Proficiency testing
Drinking water Microbiology

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Linnea Blom

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Author
Linnea Blom

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Editor in chief
Maria Sitell, head of the Unit for Microbiology, Swedish Food Agency

Responsible for the scheme
Linnea Blom, microbiologist, Unit for Microbiology, Swedish Food Agency

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SWEDISH FOOD AGENCY, DEPARTMENT OF BIOLOGY, BOX 622, SE-751 26 UPPSALA, SWEDEN

Contents

Abbreviations

Media

ACTA	Actinomycete Isolation Agar (SS 028212)
CCA	Chromogenic Coliform Agar (EN ISO 9308-1:2014)
Colilert	Colilert™ Quanti-Tray™ (IDEXX Inc.; EN ISO 9308-2:2014)
DRBC	Dichloran Rose Bengal Chloramphenicol Agar
LES	m-Endo Agar LES (SS 028167)
LTLSB	Lactose tryptone lauryl sulphate broth (SS 028167)
m-FC	m-FC Agar (SS 028167)
OGYE	Oxytetracyclin Glucose Yeast Extract Agar
PCA	Plate count agar
R2A	Reasoner's 2 Agar (Standard Methods, 9215 Heterotrophic Plate Count)
RBCC	Rose Bengal Agar with both chlortetracycline and chloramphenicol (SS 028192)
TSC	Tryptose Sulfite Cycloserine agar (EN ISO 14189:2016)
YeA	Yeast extract Agar (EN ISO 6222:1999)

Other abbreviations

MF	Membrane filter (method)
MPN	Most Probable Number (quantification based on statistical distributions)
ISO	International Organization for Standardization
EN	European standard from "Comité Européen de Normalisation" (CEN)
DS, NS, SFS, SS	National standards from Denmark, Norway, Finland and Sweden
SLV	Livsmedelsverket/Swedish Food Agency, Sweden

Analyses in this PT round

Quantitative analyses

Coliform bacteria

Suspected thermotolerant coliform bacteria (not assessed)

Escherichia coli

Clostridium perfringens

Moulds

Yeasts

Actinomycetes

Culturable microorganisms, three days incubation at 22 °C

Slow-growing bacteria, seven days incubation at 22 °C

Method

Reporting of results and method information

It is the responsibility of the individual participants to correctly report results according to the instructions. Incorrectly reported results, for example results reported for the wrong sample, cannot be correctly processed. Incorrectly reported results are as a general rule excluded but may – after manual assessment by the Swedish Food Agency in each individual case – still be included and processed.

It is also mandatory for the participants to report method information for all analyses. This method information is sometimes contradictory or difficult to interpret. For example when manual comments by the participant contradict the reported method information. In such cases, the reported method information provided by the participants is generally used in method comparisons "as it is". Alternatively, method data that are difficult to interpret may be excluded or added to the group "Other", together with results from methods and media that are only used by 1–2 participants.

Standard deviation and assigned value

Evaluation of the participants' results and statistical calculations are carried out on square root transformed results. Results reported by participants as "> value" or "< value" are not evaluated.

A robust statistical approach is used to determine the mean value and standard deviation. Algorithm A with iterated scale as described in ISO 13528:2022 [1] is used to determine the robust mean (m_{PT}) and robust standard deviation (s_{PT}) of the participants' results. Results that are obviously erroneous are excluded prior to determining m_{PT} and s_{PT} (blunder removal). For evaluated parameters, the assigned value consists of m_{PT}. It is regarded as the true, normative value.

For small datasets, there is an increased uncertainty associated with determining the robust mean (m_{PT}) and robust standard deviation (s_{PT}) of the participants' results. Therefore, when fewer than 12 participants have reported evaluated results, the statistical measures for performance evaluation will be provided *only as an information* to the participants.

Outliers

Outliers are results that deviate from the other results in a way that cannot be explained by normal variation. Results within $m_{PT} \pm 3s_{PT}$ are considered acceptable, whereas results outside this interval are considered as outliers. When fewer than 12 participants have reported results, as well as in some individual cases, subjective adjustments are made to set acceptance limits based on prior knowledge of the samples contents.

Results from different methods

Non-robust median values (*Med*) and coefficient of variation (*CV*) are calculated to assist in the evaluation of the results from different methods. These are shown in tables in the report, in connection with the respective analyses. In these instances, *Med* and *CV* are calculated from the respective method groups' results, with outliers and false results excluded. For method groups with fewer than 5 results, only the number of false results and outliers are provided.

Coefficient of variation

The coefficient of variation (*CV*) is a relative measure and is calculated as:

$$CV = 100 \times \frac{s_{\mathrm{PT}}}{m_{\mathrm{PT}}}$$

The *CV* for square root transformed results is given as a measure of dispersion. When the dispersion is <10 % it is regarded as very small, 10–20 % as small, 20–30 % as medium, 30–40 % as large and >40 % as very large.

Measurement uncertainty for the assigned value

The standard uncertainty (u_{PT}) of the assigned value (m_{PT}) is estimated from the standard deviation (s_{PT}) and the number of evaluated results (n):

$$u_{\mathrm{PT}} = 1{,}25 \times \frac{s_{\mathrm{PT}}}{\sqrt{n}}$$

The measurement uncertainty is considered negligible compared to the standard deviation (which is used for evaluating the participants' results) when:

$$u_{\mathrm{PT}} < 0{,}3 s_{\mathrm{PT}}$$

In annex 1 the relative standard uncertainty (u_{rel}) of m_{PT} is also provided.

$$u_{\mathrm{rel,mPT}}(\%) = 100 \times \frac{s_{\mathrm{PT}}}{\sqrt{n} \cdot m_{\mathrm{PT}}}$$

Z-scores

To allow comparison of the results from different analyses and samples, results are transformed into standard values (*z*-scores). *Z*-scores are calculated as:

$$z = \frac{x_{\mathrm{lab}} - m_{\mathrm{PT}}}{s_{\mathrm{PT}}}$$

where x_{lab} is the square root transformed result of the individual participant.

Z-scores for individual analyses are shown in Annex 2 and can be used as a tool by participants when following up on the results. For quantitative analyses, a *z*-score is either positive or negative, depending on whether the participants result is higher or lower than m_{PT}.

In evaluations of the analytical results, the following guidelines can be used:

$\|z\| \leq 2$	indicates that the result is acceptable
$2 < \|z\| < 3$	indicates a warning that the result may be deviating, and might motivate an action in the follow-up process
$\|z\| \geq 3$	indicates that the result is regarded as deviating and should lead to an action in the follow-up process

Table legends

N	number of participants that reported results for the analysis
n	number of participants with acceptable result (false results and outliers excluded)
m_{PT}	assigned value, robust mean value in cfu / MPN 100 ml^{-1} or cfu ml^{-1}, re-transformed to the cfu / MPN scale
Med	median in cfu /MPN100 ml^{-1}
CV	coefficient of variation in percent
F	number of false positive or false negative results
<	number of low outliers
>	number of high outliers

Figure legends

▒	results within the interval of acceptance
■	outlier
□	false negative result
*	value outside the x-axis scale

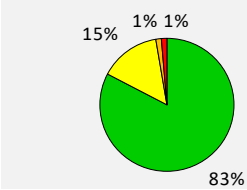
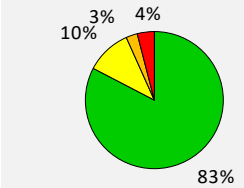
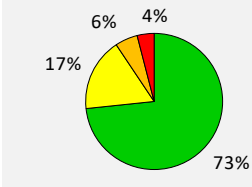
Results

General outcome

Samples were sent to 75 participants: 36 in Sweden, 38 in European countries, and one outside of Europe. Of the 73 participants that reported results, 41 (56 %) provided at least one result that received an annotation.

Individual results are listed in Annex 1. *Z*-scores for individual results are listed in Annex 2.

Table 1. Composition of the test material and proportion of deviating results (N: number of reported results, F: false positive or false negative, X: outliers)

	Sample A				Sample B				Sample C			
% participants with 0 annotations 1 annotation 2 annotations >2 annotations												
Microorganisms	*Escherichia coli* *Klebsiella oxytoca* *Clostridium perfringens* *Streptomyces species* *Pseudomonas brenneri*				*Escherichia coli* *Citrobacter freundii* *Clostridium bifermentans* *Phialophora fastigiata* *Rhodotorula minuta* *Sphingomonas sp.*				*Klebsiella pneumoniae* *Acremonium strictum* *Hanseniaspora uvarum* *Sphingomonas sp.* *Staphylococcus warneri*			
Analysis	**Target organism**	**N**	**F**	**X**	**Target organism**	**N**	**F**	**X**	**Target organism**	**N**	**F**	**X**
Coliform bacteria	***E. coli*** ***K. oxytoca***	102	0	3	***E. coli*** ***C. freundii***	101	0	5	***K. pneumoniae***	100	0	3
Susp. thermotol. coliform bact.	***E. coli***	25	0	0	***E. coli***	24	0	0	***K. pneumoniae***	23	0	0
E. coli	***E. coli***	106	0	5	***E. coli***	108	0	2	-	106	6	0
Presumptive C. perfringens	***C. perfringens***	37	0	1	***C. bifermentans***	36	2	2	-	36	3	0
Clostridium perfringens	***C. perfringens***	22	1	1	(*C. bifermentans*)	23	4	0	-	24	3	0
Moulds	-	33	0	0	***P. fastigiata***	33	0	1	***A. strictum***	33	13	0
Yeasts	-	33	1	0	***R. minuta***	33	0	2	***H. uvarum***	33	0	1
Actinomycetes	***Streptomyces sp.***	27	1	1	-	26	1	0	-	26	2	0
Culturable microorganisms 22 °C, 3 days	***P. brenneri***	72	0	1	***E. coli*** ***C. freundii***	72	0	2	***S. warneri*** ***K. pneumoniae***	72	0	0
Slow-growing microorganisms	***P. brenneri***	42	0	3	***Sphingomonas sp.***	42	0	2	***Sphingomonas sp.***	42	0	0

- no target organism or no value; **microorganism** = main target organism; microorganism = few colonies; (*microorganism*) = false positive before confirmation

The results are not evaluated

Coliform bacteria

Sample A

The strains of *E. coli* and *K. oxytoca* were target organisms. Both strains form typical colonies with a metallic sheen on m-Endo Agar LES (LES). On Chromocult Coliform Agar (CCA), *E. coli* and *K. oxytoca* form blue and pink colonies, respectively. The strains possess the enzyme β-galactosidase and are detected as coliform bacteria with Colilert/Colilert-18.

In total, 102 results were evaluated. Three low outliers were identified.

Sample B

The strains of *E. coli* and *C. freundii* were target organisms. Both strains possess the enzyme β-galactosidase and form typical colonies on most MF media at 35/36/37 °C.

In total, 101 results were evaluated. One high and four low outliers were identified.

Sample C

The strain of *K. pneumoniae* was target organism. *K. pneumoniae* possesses the enzyme β-galactosidase and forms typical colonies on most MF media at 35/36/37 °C.

In total, 100 results were evaluated. Three low outliers were identified.

General remarks

For MF methods, most participants followed (EN) ISO 9308-1:2014 using the enzyme-based chromogenic medium CCA. CCA is suitable for waters with low bacterial background flora due to the low selectivity of the medium. On CCA, β-D-galactosidase positive colonies (pink to red) are counted as presumptive coliform bacteria. β-D-galactosidase and β-D-glucuronidase positive colonies (dark blue to violet) are counted as *E. coli*. Total coliform bacteria are the sum of oxidase-negative presumptive coliform bacteria and *E. coli*. ISO 9308-1:2014 was last reviewed and confirmed by ISO in 2019 and remains current. An amendment of the incubation time and performance testing of CCA is available (ISO 9308-1:2014/Amd 1:2016).

SS 028167 and SFS 3016 are Nordic national standards based on incubation on LES. On LES, coliform bacteria form red colonies with a metallic sheen, which is due to the production of aldehyde from the fermentation of lactose. The presumptive coliform bacteria are confirmed by a negative oxidase test.

MPN methods are based on the growth of target organisms in a liquid medium and calculation of the MPN of organisms is done by reference to MPN tables. For MPN methods, most participants followed (EN) ISO 9308-2:2012 using Colilert-18 or equivalent defined substrate technology. The standard was last reviewed by ISO in 2023 and remains current. As with CCA, Colilert-18 is based on the activity of β-D-galactosidase. β-D-galactosidase cleaves ortho-nitrophenol galactoside (ONPG) and changes the coloration of the wells to yellow.

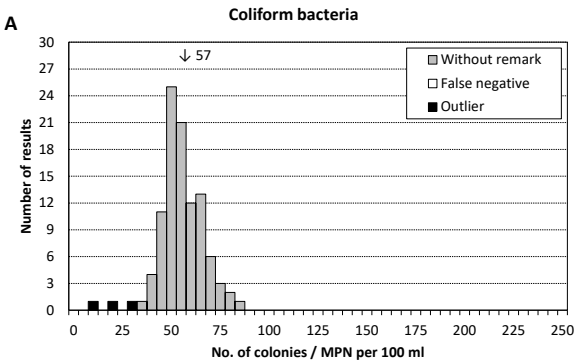
A somewhat higher median was observed for methods based on MPN methodology, particularly for samples B and C. The same observation has been made in previous PT rounds and can be considered as an expected result.

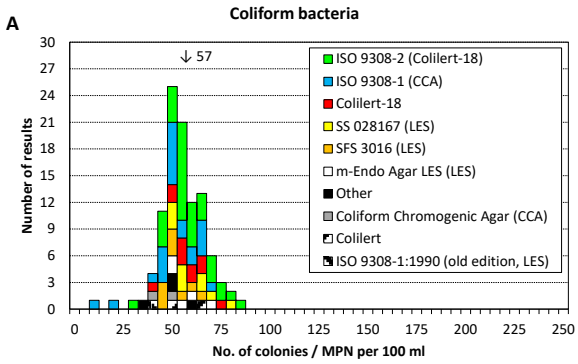
Table 2. Results from analysis of coliform bacteria.

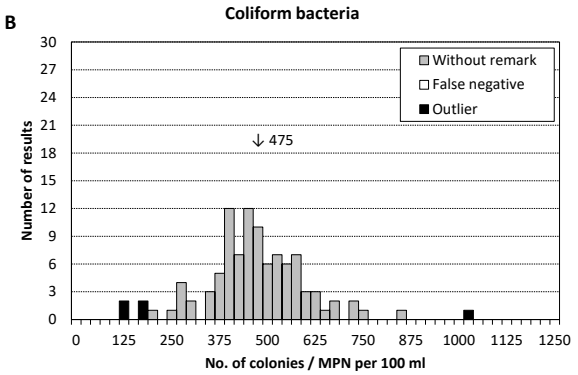
Method	Sample A							Sample B							Sample C						
	N	*n*	m_{PT}	*CV*	*F*	<	>	*N*	*n*	m_{PT}	*CV*	*F*	<	>	*N*	*n*	m_{PT}	*CV*	*F*	<	>
All results	**102**	**99**	**57**	**9**	**0**	**3**	**0**	**101**	**96**	**475**	**12**	**0**	**4**	**1**	**100**	**97**	**1233**	**10**	**0**	**3**	**0**
ISO 9308-2 (Colilert-18)	35	34	59	8	0	1	0	34	34	517	13	0	0	0	33	33	1376	9	0	0	0
ISO 9308-1 (CCA)	23	21	52	7	0	2	0	22	20	442	10	0	2	0	23	21	1100	8	0	2	0
Colilert-18	11	11	59	9	0	0	0	12	11	500	8	0	0	1	11	11	1326	4	0	0	0
SS 028167 (LES)	10	10	58	7	0	0	0	10	10	455	9	0	0	0	9	9	1290	9	0	0	0
SFS 3016 (LES)	9	9	51	7	0	0	0	10	10	482	12	0	0	0	10	10	1175	11	0	0	0
m-Endo Agar LES (LES)	5	5	57	6	0	0	0	5	5	440	6	0	0	0	6	6	1200	7	0	0	0
Other	4	4	-	-	0	0	0	3	1	-	-	0	2	0	3	2	-	-	0	1	0
Coliform Chromogenic Agar	2	2	-	-	0	0	0	2	2	-	-	0	0	0	2	2	-	-	0	0	0
Colilert	2	2	-	-	0	0	0	2	2	-	-	0	0	0	2	2	-	-	0	0	0
ISO 9308-1:1990 (LES)	1	1	-	-	0	0	0	1	1	-	-	0	0	0	1	1	-	-	0	0	0

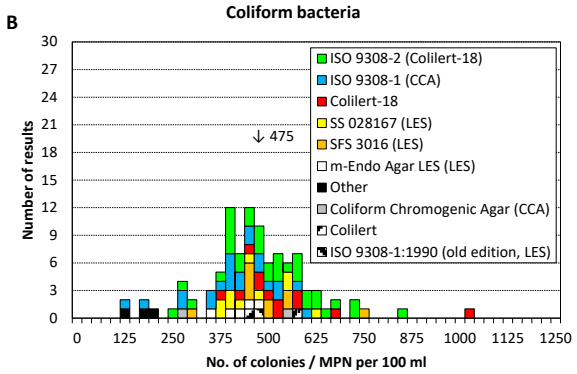
For "All results", m_{PT} = assigned value, robust mean value in cfu / MPN 100 ml^{-1}, re-transformed to the cfu /MPN scale

For individual methods, m_{PT} = median value in cfu / MPN 100 ml^{-1}









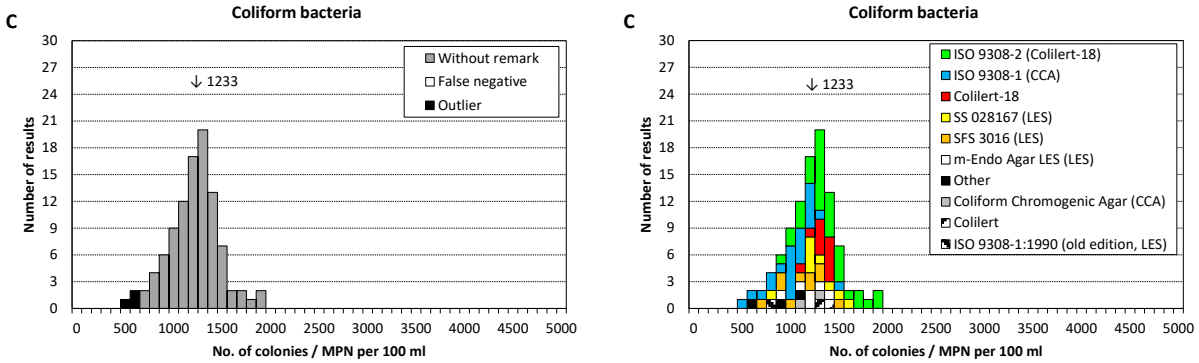


Figure 1. Results from analysis of coliform bacteria

Suspected thermotolerant coliform bacteria

Sample A

The strain of *E. coli* was target organism. On m-FC Agar, it forms typical blue colonies at 44/44.5 °C.

In total, 25 results were reported.

Sample B

The strain of *E. coli* (not identical to that in sample A) was target organism. On m-FC Agar, it forms typical blue colonies at 44/44.5 °C.

In total, 24 results were reported.

Sample C

The strain of *K. pneumoniae* was target organism. On m-FC Agar, it forms blue colonies at 44/44.5 °C.

In total, 23 participants reported results. Three zero results were reported by two participants.

General remarks

The parameter suspected thermotolerant coliform bacteria is not evaluated and the median value for performance evaluation is provided only as an information.

In total, 25 results were reported. Most participants used m-FC. The elevated incubation temperature (44/44.5 °C) and the addition of rosolic acid makes m-FC selective for thermotolerant coliform bacteria.

ISO is currently developing a Committee Draft (CD) standard for a membrane filtration method of *E. coli* in water with high levels of background bacteria.

Table 3. Results from analysis of suspected thermotolerant coliform bacteria.

Method	Sample A							Sample B							Sample C						
	N	*n*	*Med**	*CV*	*F*	*<*	*>*	*N*	*n*	*Med**	*CV*	*F*	*<*	*>*	*N*	*n*	*Med**	*CV*	*F*	*<*	*>*
All results	**25**	**25**	**14**	-	-	-	-	**24**	**24**	**255**	-	-	-	-	**23**	**23**	**1100**	-	-	-	-
SS 028167 (m-FC)	7	7	13	-	-	-	-	7	7	220	-	-	-	-	7	7	1100	-	-	-	-
SFS 4088 (m-FC)	7	7	14	-	-	-	-	6	6	184	-	-	-	-	7	7	1100	-	-	-	-
Other	7	7	30	-	-	-	-	7	7	304	-	-	-	-	5	5	550	-	-	-	-
MacConkey Agar	1	1	-	-	-	-	-	1	1	-	-	-	-	-	1	1	-	-	-	-	-
m-FC Agar (m-FC)	1	1	-	-	-	-	-	1	1	-	-	-	-	-	1	1	-	-	-	-	-
ISO 9308-1:1990 (old edition, m-FC)	1	1	-	-	-	-	-	1	1	-	-	-	-	-	1	1	-	-	-	-	-
NS 4792 (m-FC)	1	1	-	-	-	-	-	1	1	-	-	-	-	-	1	1	-	-	-	-	-

Med = Median value in cfu 100 ml^{-1}

* The samples are not evaluated. The values are shown only as an information to the participants.

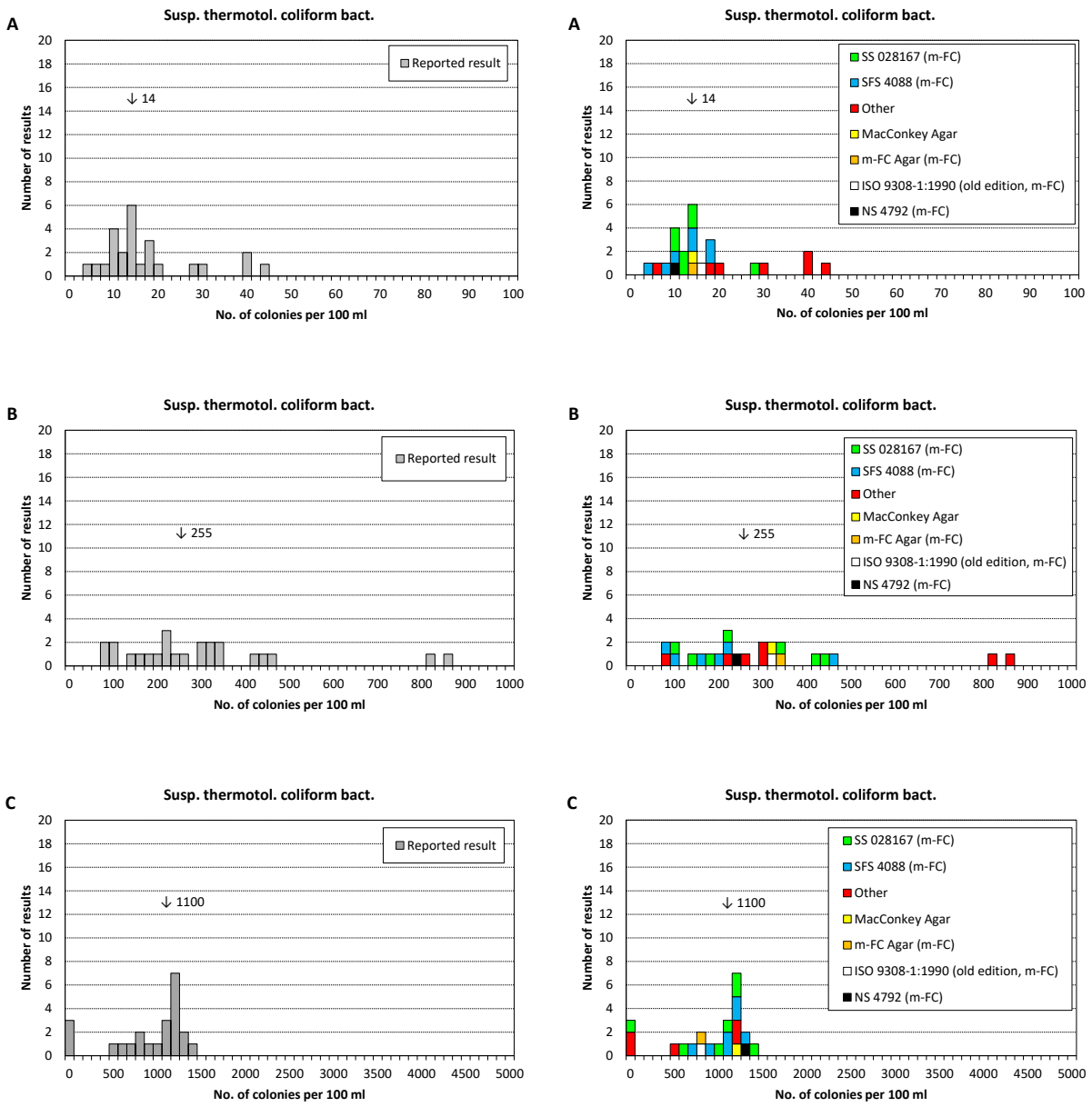


Figure 2. Results from analysis of *suspected thermotolerant coliform bacteria*

Escherichia coli

Sample A

The strain of *E. coli* was target organism. It forms typical colonies with a metallic sheen on LES and blue colonies on CCA. It possesses the enzyme β-glucuronidase and is detected as *E. coli* with Colilert/Colilert-18. The strain is positive for indole production and it produces gas in Lactose-Tryptone-Lauryl Sulphate Broth (LTLSB).

The strain of *K. oxytoca* is β-glucuronidase negative but indole positive. If the method used is based on indole-production instead of β-glucuronidase activity as a criterion for identifying *E. coli*, the strain could be classified as *E. coli.*

In total, 106 results were evaluated. One low and four high outliers were identified.

Sample B

The strain of *E. coli* (not identical to that in sample A) was target organism. It has a typical appearance on most MF media, as well as with MPN methods at 35/36/37 °C. The strain is positive for indole production and β-glucuronidase activity, and it produces gas in LTLSB.

In total, 108 results were evaluated. One low and one high outlier were identified.

Sample C

No target organism was present in the sample. However, the strain of *K. pneumoniae* was included in the sample as a thermotolerant coliform bacterium. The strain is negative for both indole production and β-glucuronidase activity.

In total, 106 results were evaluated. Six false positive results were reported from four participants.

General remarks

Most participants followed (EN) ISO 9308-2:2012, (EN) ISO 9308-1:2014 and/or Nordic national standards (see table 4). (EN) ISO 9308 defines *E. coli* as a member of the Enterobacteriaceae that possesses both β-D-galactosidase and β-D-glucuronidase enzymes. On CCA, β-D-galactosidase and β-D-glucuronidase positive strains appear as dark blue to violet colonies. On Colilert, yellow wells that also exhibit any degree of fluorescence are regarded as positive for *E. coli*. No further confirmation is needed.

When colonies are isolated from LES or m-FC, confirmation is required. Since EN ISO 9308-1:2014 only requires expression of β-D-glucuronidase, some participants have modified their standard accordingly. Depending on the method, tests for gas production, indole production and/or β-glucuronidase activity are usually performed from oxidase-negative presumptive colonies.

The primary MF growth media CCA and LES are incubated at 35/36/37 °C and m-FC at 44/44.5 °C.

Table 4. Results from analysis of *Escherichia coli* with MF methods.

Method	Sample A							Sample B							Sample C						
	N	*n*	m_{PT}	*CV*	*F*	<	>	*N*	*n*	m_{PT}	*CV*	*F*	<	>	*N*	*n*	m_{PT}	*CV*	*F*	<	>
All results	**106**	**101**	**16**	**16**	**0**	**1**	**4**	**108**	**106**	**278**	**15**	**0**	**1**	**1**	**106**	**100**	**-**	**-**	**6**	**-**	**-**
ISO 9308-2 (Colilert-18)	35	35	17	16	0	0	0	35	35	292	15	0	0	0	34	33	-	-	1	-	-
ISO 9308-1 (CCA)	24	21	15	16	0	1	2	25	24	242	12	0	1	0	25	24	-	-	1	-	-
Colilert-18	11	11	15	11	0	0	0	11	11	351	9	0	0	0	11	9	-	-	2	-	-
SS 028167 (LES)	8	7	17	16	0	0	1	8	7	270	7	0	0	1	8	8	-	-	0	-	-
SFS 3016 (LES)	8	8	14	16	0	0	0	8	8	305	16	0	0	0	8	7	-	-	1	-	-
SS 028167 (m-FC)	6	6	12	25	0	0	0	6	6	191	22	0	0	0	6	6	-	-	0	-	-
m-Endo Agar LES (LES)	5	5	17	6	0	0	0	6	6	260	16	0	0	0	4	4	-	-	0	-	-
Chromocult Coliform Agar	2	2	-	-	0	0	0	2	2	-	-	0	0	0	2	2	-	-	0	-	-
Colilert	2	2	-	-	0	0	0	2	2	-	-	0	0	0	2	2	-	-	0	-	-
SFS 4088 (m-FC)	1	1	-	-	0	0	0	1	1	-	-	0	0	0	2	2	-	-	0	-	-
Other	1	1	-	-	0	0	0	1	1	-	-	0	0	0	1	1	-	-	0	-	-
m-FC Agar (m-FC)	1	1	-	-	0	0	0	1	1	-	-	0	0	0	1	1	-	-	0	-	-
ISO 9308-1:1990 (LES)	1	0	-	-	0	0	1	1	1	-	-	0	0	0	1	0	-	-	1	-	-
NS 4792 (m-FC)	1	1	-	-	0	0	0	1	1	-	-	0	0	0	1	1	-	-	0	-	-

For "All results", m_{PT} = assigned value, robust mean value in cfu / MPN 100 ml^{-1}, re-transformed to the cfu /MPN scale

For individual methods, m_{PT} = median value in cfu / MPN 100 ml^{-1}

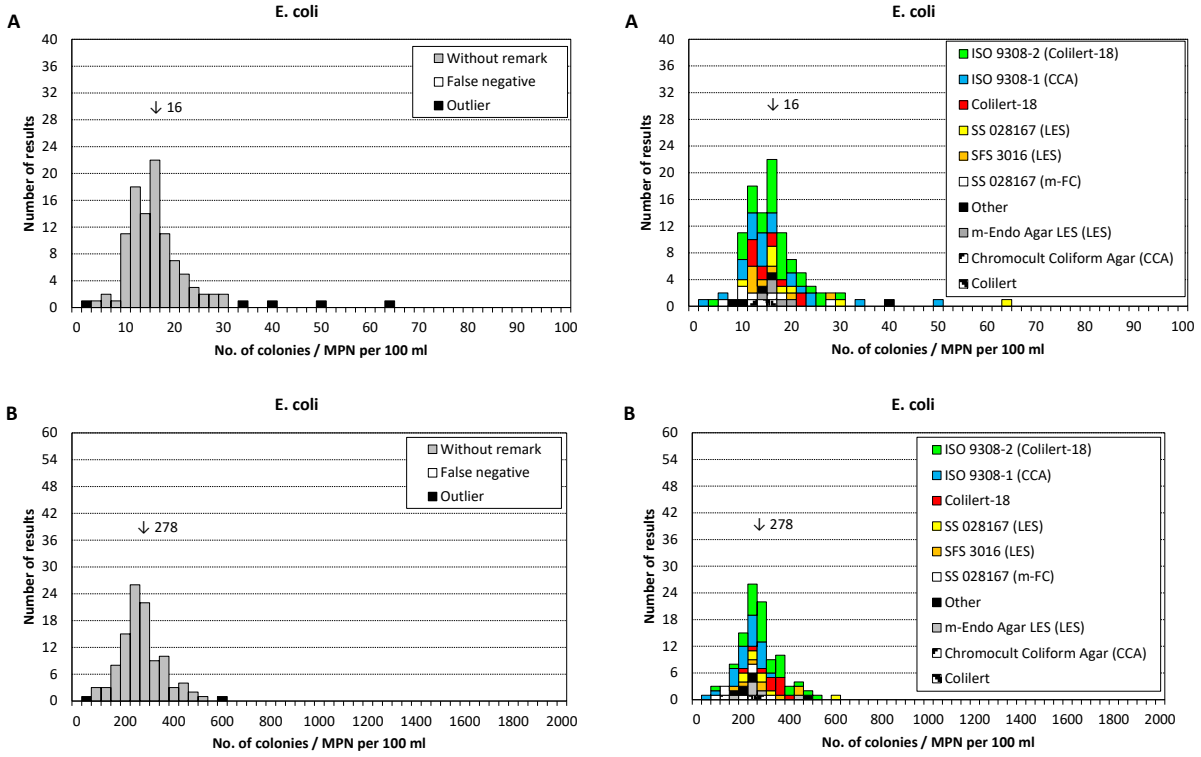


Figure 3. Results from analysis of Escherichia coli. The group "Other" includes the reporting of SFS 4088 (m-FC), m-FC Agar, ISO 9308-1:1990 (old edition, LES), NS 4792 (m-FC) and unknown methods.

Presumptive and confirmed *Clostridium perfringens*

Sample A

The strain of *C. perfringens* was target organism. On Tryptose Sulfite Cycloserine agar (TSC), the colour of the colonies can vary from faint yellow-brown to completely black depending on the condition and reduction potential of the medium.

In total, 37 results were evaluated for presumptive *C. perfringens.* One low outlier was reported.

For *C. perfringens,* 22 results were evaluated. One false negative result and one low outlier were identified.

Sample B

No target organism was present in the sample for *C. perfringens*. However, the strain of *C. bifermentans* was included in the sample as presumptive *C. perfringens.* On TSC, it forms small faint yellow-brown to black colonies. The strain does not possess the enzyme acid phosphatase and should not be reported as confirmed *C. perfringens.*

In total, 36 results were evaluated for presumptive *C. perfringens.* The results varied considerably, and the dispersion (CV) was large. The lower acceptance limit has therefore manually been set to 1 cfu / 100 ml. Two false negative results and two high outliers were identified.

For *C. perfringens,* 23 results were evaluated. Four false positive results were identified.

Sample C

No target organism was present in the sample.

In total, 36 results were evaluated for presumptive *C. perfringens.* Three false positive result were identified.

For *C. perfringens,* 24 results were evaluated. Three false positive results were identified.

General remarks

The parameter *C. perfringens* includes spores and vegetative cells of *C. perfringens* and no sample pasteurisation should be done before analyses. Participants may report presumptive (non-confirmed) or confirmed *C. perfringens.*

Most participants followed (EN) ISO 14189:2013, which was last reviewed by ISO in 2024 and remains current. ISO 14189 is a TSC-based method that enables the detection and enumeration of *C. perfringens* in different types of water. Presumptive *C. perfringens* are defined as bacteria that produce all shades of black or grey to yellow brown colonies on TSC after anaerobic incubation. *C. perfringens* is presumptive

C. perfringens that possess the enzyme acid phosphatase. Due to the presence of health hazardous substances in the confirmation reagent, some laboratories report only presumptive *C. perfringens*.

Two participants reported the use of TSC following the draft standard ISO/CD 6461-2:2002.

Table 5. Results from analysis of presumptive *C. perfringens*

Method	Sample A							Sample B							Sample C						
	N	*n*	m_{PT}	*CV*	*F*	<	>	*N*	*n*	m_{PT}	*CV*	*F*	<	>	*N*	*n*	m_{PT}	*CV*	*F*	<	>
All results	**37**	**36**	**4015**	**11**	**0**	**1**	**0**	**36**	**32**	**85**	**35**	**2**	**0**	**2**	**36**	**33**	-	-	**3**	-	-
ISO 14189 (TSC)	35	34	4100	12	0	1	0	35	31	94	34	2	0	2	35	32	-	-	3	-	-
ISO/CD 6461-2:2002-12-20, Mod.	2	2	-	-	0	0	0	1	1	-	-	0	0	0	1	1	-	-	0	-	-

For "All results", m_{PT} = assigned value, robust mean value in cfu 100 ml^{-1}, re-transformed to the cfu scale

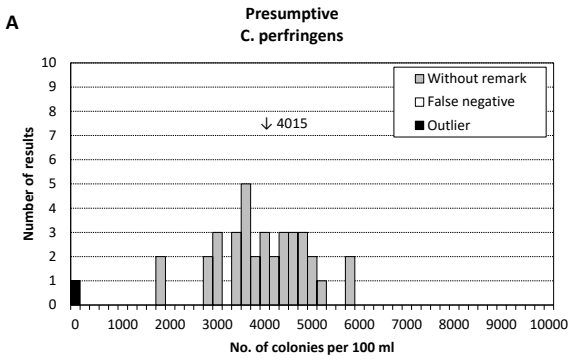
For individual methods, m_{PT} = median value in cfu 100 ml^{-1}

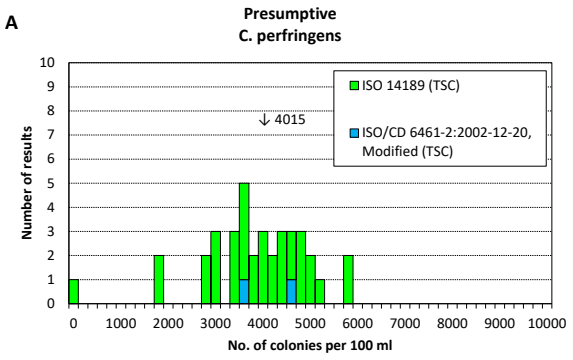
Table 6. Results from analysis of *C. perfringens*

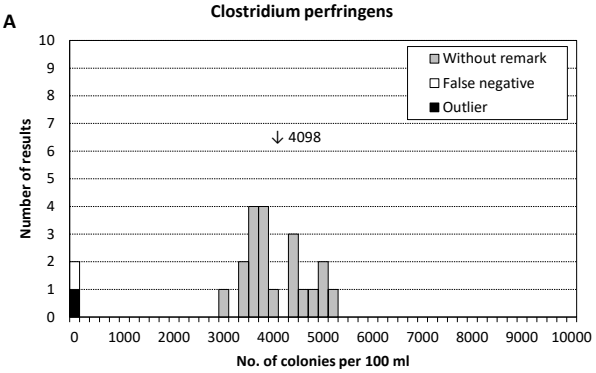
Method	Sample A							Sample B							Sample C						
	N	*n*	m_{PT}	*CV*	*F*	<	>	*N*	*n*	m_{PT}	*CV*	*F*	<	>	*N*	*n*	m_{PT}	*CV*	*F*	<	>
All results	**22**	**20**	**4098**	**8**	**1**	**1**	**0**	**23**	**19**	-	-	**4**	-	-	**24**	**21**	-	-	**3**	-	-
ISO 14189 (TSC)	20	18	3915	7	1	1	0	20	19	-	-	1	-	-	21	18	-	-	3	-	-
ISO/CD 6461-2:2002-12-20, Mod	1	1	-	-	0	0	0	2	0	-	-	2	-	-	2	2	-	-	0	-	-
Tryptose Sulfite Cycloserine Agar	1	1	-	-	0	0	0	1	0	-	-	1	-	-	1	1	-	-	0	-	-

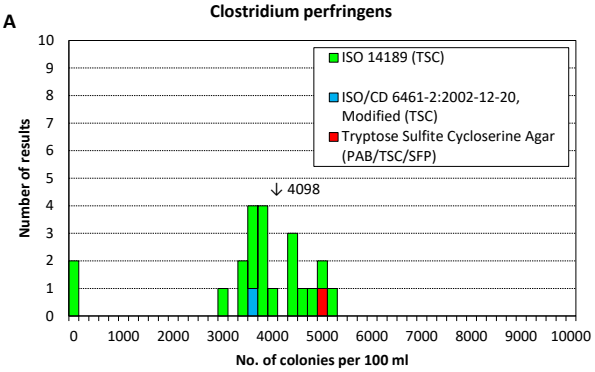
For "All results", m_{PT} = assigned value, robust mean value in cfu 100 ml^{-1}, re-transformed to the cfu scale

For individual methods, m_{PT} = median value in cfu 100 ml^{-1}









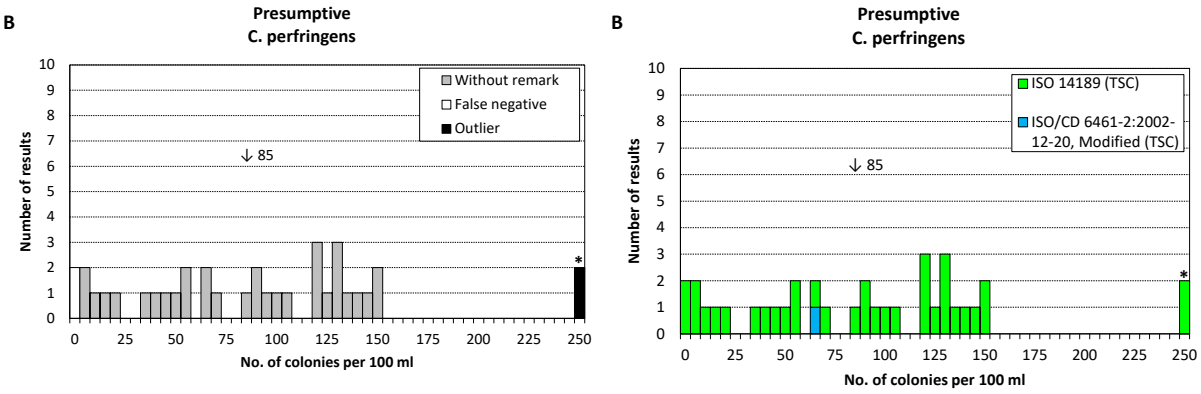


Figure 4. Results from analysis of presumptive and confirmed *Clostridium perfringens*.

Moulds and yeasts

Sample A

No target organism was present in the sample.

In total, 33 results were evaluated for moulds and yeast respectively. All of these were correct negative results.

Sample B

The strains of *P. fastigiata* and *R. minuta* were target organisms for moulds and yeasts respectively.

In total, 33 results were evaluated for moulds. One low outlier was reported.

For yeasts, 33 results were evaluated. Two low outliers were identified.

Sample C

The strains of *A. strictum* and *H. uvarum* were target organisms for moulds and yeasts respectively.

In total, 33 results were evaluated for moulds. Thirteen false negative results were reported. The reason for the false negative results is likely that the strain of *A. strictum* forms small, undeveloped colonies with pale mycelium without mature spores (colourless colonies) after seven days of incubation.

For yeasts, 33 results were evaluated. One high outlier was reported.

General remarks

Most participants followed the Swedish standard SS 028192. This standard is also partly used in Finland under the national designation SFS 5507. SS 028192 is based on incubation on Rose Bengal agar with chlortetracycline and chloramphenicol (RBCC) at 25 °C for seven days.

Most participants used RBCC, but the use of Dichloran Rose Bengal Chloramphenicol Agar (DRBC) and Oxytetracyclin Glucose Yeast Extract Agar (OGYE) was also reported.

For sample C, the proportion of false negative results for moulds was higher for methods not based on RBCC. This could be attributed to the substrate itself, or to the magnification used during examination. *A. strictum* develops small and pale colonies and magnification is usually needed during examination of the plates.

Table 7. Results from analysis of moulds.

Method	Sample A							Sample B							Sample C						
	N	*n*	m_{PT}	*CV*	*F*	<	>	*N*	*n*	m_{PT}	*CV*	*F*	<	>	*N*	*n*	m_{PT}	*CV*	*F*	<	>
All results	**33**	**33**	**-**	**-**	**0**	**-**	**-**	**33**	**32**	**122**	**19**	**0**	**1**	**0**	**33**	**20**	**21**	**28**	**13**	**0**	**0**
SS 028192 (RBCC)	11	11	-	-	0	-	-	11	10	133	20	0	1	0	11	8	26	33	3	0	0
NS (SS) 028192 (RBCC)	4	4	-	-	0	-	-	4	4	-	-	0	0	0	4	4	-	-	0	0	0
Other	3	3	-	-	0	-	-	3	3	-	-	0	0	0	3	1	-	-	2	0	0
SFS 5507 (DRBC)	3	3	-	-	0	-	-	3	3	-	-	0	0	0	3	1	-	-	2	0	0
SFS 5507 (RBCC)	3	3	-	-	0	-	-	3	3	-	-	0	0	0	3	2	-	-	1	0	0
RBCC	3	3	-	-	0	-	-	3	3	-	-	0	0	0	3	3	-	-	0	0	0
DRBC	2	2	-	-	0	-	-	2	2	-	-	0	0	0	2	1	-	-	1	0	0
NMKL 98:2005 modified (DRBC)	2	2	-	-	0	-	-	2	2	-	-	0	0	0	2	0	-	-	2	0	0
SS 028192 modified (DRBC)	1	1	-	-	0	-	-	1	1	-	-	0	0	0	1	0	-	-	1	0	0
OGYE	1	1	-	-	0	-	-	1	1	-	-	0	0	0	1	0	-	-	1	0	0

For "All results", m_{PT} = assigned value, robust mean value in cfu 100 ml^{-1}, re-transformed to the cfu scale.

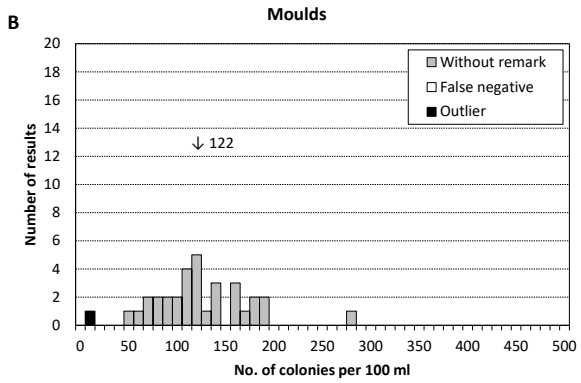
For individual methods, m_{PT} = median value in cfu 100 ml^{-1}

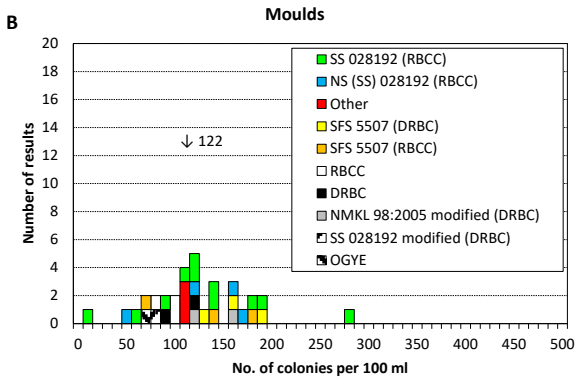
Table 8. Results from analysis of yeasts.

Method	Sample A							Sample B							Sample C						
	N	*n*	m_{PT}	*CV*	*F*	<	>	*N*	*n*	m_{PT}	*CV*	*F*	<	>	*N*	*n*	m_{PT}	*CV*	*F*	<	>
All results	**33**	**32**	**-**	**-**	**1**	**-**	**-**	**33**	**31**	**174**	**11**	**0**	**2**	**0**	**33**	**32**	**31**	**14**	**0**	**0**	**1**
SS 028192 (RBCC)	11	11	-	-	0	-	-	11	10	176	9	0	1	0	11	11	29	12	0	0	0
NS (SS) 028192 (RBCC)	4	4	-	-	0	-	-	4	3	-	-	0	1	0	4	4	-	-	0	0	0
Other	3	3	-	-	0	-	-	3	3	-	-	0	0	0	3	3	-	-	0	0	0
SFS 5507 (DRBC)	3	3	-	-	0	-	-	3	3	-	-	0	0	0	3	3	-	-	0	0	0
SFS 5507 (RBCC)	3	3	-	-	0	-	-	3	3	-	-	0	0	0	3	3	-	-	0	0	0
RBCC	3	2	-	-	1	-	-	3	3	-	-	0	0	0	3	3	-	-	0	0	0
DRBC	2	2	-	-	0	-	-	2	2	-	-	0	0	0	2	1	-	-	0	0	1
NMKL 98:2005 modified (DRBC)	2	2	-	-	0	-	-	2	2	-	-	0	0	0	2	2	-	-	0	0	0
SS 028192 modified (DRBC)	1	1	-	-	0	-	-	1	1	-	-	0	0	0	1	1	-	-	0	0	0
OGYE	1	1	-	-	0	-	-	1	1	-	-	0	0	0	1	1	-	-	0	0	0

For "All results", m_{PT} = assigned value, robust mean value in cfu 100 ml^{-1}, re-transformed to the cfu scale

For individual methods, m_{PT} = median value in cfu 100 ml^{-1}





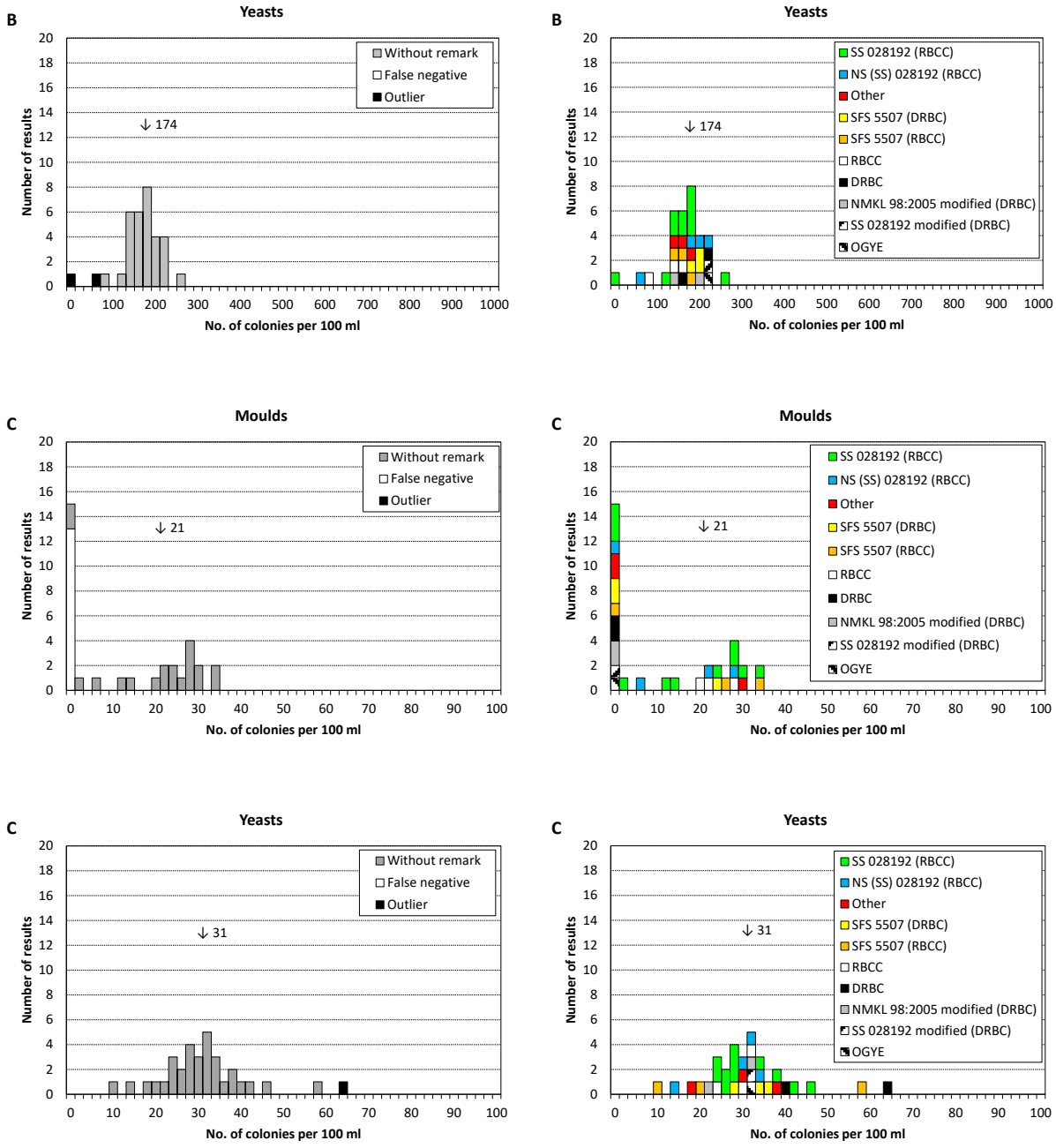


Figure 5. Results from analysis of moulds and yeasts.

Actinomycetes

Sample A

One actinomycete within the group *Streptomyces* sp. was target organism.

In total, 27 results were evaluated. One false negative result and one low outlier were identified.

Sample B

No target organism was present in the sample.

In total, 26 results were evaluated. One false positive result was reported.

Sample C

No target organism was present in the sample.

In total, 26 results were evaluated. Two false positive results were reported.

General remarks

Actinomycetes can impart odour or taste to drinking water. In Sweden, actinomycetes is included as a parameter for monitoring of drinking water according to a Swedish Food Agency regulation (LIVSFS 2022:12). The parameter is analysed according to the Swedish standard for actinomycetes in water, SS 028212 (1994), using Actinomycete Isolation Agar (ACTA) including cycloheximide. Five participants used Plate Count Agar (PCA), with natamycin as the selective substance.

Table 9. Results from analysis of *Actinomycetes*

Method	Sample A							Sample B							Sample C						
	N	*n*	m_{PT}	*CV*	*F*	<	>	*N*	*n*	m_{PT}	*CV*	*F*	<	>	*N*	*n*	m_{PT}	*CV*	*F*	<	>
All results	**27**	**25**	**72**	**9**	**1**	**1**	**0**	**26**	**25**	**-**	**-**	**1**	**-**	**-**	**26**	**24**	**-**	**-**	**2**	**-**	**-**
SS 028212 (ACTA)	21	20	71	9	0	1	0	21	20	-	-	1	-	-	21	19	-	-	2	-	-
THG (PCA) agar, containing Natamycin	5	4	-	-	1	0	0	4	4	-	-	0	-	-	4	4	-	-	0	-	-
Other	1	1	-	-	0	0	0	1	1	-	-	0	-	-	1	1	-	-	0	-	-

For "All results", m_{PT} = assigned value, robust mean value in cfu 100 ml^{-1}, re-transformed to the cfu scale

For individual methods, m_{PT} = median value in cfu 100 ml^{-1}

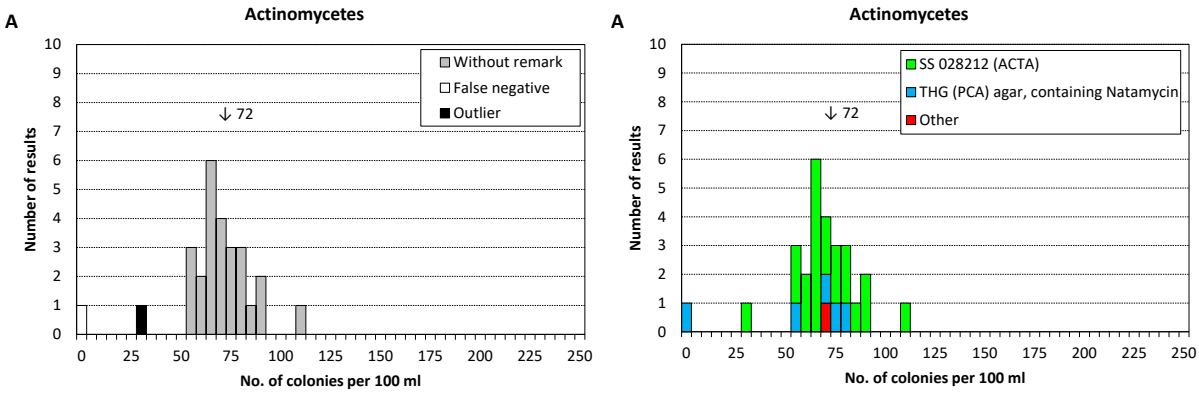


Figure 6. Results from analysis of actinomycetes.

Culturable microorganisms, 72 hours incubation at 22 °C

Sample A

The strain of *P. brenneri* was the main target organism.

In total, 72 results were evaluated. One low outlier was identified

Sample B

The strains of *E. coli and C. freundii* were main target organisms.

In total, 72 results were evaluated. Two high outliers were identified.

Sample C

The strains of *S. warneri* and *K. pneumoniae* were the main target organisms.

In total, 72 results were evaluated. The dispersion (CV) was large and no outliers were identified.

General remarks

Most participants followed (EN) ISO 6222:1999, which describes a pour-plate method with Yeast extract Agar (YeA). With this standard, culturable microorganisms are defined as all aerobic bacteria, yeasts and moulds that form colonies in the medium. ISO 6222:1999 was last reviewed by ISO in 2021 and remains current.

Some laboratories have modified the standard and use PCA instead of YeA. No differences were observed between these media in samples A and B. However, in sample C, PCA exhibited a lower median than YeA.

Table 10. Results from analysis of culturable microorganisms, 72 hours incubation at 22±2 °C.

Method	Sample A							Sample B							Sample C						
	N	*n*	m_{PT}	*CV*	*F*	<	>	*N*	*n*	m_{PT}	*CV*	*F*	<	>	*N*	*n*	m_{PT}	*CV*	*F*	<	>
All results	**72**	**71**	**53**	**21**	**0**	**1**	**0**	**72**	**70**	**7**	**22**	**0**	**0**	**2**	**72**	**72**	**58**	**35**	**0**	**0**	**0**
ISO 6222 (YeA, pour plate)	53	53	60	19	0	0	0	53	53	6	21	0	0	0	53	53	77	28	0	0	0
ISO 6222 modified (PCA, pour plate)	9	8	52	15	0	1	0	9	7	7	17	0	0	2	9	9	47	36	0	0	0
Other	3	3	-	-	0	0	0	3	3	-	-	0	0	0	3	3	-	-	0	0	0
3M™ Petrifilm™ Aerobic Count Plate	3	3	-	-	0	0	0	3	3	-	-	0	0	0	3	3	-	-	0	0	0
Plate Count Agar (PCA, pour plate)	2	2	-	-	0	0	0	2	2	-	-	0	0	0	2	2	-	-	0	0	0
Yeast extract Agar (YeA, pour plate)	2	2	-	-	0	0	0	2	2	-	-	0	0	0	2	2	-	-	0	0	0

For “All results”, m_{PT} = assigned value, robust mean value in cfu ml^{-1}, re-transformed to the cfu scale

For individual methods, m_{PT} = median value in cfu ml^{-1}

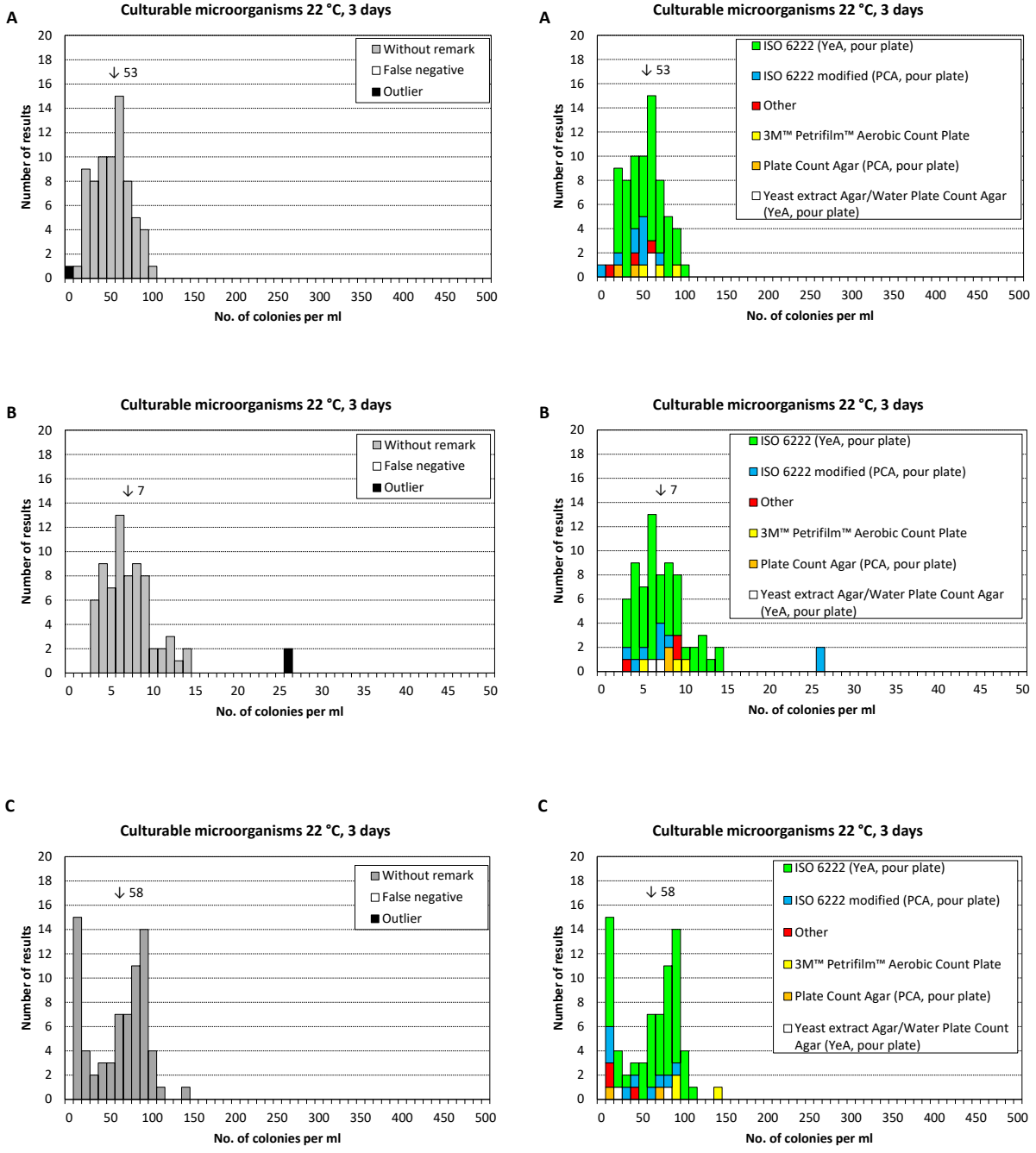


Figure 7. Results from analysis of culturable microorganisms, 72 hours incubation at 22 °C

Slow-growing bacteria 22 °C, 7 days

Sample A

No specific slow-growing bacteria were included in the sample but the strain of *P. brenneri* will form colonies on Yeast extract Agar (YeA) and Reasoner's 2 Agar (R2A) at 22 °C after 7 days.

In total, 42 results were evaluated. One high and two low outliers were identified.

Sample B

The strain of *Sphingomonas* sp. was the main target organism.

In total, 42 results were evaluated. Two low outliers were identified.

Sample C

The strain of *Sphingomonas* sp. was the main target organism.

In total, 42 results were evaluated. No outliers were identified.

General remarks

The parameter slow growing bacteria indicates microbiological growth in water treatment plants and distribution systems. In Sweden, slow-growing bacteria is included as a parameter for drinking water monitoring according to a Swedish Food Agency regulation (LIVSFS 2022:12). Before 2003 a Swedish standard was available, but the parameter is currently analysed according to a modified version of (EN) ISO 6222:1999. The modifications are a prolonged incubation time (seven days) and that only bacteria should be included in the result. A Draft International Standard (DIS) is currently under development ("Water quality — Enumeration of culturable microorganisms — Colony count by spread plate inoculation on R2A medium"). It is based on the low nutrient media R2A and a spread-plate technique.

Samples B and C included a slow-growing *Sphingomonas* sp. bacterium. It often forms small colonies, and magnification is usually needed during examination of the plates.

Most participants (81%) used YeA and six participants used R2A.

Table 11. Results from analysis of slow-growing bacteria 22 °C, 7 days.

Method	Sample A							Sample B							Sample C						
	N	*n*	m_{PT}	*CV*	*F*	<	>	*N*	*n*	m_{PT}	*CV*	*F*	<	>	*N*	*n*	m_{PT}	*CV*	*F*	<	>
All results	**42**	**39**	**64**	**19**	**0**	**2**	**1**	**42**	**40**	**110**	**18**	**0**	**2**	**0**	**42**	**42**	**175**	**17**	**0**	**0**	**0**
ISO 6222 modified (YeA, pour plate)	31	31	65	15	0	0	0	31	30	119	17	0	1	0	31	31	175	14	0	0	0
Reasoner's 2A (R2A) agar, spread plate	5	3	-	-	0	1	1	5	5	115	9	0	0	0	5	5	209	24	0	0	0
Yeast extract Agar (YeA), pour plate	3	3	-	-	0	0	0	3	3	-	-	0	0	0	3	3	-	-	0	0	0
Other	2	1	-	-	0	1	0	2	1	-	-	0	1	0	2	2	-	-	0	0	0
Reasoner's 2A (R2A) agar, pour plate	1	1	-	-	0	0	0	1	1	-	-	0	0	0	1	1	-	-	0	0	0

For "All results", m_{PT} = assigned value, robust mean value in cfu ml^{-1}, re-transformed to the cfu scale

For individual methods, m_{PT} = median value in cfu ml^{-1}

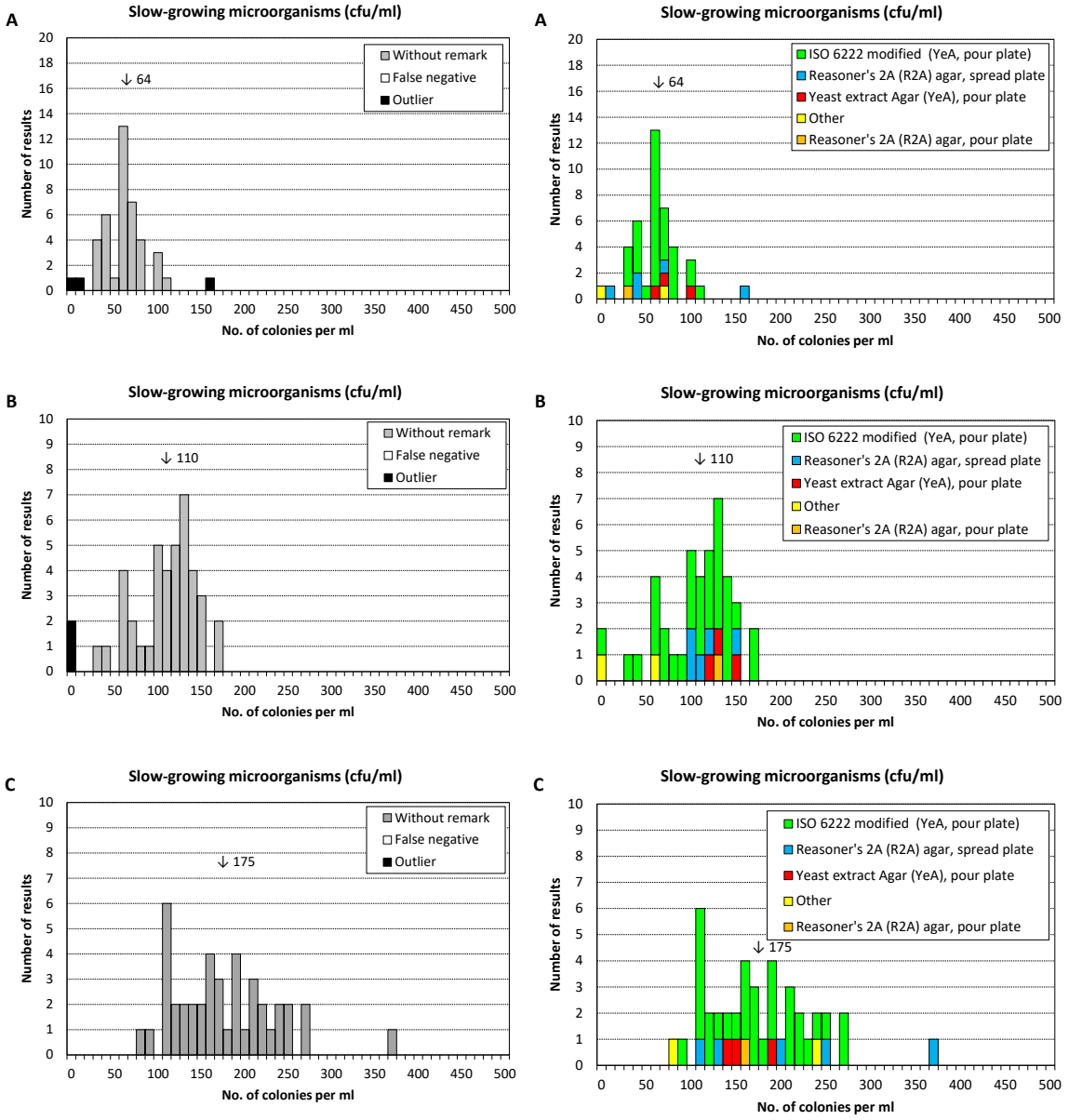


Figure 8. Results from analysis of slow-growing bacteria

Outcome of the results of individual participants - assessment

Reporting and evaluation of results

The results of all participants are listed in Annex 1, together with the minimum and maximum accepted values for each analytical parameter. Outliers and false results are highlighted in yellow and red, respectively, with bold font.

Participants are not grouped or ranked based on their results. The performance of an individual participant can be broadly assessed by the numbers of outliers and false results, and by the *z*-scores.

Information on the results processing and recommendations for follow-up work are given in the Scheme Protocol [2].

Samples for follow-up analyses can be ordered at: **https://laboratory.livsmedelsverket.se**

Box plots

Box plots are based on the *z*-scores listed in Appendix 2 and give a comprehensive view of the performance of each participant. The range of *z*-scores is indicated by the size of the box and, for most participants, by lines and/or circles above and beneath the box. A small range of values, centred around zero, indicates that the results of the individual participant are in general close to m_{PT} for the different analyses.

The different parts of a box plot are shown in figure 9.

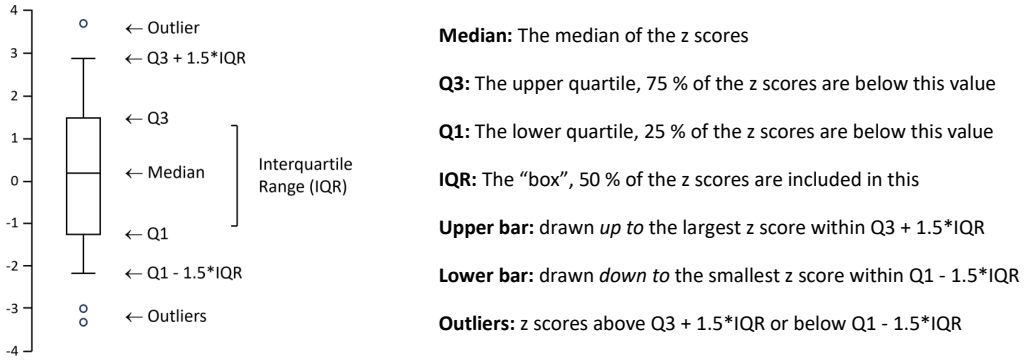
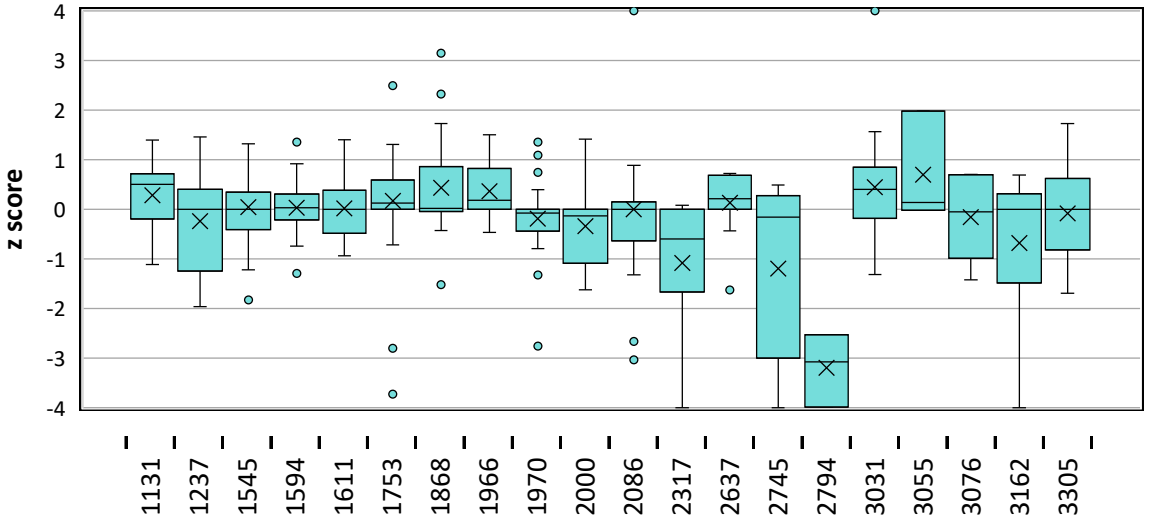


Figure 9. Schematic explanation of a box plot.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4
3
2
1
0
-1
-2
-3
-4
1131
1237
1545
1594
1611
1753
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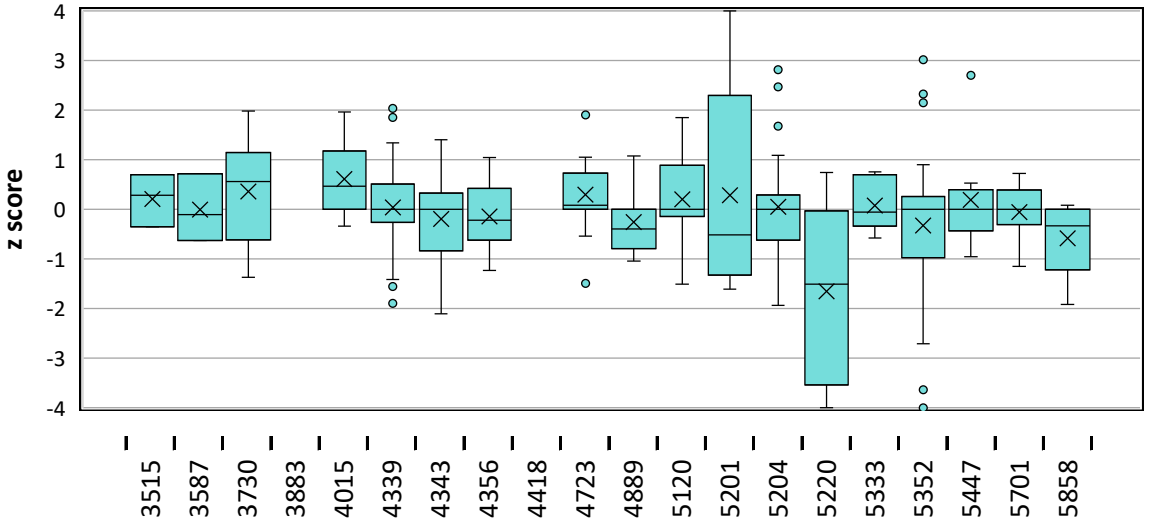
2745
2794
3031
3055
3076
3162
3305


z score
4
3
2
1
0
-1
-2
-3
-4
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3587
3730
3883
4015
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4343
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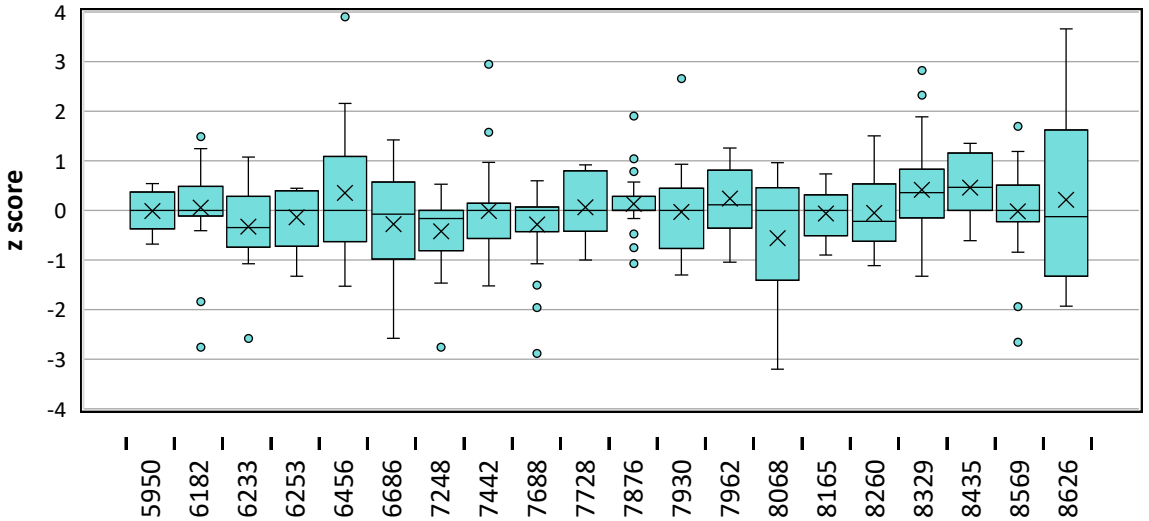
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7728
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8165
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8329
8435
8569
8626

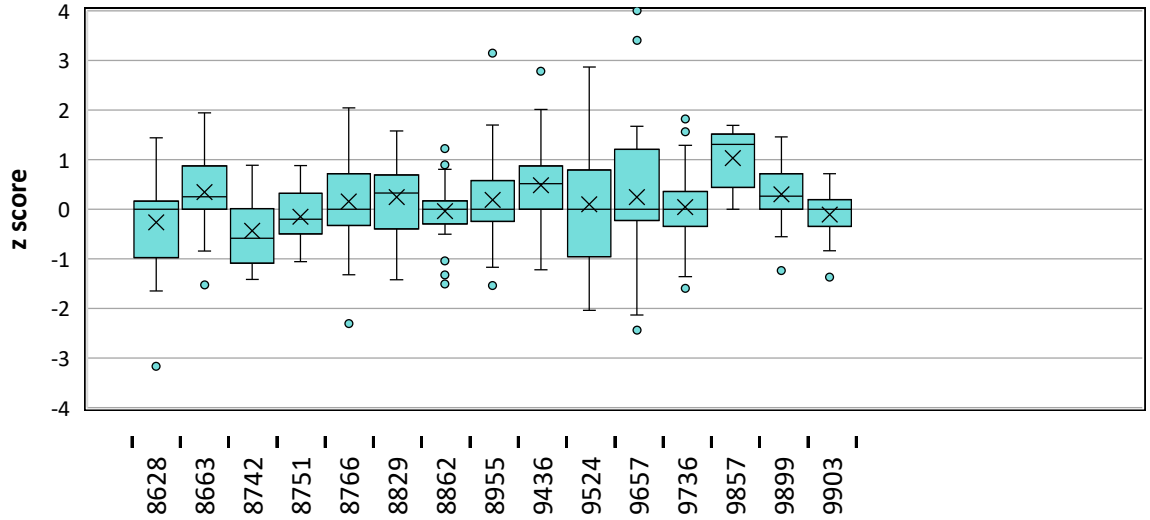

Figure 10. Box plots of each participant's z-scores.

Test material and quality control

Test material

Each participant received three samples with freeze-dried microorganisms, designated A–C. The test material was freeze-dried in 0.5 ml portions in glass vials, as described by Peterz and Steneryd [3]. Before analysing the samples, the contents of each vial should be reconstituted in 800 ml of sterile diluent. The microorganism content of the samples and the concentrations determined at the Swedish Food Agency are listed in the table below.

Table 12. Microorganisms and approximate concentrations in the samples.

Sample	Microorganism	Strain			
		SLV no.[1]	Origin	Reference[2]	cfu / 100 ml[3]
A	*Escherichia coli*	084	Drinking water	-	17
	Klebsiella oxytoca	553	Water	-	39
	Clostridium perfringens	442	-	CCUG 43593	3820
	Streptomyces species	548	Resevoir	DSMZ, verified	83
	Pseudomonas brenneri	535	Drinking water	CCUG 45106	98*
B	*Escherichia coli*	082	Drinking water	CCUG 45097	267
	Citrobacter freundii	424	Well water	-	215
	Clostridium bifermentans	009	Fish	CCUG 43592	104
	Phialophora fastigiata	504	Water	CBS, verified	131
	Rhodotorula minuta	506	Drinking water	CBS 970818	190
	Sphingomonas sp.	547	Water	-	121*
C	*Klebsiella pneumoniae*	186	Vegetarian kebab	CCUG 45102	1118
	Acremonium strictum	502	Water	CBS, verified	18
	Hanseniaspora uvarum	555	-	CF SQE 77[#]	29
	Sphingomonas sp.	547	Water	-	176*
	Staphylococcus warneri	189	Minced meat	CCUG 45143	45*

[1] Internal strain identification no. at the Swedish Food Agency

[2] Culture collection: CBS: Centraalbureau voor Schimmelcultures (Westerdijk Institute), CCUG: Culture Collection University of Gothenburg

[3] cfu = colony forming units

* indicates cfu per ml

[#] Designation in an older culture collection

Quality control of the samples

Quality control and evaluation of sample homogeneity is performed on 10 randomly chosen vials in conjunction with manufacture, or on 5 vials if the batch is previously approved for homogeneity. Homogeneity of a test material is approved if, for each analysis, the p value of a one-way analysis of variance (ANOVA) fulfils the criterion $p \geq 0.05$. If the ANOVA yields $p < 0.05$, the PT test item batch is still considered homogenous, if $s_{bb} < s_R/3$, where:

s_{bb}: the between-vial standard deviation from the ANOVA

s_R: the expected laboratory variation, generally assumed to be 1.25 for the Drinking water scheme.

See the Scheme protocol [2] for more information regarding the evaluation of homogeneity.

Table 13. Concentration mean (m), between-vial variation (sbb) and p values from the quality control of the samples; m is expressed in square root cfu (colony forming units) per 100 ml of sample for MF methods and per 1 ml for pour plate methods

Analysis and method	A[1]			B			C[1]		
	m	s_{bb}	*p*	*m*	s_{bb}	*p*	*m*	s_{bb}	*p*
Coliform bacteria SS-EN ISO 9308-1:2014	56	0.00	0.62	49[c]	0.25	0.25	11[b]	0.26	0.14
Suspected thermotolerant coliform bact. SS 028167	15	0.40	0.09	24[c]	0.00	0.69	12[b]	0.00	0.88
Escherichia coli SS-EN ISO 9308-1:2014	17	0.00	0.65	27[c]	0.00	0.64	-	-	-
Presumptive Clostridium perfringens EN ISO 14189:2016	38[b]	0.00	0.58	10[c]	0.27	0.28	-	-	-
Moulds SS 028192	-	-	-	13[c]	0.30	0.13	18	0.00	0.82
Yeasts SS 02819	-	-	-	19[c]	0.00	0.72	29	0.00	0.63
Actinomycetes SS 028212	41[d]	0.37	0.21	-	-	-	-	-	-
Culturable microorganisms, 72 h 22 °C SS-EN ISO 6222:1999	94	0.24	0.18	7	0.00	0.99	52	0.31	0.32
Slow-growing bacteria, 7d 22 °C SS-EN ISO 6222:1999 modified	95	0.28	0.13	128	0.00	0.51	22[a]	0.38	0.05

– No target organism or no value

[1] n = 5 vials analysed in duplicate

[a] cfu per 0.1 ml of sample

[b] cfu per 1 ml of sample

[c] cfu per 10 ml of sample

[d] cfu per 50 ml of sample

References

1. ISO 13528:2022 Statistical methods for use in proficiency testing by interlaboratory comparison.
2. Ilbäck J and Blom L. 2024. Protocol – Microbiological Proficiency Testing, Swedish Food Agency.
3. Peterz, M., Steneryd. A.C. 1993. Freeze-dried mixed cultures as reference samples in quantitative and qualitative microbiological examinations of food. *Journal of Applied Bacteriology*. 74:143–148.

Appendix 1. Results of the participating laboratories

Lab no.	Coliform bacteria			Susp. thermotol. coliform bact.			E. coli			Presumptive C. perfringens			Clostridium perfringens			Moulds			Yeasts			Actinomycetes			Culturable microorganisms 22 °C, 3 days			Slow-growing microorganisms			Lab no.
	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	
1131-1	70	548	1376	-	-	-	12	326	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	64	6	22	64	171	222	1131-1
1131-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1131-2
1131-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1131-3
1237-1	42	280	1300	14	320	1200	12	140	0	-	-	-	5100	150	0	-	-	-	-	-	-	-	-	-	21	8	76	-	-	-	1237-1
1237-2	53	590	1300	-	-	-	16	340	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1237-2
1237-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1237-3
1545-1	69	470	1240	19	235	1240	19	235	0	5000	56	0	5000	0	0	0	80	0	0	225	33	71	0	0	37	9	38	38	121	196	1545-1
1545-2	70	498	1480	13	148	1210	14	261	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1545-2
1545-3	-	-	-	-	-	-	13	148	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1545-3
1594-1	58	540	1300	-	-	-	15	310	0	-	-	-	-	-	-	0	75	0	0	-	33	73	-	0	28	6	86	-	-	-	1594-1
1594-2	51	505	1300	-	-	-	21	220	0	-	-	-	-	-	-	-	-	-	-	230	-	-	-	-	-	-	-	-	-	-	1594-2
1594-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1594-3
1611-1	59	650	1300	-	-	-	15	390	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5	87	46	77	129	1611-1
1611-2	53	520	1300	-	-	-	15	310	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	44	-	-	-	-	-	1611-2
1611-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1611-3
1753-1	85	637	1892	-	-	-	19	367	0	1900	94	0	-	-	-	0	127	28	0	182	25	33	0	0	62	6	110	64	133	212	1753-1
1753-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1753-2
1753-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1753-3
1868-1	65	445	1314	-	-	-	17	286	0	4900	67	0	-	-	-	0	123	0	0	164	64	94	0	0	98	8	13	101	136	199	1868-1
1868-2	82	427	1214	-	-	-	26	268	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1868-2
1868-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1868-3
1966-1	56	423	1350	-	-	-	21	270	0	4410	144	0	-	-	-	0	171	28	0	207	30	75	0	0	83	12	87	87	116	174	1966-1
1966-2	53	568	1376	-	-	-	16	376	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1966-2
1966-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1966-3
1970-1	57	440	1200	20	260	1200	20	260	0	3600	67	0	3600	67	0	0	90	1	0	230	41	-	-	-	49	8	17	-	-	-	1970-1
1970-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1970-2
1970-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1970-3
2000-1	57	350	880	-	-	-	24	190	0	-	-	-	3700	0	0	-	-	-	-	-	-	-	-	-	36	6	66	-	-	-	2000-1
2000-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2000-2
2000-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2000-3
2086-1	51	218	1136	44	864	-	-	219	0	4100	500	0	3800	500	0	0	110	0	0	149	39	-	-	-	57	26	68	66	76	118	2086-1
2086-2	60	190	960	40	820	-	-	290	0	-	-	0	-	-	0	0	110	0	0	190	30	-	-	-	50	26	89	67	65	115	2086-2
2086-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2086-3
2317-1	52	291	1082	-	-	-	16	191	0	9	0	0	9	0	0	-	-	-	-	-	-	-	-	-	26	7	11	-	-	-	2317-1
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2317-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2317-3
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2637-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2637-3
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2745-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2745-3
2794-1	35	127	615	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2794-1
2794-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2794-2
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3031-2	50	579	1414	-	-	-	13	260	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3031-2
3031-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3031-3
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3055-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3055-3
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3076-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3076-3
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3162-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3162-3
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3305-2	57	310	1600	-	-	-	26	200	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3305-2
3305-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3305-3

Appendix 1. Results of the participating laboratories

Lab no.	Coliform bacteria			Susp. thermotol. coliform bact.			E. coli			Presumptive C. perfringens			Clostridium perfringens			Moulds			Yeasts			Actinomycetes			Culturable microorganisms 22 °C, 3 days			Slow-growing microorganisms			Lab no.
	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	
3515-1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	60	9	45	-	-	-	3515-1
3515-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3515-2
3515-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3515-3
3587-1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	51	5	91	-	-	-	3587-1
3587-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3587-2
3587-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3587-3
3730-1	54	375	1500	11	220	1400	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	67	14	16	68	144	254	3730-1
3730-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3730-2
3730-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3730-3
3883-1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3883-1
3883-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3883-2
3883-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3883-3
4015-1	68	727	1553	-	-	-	20	461	**4**	5300	85	**1**	-	-	-	0	144	**0**	0	171	28	86	0	0	55	12	59	61	155	228	4015-1
4015-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4015-2
4015-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4015-3
4339-1	46	450	1200	10	110	760	28	450	0	-	-	-	4400	0	0	0	190	**0**	0	180	36	-	-	-	26	6	98	32	130	160	4339-1
4339-2	40	490	1200	-	-	-	12	370	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4339-2
4339-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4339-3
4343-1	62	411	1553	-	-	-	17	210	0	3500	6	0	-	-	-	0	93	13	0	141	27	91	0	0	75	4	23	79	125	128	4343-1
4343-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4343-2
4343-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4343-3
4356-1	48	450	1200	5	98	1100	13	300	**300**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	29	6	84	-	-	-	4356-1
4356-2	56	440	1400	-	-	-	13	370	**370**	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4356-2
4356-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4356-3
4418-1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4418-1
4418-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4418-2
4418-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4418-3
4723-1	57	579	1730	-	-	-	20	299	0	5900	127	0	-	-	-	0	64	15	0	182	29	73	0	**10**	80	7	71	82	129	167	4723-1
4723-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4723-2
4723-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4723-3
4889-1	54	390	1500	-	-	-	12	200	0	-	-	-	3700	0	0	-	-	-	-	-	-	-	-	-	77	4	35	-	-	-	4889-1
4889-2	48	410	1400	-	-	-	16	240	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4889-2
4889-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4889-3
5120-1	59	520	1200	19	-	1100	24	290	0	-	-	-	5200	0	0	0	180	35	0	160	20	78	0	0	29	3	100	-	-	-	5120-1
5120-2	51	560	1500	-	-	-	15	450	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5120-2
5120-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5120-3
5201-1	-	-	-	-	-	-	**51**	237	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	23	4	84.83	-	-	-	5201-1
5201-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5201-2
5201-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5201-3
5204-1	54	390	1400	-	-	-	11	234	0	4100	93	0	-	-	-	0	118	31	0	182	26	59	0	0	59	4	77	60	48	135	5204-1
5204-2	50	687	1986	-	-	-	22	517	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5204-2
5204-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5204-3
5220-1	**21**	**144**	1000	-	-	-	**2**	**45**	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**1**	3	78	**3**	**6**	80	5220-1
5220-2	47	461	1414	-	-	-	10	291	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	12	3	13	**12**	128	116	5220-2
5220-3	54	-	-	-	-	-	8	161	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5220-3
5333-1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	41	7	89	-	-	-	5333-1
5333-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	49	6	93	-	-	-	5333-2
5333-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5333-3
5352-1	50	530	1100	30	310	0	**35**	300	0	2900	18	0	-	-	-	0	**13**	28	0	**17**	29	84	0	0	33	5	98	34	86	111	5352-1
5352-2	80	410	1290	11	100	0	30	310	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	44	115	130	5352-2
5352-3	-	-	-	-	-	-	11	100	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5352-3
5447-1	-	-	-	-	-	-	-	-	-	3500	120	0	3500	0	0	-	-	-	-	-	-	-	-	-	-	-	-	70	100	370	5447-1
5447-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5447-2
5447-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5447-3
5701-1	54	440	1240	-	-	-	18	340	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	63	6	21	-	-	-	5701-1
5701-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5701-2
5701-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5701-3
5858-1	49	280	1030	-	-	-	14	169	0	-	-	-	3930	0	0	-	-	-	-	-	-	-	-	-	54	7	17	-	-	-	5858-1
5858-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5858-2
5858-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5858-3

Appendix 1. Results of the participating laboratories

Lab no.	Coliform bacteria			Susp. thermotol. coliform bact.			E. coli			Presumptive C. perfringens			Clostridium perfringens			Moulds			Yeasts			Actinomycetes			Culturable microorganisms 22 °C, 3 days			Slow-growing microorganisms			Lab no.
	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	
5950-1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	64	0	0	-	-	-	77	100	194	5950-1
5950-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5950-2
5950-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5950-3
6182-1	58	536	1326	-	-	-	14	376	0	3700	11	0	-	-	-	0	162	1	0	236	33	69	0	0	62	11	93	63	112	167	6182-1
6182-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	6182-2
6182-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	6182-3
6233-1	50	450	700	-	-	-	12	250	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	60	9	90	-	-	-	6233-1
6233-2	68	400	1090	-	-	-	11	238	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	6233-2
6233-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	6233-3
6253-1	61	380	1100	-	-	-	18	270	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	64	8	17	-	-	-	6253-1
6253-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	6253-2
6253-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	6253-3
6456-1	46	1030	1318	-	-	-	22	372	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	40	5	18	-	-	-	6456-1
6456-2	79	755	900	-	-	-	16	270	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	6456-2
6456-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	6456-3
6686-1	62.4	478	1445	-	-	-	13.7	406	0	4800	130	0	-	-	-	-	-	-	-	-	-	-	-	-	50	4	11	-	-	-	6686-1
6686-2	48	350	700	-	-	-	12	240	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	6686-2
6686-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	6686-3
7248-1	54	480	964	14	340	846	16	240	0	3700	120	0	-	-	-	0	86	23	0	85	31	55	0	0	38	8	52	40	69	115	7248-1
7248-2	46	461	1120	-	-	-	14	219	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7248-2
7248-3	-	-	-	-	-	-	17	238	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7248-3
7442-1	48	495	1057	-	-	-	25	276	0	4600	56	0	-	-	-	-	-	-	-	-	-	114	0	0	64	3	13	65	151	143	7442-1
7442-2	55	464	1212	-	-	-	12	280	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7442-2
7442-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7442-3
7688-1	63	470	1100	-	-	-	19	260	0	3900	21	0	3900	0	0	0	140	27	0	180	11	0	0	0	43	3	77	-	-	-	7688-1
7688-2	57	276	1300	-	-	-	11	248	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7688-2
7688-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7688-3
7728-1	66	410	1200	-	-	-	21	280	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	33	6	91	-	-	-	7728-1
7728-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7728-2
7728-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7728-3
7876-1	57	480	1200	15	450	1200	16	280	0	5900	150	0	-	-	-	0	140	35	0	170	38	74	0	0	60	7	84	47	104	185	7876-1
7876-2	-	-	-	-	-	-	11	240	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7876-2
7876-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7876-3
7930-1	50	470	970	-	-	-	12	270	0	4600	150	0	4600	0	0	0	78	0	0	140	58	-	-	-	29	9	91	-	-	-	7930-1
7930-2	45	410	1300	-	-	-	18	290	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7930-2
7930-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7930-3
7962-1	55	570	1150	15	168	990	13	390	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	43	4	96	-	-	-	7962-1
7962-2	66	488	1414	-	-	-	22	326	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7962-2
7962-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7962-3
8068-1	30	267	969	9	200	1300	5	93	0	-	-	-	4400	0	0	0	160	24	0	209	35	-	-	-	39	4	104	-	-	-	8068-1
8068-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8068-2
8068-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8068-3
8165-1	52	400	1127	-	-	-	15	209	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8165-1
8165-2	58	515	1289	-	-	-	19	341	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8165-2
8165-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8165-3
8260-1	51	440	1045	-	-	-	13	245	0	4550	73	0	-	-	-	-	-	-	-	-	-	-	-	-	73	12	22	76	132	147	8260-1
8260-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8260-2
8260-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8260-3
8329-1	77	580	1987	-	-	-	30	308	0	4400	135	0	-	-	-	0	109	28	0	143	24	-	-	-	78	5	17	79	143	193	8329-1
8329-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8329-2
8329-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8329-3
8435-1	71	620	1100	-	-	-	22	230	0	-	-	-	4400	0	0	-	-	-	-	-	-	-	-	-	77	11	79	-	-	-	8435-1
8435-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8435-2
8435-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8435-3
8569-1	56	476	1210	-	-	-	16	272	0	1990	9	0	-	-	-	-	-	-	-	-	-	-	-	-	84	7	105	110	138	236	8569-1
8569-2	53	494	1317	-	-	-	12	250	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8569-2
8569-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8569-3
8626-1	42	480	820	17	320	830	40	480	820	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	46	7	47	-	-	-	8626-1
8626-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8626-2
8626-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8626-3

Appendix 1. Results of the participating laboratories

Lab no.	Coliform bacteria			Susp. thermotol. coliform bact.			E. coli			Presumptive C. perfringens			Clostridium perfringens			Moulds			Yeasts			Actinomycetes			Culturable microorganisms 22 °C, 3 days			Slow-growing microorganisms			Lab no.
	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	
8628-1	68	410	-	10	250	1300	21	190	0	-	-	-	3100	0	**800**	0	120	**0**	0	140	33	-	-	-	54	4	64	65	133	270	8628-1
8628-2	-	-	**600**	-	-	-	10	250	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8628-2
8628-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8628-3
8663-1	66	460	900	14	470	1200	17	460	0	4300	120	0	**0**	0	0	-	-	-	-	-	-	-	-	-	90	8	96	-	-	-	8663-1
8663-2	50	610	1700	-	-	-	12	310	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8663-2
8663-3	68	580	1400	-	-	-	16	270	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8663-3
8742-1	49	470	1100	-	-	-	10	280	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	26	5	100	-	-	-	8742-1
8742-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8742-2
8742-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8742-3
8751-1	53	453	1370	-	-	-	15	238	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	43	8	62	41	100	209	8751-1
8751-2	66	384	-	-	-	-	15	222	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8751-2
8751-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8751-3
8766-1	63	739	1147	28	427	1100	10	418	0	5000	145	0	-	-	-	0	164	**0**	0	200	22	68	0	0	64	6	68	53	39	154	8766-1
8766-2	69	564	1200	-	-	-	17	255	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8766-2
8766-3	-	-	-	-	-	-	28	245	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8766-3
8829-1	52	550	1100	-	-	-	17	300	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	70	9	140	73	62	240	8829-1
8829-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8829-2
8829-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8829-3
8862-1	63	419	1000	-	-	-	14	255	0	3900	102	0	3900	0	0	0	127	23	0	181	35	84	0	0	85	3	17	84	148	176	8862-1
8862-2	55	449	1126	-	-	-	16	247	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8862-2
8862-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8862-3
8955-1	60	690	1300	18	220	1200	16	280	0	3700	53	0	3700	0	0	0	110	31	0	160	19	80	0	-	66	6	56	**160**	150	250	8955-1
8955-2	72	350	1400	-	-	-	15	280	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8955-2
8955-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8955-3
9436-1	59	564	1600	14	355	1000	16	345	0	3000	130	0	-	-	-	0	280	**0**	0	260	24	63	-	0	76	13	45	69	138	217	9436-1
9436-2	68	536	1414	-	-	-	23	351	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	9436-2
9436-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	-	-	-	-	-	-	-	9436-3
9524-1	44	590	800	-	-	-	10	240	0	3500	47	**1700**	3500	0	**1700**	-	-	-	-	-	-	-	-	-	59	8	95	-	-	-	9524-1
9524-2	79	862	1008	-	-	-	19	529	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	9524-2
9524-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	9524-3
9657-1	61	597	1539	12	182	600	17	385	0	3000	**0**	0	-	-	-	0	191	2	0	191	47	65	**67**	**23**	68	6	60	63	102	175	9657-1
9657-2	72	627	800	-	-	-	**64**	**627**	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	9657-2
9657-3	-	-	-	-	-	-	7	146	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	9657-3
9736-1	59	537	1307	-	-	-	16	292	0	2892	108	0	-	-	-	0	182	**0**	0	135	43	68	0	0	103	6	18	106	91	94	9736-1
9736-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	9736-2
9736-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	9736-3
9857-1	73	649	1414	-	-	-	16	387	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	99	10	73	105	174	271	9857-1
9857-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	9857-2
9857-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	9857-3
9899-1	65	505	1298	-	-	-	15	315	0	3750	130	0	-	-	-	0	124	25	0	154	34	68	0	0	81	8	19	81	143	249	9899-1
9899-2	58	605	1545	-	-	-	19	410	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	9899-2
9899-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	9899-3
9903-1	53	400	1382	-	-	-	17	177	0	3000	43	0	-	-	-	0	108	21	**2**	175	33	68	0	0	61	9	91	61	118	168	9903-1
9903-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	9903-2
9903-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	9903-3
N	102	101	100	25	24	23	106	108	106	37	36	36	22	23	24	33	33	33	33	33	33	27	26	26	72	72	72	42	42	42	**N**
n	99	96	97	25	24	23	101	106	100	36	32	33	20	19	21	33	32	20	32	31	32	25	25	24	71	70	72	39	40	42	**n**
m_{PT}	**7.55**	**21.79**	**35.12**	-	-	-	**4.00**	**16.66**	-	**63.37**	**9.24**	-	**64.02**	-	-	-	**11.05**	**4.57**	-	**13.21**	**5.55**	**8.50**	-	-	**7.31**	**2.60**	**7.64**	**7.97**	**10.50**	**13.23**	m_{PT}
s_{PT}	**0.65**	**2.64**	**3.36**	-	-	-	**0.64**	**2.46**	-	**7.07**	**3.22**	-	**5.07**	-	-	-	**2.04**	**1.30**	-	**1.45**	**0.78**	**0.74**	-	-	**1.56**	**0.58**	**2.66**	**1.49**	**1.85**	**2.22**	s_{PT}
u_{PT}	0.080	0.328	0.420	-	-	-	0.077	0.296	-	1.472	0.691	-	1.417	-	-	-	0.445	0.362	-	0.315	0.169	0.181	-	-	0.230	0.085	0.391	0.286	0.356	0.429	u_{PT}
***CV* (%)**	9	12	10	-	-	-	16	15	-	11	35	-	8	-	-	-	19	28	-	11	14	9	-	-	21	22	35	19	18	17	***CV* (%)**
$u_{rel,mPT}$ (%	0.8	1.2	1.0	-	-	-	1.5	1.4	-	1.9	6.0	-	1.8	-	-	-	3.2	6.3	-	1.9	2.4	1.7	-	-	2.5	2.6	4.1	2.9	2.7	2.6	$u_{rel,mPT}$ (%
F+	0	0	0	-	-	-	0	0	6	0	0	3	0	4	3	0	0	0	1	0	0	0	1	2	0	0	0	0	0	0	***F+***
F-	0	0	0	-	-	-	0	0	0	0	2	0	1	0	0	0	0	13	0	0	0	1	0	0	0	0	0	0	0	0	***F-***
<	3	4	3	-	-	-	1	1	0	1	0	0	1	0	0	0	1	0	0	2	0	1	0	0	1	0	0	2	2	0	**<**
>	0	1	0	-	-	-	4	1	0	0	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2	0	1	0	0	**>**
Min	14	127	550	5	95	0	2	45	0	9	0	0	0	0	0	0	13	0	0	17	11	0	0	0	1	3	11	3	6	80	***Min***
Max	85	1 030	1 987	44	864	1 400	64	627	820	5 900	610	1 700	5 200	500	1 700	0	280	35	2	260	64	114	67	23	103	26	140	160	174	370	***Max***
Med	57	477	1 290	14	255	1 100	16	271	0	4 100	93	0	3 915	0	0	0	123	24	0	180	30	73	0	0	57	6	74	65	122	174	***Med***

Appendix 1. Results of the participating laboratories

Lab no.	Coliform bacteria			Susp. thermotol. coliform bact.			E. coli			Presumptive C. perfringens			Clostridium perfringens			Moulds			Yeasts			Actinomycetes			Culturable microorganisms 22 °C, 3 days			Slow-growing microorganisms			Lab no.
	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	
m_{PT}	**57**	**475**	**1 233**	-	-	-	**16**	**278**	-	**4 015**	**85**	-	**4 098**	-	-	-	**122**	**21**	-	**174**	**31**	**72**	-	-	**53**	**7**	**58**	**64**	**110**	**175**	m_{PT}
Lower	32	193	628	5	95	0	5	87	0	1 779	1	0	2 383	0	0	-	25	1	0	79	11	40	0	0	7	1	0	13	25	44	***Lower***
Upper	90	882	2 042	44	864	1 400	34	577	0	7 152	357	0	6 275	0	0	-	295	71	0	308	62	114	0	0	143	18	243	154	257	396	***Upper***

N = number of reported results
n = results without annotation
CV = coefficient of variation

Min = lowest reported result
Max = highest reported result
$u_{rel,mPT}$ = relative standard uncertainty of m_{PT}

Med = median value
m_{PT} = assigned value

s_{PT} = standard deviation
u_{PT} = measurement uncertainty

< = low outlier
> = high outlier

Lower = lowest accepted value
Upper = highest accepted value

F+ = false positive
F- = false negative

False positive or false negative
Outside the acceptance limits
Results "larger than" are not evalutated
The parameter is not evaluated
The result is not evaluated
u_{PT} > 0,3 s_{PT} and/or > 20 % outliers and/or fewer than 12 evaluated results
Result The result is excluded prior determining m_{PT} and s_{PT}

Appendix 2. Z-scores of all participants

Lab no.	Coliform bacteria			Susp. thermotol. coliform bact.			E. coli			Presumptive C. perfringens			Clostridium perfringens			Moulds			Yeasts			Actinomycetes			Culturable microorganisms 22 °C, 3 days			Slow-growing microorganisms			Lab no.
	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	
1131-1	1.258	0.613	0.588				-0.843	0.567	0																0.443	-0.261	-1.111	0.019	1.395	0.749	1131-1
1131-2																															1131-2
1131-3																															1131-3
1237-1	-1.653	-1.915	0.279				-0.843	-1.964	0				1.460		0										-1.748	0.397	0.406				1237-1
1237-2	-0.419	0.946	0.279				0.000	0.723	0																						1237-2
1237-3																															1237-3
1545-1	1.165	-0.042	0.028				0.565	-0.542	0	1.039	-0.547	0	1.321	0	0	0	-1.029		0	1.237	0.244	-0.100	0	0	-0.786	0.695	-0.556	-1.217	0.270	0.345	1545-1
1545-2	1.258	0.199	0.998				-0.406	-0.206	0																						1545-2
1545-3							-0.620	-1.828	0																						1545-3
1594-1	0.099	0.548	0.279				-0.199	0.384	0							0	-1.168		0		0.244	0.059		0	-1.293	-0.261	0.615				1594-1
1594-2	-0.633	0.258	0.279				0.917	-0.744	0											1.352											1594-2
1594-3																															1594-3
1611-1	0.200	1.403	0.279				-0.199	1.255	0																	-0.632	0.635	-0.801	-0.935	-0.844	1611-1
1611-2	-0.419	0.383	0.279				-0.199	0.384	0																-0.433						1611-2
1611-3																															1611-3
1753-1	**2.574**	1.306	**2.495**				0.565	1.015	0	**-2.799**	0.140	0				0	0.108	0.555	0	0.195	-0.714	**-3.725**	0	0	0.362	-0.261	1.072	0.019	0.559	0.597	1753-1
1753-2																															1753-2
1753-3																															1753-3
1868-1	0.788	-0.264	0.336				0.194	0.101	0	0.939	-0.329	0				0	0.020		0	-0.278	**3.148**	1.616	0	0	1.661	0.397	-1.519	1.399	0.629	0.393	1868-1
1868-2	**2.321**	-0.427	-0.083				1.729	-0.119	0																						1868-2
1868-3																															1868-3
1966-1	-0.106	-0.463	0.483				0.917	-0.094	0	0.430	0.855	0				0	0.992	0.555	0	0.814	-0.100	0.216	0	0	1.155	1.501	0.635	0.912	0.146	-0.019	1966-1
1966-2	-0.419	0.773	0.588				0.000	1.109	0																						1966-2
1966-3																															1966-3
1970-1	-0.003	-0.309	-0.143				0.743	-0.219	0	-0.476	-0.329	0	-0.793		0	0	-0.764	**-2.757**	0	1.352	1.092				-0.198	0.397	-1.324				1970-1
1970-2																															1970-2
1970-3																															1970-3
2000-1	-0.003	-1.167	-1.625				1.414	-1.170	0				-0.629	0	0										-0.839	-0.261	0.182				2000-1
2000-2																															2000-2
2000-3																															2000-3
2086-1	-0.633	**-2.661**	-0.422					-0.758	0	0.094	**4.000**	0	-0.468		0	0	-0.274		0	-0.692	0.888				0.154	**4.000**	0.228	0.102	-0.965	-1.066	2086-1
2086-2	0.300	**-3.032**	-1.232					0.149	0			0			0	0	-0.274		0	0.398	-0.100				-0.153	**4.000**	0.675	0.144	-1.320	-1.129	2086-2
2086-3																															2086-3
2317-1	-0.526	-1.792	-0.663				0.000	-1.156	0	**-4.000**		0	**-4.000**	0	0										-1.417	0.079	-1.628				2317-1
2317-2																															2317-2
2317-3																															2317-3
2637-1	0.200	0.216	0.684				0.382	0.723	0	0.631					0										-0.433	0.695	-1.628				2637-1
2637-2																															2637-2
2637-3																															2637-3
2745-1	**-4.000**	**-3.060**	**-3.476**				**-2.130**	**-2.812**	0																0.280	0.079	0.491	0.266	0.319	-0.316	2745-1
2745-2																															2745-2
2745-3																															2745-3
2794-1	**-2.525**	**-3.984**	**-3.075**																												2794-1
2794-2																															2794-2
2794-3																															2794-3
3031-1	0.399	0.466	-0.143				-1.317	0.832		0.094	**4.000**		0.003	0											1.563	0.976	0.735				3031-1
3031-2	-0.742	0.860	0.740				-0.620	-0.219																							3031-2
3031-3																															3031-3
3055-1																									-0.019	1.983	0.136				3055-1
3055-2																															3055-2
3055-3																															3055-3
3076-1																									-0.839	0.695	0.554	-0.654	-1.422	0.704	3076-1
3076-2																															3076-2
3076-3																															3076-3
3162-1	0.692	-0.575	0.656				0.565	-1.536	0	0.312	0.172					0	-1.810	-1.487		**-3.302**	**-2.165**	0.448	0	0	-0.839	-1.042	0.675	-1.217	**-4.000**	-1.150	3162-1
3162-2																			0												3162-2
3162-3																															3162-3
3305-1	0.595	-1.693	-1.042				-0.620	-1.170	0	0.837	-1.007	0	1.039	0	0	0	0.173		0	0.645	-0.218	-1.375	0	0	0.678	-0.632	0.793				3305-1
3305-2	-0.003	-1.584	1.454				1.729	-1.025	0																						3305-2
3305-3																															3305-3

Appendix 2. Z-scores of all participants

Lab no.	Coliform bacteria			Susp. thermotol. coliform bact.			E. coli			Presumptive C. perfringens			Clostridium perfringens			Moulds			Yeasts			Actinomycetes			Culturable microorganisms 22 °C, 3 days			Slow-growing microorganisms			Lab no.
	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	
3515-1																									0.280	0.695	-0.351				3515-1
3515-2																															3515-2
3515-3																															3515-3
3587-1																									-0.107	-0.632	0.715				3587-1
3587-2																															3587-2
3587-3																															3587-3
3730-1	-0.314	-0.919	1.075																						0.562	1.983	-1.371	0.184	0.812	1.216	3730-1
3730-2																															3730-2
3730-3																															3730-3
3883-1																															3883-1
3883-2																															3883-2
3883-3																															3883-3
4015-1	1.072	1.959	1.277				0.743	1.955		1.335	-0.008					0	0.465		0	-0.091	-0.339	1.045	0	0	0.069	1.501	0.015	-0.109	1.055	0.839	4015-1
4015-2																															4015-2
4015-3																															4015-3
4339-1	-1.188	-0.219	-0.143				**2.032**	1.851	0				0.457	0	0	0	1.338		0	0.144	0.573				-1.417	-0.261	0.851	-1.559	0.488	-0.263	4339-1
4339-2	-1.894	0.131	-0.143				-0.843	1.046	0																						4339-2
4339-3																															4339-3
4343-1	0.497	-0.575	1.277				0.194	-0.883	0	-0.595	**-2.109**	0				0	-0.687	-0.746	0	-0.921	-0.462	1.405	0	0	0.866	-1.042	-1.071	0.617	0.368	-0.863	4343-1
4343-2																															4343-2
4343-3																															4343-3
4356-1	-0.963	-0.219	-0.143				-0.620	0.268																	-1.233	-0.261	0.574				4356-1
4356-2	-0.106	-0.309	0.684				-0.620	1.046																							4356-2
4356-3																															4356-3
4418-1																															4418-1
4418-2																															4418-2
4418-3																															4418-3
4723-1	-0.003	0.860	1.928				0.743	0.256	0	1.902	0.629	0				0	-1.491	-0.540	0	0.195	-0.218	0.059	0		1.048	0.079	0.296	0.729	0.464	-0.140	4723-1
4723-2																															4723-2
4723-3																															4723-3
4889-1	-0.314	-0.773	1.075				-0.843	-1.025	0				-0.629	0	0										0.940	-1.042	-0.649				4889-1
4889-2	-0.963	-0.584	0.684				0.000	-0.476	0																						4889-2
4889-3																															4889-3
5120-1	0.200	0.383	-0.143				1.414	0.149	0				1.597	0	0	0	1.158	1.037	0	-0.386	-1.394	0.448	0	0	-1.233	-1.507	0.889				5120-1
5120-2	-0.633	0.709	1.075				-0.199	1.851	0																						5120-2
5120-3																															5120-3
5201-1							**4.000**	-0.515																	-1.611	-1.042	0.591				5201-1
5201-2																															5201-2
5201-3																															5201-3
5204-1	-0.314	-0.773	0.684				-1.074	-0.555	0	0.094	0.124	0				0	-0.091	0.769	0	0.195	-0.587	-1.107	0	0	0.239	-1.042	0.427	-0.152	-1.934	-0.726	5204-1
5204-2	-0.742	1.674	**2.813**				1.086	**2.470**	0																						5204-2
5204-3																															5204-3
5220-1	**-4.000**	**-3.708**	-1.042				**-4.000**	**-4.000**	0																**-4.000**	-1.507	0.449	**-4.000**	**-4.000**	-1.929	5220-1
5220-2	-1.075	-0.121	0.740				-1.317	0.161	0																**-2.465**	-1.507	-1.519	**-3.035**	0.440	-1.108	5220-2
5220-3	-0.314						-1.842	-1.616	0																						5220-3
5333-1																									-0.581	0.079	0.675				5333-1
5333-2																									-0.198	-0.261	0.754				5333-2
5333-3																															5333-3
5352-1	-0.742	0.466	-0.582				**3.014**	0.268	0	-1.346	-1.553	0				0	**-3.640**	0.555	0	**-4.000**	-0.218	0.899	0	0	-1.003	-0.632	0.851	-1.442	-0.665	-1.213	5352-1
5352-2	**2.149**	-0.584	0.237				**2.324**	0.384	0																			-0.901	0.121	-0.824	5352-2
5352-3							-1.074	**-2.709**	0																						5352-3
5447-1										-0.595	0.531	0	-0.958	0	0													0.266	-0.271	**2.699**	5447-1
5447-2																															5447-2
5447-3																															5447-3
5701-1	-0.314	-0.309	0.028				0.382	0.723	0																0.403	-0.261	-1.151				5701-1
5701-2																															5701-2
5701-3																															5701-3
5858-1	-0.852	-1.915	-0.902				-0.406	-1.489	0				-0.262	0	0										0.025	0.079	-1.324				5858-1
5858-2																															5858-2
5858-3																															5858-3

Appendix 2. Z-scores of all participants

Lab no.	Coliform bacteria			Susp. thermotol. coliform bact.			E. coli			Presumptive C. perfringens			Clostridium perfringens			Moulds			Yeasts			Actinomycetes			Culturable microorganisms 22 °C, 3 days			Slow-growing microorganisms			Lab no.
	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	
5950-1																						-0.676	0	0				0.540	-0.271	0.313	5950-1
5950-2																															5950-2
5950-3																															5950-3
6182-1	0.099	0.515	0.385				-0.406	1.109	0	-0.359	-1.840	0				0	0.821	**-2.757**	0	1.488	0.244	-0.262	0	0	0.362	1.244	0.754	-0.024	0.044	-0.140	6182-1
6182-2																															6182-2
6182-3																															6182-3
6233-1	-0.742	-0.219	**-2.581**				-0.843	-0.346	0																0.280	0.695	0.695				6233-1
6233-2	1.072	-0.678	-0.627				-1.074	-0.502	0																						6233-2
6233-3																															6233-3
6253-1	0.399	-0.870	-0.582				0.382	-0.094	0																0.443	0.397	-1.324				6253-1
6253-2																															6253-2
6253-3																															6253-3
6456-1	-1.188	**3.901**	0.353				1.086	1.067	0																-0.631	-0.632	-1.279				6456-1
6456-2	**2.063**	**2.153**	-1.525				0.000	-0.094	0																						6456-2
6456-3																															6456-3
6686-1	0.536	0.027	0.862				-0.469	1.418	0	0.837	0.670	0													-0.153	-1.042	-1.628				6686-1
6686-2	-0.963	-1.167	**-2.581**				-0.843	-0.476	0																						6686-2
6686-3																															6686-3
7248-1	-0.314	0.045	-1.213				0.000	-0.476	0	-0.359	0.531	0				0	-0.868	0.173	0	**-2.755**	0.017	-1.465	0	0	-0.734	0.397	-0.162	-1.109	-1.188	-1.129	7248-1
7248-2	-1.188	-0.121	-0.493				-0.406	-0.758	0																						7248-2
7248-3							0.194	-0.502	0																						7248-3
7442-1	-0.963	0.173	-0.777				1.573	-0.020	0	0.631	-0.547	0										**2.943**	0	0	0.443	-1.507	-1.519	0.061	0.968	-0.573	7442-1
7442-2	-0.209	-0.095	-0.091				-0.843	0.029	0																						7442-2
7442-3																															7442-3
7688-1	0.595	-0.042	-0.582				0.565	-0.219	0	-0.130	-1.447	0	-0.309	0	0	0	0.383	0.482	0	0.144	**-2.881**		0	0	-0.482	-1.507	0.427				7688-1
7688-2	-0.003	-1.961	0.279				-1.074	-0.372	0																						7688-2
7688-3																															7688-3
7728-1	0.883	-0.584	-0.143				0.917	0.029	0																-1.003	-0.261	0.715				7728-1
7728-2																															7728-2
7728-3																															7728-3
7876-1	-0.003	0.045	-0.143				0.000	0.029	0	1.902	0.932	0				0	0.383	1.037	0	-0.117	0.785	0.138	0	0	0.280	0.079	0.574	-0.752	-0.164	0.165	7876-1
7876-2							-1.074	-0.476	0																						7876-2
7876-3																															7876-3
7930-1	-0.742	-0.042	-1.184				-0.843	-0.094	0	0.631	0.932	0	0.751	0	0	0	-1.084		0	-0.950	**2.653**				-1.233	0.695	0.715				7930-1
7930-2	-1.302	-0.584	0.279				0.382	0.149	0																						7930-2
7930-3																															7930-3
7962-1	-0.209	0.789	-0.360				-0.620	1.255	0																-0.482	-1.042	0.812				7962-1
7962-2	0.883	0.114	0.740				1.086	0.567	0																						7962-2
7962-3																															7962-3
8068-1	**-3.202**	**-2.064**	-1.189				**-2.774**	**-2.854**	0				0.457	0	0	0	0.783	0.252	0	0.862	0.465				-0.682	-1.042	0.963				8068-1
8068-2																															8068-2
8068-3																															8068-3
8165-1	-0.526	-0.678	-0.462				-0.199	-0.897	0																						8165-1
8165-2	0.099	0.342	0.233				0.565	0.734	0																						8165-2
8165-3																															8165-3
8260-1	-0.633	-0.309	-0.832				-0.620	-0.411	0	0.578	-0.218	0													0.792	1.501	-1.111	0.502	0.535	-0.499	8260-1
8260-2																															8260-2
8260-3																															8260-3
8329-1	1.888	0.868	**2.817**				**2.324**	0.361	0	0.420	0.737	0				0	-0.298	0.555	0	-0.863	-0.844				0.976	-0.632	-1.324	0.617	0.789	0.296	8329-1
8329-2																															8329-2
8329-3																															8329-3
8435-1	1.350	1.177	-0.582				1.086	-0.608	0				0.457	0	0										0.940	1.244	0.470				8435-1
8435-2																															8435-2
8435-3																															8435-3
8569-1	-0.106	0.010	-0.100				0.000	-0.069	0	**-2.654**	-1.938	0													1.190	0.079	0.982	1.694	0.675	0.957	8569-1
8569-2	-0.419	0.165	0.349				-0.843	-0.346	0																						8569-2
8569-3																															8569-3
8626-1	-1.653	0.045	-1.932				**3.656**	**2.133**																	-0.338	0.079	-0.295				8626-1
8626-2																															8626-2
8626-3																															8626-3

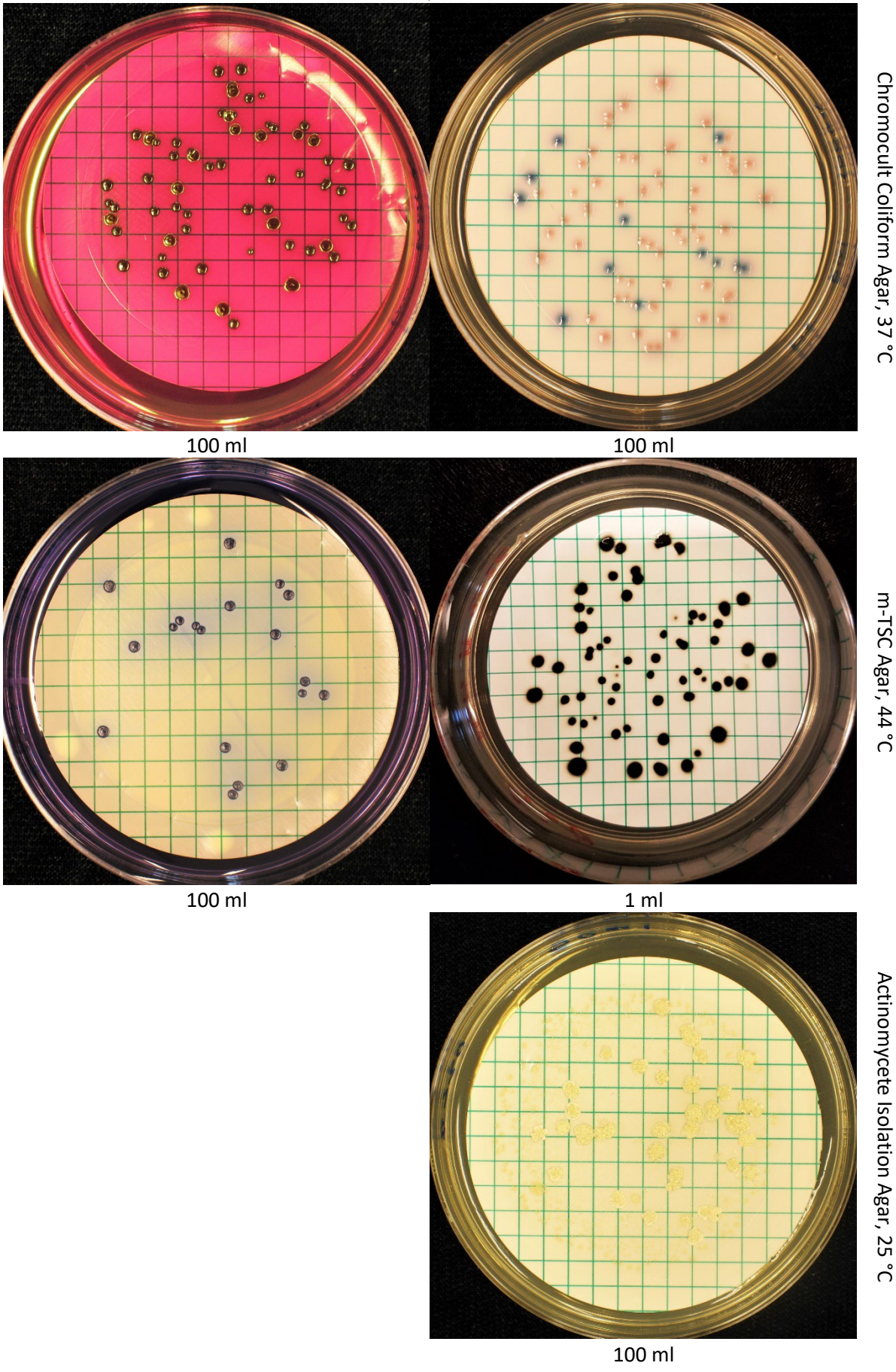
Appendix 2. Z-scores of all participants

Lab no.	Coliform bacteria			Susp. thermotol. coliform bact.			E. coli			Presumptive C. perfringens			Clostridium perfringens			Moulds			Yeasts			Actinomycetes			Culturable microorganisms 22 °C, 3 days			Slow-growing microorganisms			Lab no.
	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	
8628-1	1.072	-0.584					0.917	-1.170	0				-1.645	0		0	-0.046		0	-0.950	0.244				0.025	-1.042	0.136	0.061	0.559	1.438	**8628-1**
8628-2			**-3.165**				-1.317	-0.346	0																						**8628-2**
8628-3																															**8628-3**
8663-1	0.883	-0.130	-1.525				0.194	1.946	0	0.312	0.531	0		0	0										1.396	0.397	0.812				**8663-1**
8663-2	-0.742	1.101	1.820				-0.843	0.384	0																						**8663-2**
8663-3	1.072	0.868	0.684				0.000	-0.094	0																						**8663-3**
8742-1	-0.852	-0.042	-0.582				-1.317	0.029	0																-1.417	-0.632	0.889				**8742-1**
8742-2																															**8742-2**
8742-3																															**8742-3**
8751-1	-0.419	-0.192	0.564				-0.199	-0.502	0																-0.482	0.397	0.088	-1.056	-0.271	0.550	**8751-1**
8751-2	0.883	-0.831					-0.199	-0.717																							**8751-2**
8751-3																															**8751-3**
8766-1	0.595	**2.042**	-0.373				-1.317	1.538	0	1.039	0.868	0				0	0.860		0	0.645	-1.113	-0.343	0	0	0.443	-0.261	0.228	-0.466	**-2.304**	-0.370	**8766-1**
8766-2	1.165	0.741	-0.143				0.194	-0.282	0																						**8766-2**
8766-3							**2.032**	-0.411	0																						**8766-3**
8829-1	-0.526	0.629	-0.582				0.194	0.268	0																0.678	0.695	1.578	0.385	-1.422	1.016	**8829-1**
8829-2																															**8829-2**
8829-3																															**8829-3**
8862-1	0.595	-0.500	-1.042				-0.406	-0.282	0	-0.130	0.265	0	-0.309	0	0	0	0.108	0.173	0	0.169	0.465	0.899	0	0	1.225	-1.507	-1.324	0.803	0.901	0.015	**8862-1**
8862-2	-0.209	-0.228	-0.466				0.000	-0.385	0																						**8862-2**
8862-3																															**8862-3**
8955-1	0.300	1.695	0.279				0.000	0.029	0	-0.359	-0.610	0	-0.629	0	0	0	-0.274	0.769	0	-0.386	-1.540	0.600	0		0.523	-0.261	-0.059	**3.149**	0.946	1.159	**8955-1**
8955-2	1.441	-1.167	0.684				-0.199	0.029	0																						**8955-2**
8955-3																															**8955-3**
9436-1	0.200	0.741	1.454				0.000	0.777	0	-1.216	0.670	0				0	**2.780**		0	**2.014**	-0.844	-0.761		0	0.903	1.746	-0.351	0.225	0.675	0.673	**9436-1**
9436-2	1.072	0.515	0.740				1.252	0.843	0																						**9436-2**
9436-3																							0								**9436-3**
9524-1	-1.418	0.946	**-2.036**				-1.317	-0.476	0	-0.595	-0.742		-0.958	0											0.239	0.397	0.793				**9524-1**
9524-2	**2.063**	**2.866**	-1.004				0.565	**2.577**	0																						**9524-2**
9524-3																															**9524-3**
9657-1	0.399	1.001	1.224				0.194	1.203	0	-1.216		0				0	1.356	**-2.438**	0	0.423	1.675	-0.592			0.601	-0.261	0.040	-0.024	-0.217	-0.002	**9657-1**
9657-2	1.441	1.230	**-2.036**				**4.000**	**3.407**	0																						**9657-2**
9657-3							**-2.130**	-1.862	0																						**9657-3**
9736-1	0.200	0.523	0.307				0.000	0.173	0	-1.357	0.356	0				0	1.194		0	-1.098	1.291	-0.343	0	0	1.821	-0.261	-1.279	1.564	-0.521	-1.591	**9736-1**
9736-2																															**9736-2**
9736-3																															**9736-3**
9857-1	1.531	1.395	0.740				0.000	1.224	0																1.693	0.976	0.340	1.531	1.456	1.452	**9857-1**
9857-2																															**9857-2**
9857-3																															**9857-3**
9899-1	0.788	0.258	0.270				-0.199	0.442	0	-0.301	0.670	0				0	0.042	0.330	0	-0.552	0.355	-0.343	0	0	1.084	0.397	-1.235	0.692	0.789	1.145	**9899-1**
9899-2	0.099	1.063	1.247				0.565	1.458	0																						**9899-2**
9899-3																															**9899-3**
9903-1	-0.419	-0.678	0.612				0.194	-1.365	0	-1.216	-0.834	0				0	-0.321	0.008		0.014	0.244	-0.343	0	0	0.321	0.695	0.715	-0.109	0.196	-0.122	**9903-1**
9903-2																															**9903-2**
9903-3																															**9903-3**

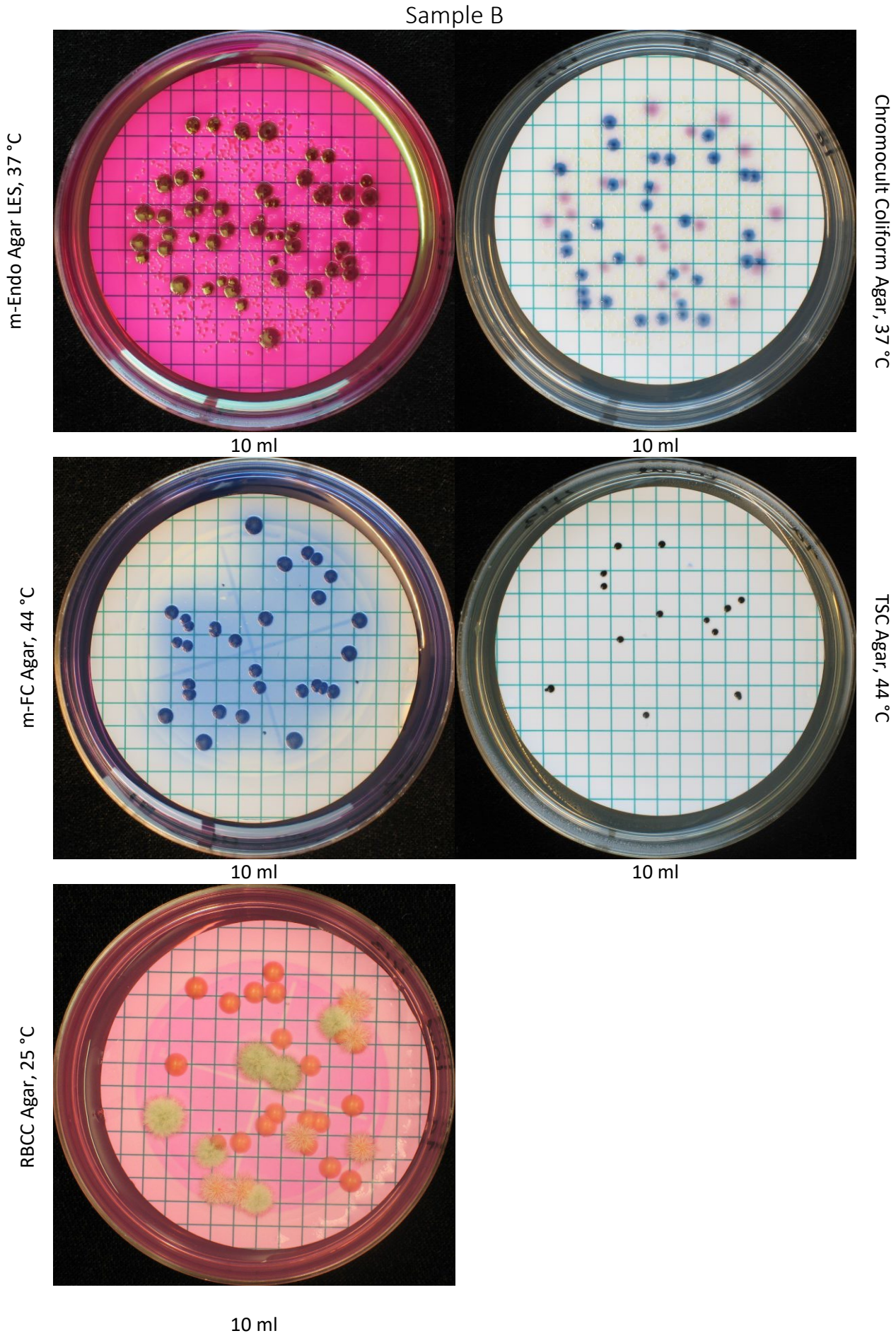
|z| ≥ 3,0 ("Unacceptable" or "Action")
2,0 < |z| < 3,0 ("Warning")
The parameter is not evaluated
The result is not evaluated

Appendix 3. Photos

Sample A



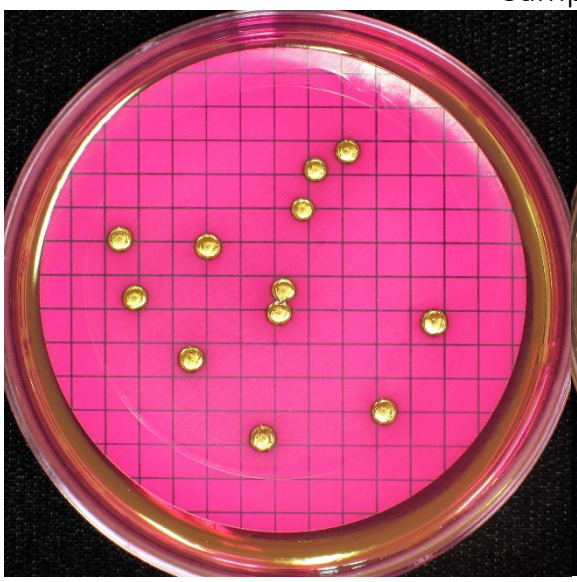
Appendix 3. Photos



Appendix 3. Photos

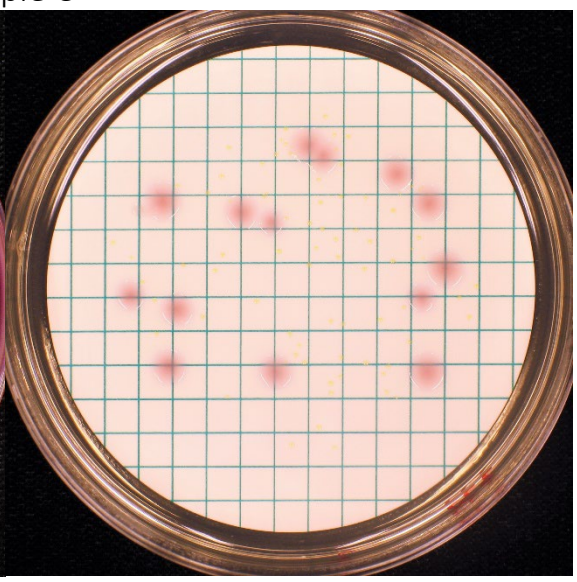
Sample C

m-Endo Agar LES, 37 °C



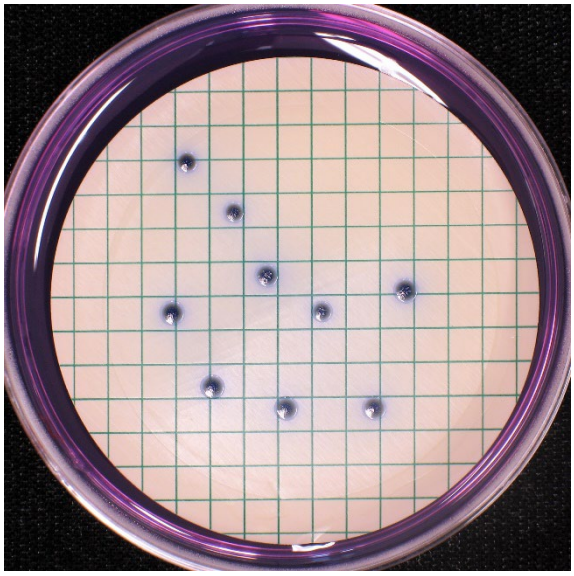
1 ml

Chromocult Coliform Agar, 37 °C



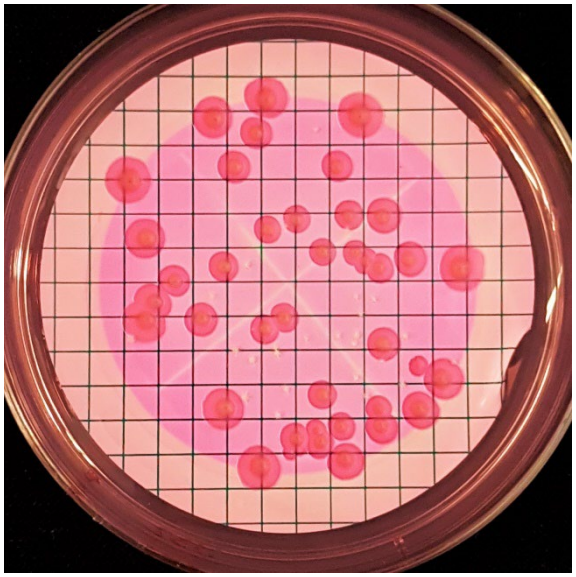
1 ml

m-FC Agar, 44 °C



1 ml

RBCC Agar, 25 °C



100 ml

Internal and external control for microbiological analyses of food and drinking water

All analytical activities require work of a high standard that is accurately documented. For this purpose, most participants carry out some form of internal quality assurance, but the analytical work also needs to be evaluated by an independent party. Such external quality control of laboratory competence is commonly required by accreditation bodies and can be done by taking part in proficiency testing (PT).

In a PT, identical test material is analysed by a number of participants. After reporting of results by the participants, the organiser evaluates the results and compiles them in a report.

The Swedish Food Agency's PT program offers

- External and independent evaluation of participants analytical competence.
- Improved knowledge of analytical methods with respect to various types of organisms.
- Expert support.
- Tool for inspections regarding accreditation.

For more information, visit our website: www.livsmedelsverket.se/en/PT-micro

The Swedish Food Agency's reference material

As a complement to the proficiency testing, but without specific accreditation, the Swedish Food Agency also manufactures a number of reference materials (RM) for internal quality control of food and drinking water microbiological analyses, including pathogens.

For more information, visit our website: www.livsmedelsverket.se/en/RM-micro

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