be found in Appendix 1.

Participation

A total of 196 laboratories responded to the pre-notification and were enrolled in the WHO EQAS. When the deadline for submitting results was reached, 182 laboratories in 81 countries had uploaded data.

The following countries provided data for at least one of the EQAS components (Appendix 1): Argentina, Australia (3), Bahrain, Barbados, Belgium, Bolivia, Brazil (2), Brazil, Brunei Darussalam, Bulgaria, Cambodia, Cameroon, Canada (12), Chile (2), China (18), Colombia (3), Congo, Democratic Republic of the, Costa Rica (2), Croatia, Cyprus, Czech Republic (2), Ecuador (2), Egypt, El Salvador, Gambia (2), Germany (2), Greece (2), Guatemala (2), Honduras, Hungary, India (4), Iran, Islamic rep. Of (3), Iraq, Ireland, Israel, Italy (16), Ivory Coast, Jamaica, Japan, Kenya (3), Korea, Rep of (2), Kosovo, Lao PDR, Luxembourg (2), Madagascar, Malaysia (6), Malta (2), Mauritius, Mexico (2), Morocco (2), New Zealand, Nigeria, Norway, Oman, Panama (2), Paraguay, Peru, Philippines, Poland (4), Portugal, Senegal, Serbia (2), Singapore, Slovakia, Slovenia, South Africa, Spain, Sri Lanka (2), Suriname, Sweden, Taiwan, Thailand (15), Trinidad and Tobago, Turkey (2), Ukraine, United Kingdom, United States of America (5), Uruguay, Venezuela (2), Viet Nam (2), Zambia, Zimbabwe.

The level participation in the WHO EQAS 2016 was the same as at the WHO EQAS 2015.

Salmonella EQAS components

The acceptance threshold for the EQAS *Salmonella* serotyping component was met by 73% (n = 106) of the 146 participating laboratories (Table 1). In addition, 89% (n = 130) of the laboratories tested all eight strains with a total at 90% (n = 1.004) of all tests being correct, representing a slight increase compared to 2015 to one of the best performances observed since the initiation of the EQAS (Table 2). The ability to correctly serotype the internal control strain continued to decrease in 2016 to the lowest level since 2001 at 84%, most likely due to many new laboratories participating in 2016. In 2016, the participation in testing the internal control strain increased from 125 to the highest ever recorded, 159 (Table 3). On a region-based categorization of participating laboratories, the Caribbean and Africa both correctly serotyped between 60% and 62% of the test strains whereas Southeast Asia, Latin America, Central Asia & Middle East correctly serotyped between 79% and 88% of the test strains. The performance of correct serotyping in Europe, China, North America was between 93 and 99% but reached 100% correct serotyping of all eight strains in only Oceania.

In 2016, Russia was the only region not participating (Table 4). In all regions, either a marked or consistent improvement was observed and in line with the other data presented.

The main problem regarding the *Salmonella* serotyping appeared to be associated with all strains included the 2016 trial except for the internal control, WHO S-16.3 (Enteritidis; I 9,12:g,m:-).

WHO 2016 S-16.1 (Bovismorbificans / Hindmarsh, I 6,8:r:1,5), WHO 2016 S-16.2 (Infantis, I 6,7:r:1,5), WHO 2016 S-16.4 (Uganda, I 3,10:l,z13;1,5), WHO 2016 S-16.5 (Stanley, I 4,5,12:d;1,2), WHO 2016 S-16.6 (Heidelberg, I 4,12:r:1,2), WHO 2016 S-16.7 (Altendorf, I 4,12,27:c:1,7), and WHO 2016 S-16.8 (Plymouth, I 9,46:d:z6) revealed considerable levels of deviations, 17.9%, 28.0%, 25.5%, 15.7%, 17.6%, 21.0%, and 26.3%, respectively (Table 5). The level of deviation is surprising since the serovars included the 2016 should not pose major difficulties since the somatic O antigen all belong to the major serogroups such as O:4, O:3,10, O:7, O:8, O:9, O:9,46 and the flagella antigens to well know polyvalent antisera HMA, HMB, and HMD, respectively. It is a concern that many laboratories had difficulties at serotyping that many of the major serovars such as Infantis, Stanley, and Heidelberg which are all well-known often to be multidrug resistant.

Concerning the *Salmonella* AST component for the EQAS 2016, the performance slightly increased compared to the EQAS of 2015, with a low deviations of 2% minor, 2% major, and 1% very major deviations. Thus, the percentages of critical deviation was 3% (Table 6). Deviations categorized by the tested antimicrobials revealed that ciprofloxacin (CIP), gentamicin (GEN), meropenem (MERO), sulfamethoxazole (SMX) and tetracycline (TET) caused most of the difficulties observed with the following total percentage deviations: 10%, 6%, 6%, 8% and 6%, respectively (Table 7). The deviation to CIP is most likely due to the often observed double zone when performing disk diffusion and to SMX the bacteriostatic effect. TET, however, also often pose difficulties using disk diffusion whereas this is not reflected conducting MIC determination. For the four antimicrobials, CIP, MERO, SMX and TET the deviations resulted in that less than 90% of the laboratories submitted the correct and expected susceptibility interpretation. Thus, it is a concern that 27 laboratories of 106 incorrectly interpreted WHO 2016 S-16.2 (Infantis, I 6,7:r:1,5) as susceptible to MERO, a carbapenem (Table 8). On a region-based categorization of participating laboratories, Africa obtained the highest percentages of total deviations, 9.9 where as China, Southeast Asia, Latin America, Europe, Central Asia & Middle East, North America, and Oceania obtained a slightly lover percentage of total deviations between 0.9% to 6.5%. The performance of 100% correctly antimicrobial susceptibility testing all eight strains was observed in the Caribbean. Russia did not participate in the 2016 EQAS (Table 9).

For the 150 laboratories performing the *Salmonella* AST component (MIC (n = 30)/Disk diffusion (n = 76)), only 71% (106 laboratories) reported data for AST of the control strain *E. coli* ATCC 25922. This is a very alerting number and an almost 10 percentage-point decrease compared to 2015 (Table 10). It is of extreme importance to once again emphasize that this component represents the true indicator for the laboratory as to the performance of AST. It is noteworthy that the WHO EQAS organizers provide free of charge the control strain *E. coli* ATCC 25922 for all new participants in the AST component, why there should not be any excuses not to test this strain.

Shigella EQAS components

The *Shigella* components included in the WHO EQAS consist of serogrouping (i.e. the identification of the species), serotyping (i.e. the further typing of the species), and AST.

For the *Shigella* serogrouping component in EQAS 2016, the deviations observed ranged from 0.0% to 4.9%, for the four *Shigella* strains. This is an acceptable level as the 4.9% was related to one of the four strains whereas the remaining three isolates revealed a maximum deviation of 1.6% (Table 11).

The serotyping component was performed by a total of 77 laboratories for all of the four strains, WHO 2016 SH-16.1 (*S. flexneri,* 1b), WHO 2016 SH-16.2 (*S. boydii,*4), WHO 2016 SH-16.3 (*S. flexneri,*2b), and WHO 2016 SH-16.4 (*S. flexneri,*3a) with deviating results observed between 36.9% and 43.1%, respectively (Table 11).

According to the geographical distribution of the participating laboratories the results, on a region-based categorization, ranged from 69.2% (Africa) to 93.3% correctly serotyped strains by the Oceania region. No participation from Russia and the Caribbean in this trial (Table 12).

For the results of the *Shigella* AST component, the number of participating laboratories was somehow at the same level as in previous years, with 112 participating laboratories in EQAS 2016. The results obtained were in 96% of the cases in agreement with the expected results and a slightly better than in previous years. Minor, major and very major deviations were observed in 1%, 1%, and 1% of the reported results, respectively (Table 13). Categorizing the tested antimicrobials according to the deviations revealed again as in 2015 that CIP (7.1%) and (CHL) (7.1%) but also SMX (4.1%) and GEN (4.2%) caused difficulties in the AST component (Table 14). The deviations to CIP and SMX was not surprising as the same explanation given for *Salmonella* also comply to *Shigella* (Table 14). For the four antimicrobials, CAZ, CIP, CHL, and SMX the deviations resulted in that less than 90% of the laboratories submitted the correct and expected susceptibility interpretation (Table 15).

A region-based categorization of the results revealed correct test results between 90.3% (Africa) and 98.7% (North America), with Central Asia & Middle East having most critical deviations (7.2%). No participation from Russian in this trial (Table 16).

ESBL EQAS component

A part of the EQAS is to detect and confirm ESBL production in the *Salmonella* and *Shigella* strains. If participating in this component of the EQAS, all strains showing reduced susceptibility to cefotaxime (CTX), ceftazidime (CAZ) ceftriaxone (CRO) and/or meropenem (MERO) should be tested for ESBL, AmpC and carbapenemase production.

For the EQAS 2016, three AmpC-, ESBL-, carbapenemase-producers were included with two *Salmonella* strains (WHO 2016 S-16.2, Infantis and WHO 2016 S-16.6, Heidelberg) and one *Shigella* isolate (WHO 2016 SH-16.3, *S. flexneri* serovar 2b). The *Salmonella* isolate, WHO 2016

S-16.2, Infantis was a carbapenemase-producer whereas WHO 2016 S-16.6, Heidelberg was an AmpC-phenotype. The *Shigella* strain included was an ESBL-producer (WHO 2016 SH-16.3, *S. flexneri* serovar 2b). For the two *Salmonella* strains, the genes accounting for the phenotypes were: $bla_{\text{VIM-1}}$ (WHO 2016 S-16.2) and $bla_{\text{CMY-2}}$ (WHO 2016 S-16.6) and the confirmatory tests (CAZ/Cl:CAZ and CTX/Cl:CTX) showed 32% and 24% of deviations in reporting correct results (based on assigned phenotype), respectively. For the *Shigella* strain; WHO 2016 SH-16.3 ($bla_{\text{OXA-1}}$ and $bla_{\text{CTX-M14}}$), deviations of the confirmatory test result as and ESBL-producer was observed to be 4%.

Campylobacter EQAS components

A total of 95 laboratories participated in the identification of the *C. jejuni* WHO 2016 C-16.1 and *C. coli* WHO 2016 C-16.2 strain with a result of 94% and 91% correct species identification, respectively (Table 18). On a region-based characterization, the accuracy in *Campylobacter* identification ranged from 79% (Southeast Asia) to 100% (Africa, Central Asia & Middle East, Caribbean, Oceania, and China regions). No participation from Russia (Table 19).

Concerning the *Campylobacter* AST component in the EQAS 2016, 49 laboratories participated. The overall performance of the AST showed 4.2% major deviations, and 4.0% very major deviations, summing up to a total of 8.2% critical deviations, a two percent-point decrease compared to 2015 (Table 20). From the categorization of the antimicrobials, the results showed problems when testing all of the antimicrobials with most critical deviations to streptomycin with a level of critical deviations at 17.2% (Table 21). For the three antimicrobials, CIP, NAL, and TET the deviations resulted in less than 90% of the laboratories submitting the correct and expected susceptibility interpretation (Table 22).

On a region-based characterization, the performance in Central Asia & Middle East and Caribbean were noteworthy, with a deviation level of 60.0% (n = 1) and 26.7% (n = 2) critical deviations, respectively. In contrast, the North America and Oceanic region perfectly performed the test without deviations. Latin America, China, Europe, and Southeast Asia reported deviations at 3.1 and 15.8%, respectively. In EQAS 2016, no laboratories in the Africa and the Russian region participated in the *Campylobacter* AST component (Table 23).

For the QC strain *Campylobacter jejuni* ATCC 33560 only 42 laboratories reported AST results. Again, we have to emphasize the importance of including this component as it represents the true indicator for the laboratory's performance of AST. For gentamicin (GEN) which has previously shown to cause problems for the participants, the percentage of laboratories reporting a correct AST result for this compound increased once again from 86% to 93% compared to 2015 (Table 24).

Identification of unknown culture EQAS component

For this part of the EQAS, an unknown culture is provided for identification. In EQAS 2016, the unknown strain was the Gram positive *Listeria monocytogenes*.

A total of 137 laboratories participated in this component, with 86.1% identifying the strain correctly.

3. List of Appendices

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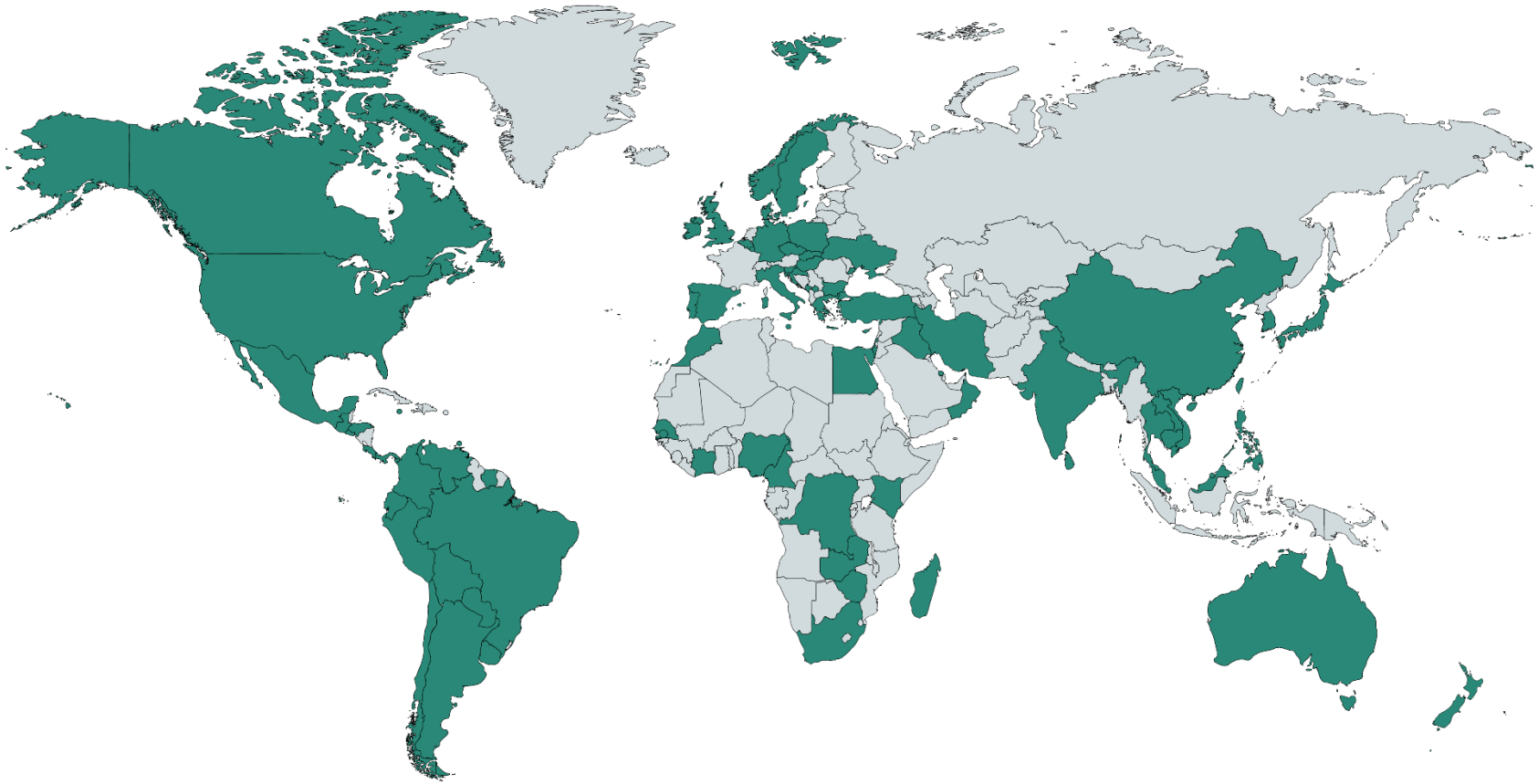
Appendix 4: WHO EQAS 2016 Protocol

Appendix 5a: Subculture and Maintenance of Quality Control Strains

Appendix 5b: Instructions for Opening and Reviving Lyophilized Cultures

Figure and Tables

Figure 1. Countries participating* in the WHO EQAS 2016



*marked in green

List of Countries in the 10 Regions

Africa

Algeria
Angola
Benin
Botswana
Burkina Faso
Burundi
Cameroon
Cameroun
Cape Verde
Central African Republic
Chad
Comoros
Congo (Brazzaville)
Congo, Democratic Republic of the
Cote d'Ivoire (Ivory Coast)
Djibouti
Egypt
Equatorial Guinea
Eritrea
Ethiopia
Gabon
Gambia
Ghana
Guinea
Guinea-Bissau
Kenya
Lesotho
Liberia
Libyan Arab Jamahiriya
Madagascar
Malawi
Mali
Mauritania
Mauritius
Mayotte
Morroco
Mozambique
Namibia
Niger
Nigeria
Reunion
Rwanda
Saint Helena
Sao Tome and Principe
Senegal
Seychelles
Sierra Leone
Somalia
South Africa
South Sudan
Sudan
Swaziland
Tanzania, United Republic of
Togo
Tunisia
Uganda
Western Sahara
Zambia
Zimbabwe

Caribbean

Anguilla
Antigua and Barbuda
Aruba
Bahamas
Barbados
Bonaire, Saint Eustatius and Saba
British Virgin Islands
Cayman Islands
Cuba
Curaçao
Dominica
Dominican Republic
Grenada
Guadeloupe
Haiti
Jamaica
Martinique
Monserrat
Puerto Rico
Saint Lucia
Saint Martin
Saint Vincent and the Grenadines
Saint-Barthélemy
Sint Maarten
St. Kitts and Nevis
Trinidad and Tobago
Turks and Caicos Islands
Virgin Islands (US)

Central Asia & Middle East

Afganistan
Armenia
Azerbaijan
Bahrain
Bangladesh
Bhutan
Georgia
Hong Kong
India
Indonesia
Iran, Islamic rep. Of
Iraq
Israel
Jordan
Kazakhstan
Kuwait
Kyrgyzstan
Lebanon
Macao
Maldives
Mongolia
Myanmar (ex-Burma)
Nepal
Oman
Pakistan
Palestine
Qatar
Saudi Arabia
Syria
Tajikistan
Timor Leste (West)
Turkmenistan
United Arab Emirates
Uzbekistan
Yemen

China

China

Europe

Albania
Andorra
Austria
Guerney and Alderney
Hungary
Iceland
Norway
Poland
Portugal

Belarus
Belgium
Bosnia
Bulgaria
Croatia
Cyprus
Czech Republic
Denmark
Estonia
European Union
Faroe Islands
Finland
France
Germany
Gibraltar
Greece
Ireland
Italy
Jersey
Kosovo
Latvia
Liechtenstein
Lithuania
Luxembourg
Macedonia
Malta
Man, Island of
Moldova
Monaco
Montenegro
Netherlands
Romania
San Marino
Serbia
Slovak Republic
Slovakia
Slovenia
Spain
Svalbard and Jan Mayen Islands
Sweden
Switzerland
Turkey
Ukraine
United Kingdom
Vatican City State (Holy See)

Latin America

Argentina
Bolivia
Brazil
Chile
Colombia
Costa Rica
Ecuador
El Salvador
Falkland Islands (Malvinas)
French Guiana
Guatemala
Guyana
Honduras
Mexico
Nicaragua
Panama
Paraguay
Peru
Suriname
Uruguay
Venezuela

North America

Bermuda
Canada
Greenland
Saint Pierre and Miquelon
United States of America

Oceania

Australia
Kiribati
New Zealand
Solomon, Islands
Fiji
Marshall Islands
Papua New Guinea
Tonga
French Polynesia
Micronesia
Samoa
Tuvalu
Guam
New Caledonia
Samoa, American
Vanuatu

Russia

Russia

Southeast Asia

Brunei Darussalam
Cambodia
Japan
Korea, North
Korea, Rep of
Lao PDR
Malaysia
Philippines
Singapore
Sri Lanka
Taiwan
Thailand
Viet Nam

Table 1. Ability of EQAS participating laboratories to serotype the test *Salmonella* strains

Number of strains correctly serotyped	Participating laboratories													
	EQAS 2000		EQAS 2001		EQAS 2002		EQAS 2003		EQAS 2004		EQAS 2006		EQAS 2007	
	No.	%	No.	%	No.	%	No.	%	No.	%	No.	%	No.	%
8	9	24	34	35	52	53	66	47	41	32	42	32	66	47
7	9	24	13	14	19	19	29	21	14	11	35	27	29	21
6	4	11	9	9	12	12	13	9	16	13	19	15	13	9
5	3	8	9	9	4	4	11	8	16	13	12	9	11	8
4	3	8	4	4	1	1	7	5	11	9	7	5	7	5
3	4	11	8	8	4	4	6	4	10	8	5	4	6	4
2	2	5	3	3	5	5	2	1	10	8	3	2	2	1
1	2	5	5	5	1	1	6	4	5	4	4	3	6	4
0	1	3	11	11	1	1	0	0	4	3	3	2	0	0
In total	37	100	96	100	99	100	127	100	127	100	130	100	140	100
	Participating laboratories													
	EQAS 2008		EQAS 2009		EQAS 2010		EQAS 2011		EQAS 2012		EQAS 2013		EQAS 2014	
	No.	%	No.	%	No.	%	No.	%	No.	%	No.	%	No.	%
8	50	33	76	50	91	61	82	67	68	47	52	41	70	47
7	36	24	29	19	16	11	17	14	29	20	29	23	32	21
6	11	7	7	5	12	8	10	8	14	10	15	12	17	11
5	14	9	13	8	9	6	2	2	9	6	8	6	6	4
4	12	8	5	3	6	5	4	3	5	3	7	6	5	3
3	9	6	7	5	2	1	4	3	6	4	7	6	7	5
2	8	6	5	3	2	1	1	1	10	7	6	5	4	3
1	9	6	6	4	7	5	3	2	2	1	2	2	4	3
0	2	1	5	3	3	2	0	0	1	1	0	0	4	3
In total	151	100	153	100	148	100	123	100	144	100	126	100	149	100
	Participating laboratories													
	EQAS 2015		EQAS 2016		**Average EQAS 2000 - 2016**									
	No.	%	No.	%	**No.**	**%**								
8	65	43	84	58	**59**	**45**								
7	25	17	22	15	**24**	**19**								
6	17	11	18	12	**13**	**10**								
5	22	15	5	3	**10**	**7**								
4	5	3	5	3	**6**	**5**								
3	2	1	5	3	**6**	**5**								
2	4	3	3	2	**4**	**4**								
1	7	5	4	3	**5**	**4**								
0	4	3	0	0	**2**	**2**								
In total	151	100	146	100	**128**	**100**								

Table 2. EQAS participating laboratories' performance of *Salmonella* serotyping

EQAS iteration	Labs serotyping all provided strains		Correct test results	
	No.	%	No.	%
2000	34	92	165	76
2001	79	82	513	72
2002	80	81	668	91
2003	69	54	692	80
2004	78	61	701	81
2006	105	81	808	85
2007	109	78	920	88
2008	100	66	888	83
2009	119	83	974	86
2010	129	87	998	89
2011	109	89	878	92
2012	122	81	936	83
2013	74	59	812	89
2014	85	57	969	92
2015	104	69	948	87
2016	130	89	1004	90
Average	99	76	805	85

Table 3. EQAS participating laboratories' performance of internal quality control strain (WHO S-16.3, *Salmonella* Enteritidis) serotyping).

EQAS iteration	Labs serotyping *S.* Enteritidis correctly	
	No.	%
2000	34	92
2001	64	84
2004	113	95
2006	116	94
2007	135	96
2008	139	96
2009	141	93
2010	138	97
2011	128	98
2012	139	96
2013	130	96
2014	145	98
2015	125	93
2016	159	89
Average	122	94

Table 4. Region-based categorization of EQAS participants' performance of *Salmonella* serotyping

Region	EQAS iteration	No. of labs	No. of strains serotyped	% strains correctly serotyped	Countries participating in EQAS 2016
Africa	2001	6	37	73.0	Cameroun, Egypt, Madagascar, Mauritius, Morocco (2), South Africa, The Gambia
	2002	9	62	87.1	
	2003	11	70	71.4	
	2004	9	51	62.7	
	2006	16	95	71.6	
	2007	11	73	80.8	
	2008	10	71	49.3	
	2009	15	94	75.5	
	2010	13	83	67.5	
	2011	10	57	79.2	
	2012	10	65	60.0	
	2013	8	51	74.5	
	2014	11	63	76.2	
	2015	12	68	61.8	
	2016	**8**	**58**	**62.1**	
Central Asia & Middle East	2001	10	60	50.0	Bahrain, India, Iraq, Israel, Oman
	2002	5	30	83.3	
	2003	5	35	54.3	
	2004	5	33	54.5	
	2006	5	35	74.3	
	2007	5	40	55.0	
	2008	5	34	61.8	
	2009	5	32	46.9	
	2010	5	22	75.9	
	2011	3	23	95.8	
	2012	4	30	56.7	
	2013	5	38	52.6	
	2014	7	37	75.7	
	2015	7	44	77.3	
	2016	**5**	**38**	**78.9**	
Caribbean	2001	0	0	0	Barbados, Trinidad and Tobago
	2002	0	0	0	
	2003	3	18	61.1	
	2004	2	8	87.5	
	2006	3	14	78.6	
	2007	2	9	77.8	
	2008	3	14	78.6	
	2009	3	12	83.3	
	2010	2	13	92.9	
	2011	1	7	87.5	
	2012	2	16	62.5	
	2013	1	5	100.0	
	2014	3	15	60.0	
	2015	5	24	58.3	
	2016	**2**	**16**	**60**	
Europe	2001	43	323	80.5	Belgium, Bulgaria, Croatia, Cyprus, Czech Republic (2), Germany (2), Greece (3), Hungary, Ireland, Italy (16), Luxembourg (2), Malta, Norway, Poland (3), Portugal, Serbia (2), Slovak Republic, Spain, Sweden, Turkey (2), Ukraine, United Kingdom
	2002	50	384	90.0	
	2003	60	401	84.8	
	2004	57	392	84.7	
	2006	52	403	86.4	
	2007	54	415	89.4	
	2008	50	379	82.3	
	2009	47	362	93.1	
	2010	45	332	94.1	
	2011	42	314	94.6	
	2012	47	368	92.9	
	2013	42	309	94.5	
	2014	52	391	96.2	
	2015	48	371	93.8	
	2016	**46**	**362**	**93.4**	

Table 4 (continued). Region-based categorization of EQAS participants' performance of *Salmonella* serotyping

Region	EQAS iteration	No. of labs	No. of strains serotyped	% strains correctly serotyped	Countries participating in EQAS 2016
North America	2001	4	32	87.5	Canada (9), United States of America (4)
	2002	2	16	100.0	
	2003	6	41	95.1	
	2004	8	55	81.8	
	2006	10	80	96.3	
	2007	12	94	97.9	
	2008	11	84	95.2	
	2009	12	90	92.2	
	2010	13	103	100.0	
	2011	11	81	97.6	
	2012	14	101	93.1	
	2013	13	92	97.8	
	2014	13	84	100.0	
	2015	13	93	100.0	
	2016	**13**	**100**	**99.0**	
Oceania	2001	4	30	100.0	Australia (3), New Zealand
	2002	6	43	93.0	
	2003	6	46	93.5	
	2004	5	38	97.4	
	2006	5	37	94.6	
	2007	4	32	100.0	
	2008	4	30	93.3	
	2009	4	32	96.9	
	2010	4	32	100.0	
	2011	4	32	100.0	
	2012	4	32	100.0	
	2013	4	31	100.0	
	2014	4	32	100.0	
	2015	4	31	100.0	
	2016	**4**	**32**	**100.0**	
Russia	2001	1	8	12.5	- none -
	2002	1	8	62.5	
	2003	1	7	14.3	
	2004	4	26	69.2	
	2006	5	40	80.0	
	2007	8	51	80.4	
	2008	6	40	90.0	
	2009	7	49	91.8	
	2010	8	54	87.1	
	2011	7	48	87.3	
	2012	6	48	87.5	
	2013	2	16	75.0	
	2014	4	30	93.3	
	2015	3	24	100.0	
	2016	**-**	**-**	**-**	
Latin America	2001	11	78	57.7	Argentina, Bolivia, Brazil (2), Chile (2), Colombia (3), Costa Rica (2), Ecuador (2), Honduras, Mexico (2), Panama (2), Paraguay, Peru, Uruguay, Venezuela (2)
	2002	11	82	87.8	
	2003	13	83	75.9	
	2004	15	88	79.5	
	2006	13	84	84.5	
	2007	15	107	88.8	
	2008	17	120	71.7	
	2009	21	150	77.3	
	2010	22	132	80.0	
	2011	23	144	83.7	
	2012	25	182	73.1	
	2013	22	154	83.1	
	2014	24	166	84.9	
	2015	20	133	84.2	
	2016	**23**	**165**	**87.9**	

Table 4 (continued). Region-based categorization of EQAS participants' performance of *Salmonella* serotyping

Region	EQAS iteration	No. of labs	No. of strains serotyped	% strains correctly serotyped	Countries participating in EQAS 2016
Southeast Asia	2001	15	113	54.0	Brunei Darussalam, Cambodia, Japan, Korea, Rep of (2), LAO PDR, Malaysia (5), Philippines, Singapore, Sri Lanka, Taiwan, Thailand (11), Viet Nam (2)
	2002	12	90	92.2	
	2003	15	100	81.0	
	2004	17	130	81.5	
	2006	15	117	84.6	
	2007	19	140	91.4	
	2008	18	125	81.6	
	2009	23	180	81.1	
	2010	24	172	90.5	
	2011	23	180	98.4	
	2012	28	207	77.8	
	2013	22	163	89.6	
	2014	22	166	94.6	
	2015	24	179	88.3	
	2016	**28**	**211**	**87.7**	
China	2001	4	32	96.9	China (17)
	2002	3	24	100.0	
	2003	8	60	75.0	
	2004	7	46	78.3	
	2006	6	48	85.4	
	2007	10	80	91.3	
	2008	15	108	94.4	
	2009	16	126	95.2	
	2010	10	74	92.5	
	2012	10	78	80.8	
	2013	7	54	92.6	
	2014	9	71	93.0	
	2015	15	118	78.0	
	2016	**17**	**136**	**95.6**	

Table 5. *Salmonella* serogroups (SG), serotypes (ST) and deviations (D), WHO EQAS 2016

Strain ID	Correct serotype		No. of labs reporting SG	% D_{SG}	No. of labs reporting ST	% D_{ST}	Deviating results (*)
WHO 2016 S-16.1	Bovismorbificans / Hindmarsh	I 6,8:r:1,5	156	5.8	156	17.9	Bsilla (2), Chailey, Diogoye, Goldcoast, Hidalgo, Haardt, Infantis (2), Takoradi, Utah
WHO 2016 S-16.2	Infantis	I 6,7:r:1,5	157	1.9	157	28.0	Aequatoria, Austin, Bulovka, Escanaba, Grampian (2), I 6,7:-:-, IV 6,7:z36:-, Lille (2), Nigeria (3), Oranienburg, Othmarschen, Papuana (2), Paratyphi C, Rumford, Thompson (2), Virchow (3)
WHO 2016 S-16.3	Enteritidis	I 9,12:g,m;-	159	1.3	159	10.7	Dublin, Essen, Hillingdon
WHO 2016 S-16.4	Uganda	I 3,10:l,z13;1,5	157	5.1	157	25.5	Assinie, Butantan, Chittagong, Freiburg, Harrisonburg, Joal , Langensalza, Lexington, Parkroyal, Sinstorf (5), Stuivenberg (2), Tyresoe, Uganda var. 15+ (3), Ughelli
WHO 2016 S-16.5	Stanley	I 4,5,12:d;1,2	159	0.6	159	15.7	Brezany, Bury, Eppendorf (2), Paratyphi B, Typhimurium
WHO 2016 S-16.6	Heidelberg	I 4,12:r:1,2	159	0.0	159	17.6	Albert, Altendorf, Ball, Bochum, Bradford, Fyris, Saintpaul, Southampton, Typhimurium (2)
WHO 2016 S-16.7	Altendorf	I 4,12,27:c:1,7	157	0.6	157	21.0	Abony, Arechavaleta, Haifa, Indiana (2), Kubacha (2), Kaapstad, Lagos, Legon, Schwarzengrund, Tafo, Togo, Travis
WHO 2016 S-16.8	Plymouth	I 9,46:d:z6	156	23.7	156	26.3	Niloese, Tarshyne (3), Typhi (2), Zega (18)

*number of participants reporting the specified deviating result

Table 6. EQAS participating laboratories' performance of antimicrobial susceptibility testing of *Salmonella* strains

EQAS iteration	**No. of EQAS participating laboratories**	**% correct test results**	**% minor deviations** (S ↔ I or I ↔ R)^	**% major deviations** (S → R)^	**% very major deviations** (R→ S)^	**% critical deviations** (R→ S & S → R)^	**% total deviations** (S → R & R → S & S ↔ I or I ↔ R)^
2000	44	92	4	4	0	4	8
2001	108	91	6	2	1	3	9
2002	119	92	6	2	1	3	9
2003*	147	93	4	3	0	3	7
2004	152	93	4	2	1	3	7
2006	143	88	8	3	1	4	12
2007	143	93	4	2	1	3	7
2008	168	91	4	2	3	5	9
2009	153	94	3	2	1	3	6
2010	152	92	4	3	2	5	8
2011	127	91	4	2	3	5	9
2012	159	94	3	2	1	3	6
2013	145	95	3	2	0	2	5
2014	155	95	3	1	1	2	5
2015	155	92	4	2	1	4	8
2016	150	95	2	2	1	3	5
Average*	139	93	4	2	1	3	7

*Data do not include one strain which may have lost resistance due to transport or storage stress
^S, susceptible; I, intermediate; R, resistant

Table 7. EQAS participants' performance of *Salmonella* strains antimicrobial susceptibility testing categorized by antimicrobial

EQAS iteration	No. of labs	Performance	Antimicrobial∞																	
			AMC	AMP	CAZ	CHL	CIP	POD	CRO	CTX	GEN	KAN	NAL	SMX	MER	STR	SXT	TET	TMP	XNL	OVERALL average
2000	44	No. of tests	-	343	-	343	334	-			343	312	328	248		312	-	335	295	-	798
		% critical deviations*	-	6	-	4	1	-			4	4	1	3		4	-	6	1	-	6
		% total deviations^	-	8	-	7	6	-			5	16	4	5		12	-	13	1	-	14
2001	108	No. of tests	-	822	-	814	813	-			821	623	726	431		679	757	804	416	-	1778
		% critical deviations*	-	4	-	2	1	-			2	2	2	6		7	2	7	1	-	6
		% total deviations^	-	7	-	3	4	-			4	7	8	9		27	5	18	2	-	15
2002	119	No. of tests	-	918	-	903	911	-			905	680	885	495		718	724	861	499	-	1961
		% critical deviations*	-	2	-	2	0	-			2	2	2	4		4	7	3	3	-	5
		% total deviations^	-	3	-	3	2	-			16	10	4	4		34	10	7	3	-	15
2003•	147	No. of tests	-	1019	-	996	995	-			993	738	947	615		768	929	995	582	-	2210
		% critical deviations*	-	2	-	1	0	-			2	2	1	4		9	2	4	1	-	5
		% total deviations^	-	4	-	2	1	-			2	6	4	5		39	2	11	1	-	12
2004	152	No. of tests	973	1178	-	1159	1162	-	-	995	1201	-	1130	734		947	1051	1122	729	-	2653
		% critical deviations*	6	3	-	2	0	-	-	0	2	-	1	5		1	3	5	2	-	5
		% total deviations^	12	5	-	2	1	-	-	14	3	-	4	8		21	4	11	2	-	13
2006	143	No. of tests	950	1092	769	1060	1110	305	-	956	1078	-	1035	649		896	996	1054	607	225	2256
		% critical deviations*	9	2	7	3	2	1	-	7	3	-	2	6		5	3	9	1	2	8
		% total deviations^	22	3	11	15	6	26	-	15	7	-	6	7		22	5	20	2	9	21
2007	143	No. of tests	908	1114	830	1105	1101	389	-	914	1111	-	1092	678		875	971	1047	583	258	2290
		% critical deviations*	6	5	1	0	1	4	-	1	3	-	2	5		4	3	4	1	0	5
		% total deviations^	17	7	1	6	1	16	-	2	4	-	3	6		26	3	11	2	6	13
2008	168	No. of tests	-	1331	961	1226	1307	-	791	1104	1265	-	1168	718		867	1155	1249	696	-	2769
		% critical deviations*	-	3	3	1	19	-	3	3	4	-	2	4		7	3	6	2	-	8
		% total deviations^	-	8	6	11	21	-	6	6	6	-	4	5		25	4	13	2	-	16
2009	153	No. of tests	-	1206	921	1108	1190	-	775	1009	1143	-	1095	624		864	1042	1114	616	-	2541
		% critical deviations*	-	3	1	1	8	-	0	1	2	-	1	7		9	3	4	1	-	6
		% total deviations^	-	6	1	2	10	-	1	2	3	-	3	9		30	4	10	1	-	11
2010	152	No. of tests	-	1173	937	1118	1194	-	787	1026	1133	-	1096	566		800	1012	1134	604	-	2516
		% critical deviations*	-	4	2	1	3	-	4	4	5	-	1	14		19	4	5	1	-	9
		% total deviations^	-	5	3	2	3	-	8	8	6	-	2	17		55	4	9	1	-	17

Table 7 (continued). EQAS participants' performance of *Salmonella* strains antimicrobial susceptibility testing categorized by antimicrobial.

EQAS iteration	No. of labs	Performance	Antimicrobial∞																	
			AMC	AMP	CAZ	CHL	CIP	POD	CRO	CTX	GEN	KAN	NAL	SMX	MER	STR	SXT	TET	TMP	XNL	OVERALL Average
2011	127	No. of tests	-	1099	829	988	1070	-	744	909	999	-	993	542	-	682	988	1017	493	-	2271
		% critical deviations*	-	5	3	2	20	-	3	4	4	-	7	4	-	3	3	4	1	-	9
		% total deviations^	-	6	4	2	21	-	3	6	5	-	15	5	-	42	3	10	2	-	17
2012	159	No. of tests	-	1228	993	1159	1245	-	834	1058	1161	-	1136	584	-	814	1054	1163	613	-	2608
		% critical deviations*	-	3	2	1	11	-	2	4	3	-	2	5	-	2	1	2	1	-	5
		% total deviations^	-	5	2	2	12	-	3	5	4	-	4	7	-	35	2	5	1	-	12
2013	145	No. of tests	-	1121	898	1027	1134	-	763	1011	1086	-	1027	491	-	-	946	1060	545	-	2381
		% critical deviations*	-	2	3	0	2	-	1	3	3	-	2	4	-	-	2	3	2	-	4
		% total deviations^	-	3	3	1	18	-	2	6	6	-	6	5	-	-	2	5	2	-	9
2014	155	No. of tests	-	1176	1003	1072	1161	-	817	1014	1147	-	1078	561	-	-	1039	1107	541	-	2511
		% critical deviations*	-	3	3	1	3	-	1	2	3	-	1	5	-	-	2	3	2	-	4
		% total deviations^	-	4	4	2	19	-	2	3	5	-	2	6	-	-	3	5	2	-	9
2015	155	No. of tests	-	1176	1010	1064	1172	-	787	1018	1145	-	1010	514	611	-	1034	1077	591	-	2468
		% critical deviations*	-	3	9	2	1	-	3	5	3	-	4	7	1	-	2	2	2	-	6
		% total deviations^	-	5	11	22	14	-	4	6	5	-	10	9	1	-	3	5	2	-	13
2016	150	No. of tests	-	1133	988	1020	1100	-	800	968	1104	-	959	529	838	-	953	1042	599	-	2407
		% critical deviations*	-	4	4	1	1	-	2	4	4	-	1	7	5	-	2	3	2	-	8
		% total deviations^	-	5	4	2	10	-	3	4	6	-	3	8	6	-	2	6	2	-	12
Average•	139	No. of tests	944	1071	922	1010	1062	347	789	999	1040	588	982	561	725	769	977	1011	563	242	1354
		% critical deviations*	7	3	3	2	5	3	2	3	3	3	2	6	3	6	3	4	2	1	3
		% total deviations^	17	5	5	4	9	21	4	6	5	10	5	7	4	31	4	10	2	8	9

∞For antimicrobial abbreviations: see List of Abbreviations page 1

*R→ S & S → R (R, resistant; S, susceptible)

^S→R & R→S & S↔I or I↔R (I, intermediate)

• Data do not include one strain which may have lost resistance due to transport or storage stress

-, not determined

Table 8. Antimicrobial susceptibility test results (number of R/I/S) for the EQAS 2016 *Salmonella* strains*

Strain	Antimicrobial^												
	AMP	**CTX**	**CAZ**	**CRO**	**CHL**	**CIP**	**GEN**	**MER**	**NAL**	**SMX**	**TET**	**TMP**	**SXT**
WHO S-16.1	**139**/2/3	6/2/**113**	5/0/**119**	1/1/**98**	1/1/**125**	1/12/**125**	4/3/**132**	3/0/**103**	1/1/**117**	**65**/0/2	**129**/0/2	**77**/0/0	**120**/0/1
WHO S-16.2	**140**/1/1	**122**/0/0	**124**/0/0	**100**/1/0	**127**/0/0	1/9/**128**	7/5/**126**	**74**/5/27	0/1/**119**	**62**/0/3	4/3/**121**	**73**/0/1	**117**/0/2
WHO S-16.3	10/6/**125**	9/1/**111**	8/3/**113**	3/1/**96**	3/4/**121**	1/18/**119**	**132**/4/3	4/0/**101**	1/2/**117**	**58**/0/9	7/2/**123**	1/1/**72**	4/0/**116**
WHO S-16.4	5/0/**136**	3/0/**118**	5/0/**119**	1/1/**98**	2/1/**125**	0/8/**131**	6/2/**130**	2/0/**102**	0/2/**119**	9/1/**57**	2/2/**127**	4/0/**71**	1/1/**117**
WHO S-16.5	7/1/**134**	3/0/**118**	5/0/**119**	2/0/**98**	**124**/1/3	0/8/**129**	6/4/**128**	2/0/**102**	3/2/**115**	**62**/0/4	**104**/13/14	**70**/0/4	**115**/0/4
WHO S-16.6	**135**/1/3	**114**/1/5	**120**/0/1	**96**/0/3	**125**/1/1	2/16/**120**	5/1/**129**	4/0/**102**	3/2/**113**	**62**/2/3	**128**/2/0	0/0/**75**	3/2/**112**
WHO S-16.7	6/0/**136**	4/2/**115**	8/1/**114**	3/0/**98**	3/0/**125**	1/19/**116**	4/2/**132**	1/0/**102**	1/5/**115**	4/2/**60**	5/1/**125**	1/0/**74**	3/0/**117**
WHO S-16.8	5/1/**136**	5/0/**116**	5/1/**118**	2/1/**96**	2/2/**123**	1/10/**125**	4/2/**133**	2/0/**102**	1/2/**117**	1/2/**61**	2/2/**124**	1/0/**74**	0/0/**118**

^For antimicrobial abbreviations: see List of Abbreviations page 1

*In bold: expected interpretation. Grey cell: <90% of laboratories did correct interpretation. R, resistant/I, intermediate/ S, susceptible.

Table 9. Region-based categorization of EQAS participants' performance of *Salmonella* AST

Region	EQAS iteration	No. of labs	% correct test result	% minor deviations (S ↔ I or I ↔ R)^	% major deviations (S → R)^	% very major deviations (R → S)^	% critical deviations (S → R & R → S)^	% total deviations (S→R & R→S & S↔I or I↔R)^	Countries participating in the 2016 iteration
Africa	2001	7	80.1	9.6	7.7	2.5	10.2	19.8	Cameroun, Congo, Democratic Republic of the, Egypt, Ivory Coast, Kenya (3), Madagascar, Mauritius, Morocco (2), Nigeria, Senegal, South Africa, The Gambia (2), Zambia, Zimbabwe
	2002	10	94.3	4.1	1.0	0.6	1.6	5.7	
	2003	13	86.9	6.6	2.8	3.7	6.5	13.1	
	2004	11	85.7	7.2	5.2	1.9	7.1	14.3	
	2006	20	85.8	7.5	4.1	2.7	6.8	14.3	
	2007	16	90.7	4.4	4.0	0.9	4.9	9.3	
	2008	19	83.8	6.5	5.5	4.2	9.7	16.2	
	2009	22	90.1	4.5	3.6	1.8	5.4	9.9	
	2010	22	84.7	6.0	6.5	2.8	9.3	15.3	
	2011	17	87.0	5.0	4.7	3.3	8.0	13.0	
	2012	18	89.4	5.3	3.5	1.9	5.4	10.6	
	2013	16	92.0	3.2	4.0	0.9	4.9	8.0	
	2014	20	92.5	3.8	2.0	1.7	3.7	7.5	
	2015	22	86.7	7.3	4.1	1.9	6.0	13.3	
	2016	**18**	**90.1**	**4.6**	**4.2**	**1.1**	**5.3**	**9.9**	
Central Asia & Middle East	2001	10	87.7	6.3	5.2	0.8	6.0	12.3	Bahrain, India (4), Iran, Islamic rep. Of (3), Iraq, Israel, Oman
	2002	6	83.4	9.8	6.6	0.2	6.8	16.6	
	2003	8	89.9	4.5	4.0	1.6	5.6	10.1	
	2004	10	87.5	6.7	5.5	0.3	5.8	12.5	
	2006	7	79.2	10.5	9.8	0.5	10.3	20.8	
	2007	8	87.8	5.0	6.2	1.1	7.3	12.2	
	2008	12	86.1	6.5	4.0	3.4	7.4	13.9	
	2009	6	93.7	4.3	0.9	1.1	2.0	6.3	
	2010	7	95.8	2.6	0.2	1.4	1.6	4.2	
	2011	4	91.8	4.1	1.8	2.3	4.1	8.2	
	2012	8	92.8	4.4	1.6	0.7	2.3	6.6	
	2013	8	93.6	5.2	1.0	0.1	1.2	6.4	
	2014	17	91.0	4.2	2.9	2.0	4.9	9.0	
	2015	14	91.4	4.3	2.3	2.1	4.4	8.6	
	2016	**11**	**95.5**	**0.9**	**1.8**	**1.8**	**3.6**	**4.5**	
Caribbean	2001	2	83.5	9.5	7.0	0.0	7.0	16.5	Barbados, Jamaica
	2002	1	95.8	4.2	0.0	0.0	0.0	4.2	
	2003	8	91.7	6.4	1.5	0.5	2.0	8.4	
	2004	8	94.1	3.1	1.9	0.9	2.8	5.9	
	2006	5	92.1	5.4	1.6	1.0	2.6	8.0	
	2007	4	95.0	3.1	0.9	0.9	1.8	5.0	
	2008	5	90.7	5.5	0.9	2.9	3.8	9.3	
	2009	4	93.2	1.8	3.2	1.8	5.0	6.8	
	2010	4	90.9	5.4	2.7	0.7	3.4	8.8	
	2011	2	96.5	1.4	0.0	2.1	2.1	3.5	
	2012	4	91.1	1.5	6.7	0.7	7.4	8.9	
	2013	3	90.2	2.6	7.3	0.0	7.3	9.8	
	2014	4	78.3	4.7	9.4	7.6	17.0	21.7	
	2015	4	87.5	6.6	3.7	2.2	5.9	12.5	
	2016	**2**	**100.0**	**0.0**	**0.0**	**0.0**	**0.0**	**0.0**	

Table 9 (continued). Region-based categorization of EQAS participants' performance of *Salmonella* antimicrobial susceptibility testing

Region	EQAS iteration	No. of labs	% correct test result	% minor deviations (S ↔ I or I ↔ R)^	% major deviations (S → R)^	% very major deviations (R → S)^	% critical deviations (S → R & R → S)^	% total deviations (S→R & R→S & S↔I or I↔R)^	Countries participating in the 2016 iteration
Europe	2001	47	91.3	5.7	2.7	0.3	3.0	8.7	Belgium, Bulgaria, Croatia, Cyprus, Czech Republic, Greece (3), Hungary, Ireland, Italy (9), Kosova, Luxembourg (2), Malta (2), Norway, Poland (2), Portugal, Serbia (2), Slovak Republic, Spain, Turkey (2), Ukraine, United Kingdom
	2002	57	92.7	5.2	1.2	0.9	2.1	7.3	
	2003	64	92.9	3.8	1.0	2.3	3.3	7.1	
	2004	58	93.5	4.3	1.4	0.8	2.2	6.5	
	2006	54	88.7	7.0	3.8	0.6	4.4	11.3	
	2007	49	94.2	3.7	1.6	0.4	2.0	5.7	
	2008	51	91.2	4.4	2.5	1.9	4.4	8.8	
	2009	40	95.1	2.6	1.3	0.9	2.2	4.8	
	2010	39	92.4	4.1	1.2	2.3	3.5	7.6	
	2011	36	92.5	4.5	1.7	1.3	3.0	7.5	
	2012	40	95.5	2.8	1.2	0.4	1.7	4.5	
	2013	37	95.7	2.5	1.4	0.3	1.7	4.2	
	2014	40	96.6	2.1	0.8	0.5	1.3	3.4	
	2015	38	93.4	4.1	1.3	1.2	2.5	6.6	
	2016	**36**	**96.9**	**1.5**	**1.2**	**0.5**	**1.6**	**3.1**	
North America	2001	4	95.8	3.8	0.0	0.4	0.4	4.2	Canada (5), United States of America (3)
	2002	3	90.5	6.9	0.6	2.0	2.6	9.5	
	2003	7	93.4	5.2	0.0	1.4	1.4	6.6	
	2004	9	94.2	4.2	1.8	0.0	1.8	6.0	
	2006	8	94.8	2.9	1.0	1.3	2.3	5.2	
	2007	10	95.4	2.9	0.8	0.8	1.6	4.6	
	2008	14	96.4	0.6	0.4	2.6	3.0	3.6	
	2009	10	98.7	0.0	0.4	0.9	1.3	1.3	
	2010	11	94.8	2.6	0.2	2.4	2.6	5.2	
	2011	9	92.1	2.6	1.5	3.8	5.3	7.9	
	2012	10	96.0	2.1	1.0	0.9	1.9	4.0	
	2013	7	98.4	1.3	0.0	0.2	0.2	1.6	
	2014	8	96.9	2.2	0.4	0.6	0.9	3.1	
	2015	8	94.5	2.0	0.8	2.8	3.6	5.5	
	2016	**8**	**99.1**	**0.2**	**0.0**	**0.7**	**0.7**	**0.9**	
Oceania	2001	6	91.8	4.7	2.7	0.9	3.6	8.2	Australia (2), New Zealand
	2002	7	91.7	6.2	0.0	2.0	2.0	8.3	
	2003	9	94.3	2.5	1.2	2.0	3.2	5.7	
	2004	11	97.1	2.5	0.3	0.1	0.4	2.9	
	2006	7	93.4	4.6	0.9	1.1	2.0	6.6	
	2007	1	98.9	1.1	0.0	0.0	0.0	1.1	
	2008	4	93.9	3.8	0.0	2.3	2.3	6.1	
	2009	4	95.9	3.2	0.3	0.6	0.9	4.1	
	2010	4	92.5	4.6	0.6	2.3	2.9	7.5	
	2011	4	93.8	5.6	0.6	0.0	0.6	6.2	
	2012	4	95.5	3.1	0.6	0.9	1.4	4.5	
	2013	4	96.8	2.9	0.0	0.3	0.3	3.2	
	2014	5	97.4	2.0	0.0	0.6	0.6	2.6	
	2015	5	95.3	3.8	0.5	0.5	1.0	4.8	
	2016	**3**	**98.1**	**0.0**	**0.5**	**1.4**	**1.9**	**1.9**	

Table 9 (continued). Region-based categorization of EQAS participants' performance of *Salmonella* antimicrobial susceptibility testing.

Region	EQAS iteration	No. of labs	% correct test result	% minor deviations (S ↔ I or I ↔ R)^	% major deviations (S → R)^	% very major deviations (R → S)^	% critical deviations (S → R & R → S)^	% total deviations (S→R & R→S & S↔I or I↔R)^	Countries participating in the 2016 iteration
Russia	2001	1	81.9	15.3	2.8	0.0	2.8	18.1	- none -
	2002	1	84.5	9.9	5.6	0.0	5.6	15.5	
	2003	1	100.0	0.0	0.0	0.0	0.0	0.0	
	2004	4	91.2	6.6	1.5	0.7	2.2	8.8	
	2006	5	87.4	8.2	2.7	1.7	4.4	12.6	
	2007	8	88.9	5.8	4.8	0.4	5.2	11.0	
	2008	6	92.2	4.7	1.4	1.7	3.1	7.8	
	2009	6	93.8	2.1	3.3	0.8	4.1	6.2	
	2010	8	94.3	3.3	1.3	1.1	2.4	5.7	
	2011	7	90.0	4.8	3.2	2.0	5.2	10.0	
	2012	6	97.4	2.0	0.0	0.6	0.6	2.6	
	2013	2	98.2	1.8	0.0	0.0	0.0	1.8	
	2014	4	98.2	0.3	0.9	0.6	1.5	1.8	
	2015	4	98.7	1.0	0.0	0.3	0.3	1.3	
	2016	**-**	**-**	**-**	**-**	**-**	**-**	**-**	
Latin America	2001	11	90.8	6.9	1.4	1.0	2.4	9.2	Argentina, Bolivia, Brazil (2), Chile (2), Colombia (3), Costa Rica (2), Ecuador (2), El Salvador, Guatemala (2), Honduras, Mexico, Panama, Paraguay, Peru, Suriname, Uruguay, Venezuela
	2002	13	93.7	4.6	0.7	1.0	1.7	6.3	
	2003	12	90.8	4.2	2.0	3.0	5.0	9.2	
	2004	17	94.4	4.7	0.8	0.1	0.9	5.6	
	2006	16	88.7	6.3	4.5	0.6	5.1	11.3	
	2007	17	94.9	1.8	1.9	1.4	3.3	5.0	
	2008	20	93.0	3.4	1.5	2.1	3.6	7.0	
	2009	20	95.6	2.1	1.1	1.2	2.3	4.4	
	2010	23	90.8	2.1	5.6	1.4	7.1	9.2	
	2011	22	90.8	2.8	3.1	3.3	6.4	9.2	
	2012	25	94.4	1.6	3.0	1.0	4.0	5.6	
	2013	25	95.5	2.6	1.2	0.3	1.5	4.2	
	2014	24	96.5	1.9	1.1	0.6	1.7	3.5	
	2015	20	94.9	3.8	0.6	0.7	1.3	5.1	
	2016	**24**	**95.6**	**2.5**	**1.4**	**0.5**	**1.9**	**4.4**	
China	2001	4	98.9	0.8	0.0	0.3	0.3	1.1	China (16)
	2002	3	96.0	4.0	0.0	0.0	0.0	4.0	
	2003	8	90.1	3.6	2.8	3.6	6.4	10.0	
	2004	8	96.0	3.2	0.7	0.1	0.8	4.0	
	2006	6	89.6	7.0	2.9	0.5	3.4	10.4	
	2007	10	98.3	1.1	0.3	0.2	0.5	1.6	
	2008	18	92.8	3.7	0.8	2.7	3.5	7.2	
	2009	14	94.8	2.2	2.1	0.8	2.9	5.1	
	2010	9	92.1	4.5	1.6	1.8	3.4	7.9	
	2012	9	95.3	3.0	0.5	1.2	1.6	4.7	
	2013	8	96.9	2.0	0.5	0.5	1.0	3.1	
	2014	8	97.0	1.2	0.1	1.6	1.8	3.0	
	2015	15	92.8	2.0	4.0	1.1	5.1	7.2	
	2016	**16**	**96.7**	**0.4**	**1.8**	**1.1**	**2.9**	**3.3**	

^S. susceptible; I. intermediate; R. resistant

Table 9 (continued). Region-based categorization of EQAS participants' performance of *Salmonella* antimicrobial susceptibility testing.

Region	EQAS iteration	No. of labs	% correct test result	% minor deviations (S ↔ I or I ↔ R)^	% major deviations (S → R)^	% very major deviations (R → S)^	% critical deviations (S → R & R → S)^	% total deviations (S→R & R→S & S↔I or I↔R)^	Countries participating in the 2015 iteration
Southeast Asia	2001	16	88.1	7.7	2.3	1.9	4.2	11.9	Cambodia, Japan, Korea, Rep of (2), LAO PDR, Malaysia (5), Philippines, Sri Lanka (2), Taiwan, Thailand (10), Viet Nam
	2002	18	89.0	8.1	1.4	1.6	3.0	11.0	
	2003	17	87.4	5.2	4.7	2.7	7.4	12.6	
	2004	16	92.8	4.4	2.3	0.5	2.8	7.2	
	2006	15	90.0	8.1	1.2	0.8	2.0	10.0	
	2007	20	93.9	4.0	1.4	0.7	2.1	6.1	
	2008	19	90.5	4.7	2.2	2.6	4.8	9.5	
	2009	27	91.8	4.1	3.0	1.2	4.2	8.3	
	2010	25	92.8	3.8	1.5	1.9	3.4	7.2	
	2011	26	90.5	3.5	2.4	3.5	5.9	9.5	
	2012	35	91.7	3.9	3.5	0.9	4.4	8.3	
	2013	35	93.4	3.2	2.5	0.7	3.2	6.4	
	2014	8	97.0	1.2	0.1	1.6	1.8	3.0	
	2015	25	89.9	6.0	2.6	1.5	4.1	10.1	
	2016	**30**	**93.5**	**2.2**	**3.5**	**0.8**	**4.3**	**6.5**	

^S. susceptible; I. intermediate; R. resistant

Table 10. EQAS participants' performance of antimicrobial susceptibility testing of quality control strain *Escherichia coli* ATCC 25922

		Method	Perfor-mance[4,5]	AMP	CAZ	CHL	CIP	CRO	CTX	FIS (SMX)[2]	FOX	GEN	MER	NAL	STR	SXT	TET	TMP
Accepted interval[1]		**MIC (µg/ml)**		2-8	0.06-0.5	2-8	0.004-0.016	0.03-0.12	0.03-0.12	8-32	2-8	0.25-1	0.008-0.06	1-4	4-16[3]	≤0.5/9.5	0.5-2	0.5-2
		Disks (mm)		15-22	25-32	21-27	30-40	29-35	29-35	15-23	23-29	19-26	28-34	22-28	12-20	23-29	18-25	21-28
EQAS iteration (total no. of participants)	**2000** (44)	MIC & Disk	No.[4]	37	-	38	35	-	-	19	-	39	-	37	36	-	42	31
			%[5]	27	-	37	20	-	-	53	-	23	-	35	22	-	42	30
	2001 (107)	MIC & Disk	No.[4]	97	-	97	97	-	-	53	-	99	-	74	81	90	96	50
			%[5]	19	-	20	14	-	-	34	-	12	-	14	12	14	22	22
	2002 (114)	MIC & Disk	No.[4]	109	-	107	108	-	-	57	-	108	-	102	82	102	102	66
			%[5]	16	-	15	14	-	-	26	-	12	-	14	11	12	13	11
	2003 (144)	MIC & Disk	No.[4]	140	-	137	138	-	-	82	-	138	-	132	105	129	137	79
			%[5]	14	-	22	9	-	-	17	-	9	-	16	9	14	19	14
	2004 (140)	MIC & Disk	No.[4]	132	-	128	132	-	111	84	-	134	-	126	110	120	129	87
			%[5]	10	-	13	8	-	18	16	-	10	-	9	6	11	13	9
	2006 (137)	MIC & Disk	No.[4]	133	96	126	127	-	115	74	-	131	-	122	106	122	125	74
			%[5]	14	15	18	8	-	21	29	-	14	-	20	11	19	12	17
	2007 (126)	MIC & Disk	No.[4]	124	92	123	121	-	104	64	-	124	-	120	97	107	117	67
			%[5]	11	9	14	12	-	16	22	-	6	-	7	6	13	7	10
	2008 (147)	MIC & Disk	No.[4]	147	111	135	144	-	124	71	-	145	-	136	101	129	139	79
			%[5]	12	9	10	8	-	14	14	-	8	-	8	12	13	7	13
		MIC	No.[4]	33	23	24	33	-	23	18	-	31	-	23	19	22	28	16
			%[5]	0	5	0	6	-	9	11	-	0	-	0	11	9	0	13
		Disk	No.[4]	114	89	112	111	-	101	53	-	114	-	113	82	107	111	63
			%[5]	16	10	12	8	-	15	15	-	11	-	10	12	14	9	13
	2009 (129)	MIC & Disk	No.[4]	128	100	121	124	88	107	63	-	123	-	117	98	113	122	70
			%[5]	16	13	15	7	16	10	11	-	18	-	13	10	14	14	11
		MIC (27)	No.[4]	27	19	24	26	20	20	14	-	25	-	24	19	21	27	25
			%[5]	11	11	8	8	15	15	21	-	12	-	8	5	19	11	13
		Disk (102)	No.[4]	101	81	97	98	68	87	49	-	98	-	93	79	92	95	55
			%[5]	16	14	16	6	16	9	10	-	18	-	14	11	12	15	11
	2010 (116)	MIC & Disk	No.[4]	114	97	108	115	79	100	51	-	112	-	104	84	101	110	63
			%[5]	11	9	9	6	10	14	11	-	11	-	5	5	12	5	15
		MIC (24)	No.[4]	25	15	21	25	15	17	12	-	24	-	19	17	17	24	11
			%[5]	12	20	10	8	7	18	8	-	13	-	16	18	18	17	36
		Disk (91)	No.[4]	89	82	87	90	64	83	39	-	88	-	85	67	84	86	52
			%[5]	9	6	8	4	9	11	10	-	9	-	2	1	10	1	8
	2011 (112)	MIC & Disk	No.[4]	111	89	102	109	76	96	50	-	103	-	103	72	99	107	51
			%[5]	17	4	11	7	7	9	8	-	11	-	8	4	16	7	14
		MIC (23)	No.[4]	23	15	18	22	16	15	13	-	22	-	19	17	16	21	11
			%[5]	4	7	0	9	6	0	8	-	9	-	0	6	6	5	0
		Disk (89)	No.[4]	88	74	84	87	60	81	37	-	81	-	84	55	83	86	40
			%[5]	20	4	13	7	7	11	8	-	11	-	10	4	18	8	18

Table 10 (continued). EQAS participants' performance of antimicrobial susceptibility testing of quality control strain *Escherichia coli* ATCC 25922

		Method	Perfor-mance[4.5]	AMP	CAZ	CHL	CIP	CRO	CTX	FIS (SMX)[2]	FOX	GEN	MER	NAL	STR	SXT	TET	TMP
Accepted interval[1]		**MIC (µg/ml)**		2-8	0.06-0.5	2-8	0.004-0.016	0.03-0.12	0.03-0.12	8-32	2-8	0.25-1	0.008-0.06	1-4	4-16[3]	≤0.5/9.5	0.5-2	0.5-2
		Disks (mm)		15-22	25-32	21-27	30-40	29-35	29-35	15-23	23-29	19-26	28-34	22-28	12-20	23-29	18-25	21-28
EQAS iteration (total no. of participants)	**2012** (135)	MIC & Disk	No.[4]	134	111	121	131	90	115	53	-	127	-	121	89	112	129	66
			%[5]	13	12	7	6	11	10	11	-	9	-	9	8	13	10	21
		MIC (37)	No.[4]	37	26	31	35	23	28	19	-	35	-	31	26	23	35	22
			%[5]	3	4	0	3	0	4	5	-	3	-	3	8	0	0	9
		Disk (98)	No.[4]	97	85	90	96	67	87	34	-	92	-	90	63	89	94	44
			%[5]	16	14	9	7	15	11	15	-	11	-	11	8	16	14	27
	2013 (122)	MIC & Disk	No.[4]	117	100	112	119	82	107	44	-	113	-	113	-	101	114	59
			%[5]	12	7	5	7	4	8	10	-	6	-	11	-	8	8	11
		MIC (33)	No.[4]	31	25	28	32	19	27	17	-	32	-	28	-	22	32	22
			%[5]	6	4	4	13	5	11	18	-	9	-	11	-	5	6	5
		Disk (89)	No.[4]	86	75	84	87	63	80	27	-	81	-	85	-	79	82	37
			%[5]	13	8	6	5	5	6	7	-	4	-	9	-	10	7	8
	2014 (115)	MIC & Disk	No.[4]	111	99	101	108	75	97	49	-	111	-	103	-	102	104	50
			%[5]	5	7	7	6	7	14	14	-	8	-	8	-	8	7	2
		MIC (28)	No.[4]	27	21	24	27	16	22	16	-	28	-	24	-	21	25	12
			%[5]	4	5	4	15	6	14	0	-	14	-	8	-	14	0	0
		Disk (87)	No.[4]	84	78	77	81	59	75	33	-	83	-	79	-	81	79	38
			%[5]	6	8	8	4	7	15	21	-	6	-	8	-	6	9	3
	2015 (117)	MIC&Disk	No.[4]	113	101	101	112	78	99	54	75	112	74	100	-	104	106	57
			%[5]	8	5	7	7	9	6	11	9	9	12	7	-	13	8	9
		MIC (31)	No.[4]	30	26	25	30	16	25	15	20	30	19	24	-	24	27	16
			%[5]	3	8	4	13	0	12	7	10	7	11	4	-	8	7	13
		Disk (85)	No.[4]	83	75	76	82	62	74	39	55	82	55	76	-	80	79	41
			%[5]	10	4	8	5	11	4	13	9	10	13	8	-	14	8	7
	2016 (106)	MIC&Disk	No.[4]	101	93	95	101	76	94	54	84	99	88	91	-	91	97	59
			%[5]	11	5	13	9	16	15	24	7	8	10	9	-	8	10	14
		MIC (30)	No.[4]	27	24	24	27	17	24	13	22	29	25	20	-	20	25	16
			%[5]	4	4	0	7	12	4	23	0	3	4	0	-	0	8	13
		Disk (76)	No.[4]	74	69	71	74	59	70	41	62	70	63	71	-	71	72	43
			%[5]	14	6	17	9	17	19	24	10	10	13	11	-	10	11	14

[0]For antimicrobial abbreviations: see List of Abbreviations page 1

[1]CLSI standard. Performance Standards for Antimicrobial Disk and Dilution Susceptibility testing. 22nd Informational supplement. CLSI document M100-S22. 2012 Wayne. PA. USA

[2]FIS (sulfisoxazole) covers the group of SMX (sulfonamides)

[3]Quality control range developed by the manufacturer of Sensititre®

[4]No.. number of laboratories performing the analysis

[5]%. percentage of laboratories reporting erroneous results

-. not determined

Table 11. *Shigella* serotypes (ST) and deviations (D). WHO EQAS 2016

Strain	Correct serotype		No. of labs reporting correct identification	D (%)	Deviating results	No. of labs reporting correct ST	D (%)	Deviating results (*)
WHO 2016 SH-16.1	*S. flexneri*	1b	120	1.6	2	77	36.9	6
WHO 2016 SH-16.2	*S. boydii*	4	117	4.9	6	70	43.1	1(2), 2, 9
WHO 2016 SH-16.3	*S. flexneri*	2b	121	1.6	2	75	39.0	
WHO 2016 SH-16.4	*S. flexneri*	3a	123	0.0	0	71	42.3	6(2)

*number of participants reporting deviating result

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Table 12. Region-based categorization of laboratories performing *Shigella* serotyping in 2016

Region	Year	No. of laboratories	No. of strains serotyped	Strains serotyped correctly (%)	Countries participating in the 2016 iteration
Africa	2009	8	18	72.2	Ivory Coast, Kenya, Mauritius, Senegal, South Africa, Zimbabwe
	2010	7	16	62.5	
	2011	4	10	100.0	
	2012	5	18	90.0	
	2013	5	8	62.5	
	2014	6	9	55.6	
	2015	8	22	68.2	
	2016	**6**	**13**	**69.2**	
Central Asia & Middle East	2009	3	5	100.0	Bahrain, India (2), Iraq, Israel, Oman
	2010	3	6	83.3	
	2011	2	6	100.0	
	2012	3	9	81.8	
	2013	4	8	100.0	
	2014	5	10	80.0	
	2015	6	24	100.0	
	2016	**6**	**22**	**90.9**	
China	2009	13	35	100.0	China (17)
	2010	9	23	91.3	
	2011	-	-	-	
	2012	8	29	90.6	
	2013	6	11	100.0	
	2014	9	18	94.4	
	2015	14	55	87.3	
	2016	**17**	**68**	**91.2**	
Caribbean	2009	-	-	-	- none -
	2010	-	-	-	
	2011	-	-	-	
	2012	1	1	33.3	
	2013	-	-	-	
	2014	1	1	0.0	
	2015	1	3	100.0	
	2016	**-**	**-**	**-**	
Europe	2009	15	40	92.5	Belgium, Bulgaria, Czech Republic, Germany (2), Greece, Ireland, Luxembourg, Malta, Norway, Portugal, Serbia (2), Slovenia, Spain, Sweden, Turkey, Ukraine, United Kingdom
	2010	15	35	85.7	
	2011	16	42	92.9	
	2012	19	63	86.3	
	2013	18	31	96.8	
	2014	20	36	86.1	
	2015	21	74	93.2	
	2016	**19**	**73**	**91.8**	

Table 12 (continued). Region-based categorization of laboratories performing *Shigella* serotyping in 2016

Region	Year	No. of laboratories	No. of strains serotyped	Strains serotyped correctly (%)	Countries participating in the 2016 iteration
North America	2009	7	18	100.0	Canada (5), United States of America (2)
	2010	7	20	100.0	
	2011	6	16	100.0	
	2012	8	25	80.6	
	2013	8	14	100.0	
	2014	6	11	100.0	
	2015	7	26	100.0	
	2016	**7**	**25**	**92.0**	
Oceania	2009	3	8	100.0	Australia (3), New Zealand
	2010	3	8	100.0	
	2011	3	8	100.0	
	2012	3	12	100.0	
	2013	4	10	100.0	
	2014	4	7	100.0	
	2015	4	15	86.7	
	2016	**4**	**15**	**93.3**	
Russia	2009	6	18	83.3	- none -
	2010	7	20	75.0	
	2011	6	18	88.9	
	2012	5	16	80.0	
	2013	2	4	100.0	
	2014	3	6	100.0	
	2015	3	12	100.0	
	2016	**-**	**-**	**-**	
Latin America	2009	16	40	97.5	Argentina, Brazil (2), Chile (2), Costa Rica, Ecuador (2), Guatemala, Honduras, Mexico (2), Paraguay, Peru, Uruguay, Venezuela (2)
	2010	13	33	78.8	
	2011	15	37	94.6	
	2012	19	58	80.6	
	2013	16	30	93.3	
	2014	17	29	86.2	
	2015	13	45	88.9	
	2016	**17**	**62**	**83.9**	
Southeast Asia	2009	11	30	90.0	Japan, Korea, Rep of, LAO PDR, Malaysia (2), Philippines, Sri Lanka, Taiwan, Thailand (5), Viet Nam
	2010	14	32	87.5	
	2011	13	33	84.8	
	2012	14	47	90.4	
	2013	9	17	100.0	
	2014	12	22	95.5	
	2015	14	49	91.8	
	2016	**14**	**54**	**85.2**	

Table 13. EQAS participating laboratories' performance of *Shigella* strains antimicrobial susceptibility testing

EQAS iteration	No. of participating laboratories	% correct test results	% minor deviations (S ↔ I or I ↔ R)^	% major deviations (S → R)^	% very major deviations (R → S)^	% critical deviations (S → R & R → S)^	% total deviations (S → R & R → S & S ↔ I or I ↔ R)^
2008	15	95	2	2	1	3	5
2009	111	96	2	1	1	2	4
2010	114	91	2	1	6	7	9
2011	107	92	2	1	4	5	7
2012	120	91	3	1	5	6	9
2013	99	91	6	2	2	4	10
2014	116	92	4	1	3	4	8
2015	116	93	4	1	1	3	7
2016	112	96	1	1	1	3	4

^S. susceptible; I. intermediate; R. resistant

Table 14. EQAS laboratories' performance of *Shigella* strains antimicrobial susceptibility testing categorized by antimicrobial

EQAS iteration	No. of labs	Lab performance	Antimicrobial														
			AMP	CAZ	CHL	CIP	CTX	GEN	MER	NAL	SMX	STR	SXT	TET	TMP	CRO	OVERALL average
2008	15	No. of tests	52	44	51	48	48	50	-	52	7	27	52	52	4	42	529
		% critical deviations*****	1	2	1	-	2	1	-	-	-	4	2	4	-	2	1.5
		% total deviations^	1	2	1	-	2	1	-	-	-	9	2	8	-	2	2.2
2009	111	No. of tests	423	358	388	426	372	396	-	388	211	293	388	386	218	301	4548
		% critical deviations*****	2.4	0.3	2.1	0.2	1.1	2.5	-	0.5	3.8	5.8	2.3	2.8	1.8	0.3	1.9
		% total deviations^	3.8	0.3	4.6	0.9	1.1	3.5	-	1.5	3.8	18.1	3.6	7.5	1.8	0.6	3.8
2010	114	No. of tests	424	344	402	434	377	403	-	382	194	275	363	410	218	291	4517
		% critical deviations*	1.7	0.6	3.5	40.8	2.4	3.5	-	2.1	4.6	8.0	8.3	4.4	3.7	0.0	6.4
		% total deviations^	1.9	1.2	9.2	77.9	3.0	5.5	-	3.0	6.0	14.6	13.8	5.9	3.8	0.0	11.2
2011	107	No. of tests	403	322	353	396	343	359	-	369	179	246	371	376	178	289	4.184
		% critical deviations*	5.5	5.2	2.2	38.9	2.7	3.3	-	4.0	1.7	3.6	3.2	2.7	2.2	2.0	5.5
		% total deviations^	7.7	12.0	4.2	40.7	2.7	4.4	-	11.0	1.7	10.5	3.2	3.5	2.2	2.0	7.7
2012	120	No. of tests	462	376	427	464	400	430	-	442	196	291	396	426	215	337	4862
		% critical deviations*	2.6	0.8	5.6	35.3	2.0	4.9	-	1.6	1.5	9.3	6.3	5.4	1.9	0.9	6.0
		% total deviations^	3.9	0.8	11.5	38.6	3.8	6.3	-	3.2	2.0	27.1	8.1	7.5	4.2	2.1	9.2
2013	99	No. of tests	-	351	379	420	384	392	-	393	164	-	346	392	193	309	3723
		% critical deviations*	-	1.1	2.1	8.3	3.4	2.3	-	3.3	1.8	-	5.8	2.8	3.1	1.0	3.4
		% total deviations^	-	0.3	0.6	2.0	0.9	0.6	-	0.8	1.1	-	1.7	0.7	1.6	0.3	9.5
2014	116	No. of tests	441	390	386	441	389	424	-	405	188	-	413	398	189	331	4395
		% critical deviations*	2.5	9.7	2.1	7.9	1.3	4.0	-	2.5	4.8	-	3.9	3.5	5.3	2.1	4.1
		% total deviations^	2.9	14.1	3.9	34.2	1.5	5.4	-	5.2	4.8	-	4.1	6.5	6.3	3.9	8.1
2015	116	No. of tests	441	405	400	448	397	434	296	388	202	-	399	410	222	331	4773
		% critical deviations*	2.0	5.7	4.0	0.9	4.5	1.8	0.0	2.3	0.5	-	1.3	3.7	0.5	3.9	2.4
		% total deviations^	2.7	8.4	10.3	26.6	5.0	3.0	0.3	6.4	1.0	-	1.3	6.6	0.5	4.5	5.9
2016	112	No. of tests	418	391	380	310	377	409	340	361	195	-	374	390	224	339	4508
		% critical deviations*	2.6	7.2	2.6	1.0	2.7	2.9	0.3	1.9	4.1	-	1.9	2.3	3.1	2.4	2.7
		% total deviations^	2.9	7.4	7.1	7.1	2.9	4.2	0.3	3.0	4.1	-	2.1	3.3	3.1	2.4	3.9

∞For antimicrobial abbreviations: see List of Abbreviations page 1

*****R→ S & S → R (R. resistant; S. susceptible)

^S→R & R→S & S↔I or I↔R (I. intermediate)

- not determined

Table 15. Antimicrobial susceptibility test results (number of R/I/S) for the EQAS 2016 *Shigella* strains*

Strain	Antimicrobial∞												
	AMP	**CTX**	**CAZ**	**CRO**	**CHL**	**CIP**	**GEN**	**MER**	**NAL**	**SMX**	**TET**	**SXT**	**TMP**
WHO 2016 SH-16.1	**98**/0/4	2/0/**90**	2/0/**93**	1/0/**81**	1/1/**91**	1/1/**99**	3/1/**95**	0/0/**82**	0/1/**86**	**44**/0/5	**92**/1/2	**87**/0/3	**53**/0/2
WHO 2016 SH-16.2	**104**/0/2	2/0/**93**	4/0/**95**	2/0/**84**	**87**/7/2	0/6/**99**	2/1/**100**	1/0/**85**	2/0/**90**	**49**/0/0	**94**/1/3	**93**/0/2	**55**/0/2
WHO 2016 SH-16.3	**102**/0/3	**93**/1/1	18/0/**80**	**84**/0/2	**90**/2/4	*	3/2/**99**	0/0/**87**	**88**/1/3	**48**/0/1	**94**/2/3	**93**/1/1	**53**/0/3
WHO 2016 SH-16.4	**102**/1/2	5/0/**90**	4/1/**94**	3/0/**82**	**85**/7/3	2/12/**90**	4/1/**98**	0/0/**85**	2/2/**86**	**46**/0/2	**96**/1/1	**93**/0/1	**56**/0/0

∞For antimicrobial abbreviations: see List of Abbreviations page 1

In bold: expected interpretation. Grey cell: <90% of laboratories did correct interpretation. R. resistant; I. intermediate; S. susceptible.

* The results obtained from the combination of SH-16.3 and ciprofloxacin, i.e. the obtained interpretation has been disregarded. In the preparatory work for WHO SH-16.3, three independent tests towards ciprofloxacin showed an MIC-value at 1 mg/L and one test showed an MIC-value at 0.5 mg/L, therefore the expected result was set at 1 mg/L interpreted as 'resistant'. As the results were submitted and approved by the participants, it became clear that the MIC-values reported were lower than expected (consequently, the DD-zones were higher than expected). Following this observation, and 1) knowing that the differences in the obtained MIC-/DD-results could likely be due to expected method variability and 2) as the obtained MIC-/DD-results were found to vary closely around the interpretative criteria, the EQAS organizers have decided to disregard the results obtained from the combination of SH-16.3 and ciprofloxacin, i.e. the obtained interpretation will not be evaluated in neither the individual nor the overall report.

Table 16. Region-based categorization of EQAS participating laboratories' performance of antimicrobial susceptibility tests for *Shigella* strains

Region	Year	No. of labs	% correct test result	% minor deviations (S↔I or I↔R)^	% major deviations (S→R)^	% very major deviations (R→ S)^	% critical deviations (R→ S & S → R)^	% total deviations (S→R & R→S & S↔I or I↔R)^	Countries participating in the 2016 iteration
Africa	2009	17	93.3	2.4	3.5	0.8	4.3	6.8	Cameroun, Congo, Democratic Republic of the, Ivory Coast, Kenya (3), Madagascar, Mauritius, Morocco, Nigeria, Senegal, South Africa, The Gambia (2), Zambia, Zimbabwe
	2010	16	84.8	2.5	2.7	10.0	12.7	15.2	
	2011	16	86.0	1.8	3.6	8.3	11.9	13.7	
	2012	17	82.6	4.2	2.5	10.7	13.2	17.4	
	2013	14	87.6	7.2	2.5	2.7	5.2	12.4	
	2014	18	85.3	6.1	2.3	6.4	8.7	14.7	
	2015	20	91.7	4.9	1.5	1.9	3.4	8.3	
	2016	**16**	**90.3**	**3.5**	**1.1**	**5.1**	**6.2**	**9.7**	
Central Asia & Middle East	2009	5	94.8	0.9	3.0	1.3	4.4	5.2	Bahrain, India (4), Iran, Islamic rep. Of (3), Iraq, Israel, Oman
	2010	6	90.6	1.2	1.6	6.7	8.3	9.4	
	2011	4	92.9	1.6	0.5	4.9	5.4	7.1	
	2012	6	92.3	4.0	2.0	1.3	3.4	7.4	
	2013	6	86.9	8.5	3.9	0.8	4.6	13.1	
	2014	16	85.6	6.7	1.7	6.0	7.7	14.4	
	2015	13	91.7	5.2	1.6	1.6	3.1	8.3	
	2016	**11**	**91.3**	**1.5**	**5.1**	**2.1**	**7.2**	**8.7**	
Caribbean	2009	4	95.6	1.5	0.7	2.2	2.9	4.4	Barbados, Jamaica
	2010	4	88.5	1.5	3.8	6.2	10.0	11.5	
	2011	1	97.7	2.3	0.0	0.0	2.3	2.3	
	2012	3	84.6	1.9	7.7	5.8	13.5	15.4	
	2013	2	87.5	9.4	0.0	3.1	3.1	12.5	
	2014	3	76.5	5.1	7.1	11.2	18.4	23.5	
	2015	4	90.7	6.4	2.9	0.0	2.9	9.3	
	2016	**2**	**98.4**	**0.0**	**1.6**	**0.0**	**1.6**	**1.6**	
Europe	2009	22	98.1	1.1	0.7	0.1	0.8	1.9	Belgium, Bulgaria, Croatia, Cyprus, Czech Republic, Greece (2), Ireland, Italy (4), Luxembourg, Malta, Norway, Poland, Portugal, Serbia (2), Spain, Turkey, Ukraine, United Kingdom
	2010	27	93.6	1.5	0.9	3.9	4.8	6.4	
	2011	24	94.8	2.2	0.5	2.5	3.0	5.1	
	2012	24	96.6	1.7	0.4	1.4	1.7	3.4	
	2013	23	93.6	4.8	1.2	0.3	1.5	6.4	
	2014	26	96.0	3.2	0.1	0.7	0.8	4.0	
	2015	25	95.2	3.7	0.4	0.8	1.1	4.8	
	2016	**23**	**98.2**	**0.8**	**0.6**	**0.5**	**1.0**	**1.8**	

Table 16 (continued) Region-based categorization of EQAS participating laboratories' performance of antimicrobial susceptibility tests for *Shigella* strains

Region	Year	No. of labs	% correct test result	% minor deviations (S↔I or I↔R)^	% major deviations (S→R)^	% very major deviations (R→ S)^	% critical deviations (R→ S & S → R)^	% total deviations (S→R & R→S & S↔I or I↔R)^	Countries participating in the 2016 iteration
North America	2009	6	100.0	0.0	0.0	0.0	0.0	0.0	Canada (3), United States of America
	2010	7	95.0	0.0	0.0	5.0	5.0	5.0	
	2011	4	90.1	0.7	3.3	5.9	9.2	9.9	
	2012	6	89.5	0.0	2.1	8.4	10.5	10.5	
	2013	4	95.2	3.2	0.0	1.6	1.6	4.8	
	2014	3	95.4	2.8	0.0	1.9	1.9	4.6	
	2015	4	96.2	3.8	0.0	0.0	0.0	3.8	
	2016	**4**	**98.7**	**0.7**	**0.7**	**0.0**	**0.7**	**1.3**	
Oceania	2009	-	-	-	-	-	-	-	Australia, New Zealand
	2010	1	90.0	10.0	0.0	0.0	0.0	10.0	
	2011	1	92.5	5.0	0.0	2.5	2.5	7.5	
	2012	1	90.0	7.5	0.0	2.5	2.5	10.0	
	2013	1	95.5	4.5	0.0	0.0	0.0	4.5	
	2014	2	96.2	3.8	0.0	0.0	0.0	3.8	
	2015	2	95.7	2.9	1.4	0.0	1.4	4.3	
	2016	**2**	**98.6**	**0.0**	**1.4**	**0.0**	**1.4**	**1.4**	
Russia	2009	6	95.5	1.6	1.6	1.3	2.9	4.6	- none -
	2010	7	92.1	2.9	1.5	3.5	5.0	7.9	
	2011	6	94.4	3.6	0.0	2.0	2.0	5.6	
	2012	5	96.8	1.4	0.5	1.4	1.8	3.2	
	2013	2	95.2	4.8	0.0	0.0	0.0	4.8	
	2014	3	98.4	0.8	0.0	0.8	0.8	1.6	
	2015	3	100.0	0.0	0.0	0.0	0.0	0.0	
	2016	**-**	**-**	**-**	**-**	**-**	**-**	**-**	
Latin America	2009	20	98.3	1.1	0.4	0.3	0.7	1.7	Argentina, Bolivia, Brazil (2), Chile (2), Colombia, Costa Rica, Ecuador (2), El Salvador, Guatemala (2), Honduras, Mexico, Panama, Paraguay, Peru, Suriname, Uruguay, Venezuela
	2010	22	92.1	1.3	2.1	4.5	6.6	7.9	
	2011	20	94.0	1.5	1.3	3.2	4.5	6.0	
	2012	24	91.7	1.3	0.6	6.5	7.1	8.3	
	2013	23	94.1	3.9	1.2	0.8	2.0	5.9	
	2014	23	94.4	3.3	0.5	1.9	2.3	5.6	
	2015	17	93.0	3.5	1.3	2.2	3.5	7.0	
	2016	**21**	**98.2**	**0.4**	**0.2**	**1.2**	**1.4**	**1.8**	

^S. susceptible; I. intermediate; R. resistant.

Table 16 (continued) Region-based categorization of EQAS participating laboratories' performance of antimicrobial susceptibility tests for *Shigella* strains

Region	Year	No. of labs	% correct test result	% minor deviations (S↔I or I↔R)^	% major deviations (S→R)^	% very major deviations (R→ S)^	% critical deviations (R→ S & S → R)^	% total deviations (S→R & R→S & S↔I or I↔R)^	Countries participating in the 2016 iteration
Southeast Asia	2009	18	94.1	3.9	0.3	1.7	2.0	5.9	Cambodia, Japan, Korea, Rep of, LAO PDR, Malaysia (2), Philippines, Sri Lanka (2), Taiwan, Thailand (5), Viet Nam
	2010	16	90.5	2.4	0.7	6.4	7.1	9.5	
	2011	19	90.0	2.1	0.8	6.1	6.9	9.0	
	2012	27	87.1	5.1	1.9	5.6	7.6	12.7	
	2013	19	86.2	7.5	2.9	3.1	6.0	13.5	
	2014	13	92.5	4.0	1.1	2.4	3.5	7.5	
	2015	15	93.1	4.8	0.8	1.3	2.0	6.9	
	2016	**16**	**96.8**	**1.5**	**0.7**	**1.0**	**1.8**	**3.2**	
China	2009	12	96.3	2.2	1.0	0.5	1.5	3.7	China (16)
	2010	8	92.7	1.2	0.6	5.5	6.1	7.3	
	2011	-	-	-	-	-	-	-	
	2012	7	90.3	2.9	0.0	6.8	6.8	9.7	
	2013	5	92.7	3.4	0.4	3.4	3.9	7.3	
	2014	8	94.6	2.2	0.3	3.0	3.2	5.4	
	2015	13	92.9	2.2	2.3	2.6	5.0	7.1	
	2016	**16**	**97.1**	**0.8**	**1.5**	**0.6**	**2.1**	**2.9**	

^S. susceptible; I. intermediate; R. resistant.

Table 17. Proportion of laboratories that obtained the expected result. Number (n/N) and percentages of laboratories which correctly detected and confirmed the ESBL-producing *Salmonella* and *Shigella* strains.

Isolate no.	Expected interpretation	Confirmatory tests
WHO 2016 S-16.1	No ESBL, AmpC or carbapenemase	-
WHO 2016 S-16.2	Carbapenemase-phenotype	56/82 (68%)
WHO 2016 S-16.3	No ESBL, AmpC or carbapenemase	-
WHO 2016 S-16.4	No ESBL, AmpC or carbapenemase	-
WHO 2016 S-16.5	No ESBL, AmpC or carbapenemase	-
WHO 2016 S-16.6	AmpC-phenotype	61/80 (76%)
WHO 2016 S-16.7	No ESBL, AmpC or carbapenemase	-
WHO 2016 S-16.8	No ESBL, AmpC or carbapenemase	-
WHO 2016 SH-16.1	No ESBL, AmpC or carbapenemase	-
WHO 2016 SH-16.2	No ESBL, AmpC or carbapenemase	-
WHO 2016 SH-16.3	ESBL-phenotype	72/75 (96%)
WHO 2016 SH-16.4	No ESBL, AmpC or carbapenemase	-

Table 18. EQAS participating laboratories' performance of *Campylobacter* strains identification

EQAS iteration	No. of labs	Correct species	Strain no.	No. of results submitted	% correct identification	Deviating results (*)
2003	97	*C. jejuni*	# 1	93	88%	*C. coli* (9) *C. lari* (3)
	97	*C. coli*	# 2	93	84%	*C. jejuni* (7) *C. lari* (4) *C. upsaliensis* (4)
2004	109	*C. lari*	# 1	97	79%	*C. coli* (11) *C. jejuni* (8)
	109	*C. jejuni*	# 2	109	87%	*C. coli* (8) *C. lari* (4) *C. upsaliensis* (2)
2006	99	*C. jejuni*	# 1	87	90%	*C. lari* (3) *C. coli* (3) *C. upsaliensis* (3)
	99	*C. coli*	# 2	95	65%	*C. lari* (19) *C. jejuni* (11) *C. upsaliensis* (2)
2007	142	*C. lari*	# 1	98	74%	*C. jejuni* (10) *C. coli* (9) *C. upsaliensis* (7)
	142	*C. coli*	# 2	102	76%	*C. lari* (3) *C. jejuni* (20) *C. upsaliensis* (2)
2008	154	*C. lari*	# 1	109	62%	*C. coli* (14) *C. jejuni* (18) *C. upsaliensis* (7)
	154	*C. lari*	# 2	109	62%	*C. coli* (10) *C. jejuni* (19) *C. upsaliensis* (13)
2009	131	*C. coli*	# 1	87	77%	*C. upsaliensis* (10) *C. jejuni* (9) *C. lari* (1)
	131	*C. jejuni*	# 2	87	95%	*C. upsaliensis* (3) *C. lari* (1)
2010	130	*C. jejuni*	# 1	88	92%	*C. coli* (4) *C. lari* (3) *C. upsaliensis* (1)
	130	*C. coli*	# 2	84	85%	*C. jejuni* (11) *C. lari* (2) *C. upsaliensis* (2)
2011	132	*C. coli*	# 1	81	59%	*C. jejuni* (19) *C. lari* (13) *C. upsaliensis* (1)
	132	*C. coli*	# 2	79	70%	*C. jejuni* (17) *C. lari* (5) *C. upsaliensis* (2)
2012	135	*C. jejuni*	# 1	112	96%	*C. coli* (4)
	135	*C. jejuni*	# 2	103	85%	*C. coli* (10) *C. lari* (5) *C. upsaliensis* (1)
2013	123	*C. coli*	# 1	95	82%	*C. jejuni (13)* *C. lari* (3) *C. upsaliensis* (1)
	123	*C. coli*	# 2	92	84%	*C. jejuni* (9) *C. lari* (4) *C. upsaliensis* (2)
2014	101	*C. coli*	#2	101	85 %	*C. jejuni* (8) *C. lari* (6) *C. upsaliensis* (1)
2015	114	*C jejuni*	#1	112	93 %	*C.coli* (6) *C.lari,* *C.upsaliensis*
	114	*C.coli*	#2	110	89 %	*C jejuni* (8) *C.lari* (4)
2016	95	*C jejuni*	#1	94	94 %	*C.coli* (5) *C.lari*
	95	*C.coli*	#2	93	91 %	*C jejuni* (6) *C.upsaliensis* (2)

*number of participants reporting the specified deviating result

Table 19. Region-based categorization of EQAS 2016 participating laboratories' performance of *Campylobacter* strains identification

Region	Year	No. of labs	No. of strains identified	% strains correctly identified	Countries participating in the 2016 iteration
Africa	2009	9	15	53	Egypt, Kenya (2), Mauritius, Senegal, South Africa
	2010	7	13	77	
	2011	10	19	32	
	2012	9	17	82	
	2013	9	17	41	
	2014	9	9	67	
	2015	12	24	88	
	2016	**6**	**12**	**100**	
Central Asia & Middle East	2009	14	27	85	Bahrain, Iran, Islamic rep. of, Oman
	2010	13	26	89	
	2011	2	4	50	
	2012	11	22	96	
	2013	1	8	50	
	2014	7	7	57	
	2015	6	12	67	
	2016	**3**	**6**	**100**	
Caribbean	2009	2	4	100	Barbados
	2010	3	6	67	
	2011	1	2	0	
	2012	4	7	57	
	2013	2	4	100	
	2014	2	2	100	
	2015	3	6	67	
	2016	**1**	**2**	**100**	
Europe	2009	29	55	89	Bulgaria, Croatia, Cyprus, Czech Republic (2), Germany, Greece (2), Italy (8), Luxembourg (2), Malta, Poland (2), Portugal, Serbia (2), Slovenia, Spain, Turkey (2)
	2010	29	57	97	
	2011	25	48	85	
	2012	29	56	95	
	2013	26	51	88	
	2014	26	26	89	
	2015	30	60	93	
	2016	**28**	**56**	**96**	
North America	2009	10	19	90	Canada (7), United States of America (3)
	2010	11	22	86	
	2011	9	18	78	
	2012	13	26	96	
	2013	10	18	100	
	2014	10	10	100	
	2015	13	26	100	
	2016	**10**	**20**	**90**	
Oceania	2009	2	4	100	Australia, New Zealand
	2010	2	3	100	
	2011	2	4	100	
	2012	2	4	100	
	2013	2	4	100	
	2014	1	1	100	
	2015	2	4	100	
	2016	**2**	**4**	**100**	

Table 19 (continued). Region-based categorization of EQAS 2016 participating laboratories' performance of *Campylobacter* strains identification

Region	Year	No. of labs	No. of strains identified	% strains correctly identified	Countries participating in the 2016 iteration
Russia	2009	2	4	100	- none -
	2010	2	4	100	
	2011	2	4	50	
	2012	5	10	80	
	2013	1	2	100	
	2014	3	3	100	
	2015	3	6	100	
	2016	**0**	**0**	**-**	
Latin America	2009	14	26	89	Brazil (2), Colombia (2), Costa Rica, Mexico, Panama, Paraguay
	2010	19	37	78	
	2011	19	37	49	
	2012	22	40	95	
	2013	20	36	83	
	2014	22	22	86	
	2015	15	28	89	
	2016	**8**	**13**	**85**	
Southeast Asia	2009	10	20	90	Brunei Darussalam, Cambodia, Japan, Korea, Rep of, LAO PDR, Malaysia (2), Philippines, Sri Lanka, Taiwan, Thailand (7), Viet Nam (2)
	2010	14	27	93	
	2011	12	24	67	
	2012	17	33	85	
	2013	15	28	89	
	2014	13	13	92	
	2015	16	28	93	
	2016	**19**	**38**	**79**	
China	2009	12	24	92	China (18)
	2010	10	20	85	
	2011	-	-	-	
	2012	-	-	-	
	2013	5	10	90	
	2014	8	8	75	
	2015	14	28	93	
	2016	**18**	**36**	**100**	

Table 20. EQAS participants' performance of *Campylobacter* strains antimicrobial susceptibility testing

EQAS iteration	No. of labs	% correct test results	% major deviations (S → R)^	% very major deviations (R → S)^	% critical deviations (R → S & S → R)^
2009	25	91.4	4.5	4.1	8.6
2010	37	91.3	4.2	4.5	8.7
2011	38	93.8	2.8	3.4	6.2
2012	47	93.6	5.0	1.5	6.4
2013	47	92.4	5.0	2.6	7.6
2014	50	91.2	1.6	7.2	8.8
2015	56	89.5	5.2	5.2	10.5
2016	49	91.8	4.2	4.0	8.2

^S. susceptible; R. resistant

Table 21. EQAS participants' performance of *Campylobacter* antimicrobial susceptibility testing categorized by antimicrobial

EQAS iteration	No. of labs	Lab performance	Antimicrobial						
			CHL	CIP	ERY	GEN	NAL	STR	TET
2009	25	No. of tests	37	46	46	43	41	34	45
		% critical deviations*	8.1	6.5	10.9	2.3	9.8	11.8	11.1
2010	37	No. of tests	44	70	71	59	53	39	68
		% critical deviations*	4.5	7.1	11.3	10.2	7.5	10.3	8.8
2011	38	No. of tests	41	67	62	65	62	30	60
		% critical deviations*	0.0	6.0	6.5	3.1	8.1	13.3	8.3
2012	47	No. of tests	70	84	81	81	39	53	74
		% critical deviations*	4.3	6.0	6.2	7.4	5.1	11.3	5.4
2013	47	No. of tests	71	90	87	82	79	51	86
		% critical deviations*	5.6	6.7	8.0	0.0	8.9	23.5	8.1
2014	50	No. of tests	-	49	46	45	42	24	45
		% critical deviations*	-	8.2	0.0	0.0	11.9	16.7	11.1
2015	56	No. of tests	-	110	108	94	92	63	107
		% critical deviations*	-	5.5	6.5	11.7	8.7	6.3	22.4
2016	49	No. of tests	-	93	93	81	78	64	93
		% critical deviations*	-	9.7	5.4	4.9	9.0	17.2	5.4

^For antimicrobial abbreviations. See List of Abbreviations page 1

*****R→ S & S → R (R. resistant; S. susceptible)

Table 22. Antimicrobial susceptibility test results (number of R/S) for the EQAS 2016 *Campylobacter* strains*

Strain	Antimicrobial^					
	CIP	ERY	GEN	NAL	STR	TET
WHO 2016 C-16.1	**42**/0/4	**43**/0/3	**39**/0/2	**36**/0/4	**26**/0/6	**45**/0/1
WHO 2016 C-16.2	5/0/**42**	2/0/**45**	2/0/**38**	3/0/**35**	5/0/**27**	4/0/**43**

^For antimicrobial abbreviations. see List of Abbreviations page 1

*In bold: expected interpretation. Grey cell: <90% of laboratories did correct interpretation. R. resistant; S. susceptible

Table 23. Region-based categorization of EQAS 2016 participants' performance of antimicrobial susceptibility testing of *Campylobacter* strains

Region	Year	No. of labs	% correct test result	% major deviations (S → R)^	% very major deviations (S → R)^	% critical deviations (R→S & S→R)^	Countries participating in the 2016 iteration
Africa	2009	2	75.0	10.7	14.3	25.0	- none -
	2010	2	95.2	0.0	4.8	4.8	
	2011	7	85.0	3.3	11.7	15.0	
	2012	4	94.3	0.0	5.7	5.7	
	2013	5	90.9	5.5	3.6	9.1	
	2014	7	51.5	39.4	9.1	48.5	
	2015	6	71.9	12.5	15.6	28.1	
	2016	-	-	-	-	-	
Central Asia & Middle East	2009	0	-	-	-	-	Iran, Islamic rep. of
	2010	0	-	-	-	-	
	2011	1	75.0	0.0	25.0	25.0	
	2012	2	93.8	6.3	0.0	6.3	
	2013	3	93.3	3.3	3.3	6.7	
	2014	3	100.0	0.0	0.0	0.0	
	2015	3	97.1	2.9	0.0	2.9	
	2016	**1**	**40.0**	**40.0**	**20.0**	**60.0**	
China	2009	2	95.2	4.8	0.0	4.8	China (16)
	2010	1	100.0	0.0	0.0	0.0	
	2011	0	-	-	-	-	
	2012	2	88.5	7.7	3.8	11.5	
	2013	3	95.2	2.4	2.4	4.8	
	2014	6	100.0	0.0	0.0	0.0	
	2015	8	86.5	5.2	8.3	13.5	
	2016	**16**	**88.5**	**5.2**	**6.3**	**11.5**	
Caribbean	2009	0	-	-	-	-	Cuba, Jamaica
	2010	0	-	-	-	-	
	2011	0	-	-	-	-	
	2012	1	75.0	25.0	0.0	25.0	
	2013	1	100.0	0.0	0.0	0.0	
	2014	2	100.0	0.0	0.0	0.0	
	2015	2	73.3	20.0	6.7	26.7	
	2016	**2**	**73.3**	**20.0**	**6.7**	**26.7**	
Europe	2009	10	94.8	3.0	2.2	5.2	Czech Republic, Greece (2), Italy (3), Luxembourg (2), Malta, Poland, Serbia, Spain, Turkey
	2010	13	100.0	0.0	0.0	0.0	
	2011	11	100.0	0.0	0.0	0.0	
	2012	16	97.3	1.6	1.1	2.7	
	2013	16	94.9	3.5	1.5	5.1	
	2014	16	97.4	1.3	1.3	2.6	
	2015	15	97.5	2.5	0.0	2.5	
	2016	**13**	**94.1**	**5.0**	**0.8**	**5.9**	
North America	2009	2	100.0	0.0	0.0	0.0	Canada (3), United States of America (3)
	2010	5	93.8	6.3	0.0	6.3	
	2011	5	100.0	0.0	0.0	0.0	
	2012	5	100.0	0.0	0.0	0.0	
	2013	3	100.0	0.0	0.0	0.0	
	2014	4	100.0	0.0	0.0	0.0	
	2015	5	97.9	2.1	0.0	2.1	
	2016	**6**	**100.0**	**0.0**	**0.0**	**0.0**	

^S. susceptible; R. resistant

Table 23 (continued). Region-based categorization of EQAS 2016 participants' performance of antimicrobial susceptibility testing of *Campylobacter* strains

Region	Year	No. of labs	% correct test result	% major deviations (S → R)^	% very major deviations (S → R)^	% critical deviations (R→S & S→R)^	Countries participating in the 2016 iteration
Oceania	2009	0	-	-	-	-	New Zealand
	2010	0	-	-	-	-	
	2011	1	100.0	0.0	0.0	0.0	
	2012	0	-	-	-	-	
	2013	0	-	-	-	-	
	2014	0	-	-	-	-	
	2015	1	100.0	0.0	0.0	0.0	
	2016	**1**	**100.0**	**0.0**	**0.0**	**0.0**	
Russia	2009	0	-	-	-	-	- none -
	2010	1	78.6	7.1	14.3	21.4	
	2011	1	100.0	0.0	0.0	0.0	
	2012	0	-	-	-	-	
	2013	0	-	-	-	-	
	2014	0	-	-	-	-	
	2015	0	-	-	-	-	
	2016	**0**	-	-	-	-	
Latin America	2009	5	93.2	6.8	0.0	6.8	Brazil, Costa Rica, Paraguay
	2010	8	89.6	6.0	4.5	10.4	
	2011	7	96.8	0.0	3.2	3.2	
	2012	7	95.2	3.2	1.6	4.8	
	2013	7	92.4	4.5	3.0	7.6	
	2014	6	100.0	0.0	0.0	0.0	
	2015	8	93.1	4.2	2.8	6.9	
	2016	**3**	**84.2**	**0.0**	**15.8**	**15.8**	
Southeast Asia	2009	4	84.4	4.4	11.1	15.6	Korea, Rep of, Philippines, Sri Lanka, Thailand (6)
	2010	7	77.2	9.8	13.0	22.9	
	2011	5	85.1	9.0	6.0	14.0	
	2012	10	85.8	13.3	0.9	14.2	
	2013	9	84.8	10.7	4.5	15.2	
	2014	6	87.5	12.5	0.0	12.5	
	2015	8	82.9	6.1	11.0	17.1	
	2016	**9**	**96.9**	**0.0**	**3.1**	**3.1**	

^S. susceptible; R. resistant

Table 24. EQAS participants' performance of antimicrobial susceptibility testing of *Campylobacter jejuni* ATCC 33560

	Method used	Incubation conditions	Labs' performance[1, 2]	Antimicrobial[3]					
				CHL	CIP	ERY	GEN	NAL	TET
EQAS 2010 (N=20)	Microdilution	42°C / 24h	No.[1]	3	6	6	6	4	6
			%[2]	67	83	100	83	75	83
		36-37°C / 48h	No.[1]	5	8	8	8	7	8
			%[2]	80	88	88	75	86	88
	Agardilution	42°C / 24h	No.[1]	-	6	6	6	-	-
			%[2]	-	100	83	83	-	-
		36-37°C / 48h	No.[1]	-	0	0	0	-	-
			%[2]	-	0	0	0	-	-
	Overall		No.[1]	8	20	20	20	11	14
			%[2]	75	90	90	80	82	86
EQAS 2011 (N=26)	Microdilution	42°C / 24h	No.[1]	4	9	9	8	7	9
			%[2]	100	67	100	88	100	67
		36-37°C / 48h	No.[1]	6	8	6	8	7	7
			%[2]	83	88	100	75	86	86
	Agardilution	42°C / 24h	No.[1]	-	8	8	8	-	-
			%[2]	-	88	63	100	-	-
		36-37°C / 48h	No.[1]	-	1	1	1	-	-
			%[2]	-	0	0	100	-	-
	Overall		No.[1]	10	26	24	25	14	16
			%[2]	90	77	83	88	93	75
EQAS 2012 (N=34)	Microdilution	42°C / 24h	No.[1]	9	12	12	12	10	12
			%[2]	67	75	83	83	80	75
		36-37°C / 48h	No.[1]	7	9	8	8	8	8
			%[2]	100	89	100	63	88	88
	Agardilution	42°C / 24h	No.[1]	-	9	7	9	-	-
			%[2]	-	89	86	89	-	-
		36-37°C / 48h	No.[1]	-	4	4	4	-	-
			%[2]	-	50	100	100	-	-
	Overall		No.[1]	34	80	75	78	43	50
			%[2]	82	81	88	83	86	80

[1]No.. number of labs performing the analysis, [2]%. percentage of labs reporting correct results, [3]For antimicrobial abbreviations: see List of Abbreviations page 1, -. not determined

Table 24 (continued). EQAS participants' performance of antimicrobial susceptibility testing of *Campylobacter jejuni* ATCC 33560

	Method used	Incubation conditions	Labs' performance[1, 2]	Antimicrobial[3]					
				CHL	CIP	ERY	GEN	NAL	TET
EQAS 2013 (N=47)	Microdilution	42°C / 24h	**No.[1]**	6	8	8	8	7	8
			%[2]	83	88	100	88	86	100
		36-37°C / 48h	**No.[1]**	8	12	12	11	11	12
			%[2]	88	92	83	73	91	75
	Agardilution	42°C / 24h	**No.[1]**	-	9	9	8	-	-
			%[2]	-	89	67	75	-	-
		36-37°C / 48h	**No.[1]**	-	7	7	6	-	-
			%[2]	-	86	86	100	-	-
	Overall		**No.[1]**	14	36	36	33	18	20
			%[2]	86	89	83	82	89	85
EQAS 2014 (N=32)	Microdilution	42°C / 24h	**No.[1]**	-	10	10	10	10	10
			%[2]	-	90	100	80	100	90
		36-37°C / 48h	**No.[1]**	-	10	10	9	8	10
			%[2]	-	100	80	89	100	100
	Agardilution	42°C / 24h	**No.[1]**	-	7	7	7	-	-
			%[2]	-	100	71	100	-	-
		36-37°C / 48h	**No.[1]**	-	5	5	5	-	-
			%[2]	-	80	80	100	-	-
	Overall		**No.[1]**	-	32	32	31	18	20
			%[2]	-	94	84	90	100	95
EQAS 2015 (N=32)	Microdilution	42°C / 24h	**No.[1]**	-	19	19	18	17	17
			%[2]	-	68	84	94	94	76
		36-37°C / 48h	**No.[1]**	-	8	8	7	5	8
			%[2]	-	100	100	86	100	100
	Agardilution	42°C / 24h	**No.[1]**	-	7	7	5	-	-
			%[2]	-	100	71	100	-	-
		36-37°C / 48h	**No.[1]**	-	5	5	5	-	-
			%[2]	-	40	40	40	-	-
	Overall		**No.[1]**	-	39	39	35	22	25
			%[2]	-	77	79	86	95	84
EQAS 2016 (N=42)	Microdilution	42°C / 24h	**No.[1]**	-	24	24	23	23	24
			%[2]	-	88	88	96	83	83
		36-37°C / 48h	**No.[1]**	-	5	5	5	5	5
			%[2]	-	100	100	100	100	100
	Agardilution	42°C / 24h	**No.[1]**	-	9	9	9	-	-
			%[2]	-	67	78	78	-	-
		36-37°C / 48h	**No.[1]**	-	4	4	3	-	-
			%[2]	-	100	75	100	-	-
	Overall		**No.[1]**	-	42	42	40	28	29
			%[2]	-	86	86	93	86	86

[1]No.. number of labs performing the analysis, [2]%. percentage of labs reporting correct results, [3]For antimicrobial abbreviations: see List of Abbreviations page 1, -. not determined

Table 25. EQAS participating laboratories' performance of unknown strain identification

EQAS iteration	Strain ID	No. of participating labs	Percentage (%) of labs performing correct identification
2003	*E. coli* O157	115	99
2004	*Shigella flexneri*	121	94 (*Shigella);* 74 (*S. flexneri)*
2006	*Yersinia enterocolitica* O3	134	93 (*Yersinia*); 89 (*Y. enterocolitica*); 66 (*Y. enterocolitica* O3)
2007	*Vibrio parahaemolyticus*	86	83
2008	*Enterobacter sakasakii*	128	92
2009	*Vibrio mimicus*	56	48
2010	*Citrobacter spp.*	115	90
2011	*Aeromonas hydrophila*	106	83
2012	*Salmonella* Paratyphi B var. Java	134	23% (*Salmonella* spp) 7% (*Salmonella* O:B) 24% (*Salmonella* Paratyphi B var. java. In total 54% Deviations: *Citrobacter freundii* (1), *Edwardsiella* sp (1), *Escherichia fergusonii* (1), *Proteus mirabilis* (1), *Salmonella* serovar X* (24), *Salmonella* serovar Paratyphi B (34) * incorrect serovar
2013	*E. coli* O157:H16 non-VTEC	129	**82% correct**, including: *Escherichia coli* non-VTEC / O157 non-VTEC / O157:H16 non-VTEC *E. coli* non-VTEC / O157 non-VTEC / O157:H16 non-VTEC Deviations: *Escherichia coli* O157 H7 (9), *Escherichia hermannii* (2), *Shigella sonnei* (2), *E.coli* EHEC, *Escherichia coli* O114: nonmotile, *Escherichia coli* O157:H12, *Escherichia coli* O157:H16, Stx1+, *Escherichia coli* O157:H45, *Escherichia coli* O157:H7/ Verotoxin negative, *Escherichia fergusonii*, *Esherichia coli* STEC, *Vibrio mimicus*, *Citrobacter amalonaticus*
2014	*Yersinia pseudotuberculosis*	117	**75% correct**, including: *YERSINIA SPECIES* *Yersinia pseudotuberculosis* *Yersinia pseudotuberculosis* I / O1 / O:1b / API 20 E [1014100] Deviations: *Acinetobacter baumannii, Burkolderia sp., Citrobacter freundi, corynebacterium species, Sphingomonas paucimobilis, HELICOBACTER, Pasteurella maisi, Pasteurella sp., Pseudomonas luteola, Rhizobium radiobacter* (6), *Salmonella typhi, Shigella flexneri, Sphingomonas paucimobilis* (4), unknown, *Vibrio metschnikovii, Yersinia enterocolitica* (4), *Yersinia similis, Yestina pestis*
2015	*Hafnia alvei*	142	**87.3% correct**, including: *Hafnia alvei* (116), *Hafnia alvei* 1(8) Deviations: *Aeromonas* spp., *Aeromonas veronii, Serratia marcescens, Enterobacter, Enterobacter cloacae , Eschericha coli* (3), *Eschericia fergusonii, Bacillus, Hafnia alvei* ATCC 13337, *Plesiomonas shigelloides, Shigella flexneri, Shigella sonnei, Shigella* spp. (2), *Vibrio parahaemolyticus, Yokenella regensburgei*
2016	*Listeria monocytogenes*	137	**86.1% correct**, including: *Listeria monocytogenes (101), Listeria monocytogenes 1/2 a (8), Listeria monocytogenes 2a, Listeria monocytogenes IIa, Listeria monocytogenes O:1, Listeria monocytogenes O1/2, Listeria monocytogenes Serotype 1, Listeria monocytogenes Type 1, Listeria spp (3).* Deviations: *Actinomyces pyogenes, Aeromonas , Chromobacterium violaceum, Corynebacterium spp., Enterobacter agglomerans, Ewingella americana , Listeria ivanovii, Listeria monocytogenes/innocua, Listeria grayi (2), non-fermenter spp., Pantoae spp 3, Salmonella Dublin (9,12;gp), Salmonella enterica ssp enterica, Sphingomonas paucimobilis (2), Staphylococcus xylosus, Vibrio parahaemolyticus, Yersinia enterocolitica.*

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Kgs. Lyngby, Denmark, April 2016

SIGN-UP FOR EQAS 2016

Greetings to the WHO Global Foodborne Infections Network (WHO GFN) Members:

WHO GFN strives to increase the quality of laboratory-based surveillance of *Salmonella* and other foodborne pathogens by encouraging national and regional reference laboratories that attended WHO GFN training courses to participate in the External Quality Assurance System (EQAS). We are pleased to announce the launch of the 2016 EQAS cycle.

WHY PARTICIPATE IN EQAS?

EQAS provides the opportunity for proficiency testing which is considered an important tool for the production of reliable laboratory results of consistently good quality.

WHAT IS OFFERED IN EQAS?

This year, WHO EQAS offers the following components:

- Serogrouping, serotyping and antimicrobial susceptibility testing of eight *Salmonella* isolates;

- Serotyping and antimicrobial susceptibility testing of four *Shigella* isolates;

- Species identification and antimicrobial susceptibility testing of two *Campylobacter* isolates. Note that in relation to the antimicrobial susceptibility testing of *Campylobacter*, results obtained by broth micro dilution or agar dilution, only, are accepted;

- Identification of one unknown bacterial isolate.

WHO SHOULD PARTICIPATE IN EQAS 2016?

All national and regional reference laboratories which perform analysis on *Salmonella*, *Shigella* and/or *Campylobacter* and are interested in participating in an external quality assurance program are invited to participate.
We expect that all national and regional reference laboratories that attended WHO GFN Training Courses will participate in EQAS.
The WHO GFN Regional Centers in cooperation with the EQAS Coordinator will evaluate the list of laboratories that sign up for EQAS 2016. Laboratories which signed up and received bacterial isolates in year 2015 but did not submit any result should provide a consistent explanation for this if they want to participate in 2016.

COST FOR PARTICIPATING IN EQAS

There is no participation fee. Laboratories should, however, cover the expenses for parcel shipment if they can afford it. If FedEx has ‘Dangerous Goods-service’ in your country or if you have a DHL-account no, please provide your FedEx or DHL import account number (for import of UN3373 Biological Substance Category B) in the sign-up form or, alternatively, to the EQAS Coordinator (please find contact information below). We need this information at this stage to save time and resources. Participating laboratories are responsible for paying any expenses related to taxes or custom fees applied by their country.

HOW TO SIGN- UP FOR EQAS 2016

This link will open a sign-up webpage: http://eqas.food.dtu.dk/who/signup

In this webpage, you will be asked to provide the following information:

- Name of institute, department, laboratory, and contact person
- Complete mailing address for shipment of bacterial isolates (no post-office box number)
- Telephone and fax number, e-mail address
- FedEx or DHL import account number (if available)
- Approximate number of *Salmonella* isolates annually serogrouped/serotyped
- Approximate number of *Salmonella* isolates annually tested for antimicrobial susceptibility
- Availability of ATCC reference strains
- Components of EQAS 2016 you plan to participate in
- Level of reference function in your country

If you experience any problem in the sign-up webpage, please try again a few days later. If problems persist after several attempts, please contact the EQAS Coordinator Susanne Karlsmose Pedersen: E-mail suska@food.dtu.dk; fax +45 3588 6341.

TIMELINE FOR SHIPMENT OF ISOLATES AND AVAILABILITY OF PROTOCOLS

Due to increased number of participants in WHO EQAS, a number of different institutions will ship the bacterial isolates, and you will receive information concerning the institution shipping your parcel. The bacterial isolates will be shipped in August/September 2016.

In order to minimize delays, **please send a valid import permit to the EQAS coordinator**. Please apply for a permit to receive the following (according to your level of participation): "UN3373, Biological Substance Category B": eight *Salmonella* strains, four *Shigella* strains, two *Campylobacter*, one *Campylobacter* reference strain (for new participants performing antimicrobial susceptibility testing on *Campylobacter*), one *Escherichia coli* reference strain (for new participants performing antimicrobial susceptibility testing on *Salmonella* and/or *Shigella*) and an unknown isolate (enteric bacteria) in August/September 2016.

Protocols and all relevant information will be available for download from the website http://www.antimicrobialresistance.dk/233-169-215-eqas.htm.

DEADLINE FOR SUBMITTING RESULTS TO THE NATIONAL FOOD INSTITUTE

Results must be submitted to the National Food Institute (DTU Food) by **31st December 2016** through the password-protected website. An evaluation report will be generated upon submission of results. Full anonymity is ensured, and only DTU Food and the WHO GFN Regional Centre in your region will have access to your results.

Deadline for sign-up for EQAS 2016 is 27th May 2016

			Presumptive phenotype	Ampicillin AMP		Cefotaxime CTX		Synergy CTX:/CTX:Cl	Cefoxitin FOX		Ceftazidime CAZ		Synergy CAZ:/CAZ:Cl	Ceftriaxone CRO		Chloramphenicol CHL		Ciprofloxacin CIP		Gentamicin GEN		Meropenem MER		Nalidixic acid NAL		Sulfonamides SMX		Tetracycline TET		Trimethoprim TMP		Trim/Sulfa SXT	
WHO 2016 S-16.1	*Salmonella* Bovismorbificans/ *Salmonella* Hindmarsh	I 6,8:r:1,5	-	>64	RESIST	<=0.25	SUSC				<=0.5	SUSC		0.064	SUSC	<=8.0	SUSC	0.03	SUSC	<=0.5	SUSC	0.06	SUSC	<=4	SUSC	>1024	RESIST	>64	RESIST	>32	RESIST	>32	RESIST
WHO 2016 S-16.2	*Salmonella* Infantis	I 6,7:r:1,5	carbapenemase	>64	RESIST	>64	RESIST	no synergy	>64	RESIST	>128	RESIST	no synergy	64	RESIST	>128	RESIST	0.03	SUSC	1	SUSC	0.25	RESIST	<=4	SUSC	>1024	RESIST	4	SUSC	>32	RESIST	>32	RESIST
WHO 2016 S-16.3	*Salmonella* Enteritidis	I 9,12:g,m;-	-	4	SUSC	0.5	SUSC				1	SUSC		0.25	SUSC	<=8.0	SUSC	0.06	SUSC	>32	RESIST	0.06	SUSC	<=4	SUSC	>1024	RESIST	4	SUSC	<=0.25	SUSC	0.125	SUSC
WHO 2016 S-16.4	*Salmonella* Uganda	I 3,10:l,z13;1,5	-	<=1	SUSC	<=0.25	SUSC				<=0.5	SUSC		0.064	SUSC	<=8.0	SUSC	0.03	SUSC	<=0.5	SUSC	<=0.03	SUSC	8	SUSC	32	SUSC	<=2	SUSC	<=0.5	SUSC	0.125	SUSC
WHO 2016 S-16.5	*Salmonella* Stanley	I 4,5,12:d;1,2	-	2	SUSC	<=0.25	SUSC				<=0.5	SUSC		0.032	SUSC	128	RESIST	0.03	SUSC	<=0.5	SUSC	0.06	SUSC	<=4	SUSC	>1024	RESIST	32	RESIST	>32	RESIST	>32	RESIST
WHO 2016 S-16.6	*Salmonella* Heidelberg	I 4,12:r:1,2	AmpC	>64	RESIST	8	RESIST	no synergy	32	RESIST	16	RESIST	no synergy	32	RESIST	>128	RESIST	0.03	SUSC	<=0.5	SUSC	<=0.03	SUSC	<=4	SUSC	>1024	RESIST	>64	RESIST	<=0.25	SUSC	0.25	SUSC
WHO 2016 S-16.7	*Salmonella* Altendorf	I 4,12,27:c:1,7	-	2	SUSC	<=0.25	SUSC				<=0.5	SUSC		0.064	SUSC	<=8.0	SUSC	0.03	SUSC	<=0.5	SUSC	0.06	SUSC	<=4	SUSC	64	SUSC	<=2	SUSC	<=0.25	SUSC	0.06	SUSC
WHO 2016 S-16.8	*Salmonella* Plymouth	I 9,46:d:z6	-	2	SUSC	<=0.25	SUSC				<=0.5	SUSC		0.064	SUSC	<=8.0	SUSC	0.03	SUSC	<=0.5	SUSC	0.06	SUSC	<=4	SUSC	16	SUSC	<=2	SUSC	<=0.25	SUSC	0.06	SUSC
WHO 2016 SH-16.1	Shigella flexneri 1b		-	>64	RESIST	<=0.25	SUSC				<=0.5	SUSC		0.064	SUSC	<=8.0	SUSC	<=0.015	SUSC	1	SUSC	<=0.03	SUSC	<=4	SUSC	>1024	RESIST	>64	RESIST	>32	RESIST	>32	RESIST
WHO 2016 SH-16.2	Shigella boydii 4		-	>64	RESIST	<=0.25	SUSC				<=0.5	SUSC		0.032	SUSC	64	RESIST	<=0.015	SUSC	1	SUSC	<=0.03	SUSC	<=4	SUSC	>1024	RESIST	>64	RESIST	>32	RESIST	>32	RESIST
WHO 2016 SH-16.3	Shigella flexneri 2b		ESBL	>64	RESIST	32	RESIST	synergy	4	SUSC	0.5	SUSC	no synergy	32	RESIST	128	RESIST	1	RESIST	1	SUSC	<=0.03	SUSC	>128	RESIST	>1024	RESIST	>64	RESIST	>32	RESIST	>32	RESIST
WHO 2016 SH-16.4	Shigella flexneri 3a		-	>64	RESIST	<=0.25	SUSC				<=0.5	SUSC		0.032	SUSC	128	RESIST	0.03	SUSC	2	SUSC	<=0.03	SUSC	<=4	SUSC	>1024	RESIST	>64	RESIST	>32	RESIST	>32	RESIST

		Ciprofloxacin CIP		Erythromycin ERY		Gentamicin GEN		Nalidixic acid NAL		Streptomycin STR		Tetracycline TET	
WHO 2016 C-16.1	*C. jejuni*	32	RESIST	>64	RESIST	>32	RESIST	>64	RESIST	>64	RESIST	>64	RESIST
WHO 2016 C-16.2	*C. coli*	0.06	SUSC	1	SUSC	1	SUSC	<=4	SUSC	<=4	SUSC	0.5	SUSC

WHO B-16.1	*Listeria monocytogenes*

WHO Collaborating Centre
External Quality Assurance System (EQAS) 2016

DTU Food
National Food Institute

WHO Collaborating Centre
for Antimicrobial Resistance in
Foodborne Pathogens
www.antimicrobialresistance.dk

PROTOCOL for

- serotyping and antimicrobial susceptibility testing of *Salmonella*
- serotyping and antimicrobial susceptibility testing of *Shigella*
- identification and antimicrobial susceptibility testing of *Campylobacter*
- identification of an unknown enteric pathogen

HISTORY OF CHANGES; protocol version 2
Interpretative criteria for meropenem adjusted in Table 1 (changes from protocol version 1 indicated with bold and italics)

1 INTRODUCTION

In 2000, the Global Foodborne Infections Network (formerly known as WHO Global Salm-Surv) launched an External Quality Assurance System (EQAS). The EQAS is organized by the National Food Institute, Technical University of Denmark (DTU Food), in collaboration with partners and Regional Sites in WHO GFN.

Technical University of Denmark DTU

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

The WHO EQAS 2016 includes

- serotyping and antimicrobial susceptibility testing of eight *Salmonella* strains,
- serotyping and antimicrobial susceptibility testing of four *Shigella* strains,
- antimicrobial susceptibility testing of the *Escherichia coli* ATCC 25922 (NCIMB 12210) reference strain for quality control (QC),
- identification and antimicrobial susceptibility testing of two thermophilic *Campylobacter* isolates,
- antimicrobial susceptibility testing of *Campylobacter jejuni* ATCC 33560 (NCTC 11351) reference strain for QC,
- identification of one 'unknown' bacterial isolate.

All participants will receive the strains according to the information they reported in the sign-up form.

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

2 OBJECTIVES

The main objective of this EQAS is to support laboratories to assess and if necessary improve the quality of serotyping and antimicrobial susceptibility testing of enteric human pathogens, especially *Salmonella*. A further objective is to assess and improve the comparability of surveillance data on *Salmonella* serotypes and antimicrobial susceptibility reported by different laboratories. Therefore, the laboratory work for this EQAS should be done by using the methods routinely used in your laboratory.

3 OUTLINE OF THE EQAS 2016

3.1 Shipping, receipt and storage of strains

In September 2016 around 200 laboratories located worldwide will receive a parcel containing eight *Salmonella* strains, four *Shigella* strains, two *Campylobacter* strains and one 'unknown' bacterial

isolate (according to information reported in the sign-up form). An *E. coli* ATCC 25922 reference strain and a *C. jejuni* ATCC 33560 reference strain will be included for participants who signed up to perform antimicrobial susceptibility testing (AST) and did not receive them previously. All provided strains belong to UN3373, Biological substance category B. AmpC-, Extended-Spectrum Beta-Lactamase (ESBL)-, and carbapenemase-producing strains could be included in the selected material.

Please confirm receipt of the parcel through the confirmation form enclosed in the shipment

The *Salmonella* and *Shigella* strains, and the 'unknown' bacterial isolate are shipped as agar stab cultures whereas the reference strains for QC and the *Campylobacter* strains are shipped lyophilised (LYFO DISK®). See section 3.1.1 below for additional info on handling and reconstitution of the lyophilised cultures.

On arrival, the bacterial cultures must be stored in a dark place at 2°C to 8°C until handling in the laboratory.

The agar stab cultures must be subcultured and prepared for storage in your strain collection (e.g. in a -80°C freezer). This set of cultures should serve as reference if discrepancies are detected during the testing (e.g. they can be used to detect errors such as mis-labelling or contamination).

3.1.1 Instructions related to handling of LYFO DISK®

The microorganisms supplied as LYFO DISK® are packaged in re-sealable vials that contain a lyophilized pellet and a desiccant to prevent adverse accumulations of moisture.

The following instructions can be downloaded from the manufacturer's website (http://microbiologics.com/Support-Center/KWIK-STIK-trade):

1. Remove the unopened LYFO DISK® vial from 2°C to 8°C storage and allow the unopened vial to equilibrate to room temperature.
2. Aseptically remove the pellet with sterile forceps from the vial. Do not remove desiccant.
3. Place the pellet in 0.5 mL of sterile fluid (water, saline, TSB, or BHIB).
4. Crush the pellet with a sterile swab until the suspension is homogenous. Immediately heavily saturate the same swab with the hydrated material and transfer to agar medium.
5. Inoculate the primary culture plate(s) by gently rolling the swab over one-third of the plate.
6. Using a sterile loop, streak to facilitate colony isolation.
7. Using proper biohazard disposal, discard the remaining hydrated material.
8. Immediately incubate the inoculated media at temperature and conditions appropriate to the microorganism.

Materials required but not provided:

- Microorganisms require sterile tubes and 0.5 ml of sterile liquid such as, Tryptic Soy Broth, Brain Heart Infusion Broth, saline, or deionized water to hydrate the lyophilized preparation.
- Sterile swabs or inoculating loops are needed to transfer the hydrated preparation to an agar plate.
- Non-selective, nutrient or enriched agar media and specific incubation times and conditions to optimize growth and recovery.

3.2 Serotyping of *Salmonella*

The eight *Salmonella* strains should be serotyped by using the method routinely used in the laboratory. If you do not have all the necessary antisera please go as far as you can in the identification and report the serogroup, since also serogroup results will be evaluated. Serogroups should be reported using terms according to Kauffmann-White-Le Minor (Grimont and Weill, 2007. 9th ed. Antigenic formulae of the *Salmonella* serovars. WHO Collaborating Centre for Reference and Research on *Salmonella*).

Please fill in information concerning the brand of antisera used for typing in the fields available in the database for entering results. In addition, we kindly ask you to report which antisera you think are required to complete the serotyping, if relevant.

3.3 Antimicrobial susceptibility testing of *Salmonella, Shigella* and *Escherichia coli* ATCC 25922

The *Salmonella* and *Shigella* strains as well as the *E. coli* ATCC 25922 QC reference strain should be tested for susceptibility towards as many as possible of the antimicrobials mentioned in the test form. Please use the methods routinely used in your laboratory.

For reconstitution of the *E. coli* QC reference strain (NCIMB 12210) which is supplied in the form of a LYFO DISK®, see instructions in section 3.1.1 above.

Testing of gentamicin susceptibility may be valuable for monitoring purposes. Therefore we kindly ask you to disregard, for the purpose of this proficiency trial, that the Clinical and Laboratory Standards Institute (CLSI) guidelines state that *Salmonella* and *Shigella* should not be reported as susceptible to aminoglycosides.

The breakpoints used in this EQAS for interpreting MIC results are in accordance with CLSI values (Table 1). Consequently, interpretation of MIC results will lead to categorization of strains into three categories: resistant (R), intermediate (I) and susceptible (S). In the evaluation report you

receive upon result submission, you can find that obtained interpretations in accordance with the expected interpretation will be defined as 'correct', whereas deviations from the expected interpretation will be defined as 'minor' (I ↔ S or I ↔ R), 'major' (S interpreted as R) or 'very major' (R interpreted as S).

Please report the breakpoints that you routinely use in your laboratory for interpretation of antimicrobial susceptibility test results in the fields available in the database (or in the test forms).

Table 1. Interpretive breakpoint for *Salmonella* and *Shigell*a antimicrobial susceptibility testing

Antimicrobials	Reference value, MIC (µg/mL)			Reference value, Disk diffusion (mm)		
	Sensitive	Intermediate	Resistant	Resistant	Intermediate	Sensitive
Ampicillin, AMP	≤8	16	≥32	≤13	14-16	≥17
Cefotaxime, CTX*	≤1	-	>1	≤27	-	>27
Cefoxitin, FOX	≤8	16	≥32	≤14	15-17	≥18
Ceftazidime, CAZ*	≤1	-	>1	≤22	-	>22
Ceftriaxone, CRO*	≤1	-	>1	≤25	-	>25
Chloramphenicol, CHL	≤8	16	≥32	≤12	13-17	≥18
Ciprofloxacin, CIP	≤0.06**	0.12-0.5**	≥1**	≤20mm (5µg)** or <23mm (1µg)***	21-30mm (5µg)** or - (1µg)***	≥31mm (5µg)** or ≥23mm (1µg)***
Gentamicin, GEN	≤4	8	≥16	≤12	13-14	≥15
Meropenem, MER*	***≤0.12***	***-***	***>0.12***	***<27***	***-***	***≥27***
Nalidixic acid, NAL	≤16	-	≥32	≤13	14-18	≥19
Sulfonamides, SMX	≤256	-	≥512	≤12	13-16	≥17
Tetracycline, TET	≤4	8	≥16	≤11	12-14	≥15
Trimethoprim, TMP	≤8	-	≥16	≤10	11-15	≥16
Trimethoprim + sulfamethoxazole, TMP+SMX, SXT	≤2/38	-	≥4/76	≤10	11-15	≥16

Reference values used in this EQAS are according to CLSI (M100-S25), with the following exceptions:
* For the cephalosporins and meropenem, the application of the interpretative criteria is intended to indicate if the microorganism is a presumptive ESBL- or carbapenemase-producer. Reference values for the cephalosporins are according to CLSI M100-S25 Table 3A. These interpretative criteria are also applied for *Salmonella* and *Shigella* test strains for interpretation of AST results in this EQAS. ***Reference values for meropenem are based on epidemiological cut off values from www.eucast.org.***
** These breakpoints should also be applied for *Shigella* test strains for interpretation of AST results in this EQAS
*** The publication by Cavaco LM and Aarestrup FM (J. Clin. Microbiol. 2009. Sep;47(9):2751-8) provides the background for these interpretative criteria in the WHO GFN EQAS. These interpretative criteria are also applied for *Shigella* test strains for interpretation of AST results in this EQAS.

Concerning ciprofloxacin susceptibility tests, please note that for results obtained in this proficiency test, the breakpoints for *Salmonella* are applied for *Shigella* also. These breakpoints for ciprofloxacin take into consideration mechanisms of resistance due to plasmid-mediated quinolone resistance genes (e.g. *qnr*-genes) and one-point-mutation in the gyrase gene.

Important notes*: beta-lactam resistance*
The following tests for detection of ESBL-, AmpC-, and carbapenamase-producing phenotypes are optional in relation to the current WHO GFN EQAS.

If choosing to participate in this component of the EQAS, all strains displaying reduced susceptibility to cefotaxime (CTX), ceftazidime (CAZ), and/or ceftriaxone (CRO) should be tested for ESBL-, AmpC, or carbapenemase-production by confirmatory tests. Reduced susceptibility to any of the above-mentioned antimicrobials indicates that the bacterial strain is an ESBL-, AmpC, or carbapenemase-producing phenotype.

Confirmatory test for ESBL production requires the use of both cefotaxime (CTX) and ceftazidime (CAZ) alone, and in combination with a β-lactamase inhibitor (clavulanic acid). Synergy is defined either as i) by microbroth dilution methods or E-test; a ≥ 3 twofold concentration decrease in an MIC for either antimicrobial agent tested in combination with clavulanic acid vs. its MIC when tested alone (E-test 3 dilution steps difference; MIC CTX : CTX/Cl or CAZ : CAZ/Cl ratio ≥ 8) or ii) by disk diffusion; a ≥ 5 mm increase in a zone diameter for either antimicrobial agent tested in combination with clavulanic acid vs. its zone when tested alone (CLSI M100 Table 2A; Enterobacteriaceae). The presence of synergy indicates ESBL production.

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

Confirmatory test for carbapenemase production requires the testing of meropenem (MER). Reduced susceptibility to MER indicates that the bacterial strain is a carbapenemase-producer.

The classification of the phenotypic results should be based on the most recent EFSA (European Food Safety Agency) recommendations (EURL-AR Workshop 2016, http://www.crl-ar.eu/data/images/ws_april-2016/f11_efsa_criteria.pdf). The following summary of these recommendations indicate how the phenotypes should be categorized:

ESBL-phenotype:
- CTX or CAZ > 1 mg/L **AND**
- MER ≤ 0.12 mg/L **AND**
- FOX ≤ 8 mg/L **AND**
- Synergy for CTX : CTX/Cl and/or CAZ : CAZ/Cl

ESBL+AmpC-phenotype:
- CTX or CAZ > 1 mg/L **AND**
- MER ≤ 0.12 mg/L **AND**
- FOX > 8 mg/L **AND**
- Synergy for CTX : CTX/Cl and/or CAZ : CAZ/Cl

AmpC-phenotype:
- CTX or CAZ > 1 mg/L **AND**
- MER ≤ 0.12 mg/L **AND**
- FOX > 8 mg/L **AND**
- No synergy for CTX : CTX/Cl nor CAZ : CAZ/Cl

(note, presence of ESBLs is not excluded)

Carbapenemase-phenotype:
- MER > 0.12 mg/L

(note, presence of ESBLs or AmpCs is not excluded)

Other-phenotype:
- Not covered by any of the above categories **AND**
- CTX, CAZ, FOX, or MER > interpretative criteria as susceptible in Table 1 (i.e. exhibits reduced susceptibility)

No ESBL-, AmpC-, or carbapenemase:
- CTX, CAZ, FOX, and MER ≤ interpretative criteria as susceptible in Table 1 (i.e. exhibits susceptibility)

The genotype obtained by PCR and/or sequencing may be necessary to correctly categorize a bacterial test strain as either of the categories, ESBL-, AmpC, and/or carbapenemase-producer, but is not requested as part of this WHO GFN EQAS.

3.4 Handling the *Campylobacter* strains

The *Campylobacter* test strains as well as the *C. jejuni* reference strain (NCTC 11351) are supplied in the form of LYFO DISK®. To revive the strains, see instructions in section 3.1.1 above

3.5 Identification of *Campylobacter*

The two thermophilic *Campylobacter* isolates should be identified to species level.

3.6 Antimicrobial susceptibility testing of *Campylobacter* and *Campylobacter jejuni* ATCC 33560

The *Campylobacter* test strains and the *C. jejuni* reference strain ATCC33560 should be tested for susceptibility to as many antimicrobials as possible among the ones mentioned in the test form. It should be noted that only MIC methods (i.e. broth or agar dilution methods) are recommendable for AST of *Campylobacter*. Neither the use of disk diffusion nor E-test is recommendable for AST of *Campylobacter*.

In this EQAS, the breakpoints used for interpretation of MIC results for *Campylobacter* are epidemiological cut-off values according to EUCAST (European Committee on Antimicrobial Susceptibility Testing; www.eucast.org; Table 2). Consequently, only two categories of characterisation (resistant, R or susceptible, S) are allowed. In the evaluation report that you receive upon result submission, you can find that obtained interpretations in agreement with the expected interpretation, will be categorised as 'correct', whereas deviations from the expected interpretation will be categorizes as 'incorrect'.

Please report the breakpoints that you routinely use in your laboratory for interpretation of antimicrobial susceptibility test results, in the fields available in the database (or in the test form).

Note that the interpretation of antimicrobial susceptibility test results for *Campylobacter* requires knowledge of the *Campylobacter* species. If you did not sign-up for *Campylobacter* identification, but perform AST on *Campylobacter*, you are welcome to contact the EQAS Coordinator to obtain information regarding the identity of the *Campylobacter* test strains.

Table 2. Interpretive criteria for *Campylobacter* antimicrobial susceptibility testing

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

Reference values for interpretation of *Campylobacter* AST results according to EUCAST

The sub-cultured *Campylobacter* strains should be used for MIC-testing after incubation at 36-37ºC for 48 hours or at 42ºC for 24 hours. Likely, two subcultures are needed prior to MIC-testing to ensure optimal growth.

3.7 Identification of the unknown enteric pathogen

The 'unknown' isolate should be identified to species level and further typed if relevant.

4 REPORTING OF RESULTS AND EVALUATION

We recommend that you write your results in the enclosed test forms and that you read carefully the description in paragraph 5 before entering your results in the web database. For entering your results via the web, you will be guided through all steps on the screen and you will immediately be able to view and print a report evaluating your results. Results in agreement with the expected interpretation are categorised as 'correct', while results deviating from the expected interpretation are categorised as 'incorrect'.

Results must be submitted no later than 31 December 2016.

Results must be submitted directly via the Internet based database. Should you not be able to access the Internet, you may return the completed test forms scanned by e-mail to the National Food Institute, Denmark.

All results will be summarized in a report which will be publicly available. Individual results will be anonymous and will only be forwarded to the official GFN Regional Centre in your region.

We are looking forward to receiving your results.

If you have any questions or concerns, please do not hesitate to contact the WHO GFN EQAS Coordinator:

Susanne Karlsmose Pedersen
National Food Institute, Technical University of Denmark
Søltofts Plads, Building 221, DK-2800 Kgs. Lyngby - DENMARK
Tel: +45 3588 6601
E-mail: suska@food.dtu.dk

WHO Collaborating Centre
External Quality Assurance System (EQAS) 2016

DTU Food
National Food Institute

WHO Collaborating Centre for Antimicrobial Resistance in Foodborne Pathogens
www.antimicrobialresistance.dk

6 HOW TO ENTER RESULTS IN THE INTERACTIVE DATABASE

Please carefully read these instructions before entering the web page. Remember that you need by your side the completed test forms and the breakpoint values you used.

In general, you can browse back and forth in the pages of the database. Always remember to save your input before leaving a page.

1) Enter the WHO Collaborating Centre website (from http://www.antimicrobialresistance.dk), then
   a. Click on 'EQAS'
   b. Click on the link for the interactive database (http://eqas.food.dtu.dk/who)
   c. Write your username and password in lower-case letters and click on 'Login'.
      You can find your username and password in the letter following your strains.
      Your username and password will remain unchanged in future trials. Do not hesitate to contact us if you experience problems with the login.

2) Click on 'Materials and methods'
   a. Fill in the fields relative to brand of antisera (very important because we would like to compare results obtained with different brands of antisera)
   b. Fill in the fields relative to the method used for antimicrobial susceptibility testing
   c. Enter the brand of materials, e.g. Oxoid
   d. Fill in the field asking whether your institute serves as a national reference laboratory
   e. In the comment field, report which antisera you think is required to complete your serotyping, if relevant
   f. Click on 'Save and go to next page' – ALWAYS remember to save each page before leaving it!

3) In the data entry page 'Routinely used breakpoints'
   a. Fill in the fields relative to the breakpoints used routinely in your laboratory to determine the antimicrobial susceptibility category. Remember to use the operator keys in order to show – equal to (=), less than (<), less or equal to(≤), greater than (>) or greater than or equal to (≥).

4) In the data entry pages '*Salmonella* strains 1-8',
   a. SELECT the serogroup (O-group) from the drop-down list, DO NOT WRITE – Wait a few seconds – the page will automatically reload, so that the drop-down list in the field "Serotype" only contains serotypes belonging to the chosen serogroup.
   b. SELECT the serotype from the drop-down list – DO NOT WRITE – wait a few seconds and you can enter the antigenic formula (e.g. 1,4,5,12:i:1,2)

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c. Enter the zone diameters in mm or MIC values in µg/ml. Remember to use the operator keys to show e.g. equal to (=), etc.
d. Enter the interpretation as R (resistant), I (intermediate) or S (susceptible)
e. If you performed confirmatory tests for ESBL production, select the appropriate result.
f. If relevant, fill in the field related to comments (e.g. which antisera you miss for complete serotyping)
g. Click on 'Save and go to next page'

If you did not perform these tests, please leave the fields empty

5) In the data entry page '*E. coli* reference strain':
   a. Enter the zone diameters in mm or MIC values in µg/ml. Remember to use the operator keys to show e.g. equal to (=), etc.
   b. Click on 'Save and go to next page'

6) In the page 'Identification of *Campylobacter* and unknown sample':
   a. Choose the correct *Campylobacter* species from the pick list
   b. Fill in the field concerning species and type of the unknown bacterial isolate, and report the method used for identification
   c. Click on 'Save and go to next page'

   If you did not perform these tests, please leave the fields empty

7) The next page is a menu that allows you to review the input pages and approve your input *and finally see and print the evaluated results*
   a. Browse through the input pages and make corrections if necessary. Remember to click on 'save and go to next page' if you make any corrections.
   b. Approve your input. Be sure that you have filled in all the results before approval, as YOU CAN ONLY APPROVE ONCE! The approval blocks your data entry into the interactive database, but allows you to see the evaluated results.
   c. As soon as you have approved your input, an evaluation report will appear.

8) After browsing all pages in the report, you will find a new menu. You can choose 'EQAS 2016 start page', 'Review evaluated results' (a printer friendly version of the evaluation report is also available) or 'Go to WHO GFN homepage'.

End of entering your data – thank you very much!

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SUBCULTURE AND MAINTENANCE OF QUALITY CONTROL STRAINS

1.1 Purpose

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

1.2 References

M100-S24, January 2014 (Performance Standards for Antimicrobial Susceptibility Testing)

M7-A9, January 2012 (Methods for Dilution Antimicrobial Susceptibility Test for Bacteria That Grow Aerobically; Approved Standard)

1.3 Definition of Terms

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

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

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

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

1.4 Important Considerations

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

- Ideally, test values should be in the middle of the acceptable range
- Graphing QC data points over time can help identify changes in data helpful for troubleshooting problems

1.5 Storage of Reference Strains

Preparation of stock cultures

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

Working cultures

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

1.6 Frequency of Testing

Weekly vs. daily testing

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

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

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

Corrective Actions

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

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

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

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

Repeat the 30 days validation before resuming weekly testing.

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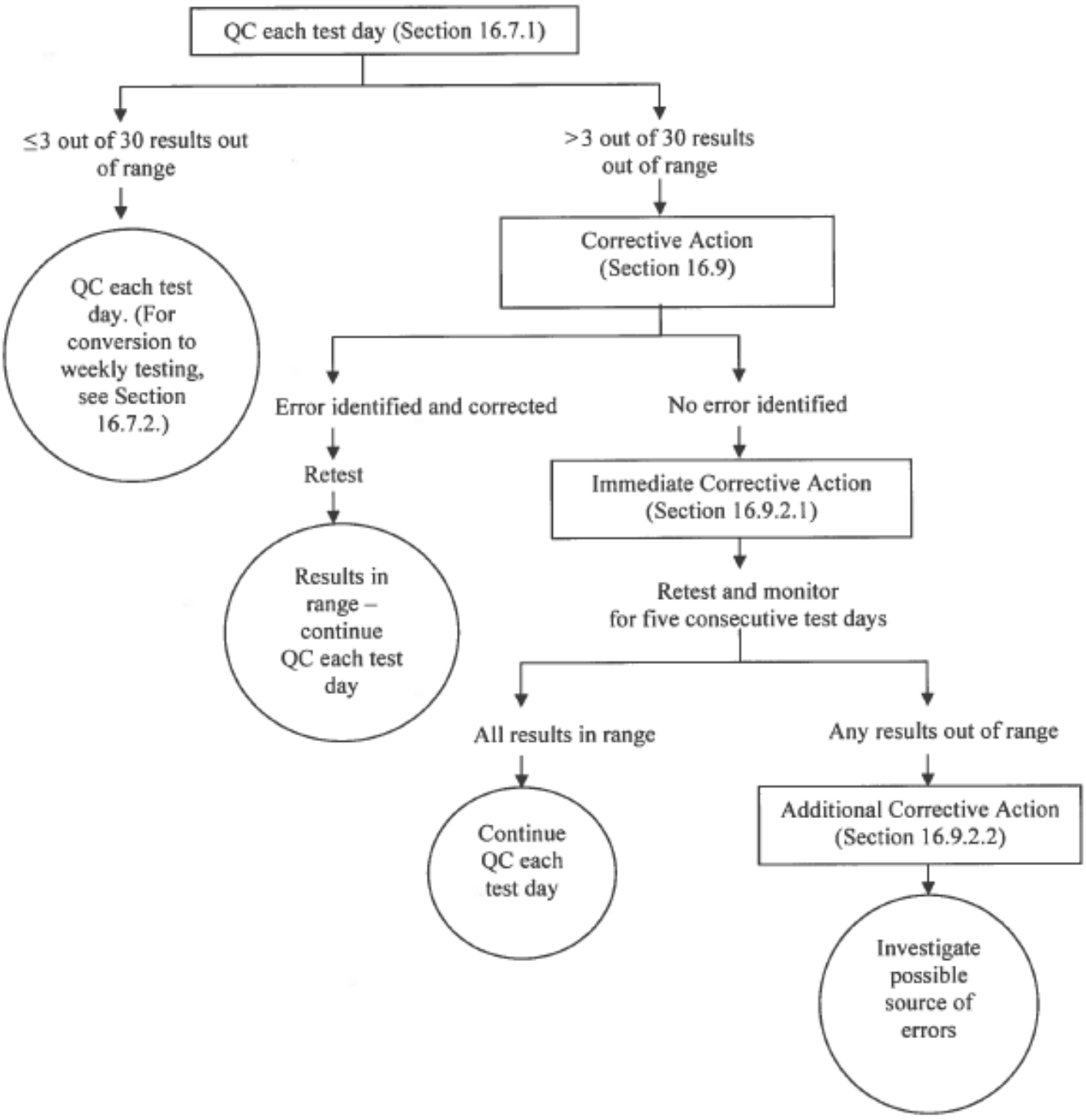
DAILY MIC QC CHART

Appendix A. Quality Control Protocol Flow Charts

Quality Control (QC) Protocol: Daily Testing



Reference: CLSI M7-A9, page 46

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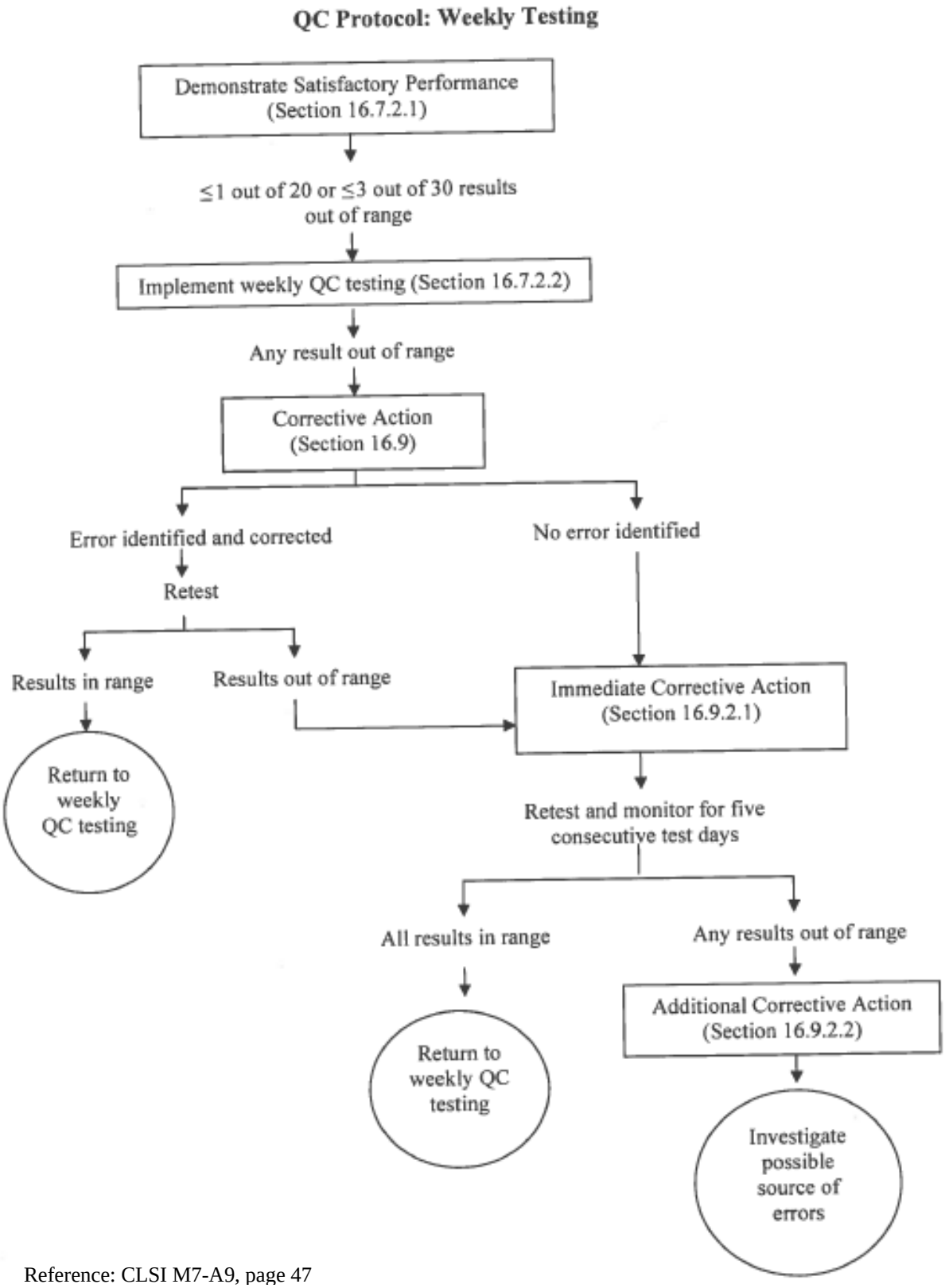
Appendix A. (Continued)



Reference: CLSI M7-A9, page 47

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INSTRUCTIONS FOR OPENING AND REVIVING LYOPHILISED CULTURES

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

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

a. Check the number of the culture on the label inside the ampoule
b. Make a file cut on the ampoule near the middle of the plug (see Figure 1)
c. Disinfect the ampoule with alcohol-dampened gauze or alcohol-dampened cotton wool from just below the plug to the pointed end
d. Apply a red-hot glass rod to the file cut to crack the glass and allow air to enter slowly into the ampoule
e. Remove the pointed end of the ampoule into disinfectant
f. Add about 0.3 ml appropriate broth to the dried suspension using a sterile Pasteur pipette and mix carefully to avoid creating aerosols. Transfer the contents to one or more suitable solid and /or liquid media
g. Incubate the inoculated medium at appropriate conditions for several days
h. Autoclave or disinfect effectively the used Pasteur pipette, the plug and all the remains of the original ampoule before discarding

Notes:

- Cultures should be grown on media and under conditions as recommended in the CCM catalogue (see http://www.sci.muni.cz)
- Cultures may need at least one subculturing before they can be optimally used in experiments
- Unopened ampoules should be kept in a dark and cool place!

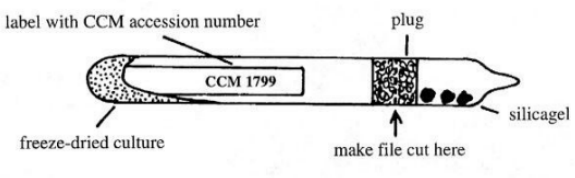

Figure 1: from CCM document 'Instructions for Opening and Reviving of Freeze-Dried Bacteria and Fungi' available on http://www.sci.muni.cz

National Food Institute
Technical University of Denmark
Kemitorvet
Building 204
DK - 2800 Kgs. Lyngby

Tel. 35 88 70 00
Fax 35 88 70 01

www.food.dtu.dk

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