Proficiency Testing

Drinking Water Microbiology

September 2019

Tommy Šlapokas

Livsmedelsverket
Swedish Food Agency

NFA PT Since 1981

New edition – Version 2

A new edition is issued because the numbers in the columns A, B och C under the heading Sample in Annex B were wrong. The correct numbers were given in the corresponding columns in Annex A. Now they are also given in the columns in Annex B.

Edition
Version 2 (2019-12-20)

Editor in chief
Maria Sitell, Head of Biology department, Swedish Food Agency

Responsible for the scheme
Tommy Šlapokas, Microbiologist, Biology department, Swedish Food Agency

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Proficiency testing

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Parameters included

Coliform bacteria and ***Escherichia coli*** with membrane filter method (MF)

Coliform bacteria and ***Escherichia coli***, (rapid methods with MPN)

Suspected thermotolerant coliform bacteria with MF (not assessed)

Intestinal enterococci with MF/MPN

Pseudomonas aeruginosa with MF/MPN

Culturable microorganisms (total count) 3 days incubation at **22±2 °C**

Culturable microorganisms (total count) 2 days incubation at **36±2 °C**

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Swedish Food Agency, Biology department, Box 622, SE-751 26 Uppsala, Sweden

Abbreviations and explanations

Microbiological media

CCA	Chromocult Coliform Agar® (Merck; EN ISO 9308-1:2014)
Colilert	Colilert® Quanti-Tray® (IDEXX Inc.; EN ISO 9308-2:2014)
Enterolert	Enterolert® Quanti-Tray® (IDEXX Inc.)
LES	m-Endo Agar LES (according to SS 028167)
LTTC	m-Lactose TTC Agar with Tergitol (according to EN ISO 9308-1:2000)
m-Ent	m-Enterococcus Agar (Slanetz & Bartley; accord. to EN ISO 7899-2:2000)
m-FC	m-FC Agar (according to SS 028167)
PACN	Pseudomonas Agar base/CN agar (with cetrimide and nalidixic acid; according to EN ISO 16266:2008)
Pseudalert	Pseudalert® Quanti-Tray® (IDEXX Inc.; ISO 16266-2:2018)
YEA	Yeast extract Agar (according to EN ISO 6222:1999)

Other abbreviations

MF	Membrane filter (method)
MPN	"Most Probable Number" (quantification based on statistical distributions)
ISO	"International Organization for Standardization" and their standards
EN	European standard from "Comité Européen de Normalisation" (CEN)
NMKL	"Nordisk Metodikkomité for næringsmidler" and their standards
DS, NS, SFS, SS	National standards from Denmark, Norway, Finland and Sweden

Legend to method comparison tables

N	total number of laboratories that reported methods and numerical results
n	number of results except false results and outliers
Mv	mean value (with outliers and false results *excluded*)
Med	median value (with outliers and false results *included*)
CV	coefficient of variation = relative standard deviation in percentage of the mean, calculated from square root transformed results
F	number of false positive or false negative results
<	number of low outliers
>	number of high outliers
	total number of results for the parameter
601	remarkably low result
278	remarkably high result or CV or many deviating results

Explanations to histograms with accepted and deviating results

	result without remark
	false negative result
	outlier
↓ 34	average without deviating results
*	over a bar means that the result is beyond the x-axis limit

Contents

General information on results evaluation

The proficiency testing program organised by the Swedish Food Agency is accredited against EN ISO/IEC 17043. This standard prescribes that results should be grouped based on the methods used. Therefore it is mandatory for participants to inform about method data. This report presents, for each parameter, method data where differences are present or could be expected.

The method information gathered is sometimes difficult to interpret. Sometimes there is inconsistency between the standard referred to and the information regarding various method details. Results from laboratories with ambiguous details are either excluded or placed in the group "Other/Unknown" in the tables, together with results from methods used only by individual laboratories. Thus, to get an as appropriate evaluation as possible of the results, it is important that correct standards and method details are reported.

Outliers and false results are not included in the calculation of mean value and measure of dispersion for the various method groups. The numbers of low and high outliers, as well as false results, are instead explicitly given in tables together with the group means etc. The mean and measure of dispersion are not shown for groups with four or fewer results, other than exceptionally when it is specifically mentioned. However, all results are shown in the method histogram when possible.

The histograms and calculation of outliers are described on page 29 under "Processing of numerical results" with further reference to the scheme protocol [1].

Results of the PT round

General outcome

Test items were sent to 94 laboratories, 34 in Sweden, 52 in other Nordic countries (Faeroe Islands, Greenland and Åland included), 3 more from EU, 1 from the rest of Europe and 4 from outside Europe. Results were reported from 90 laboratories.

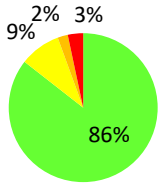
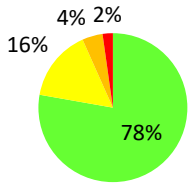
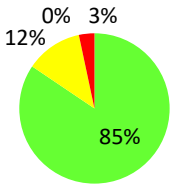
The percentages of false results and outliers are compiled in **table 1**.

Microorganisms and parameters of analyses are also compiled in table 1. For the MF analyses the parameters *suspected* coliform and thermotolerant coliform bacteria could be reported (shaded column in table 1 and table 3), as well as *suspected* intestinal enterococci and *suspected* Pseudomonas aeruginosa on primary media. The results from suspected colonies are only used for interpretations and discussions, not for assessment.

All reported results are compiled in **annex A** and results for each laboratory are also shown on our website after logging in (https://www2.slv.se/absint/).

Standardized z-scores for all evaluated results are given in **annex B** and photographs with examples of colony appearance on various media are presented in **annex C**.

Table 1 *Microorganisms in each sample and percentages of deviating results (F%: false positive or false negative, X%: outliers); parameters with grey shading are not assessed*

Sample	**A**			**B**			**C**		
Percentage of laboratories with 0 deviating results 1 deviating result 2 deviating results >2 deviating results									
No. of evaluable results	544			541			547		
No. of deviating results *	22 (4 %)			31 (6 %)			23 (4 %)		
Microorganisms / **Analysis**	*Escherichia coli* *Enterobacter cloacae* *Enterococcus faecalis* *Burkholderia cepacia*			*Escherichia coli* *Hafnia alvei* *Enterococcus faecium* *Pseudomonas aeruginosa* *Staphylococcus capitis*			*Cronobacter sakazakii* *Aeromonas hydrophila* *Pseudomonas aeruginosa* *Staphylococcus saprophyticus*		
Analysis	**Target org.**	**F%**	**X%**	**Target org.**	**F%**	**X%**	**Target org.**	**F%**	**X%**
Coliform bacteria (MF)	*E. coli* *E. cloacae*	0	1	*E. coli* *{H. alvei}*	3	3	*C. sakazakii* *[A. hydrophila]*	10	0
Susp. thermotolerant coliform bact. (MF)	*E. coli* *{E. cloacae}*	–	–	*E. coli*	–	–	*C. sakazakii*	–	–
E. coli (MF)	*E. coli*	0	7	*E. coli*	8	0	–	1	–
Coliform bacteria (rapid method)	*E. coli* *E. cloacae*	0	2	*E. coli* *H. alvei*	0	2	*C. sakazakii*	2	2
E. coli (rapid meth.)	*E. coli*	2	2	*E. coli*	3	0	–	2	0
Intestinala entero-kocker (MF)	*E. faecalis*	0	3	*E. faecium*	11	0	*[S. saprophyticus]*	6	–
Pseudomonas aeruginosa (MF)	*[B. cepacia]*	7	0	*P. aeruginosa*	2	3	*P. aeruginosa*	0	2
Culturable micro-organisms (total count), 3 days 22 °C	*B. cepacia* *E. coli* *E. cloacae* *E. faecalis*	0	5	*E. faecium* *E. coli* *H. alvei* *P. aeruginosa*	0	7	*S. saprophyticus* *A. hydrophila* *C. sakazakii* *P. aeruginosa*	0	6
Culturable micro-organisms (total count), 2 days 36 °C	*B. cepacia* *E. coli* *E. cloacae* *E. faecalis*	0	4	*S. capitis* *E. faecium* *E. coli* *H. alvei* *P. aeruginosa*	0	3	*S. saprophyticus* *A. hydrophila* *C. sakazakii* *P. aeruginosa*	0	3

* In total 32 of 90 laboratories (36 %) reported at least one deviating result

– Organism missing or numerical result irrelevant

( ) The organism contributes with only very few colonies

[ ] The organism may be presumptively false positive on the primary growth medium

{ } The organism may give different results depending on method or definition used

Coliform bacteria (MF)

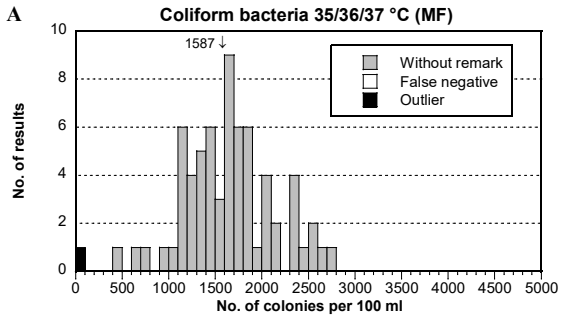
In the group Other/Unknown in the table six different media are used, based on methods for both water and food, as well as for the medical field.

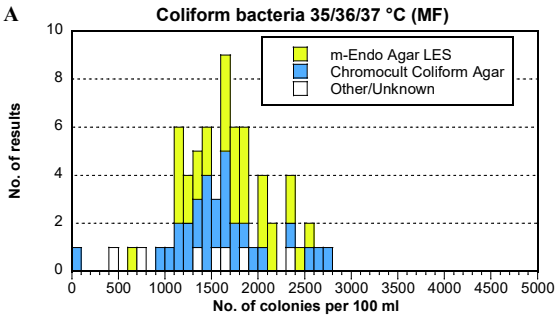
From the table it is clear that approximately the same number of laboratories used CCA and LES. The proportion that used CCA is no longer increasing in relation to LES, as has been seen since the standard EN ISO 8308-1 from 2014 was issued. The use of LTTC for coliform bacteria has ceased.

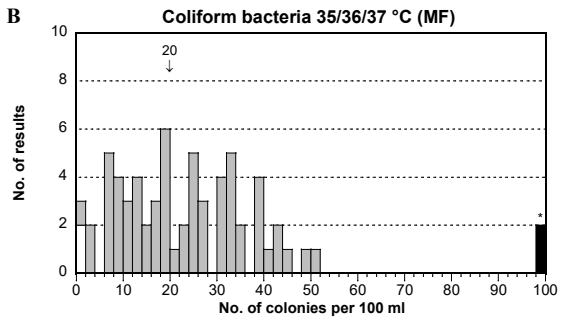
The average results for LES and CCA are approximately equal only in sample A. In both sample B and C the results are lower for CCA, as has also often been the case previously. As the media are based on different standards, the differences apply also to these standards. The heterogenic group Other/Unknown contained several low results. In sample A this group had a lower average than other groups while it contained several false negative results in sample B and C.

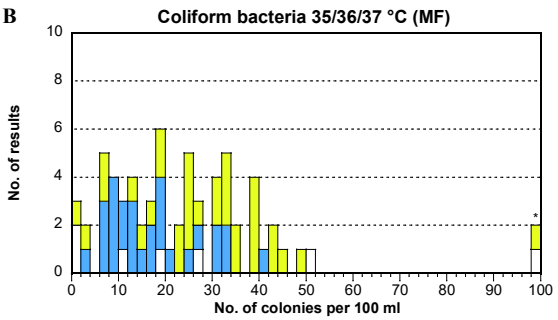
In total five coliform bacteria, including *E. coli*, were present in the samples.

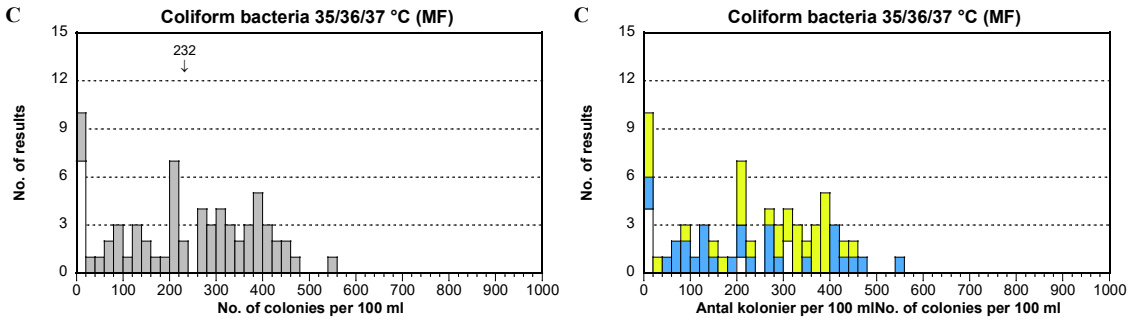
Medium	N	A						B						C					
		n	Mv	CV	F	<	>	n	Mv	CV	F	<	>	n	Mv	CV	F	<	>
Total	67	66	**1587**	15	0	0	0	62	**20**	32	2	0	2	60	**232**	33	7	0	0
m-Endo Agar LES	32	32	**1645**	13	0	0	0	31	**24**	29	0	0	1	30	**251**	31	2	0	0
Chromocult C Agar	28	27	**1599**	14	0	1	0	27	**15**	31	0	0	0	27	**207**	37	1	0	0
Other/Unknown	7	7	**1292**	27	0	0	0	4	–	–	2	0	1	3	–	–	4	0	0











Sample A

- A strain of *Escherichia coli* and a strain of *Enterobacter cloacae* were included. They appeared with for coliform bacteria typical colonies on the MF media at 37 °C, a metallic sheen on LES and blue and pinkish red, respectively, on CCA.
- The distribution of the results was good with small dispersion (CV; see page 29). One low outlier was the only deviating result.

Sample B

- One strain each of *E. coli* and *Hafnia alvei* were present as coliform bacteria. *E. coli* appeared at the Swedish Food Agency with for coliform bacteria typical colonies on the MF media at 37 °C, a typical metallic sheen on LES and blue on CCA. The colonies of *H. alvei* were red without metallic sheen on LES and light beige to pink or pale apricot coloured on CCA. This means that *H. alvei* could be included as a coliform bacterium on CCA but not on LES. The results, however, indicate the opposite, as they are lower for CCA. The colonies that have been counted from the two media seem to vary among the laboratories. Also the *Enterococcus* strain in the sample appears with small convex pink and oxidase negative colonies on CCA. By experience they should be excluded.
- The distribution of the results was quite wide with a tail to the left. The dispersion was large. Two high outliers were present that could be a result of counting errors, i.e. multiplication with 10.

Sample C

- No *E. coli* but the coliform bacteria, *Cronobacter sakazakii*, was present. This strain appeared together with a strain of *Aeromonas hydrophila* with, for coliform bacteria, typical colonies at 37 °C, i.e. with metallic sheen on LES and pinkish on CCA.
- The distribution of the accepted results was also here wide and the dispersion large. Seven false negative results were present, together with a tail of other low results. There are no clear reason for the false negative results (compare p. 14).
- *A. hydrophila* was a false positive strain but could be removed after confirmation with oxidase test because it is oxidase positive. In 9 of 42 cases the results for suspected coliform bacteria and coliform bacteria were identical. Either have the laboratories in these cases not excluded *A. hydrophila* after confirmation, or it is not even included among the suspected coliform bacteria.

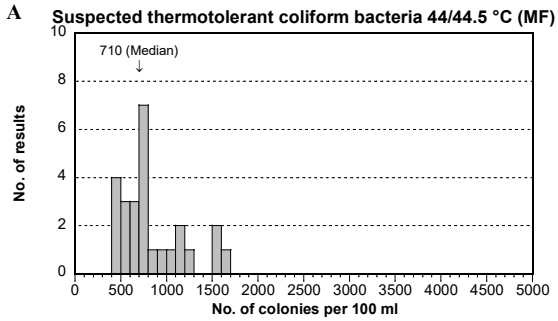
Suspected thermotolerant coliform bacteria (MF)

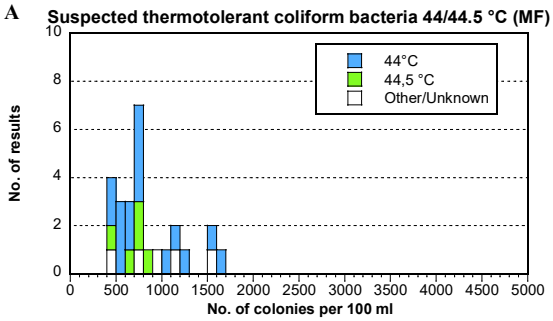
No evaluation in relation to performance is done for what is called suspected (not confirmed) colonies of a parameter. Therefore, no identification of outliers is done. The *medians* are then more robust than the means and are given in the table and in histograms. **Thus, the parameter is not included in the performance assessment**.

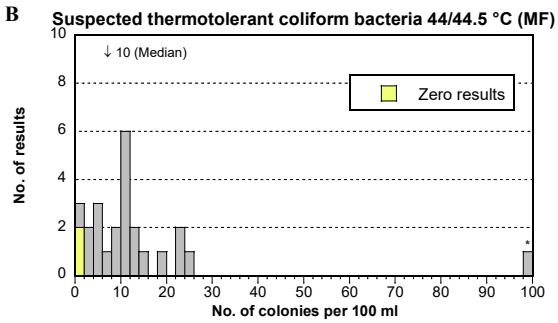
The only primary growth media used at 44 or 44.5 °C to identify suspected thermotolerant coliform bacteria is m-FC. In several cases within the group Other/Unknown primary media that are incubated at 36±2 °C have been used. In those cases 44 °C is used only for confirmation. This is not the intention with the parameter suspected thermotolerant coliform bacteria according to the definition in the instruction and on the website for the program. It is the typical colonies appearing on the membrane filter at 44/44.5 °C that should be reported. For the group Other/Unknown in sample B and C, where there are relatively low results, only minor fractions seem to have been reckoned as suspected thermotolerant coliform bacteria.

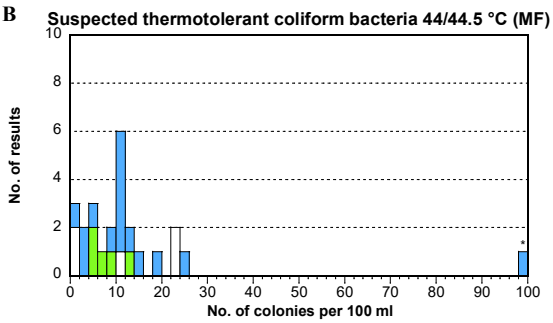
Incubation temp.	N	A						B						C					
		n	Med	CV	F	<	>	n	Med	CV	F	<	>	n	Med	CV	F	<	>
Total	26	26	**792**	–	–	–	–	25	**11**	–	–	–	–	26	**117**	–	–	–	–
44 °C	16	16	**799**	–	–	–	–	15	**15**	–	–	–	–	16	**127**	–	–	–	–
44,5 °C	5	5	**668**	–	–	–	–	5	**7**	–	–	–	–	5	**265**	–	–	–	–
Other/Unknown	5	5	**904**	–	–	–	–	5	**6**	–	–	–	–	5	**15**	–	–	–	–

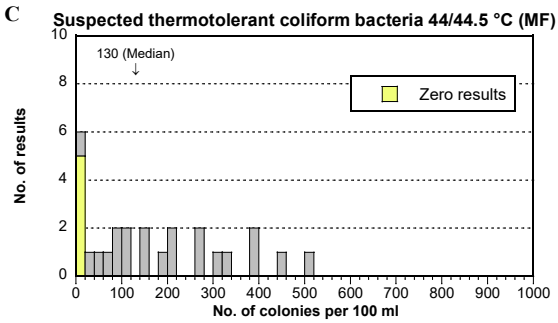
Med = Median; used here instead of mean value because it describes "suspected" colonies

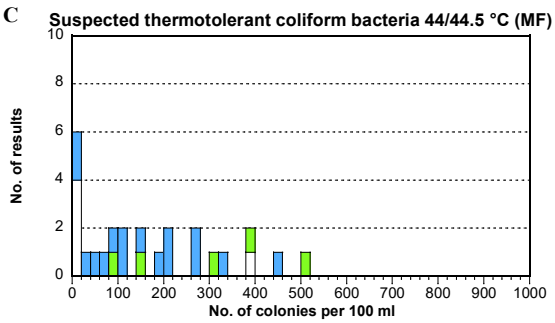












Sample A

- Two coliform bacteria were included in the sample, of which the *E. coli* strain appears as a typical suspected thermotolerant coliform bacterium; that is with blue colonies at 44/44.5 °C on m-FC.
- The distribution of the 26 results was fairly good.

Sample B

- Two coliform bacteria were included in the mixture, of which the *E. coli* strain appears as a typical suspected thermotolerant coliform bacterium; that is with blue colonies on m-FC at 44/44.5 °C. The strain of *H. alvei* doesn't grow on agar media at 44 °C.
- The distribution of the 25 results was fairly good but with some over-representation of low results. One very high result could be seen as an outlier but, no such evaluation is done.

Sample C

- One strain of *C. sakazakii* together with a strain of *A. hydrophila* appear on media for coliform bacteria at 35-37 °C. The strain of *A. hydrophila* does not grow at 44 °C while the strain of *C. sakazakii* appear there with mainly blue-grey colonies on m-FC.
- The five zero results indicate that those laboratories didn't see the colonies as bluish and therefore didn't count them as thermotolerant coliform bacteria. Even without these zero results, there is some displacement to the left compared with the results for the coliform bacteria, where there is the same strain seen. Probably this is a result of a partial inhibition on m-FC due to the high temperature. This is quite normal for most bacteria strains growing on that medium at high temperature, even *E. coli*.

Escherichia coli (MF)

To identify and quantify *E. coli,* confirmation is required when colonies are isolated from the primary cultivation media LES or m-FC. Depending on the method, tests for indole production and/or *β*-glucuronidase activity from oxidase negative presumptive strains are usually performed. A violet to blue colony on CCA indicates positive *β*-glucuronidase activity and is reckoned as a confirmed *E. coli*.

Corresponding reactions occur on other chromogenic media based on *β*-glucuronidase activity.

The primary growth media CCA, LES and others are used at 36±2 °C and m-FC at 44/44.5 °C. In addition to incubation temperature, the results are also grouped by standard. For ISO 9308-1:2014 the incubation is at 36±2 °C on CCA. For the standards from the Nordic countries (NS, SS and SFS) the majority of the results are from 36±2 °C on LES but some are also from 44/44.5 °C on m-FC. Actually, only two Finnish laboratory have stated the standard SFS 4088 (m-FC) instead of SFS 3016 for the analysis of *E. coli*. One of these has used 44 °C and the other 44.5 °C

When all results are compared, there is no differences between the different incubation temperatures for any sample. For the standards there is an indication of a lower average for CCA compared to other groups in sample A. This time there is no difference in the dispersion (CV) between CCA and LES. In contrast, the results from the Finnish standard are for some reason showing a larger dispersion than those from other standards. It might be caused by the use of different confirmation principles and that a number of laboratories have confirmed at 44.5 °C, while the majority used 44 °C.

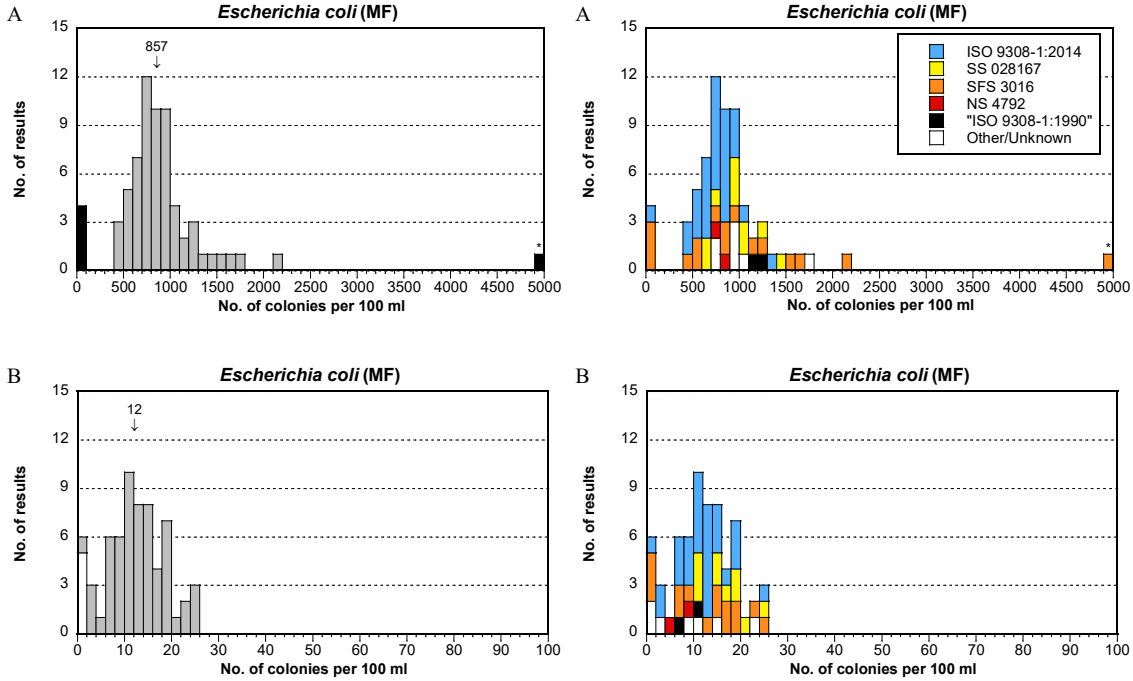
All results

Origin &Standard	**N**	**A**						**B**						**C**					
		n	**Mv**	CV	F	<	>	n	**Mv**	CV	F	<	>	n	**Mv**	CV	F	<	>
Total	67	62	**857**	17	0	4	1	60	**12**	25	5	0	0	66	**0**	–	1	–	–
Colony origin																			
36 ± 2 °C	47	44	**853**	17	0	2	1	42	**12**	26	4	0	0	46	**0**	–	1	–	–
44/44.5 °C	9	8	**837**	16	0	1	0	7	**12**	25	1	0	0	9	**0**	–	0	–	–
36 ± 2 & 44/44.5 °C	10	9	**882**	19	0	1	0	10	**12**	27	0	0	0	10	**0**	–	0	–	–
Other/Unknown	1	1	–	–	0	0	0	1	–	–	0	0	0	1	**0**	–	0	–	–
Standard																			
ISO 9308-1:2014	30	29	**747**	12	0	1	0	28	**11**	23	1	0	0	30	**0**	–	0	–	–
SS 028167	10	10	**932**	13	0	0	0	10	**15**	16	0	0	0	10	**0**	–	0	–	–
SFS 3016 (4088)	16	12	**976**	25	0	3	1	13	**13**	30	2	0	0	15	**0**	–	1	–	–
NS 4792	2	2	–	–	0	0	0	2	–	–	0	0	0	2	**0**	–	0	–	–
”ISO 9308-1:1990”	2	2	–	–	0	0	0	2	–	–	0	0	0	2	**0**	–	0	–	–
Other/Unknown	7	7	**966**	16	0	0	0	5	**11**	33	2	0	0	7	**0**	–	0	–	–

Results from the analysis of "coliform bacteria" MF at 36±2 °C

Medium	**N**	**A**						**B**						**C**					
		n	**Mv**	CV	F	<	>	n	**Mv**	CV	F	<	>	n	**Mv**	CV	F	<	>
Total	***50*#**	***47***	***844***	***17***	***0***	***2***	***1***	***45***	***12***	***26***	***4***	0	***0***	***49***	***0***	***–***	***1***	***–***	***–***
m-Endo Agar LES	18	16	**1051**	18	0	1	1	17	**14**	26	1	0	0	17	**0**	–	1	–	–
Chromocult C Agar	29	28	**749**	12	0	1	0	27	**11**	25	1	0	0	29	**0**	–	0	–	–
Other/Unknown	3	3	–	–	0	0	0	1	–	–	2	0	0	3	**0**	–	0	–	–

Compare table above – three more laboratories performed the analysis of *E. coli* than of coliform bacteria



Sample A

- One strain of *E. coli* was present together with another thermotolerant coliform bacterium, *E. cloacae*. The colonies are typical for *E. coli* on LES and m-FC that are based on lactose fermentation. On CCA the colonies are typical blue, meaning that confirmation is not necessary and therefore normally not performed. Sometimes small colonies of *E. cloacae* may appear together with *E. coli* on m-FC at 44 °C. Confirmation is necessary for colonies from LES and m-FC.
- The distribution of the results was good and the dispersion small (CV; see p. 29) except the deviating results. Four low and one high outlier were present.
- For three of the low outliers there might be a miscalculation from the plate counted to the volume 100 ml. Alternatively, the confirmation may has failed.

Sample B

- A typical strain of *E. coli* was included together with another atypical coliform bacterium, *H. alvei*. *H. alvei* shouldn't grow in broth at 44 °C, and is indole negative and lacking the enzyme *β*-glucuronidase. Thus, it cannot be mistaken for *E. coli*.
- The distribution of the results was good except a "tail" of low results, out of which five were false negative. Due to the low results, the dispersion (CV) was medium.

Sample C

- No *E. coli* was included but another coliform bacterium, *C. sakazakii*, was present together with the coliform-like bacterium, *A. hydrophila*. The latter is oxidase positive. *C. sakazakii* is indole negative and has no activity of *β*-glucuronidase. Thus, neither stain can be mistaken for *E. coli* after confirmation.
- One false positive result was reported.

Coliform bacteria & *E. coli* (rapid methods, MPN)

The rapid method used for both these parameters was exclusively Colilert® Quanti-Tray® from the manufacturer IDEXX Inc. with incubation at 35, 36 or 37 °C. Out of the about 60 laboratories that reported Colilert some used trays with 51 wells, while others used trays with 97 wells (a few of which, probably incorrectly, have reported 96 wells). The laboratories often analysed both diluted and undiluted samples. Yellow wells (ONPG positive; *β*-galactosidase activity shown) will be interpreted as coliform bacteria and yellow wells also exhibiting fluorescence (MUG positive; *β*-glucuronidase activity shown) will be interpreted as *E. coli*.

When comparing trays with different number of wells (see the table) as well as different incubation temperatures it is clear that the differences are small and inconsistent. Differences based on stated maximum incubation time were also small.

In this round it is clear that the two laboratories using "Wrong method" ("most probable numbers" in connection with a multiple tube method) instead of a rapid kit method obtained some low or high deviating results. Further, even most averages for the accepted results are low according to the table. The third laboratory in the group "Wrong method" used a presence/absence method with an evaluable result only for *E. coli* in sample C, where no deviating results were seen.

Coliform bacteria, Rapid method with MPN

Principle	N	A						B						C					
		n	**Mv**	CV	F	<	>	n	**Mv**	CV	F	<	>	n	**Mv**	CV	F	<	>
Total, Rapid meth.	62	61	**1805**	11	0	0	0	60	**21**	26	0	0	1	60	**350**	16	0	1	0
Colilert-18, 51 wells	12	11	**1804**	12	0	0	0	12	**19**	21	0	0	0	11	**313**	23	0	0	0
Colilert-18, 97 wells	45	45	**1773**	11	0	0	0	43	**22**	27	0	0	1	44	**358**	13	0	1	0
Colilert-18, 51 & 97	2	2*	**2177**	8	0	0	0	2*	**25**	15	0	0	0	2*	**389**	4	0	0	0
Colilert-24, ? wells	3	3*	**2072**	7	0	0	0	3*	**14**	29	0	0	0	3*	**348**	33	0	0	0
Wrong method#	2	1*	**920**	–	0	0	1	2*	**10**	77	0	0	0	1*	**70**	–	1	0	0

E. coli, Rapid method with MPN

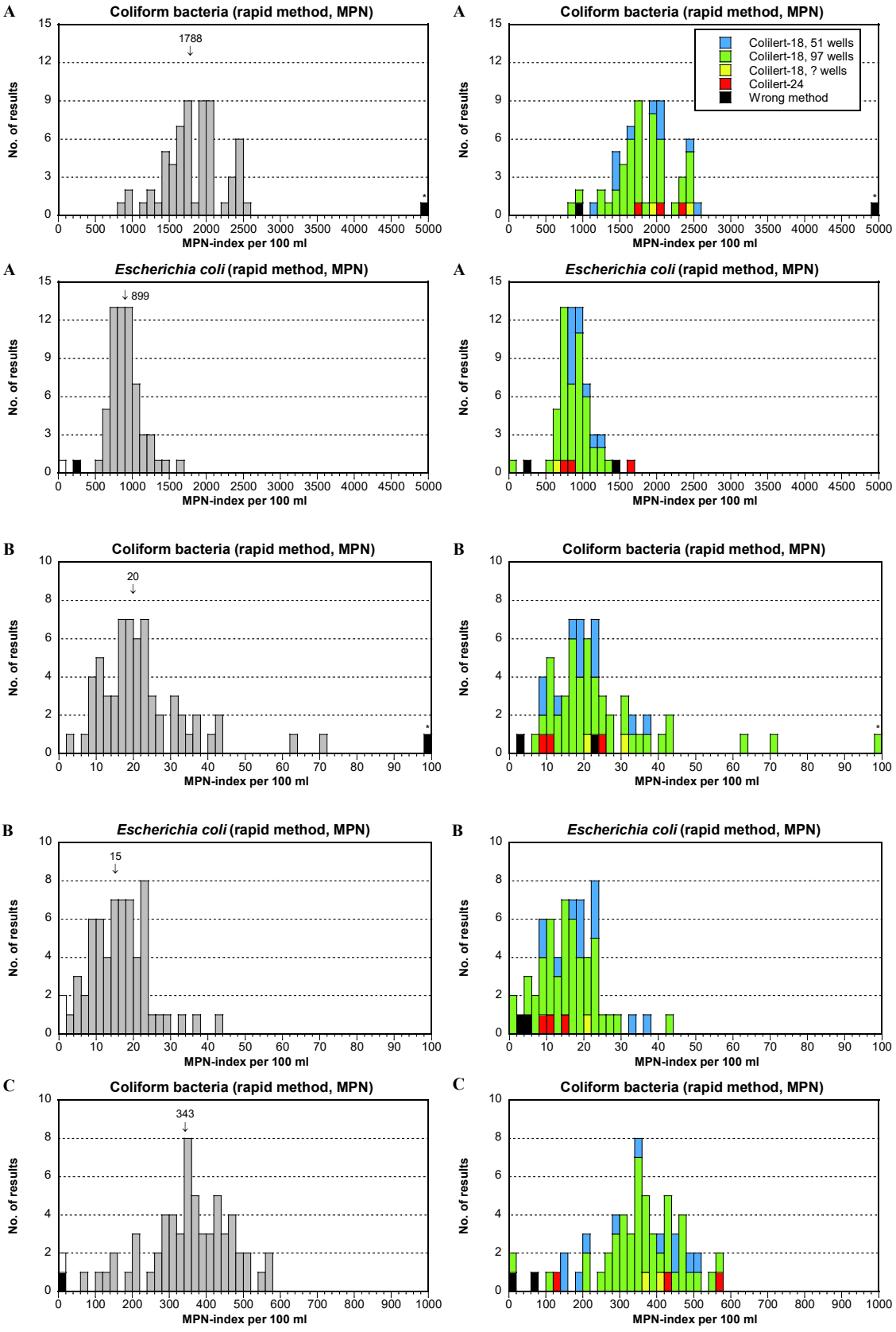
Principle	N	A						B						C					
		n	**Mv**	CV	F	<	>	n	**Mv**	CV	F	<	>	n	**Mv**	CV	F	<	>
Total, Rapid meth.	61	60	**14**	13	1	0	0	61	**0**	–	0	–	–	59	**41**	10	0	1	1
Colilert-18, 51 wells	12	11	**939**	7	0	0	0	12	**19**	22	0	0	0	12	**0**	–	0	–	–
Colilert-18, 97 wells	46	45	**876**	10	1	0	0	43	**15**	22	2	0	0	45	**0**	–	1	–	–
Colilert-18, 51 & 97	1	1*	**687**	–	0	0	0	1*	**20**	–	0	0	0	1	**0**	–	0	–	–
Colilert-24, ? wells	3	3*	**1026**	23	0	0	0	3*	**11**	14	0	0	0	3	**0**	–	0	–	–
Wrong method#	**3**	1*	**1400**	–	0	1	0	2*	**3**	32	0	0	0	**3**	**0**	**–**	**0**	**–**	**–**

* Mean value is given for comparison despite few results

\# In two cases no rapid kit method but a multiple tube method based on lactose fermentation, in the third case a qualitative presence/absence method

Sample A

- The strains of *E. coli* and *E. cloacae* grow in the medium and have the enzyme *β*-galactosidase. Therefore, they are detected as coliform bacteria by methods based


A
Coliform bacteria (rapid method, MPN)
1788
No. of results
MPN-index per 100 ml
A
Coliform bacteria (rapid method, MPN)
Colilert-18, 51 wells
Colilert-18, 97 wells
Colilert-18, ? wells
Colilert-24
Wrong method
No. of results
MPN-index per 100 ml
A
Escherichia coli (rapid method, MPN)
899
No. of results
MPN-index per 100 ml
A
Escherichia coli (rapid method, MPN)
No. of results
MPN-index per 100 ml
B
Coliform bacteria (rapid method, MPN)
20
No. of results
MPN-index per 100 ml
B
Coliform bacteria (rapid method, MPN)
No. of results
MPN-index per 100 ml
B
Escherichia coli (rapid method, MPN)
15
No. of results
MPN-index per 100 ml
B
Escherichia coli (rapid method, MPN)
No. of results
MPN-index per 100 ml
C
Coliform bacteria (rapid method, MPN)
343
No. of results
MPN-index per 100 ml
C
Coliform bacteria (rapid method, MPN)
No. of results
MPN-index per 100 ml

on this enzyme (ONPG positive) e.g. Colilert®-18/24 Quanti-Tray® where ONPG is a substrate.

- The strain of *E. coli* has the enzyme *β*-glucuronidase and is detected as *E. coli*.
- The distributions of the results were good and the dispersions small (CV; see p. 29). The only deviating results were a high outlier for coliform bacteria, as well as a low outlier and one false negative result for *E. coli*.
- The averages for both coliform bacteria and *E. coli* were only somewhat higher than for the corresponding analyses with the MF technique (compare p. 6 and 10).

Sample B

- The strains of *E. coli* and *H. alvei* grow in the medium and possess the enzyme *β*-galactosidase. Therefore, they are detected as coliform bacteria by methods based on this enzyme (ONPG positive) e.g. Colilert®-18/24 Quanti-Tray® where ONPG is a substrate. *E. coli* has the enzyme *β*-glucuronidase and is detected as *E. coli*.
- The activity of *β*-galactosidase is weak in *H. alvei*, often resulting in negative outcome after 18 hours and positive only after 22 hours. This species is completely lacking the enzyme *β*-glucuronidase and, is thus not detected as *E. coli*.
- The distribution of the results for coliform bacteria is not as dispersed as for the MF-method (lesser CV) but the means are still the same. You could expect a somewhat higher mean with the rapid method as at least the colonies of *H. alvei* on LES with the MF method are not reckoned as coliform bacteria. The outcome is instead indicating that quite a number of laboratories also with the rapid method have not detected *H. alvei* as positive. You might then question if the final reading has been earlier than after 22 hours.
- One high outlier was present for coliform bacteria.
- The average for *E. coli* was somewhat higher with the rapid method compared to the MF method, which is often the case. The dispersions were similar and medium in both cases. Two false negative results were present.

Sample C

- In this sample only one coliform bacterium, *C. sakazakii*, was present. It has the enzyme *β*-galactosidase and is detected as a coliform bacterium. *A. hydrophila* that was included in the sample, and could be taken for a coliform bacterium by the MF method before confirmation, is not detected as such by Colilert®.
- *C. sakazakii* is lacking the enzyme *β*-glucuronidase and is not detected as *E. coli*.
- The distribution of the results was good with small dispersion in average. One low outlier and one false negative result were the only deviating results.
- The average for the accepted results of the coliform bacteria was about 50 % higher with the rapid method compared to the MF method (see p. 7). This together with the tail of low results and false negative values by the MF method indicates that some laboratories had difficulties in interpreting the colonies of *C. sakazakii* by that method. Some of the laboratories seem to have been interpreted them as not being coliform bacteria.

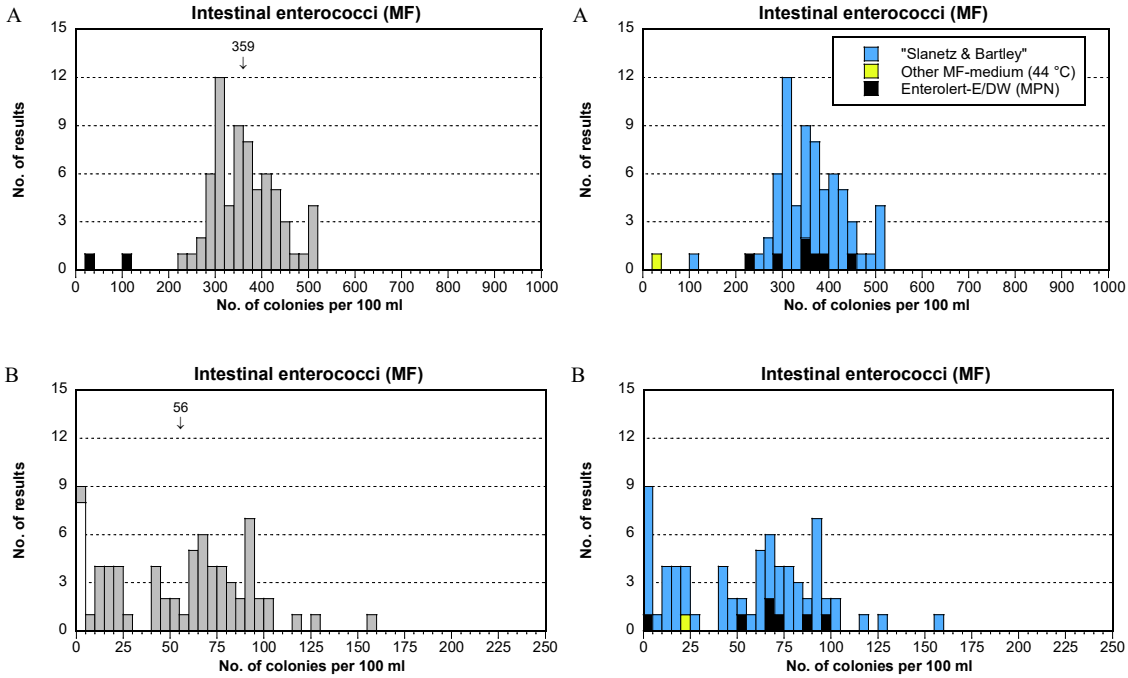
Intestinal enterococci (MF/MPN)

The MF method used for intestinal enterococci is almost exclusively EN ISO 7899-2:2000. In seven cases methods with another reference, like "according to manufacturer's instruction", have been stated. The primary growth medium was m-Enterococcus Agar (Slanetz & Bartley), here designated m-Ent, except in these seven cases and one more. In this last case the laboratory used Rapid Enterococcus Agar at 44 °C without confirmation. In the other seven cases the rapid method Enterolert®-E (Idexx Inc.) was used by five and Enterolert®-DW (Idexx Inc.) by two laboratories. The incubation temperature was 41 °C in six of these laboratories but 41.5 °C in the seventh. In all cases with the MF method and m-Ent the incubation temperature was 35, 36 or 37 °C.

The prominent method difference is the MF-method versus the rapid method. No general trend can be seen, instead the differences are sample specific (see below). There are some variants of the confirmation step for the MF methods. However, no general differences in the results relating to that could be seen. In sample B the dispersion is large for the MF methods irrespective of the variants (not shown).

Method/Medium	N	A						B						C					
		n	Mv	CV	F	<	>	n	Mv	CV	F	<	>	n	Mv	CV	F	<	>
Total	70	68	**359**	9	0	2	0	62	**56**	31	8	0	0	66	**0**	–	4	–	–
EN ISO 7899	*63*	*61*	***361***	*9*	*0*	*2*	*0*	*56*	***55***	*33*	*7*	*0*	*0*	*59*	***0***	–	*4*	–	–
Slanetz & Bartley	62	61	**361**	9	0	1	0	55	**55**	33	7	0	0	58	**0**	–	4	–	–
Other/Unknown	1	0	–	–	0	1	0	1*	**22**	–	0	0	0	1	**0**	–	0	–	–
Rapid method#, MPN	*7*	*7*	***345***	*10*	*0*	*0*	*0*	*6*	***74***	*10*	*1*	*0*	*0*	*7*	***0***	–	*0*	–	–

* Mean value is given for comparison despite only one result
\# Two variants of Enterolert® – no confirmation was performed



Sample A

- A strain of *Enterococcus faecalis* was present. The distribution of the results was good with very small dispersion (CV; see page 29). The colonies are brown-red on m-Ent and are normally confirmed as enterococci without problem.
- The results by Enterolert® were not deviant from those by the MF-method.
- Two low outliers were present, one of which was by the Rapid Enterococcus Agar (44 °C).

Sample B

- A strain of *Enterococcus faecium* was included. The distribution of the results showed two peaks (with 23 and 47 results, respectively) and was therefore wide with large dispersion. The colonies were brown-red in varying degree on m-Ent, the darkest colonies were also often even the biggest. Eight false negative results were present.
- In many instances, the darkest colonies were the only ones giving clear positive confirmation on Bile Esculin Azide Agar (BEAA). Thus, many colonies were taken as negative in the confirmation. This is the probable cause to the varying results. Extended confirmation time didn't necessarily give more positive colonies.
- The median is higher for suspected intestinal enterococci (81 cfu/100 ml) compared to for all confirmed results (66 cfu/100 ml). The median for the rightmost peak alone of the confirmed results is 74 cfu/100 ml. ***All results, except the false negative ones, are considered as acceptable due to the variation in colony colour and confirmation outcome***.
- The results by Enterolert® were generally higher (74 cfu/100 ml) because they were absent in the peak with the 23 lowest values, except the false negative one. This false negative results was obtained by the only laboratory that incubated at 41.5 °C. In principle all bacteria were detected as intestinal enterococci by Enterolert®, corresponding to the suspected ones mentioned above.

Sample C

- No enterococcus strain was included but the strain of *Staphylococcus saprophyticus* may sometimes appear on m-Ent with small, often brownish, colonies after 2 days.
- Four false positive results were present despite the small atypical colonies. No blackening at all was seen on BEAA during confirmation (see annex C).

Pseudomonas aeruginosa (MF/MPN)

EN ISO 16266:2008 with or without modification was used by 46 of the 59 laboratories that reported results. One laboratory stated the identical, but since long time withdrawn, CEN standard EN 12780:2002 without modification. Pseudalert® (Idexx Inc.) was reported by 13 laboratories. The incubation was in eleven of these cases done at 38 °C and in 2 cases at 37 °C. For the MF methods the incubation was done at 35, 36 or 37 °C.

Since unhealthy substances like mercury are included, many laboratories have replaced the confirmation tests in the standard by another method. The major modification of the method therefore concerns the confirmation. When only typical yellow-green to blue-green colonies are present, no confirmation needs to be done. In those cases there is no principal difference between what is counted whether "mod." is stated for the method or not.

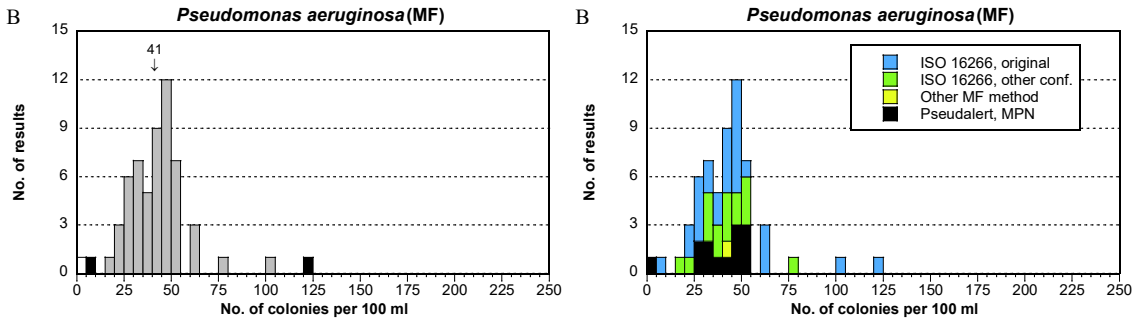
The colonies in sample C were typical, meaning no confirmation was necessary. Those in sample B were a bit more yellow-green, and could normally be deemed as *Pseudomonas aeruginosa* without confirmation. The colonies were clearly fluorescing in UV light in both the samples.

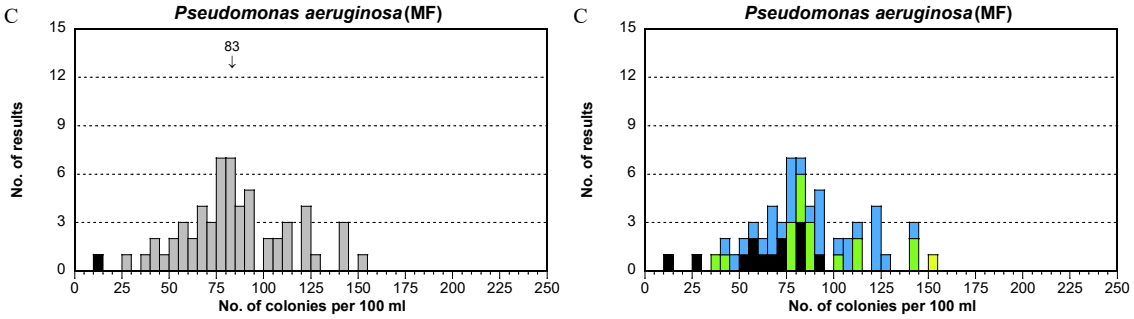
In sample C the average was lower by Pseudalert® than by the MF-methods, but the dispersions (CV) were approximately the same. In sample B no difference between methods could be seen.

Standard/Method	N	A						B						C					
		n	Mv	CV	F	<	>	n	Mv	CV	F	<	>	n	Mv	CV	F	<	>
Total	59	54	**0**	–	4	–	–	55	**41**	16	1	1	1	58	**83**	17	0	1	0
Membrane filtration	*46*	*41*	***0***	–	*4*	–	–	*43*	***41***	*18*	*0*	*1*	*1*	*46*	***88***	*16*	*0*	*0*	*0*
ISO 16266 [a]	29	24	**0**	–	4	–	–	26	**42**	18	0	1	1	29	**87**	15	0	0	0
ISO 16266, mod. [b]	16	16	**0**	–	0	–	–	16	**41**	18	0	0	0	16	**86**	17	0	0	0
Other	1	1	**0**	–	0	–	–	1	**–**	–	0	0	0	1	**–**	–	0	0	0
Pseudalert®, MPN	*13*	*13*	***0***	–	*0*	*0*	*0*	*12*	***41***	*12*	*1*	*0*	*0*	*12*	***66***	*14*	*0*	*1*	*0*

a Modification not stated for confirmation; includes EN 12780:2002

b Alternative confirmation performed, e.g. Maldi-TOF, API, phenanthroline test





Sample A

- There was no *P. aeruginosa* in the sample but instead pale yellow colonies of *Burkholderia cepacia*. Four laboratories reported them as suspected *P. aeruginosa*. Of these, one also reported the result as false positive for *P. aeruginosa*. For the remaining laboratories, confirmation has likely been done with a correct negative outcome.
- Four false positive results were reported.

Sample B

- One strain of *P. aeruginosa* with relatively light yellow-green colonies on PACN was included. The colonies showed a clear fluorescence under UV light. Due to the green colour, no confirmation is necessary according to the standard.
- The results were well accumulated and the distribution therefore good with a small dispersion (CV; see page. 29).
- On false negative result as well as one low and one high outlier were present.

Sample C

- One strain of *P. aeruginosa* with typical blue-green colonies on PACN was included. The colonies showed a clear fluorescence under UV light. No confirmation was necessary according to the standard due to the colour.
- The results appear more dispersed than they are due to the scale of the x-axis. The distribution was good, which can be seen from the small dispersion.
- One low outlier was present.

Culturable microorganisms 22 °C, 3 days

Eighty-three of the 85 laboratories performing the analysis reported EN ISO 6222:1999 as method, which prescribes the use of Yeast extract Agar (YeA). Eight laboratories used Plate Count Agar instead, simultaneously stating the use of EN ISO 6222:1999. One laboratory used YeA and yet another "Standard Methods Agar" (= PCA) in conjunction with Standard methods [5]. These two comprise the group "Other method". The majority of the laboratories have claimed counting both bacterial and fungal colonies. Only four state that they don't count fungi and three others that they count yeasts but not moulds.

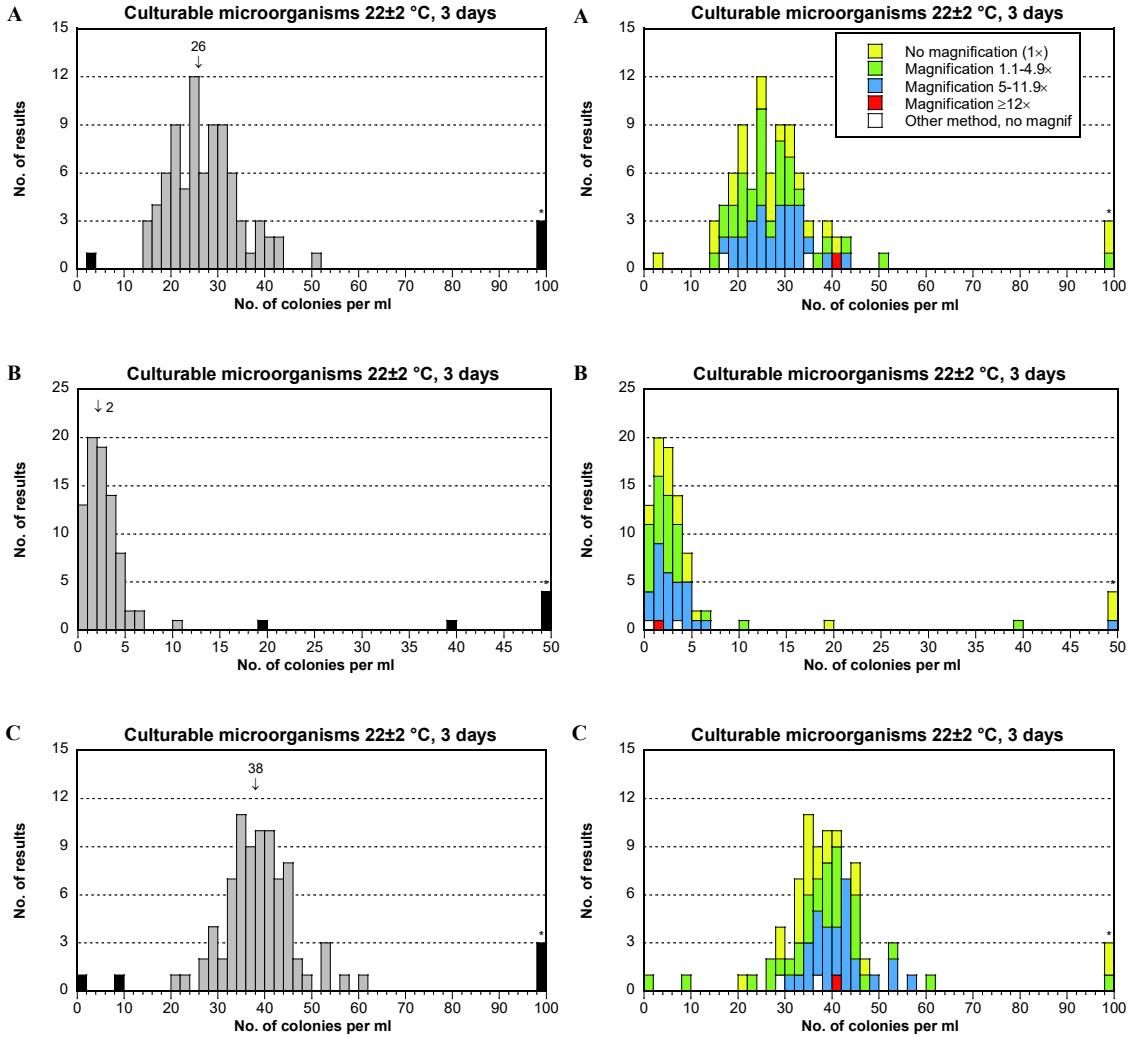
Since all except two laboratories refer to EN ISO 6222:1999, differences among method variants are relevant to discuss only for these. Results are shown for culture media and magnification at reading.

It is difficult to find any consistent method difference. Both in sample A and B, Plate Count Agar gave larger dispersion (CV) than YeA, probably due to the few results for PCA. No general difference was seen in relation to magnification. There might be a tendency to higher results in the two groups with the highest magnification, but it is not certain. The culturable microorganisms at 22 °C were easy to count in all samples. There were no small colonies present that could be difficult to discern. This explains why there were only minute differences when various magnifications were used for counting.

The distributions of the results were good for all samples and the dispersions were small (CV; see p. 29) in sample A and C. In sample B, however, the relative dispersion was very large due to the very low average content. This is quite normal. Some deviating results were reported for each sample.

Group of results	N	A						B						C					
		n	**Mv**	CV	F	<	>	n	**Mv**	CV	F	<	>	n	**Mv**	CV	F	<	>
Total, all results	85	81	**26**	14	0	1	3	79	**2**	56	0	0	6	80	**38**	9	0	2	3
EN ISO 6222	*83*	*79*	***26***	*13*	*0*	*1*	*3*	*77*	***2***	*54*	*0*	*0*	*6*	*78*	***38***	*9*	*0*	*2*	*3*
Medium																			
Yeast extract Agar	75	72	**26**	13	0	1	2	69	**2**	53	0	0	6	73	**38**	9	0	1	1
Plate Count Agar	8	7	**28**	19	0	0	1	8	**1**	69	0	0	0	5	**37**	8	0	1	2
Magnification																			
None	22	19	**25**	15	0	1	2	18	**2**	46	0	0	4	20	**35**	8	0	0	2
1.1–4.9×	31	30	**26**	15	0	0	1	30	**1**	68	0	0	1	28	**38**	11	0	2	1
5–11.9×	29	29	**27**	11	0	0	0	28	**2**	47	0	0	1	29	**41**	7	0	0	0
> 12×	1	1*	**40**	–	0	0	0	1*	**1**	–	0	0	0	1*	**40**	–	0	0	0
Other method	2	2*	**25**	–	0	0	0	2*	**1**	–	0	0	0	2*	**32**	–	0	0	0

* Mean value is given for comparison despite few results



Sample A

- The colonies consist of all the four bacteria in the sample. The two coliform bacteria are in majority.
- The distribution of the results was good, with one low and three high outliers.

Sample B

- The few colonies comprise all bacteria included, but mainly *E. faecium*.
- The distribution of the results was good despite the low average content. Six high outliers were present, out of which five were unreasonably high.

Sample C

- The colonies mainly consist of *S. saprophyticus,* but the three other strains also contributed with a few colonies.
- The distribution of the results was good but with two low and three high outliers. Two of the three high outliers are unreasonably high.

Culturable microorganisms 36 °C, 2 days

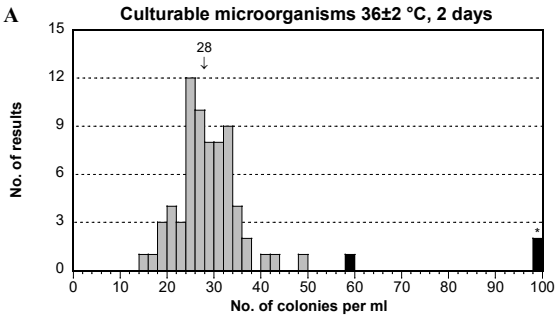
Sixty-nine of the 71 laboratories have stated the use of EN ISO 6222:1999. The two laboratories in the group "Other method" in the table have stated Standard Methods [5]. Five laboratories have reported Plate Count Agar (PCA), all in combination with EN ISO 6222:1999. The values for PCA together with EN ISO 6222:1999 are shown as comparison in the table, despite only 4 values in sample C.

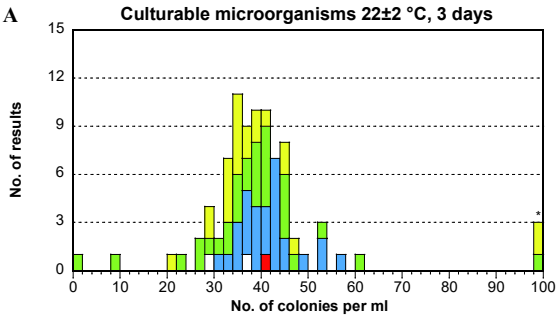
As for the analysis at 22 °C, comparisons of method variants are relevant to discuss only when EN ISO 6222:1999 was used. Also here, the results are presented in relation to culture media and magnification for reading.

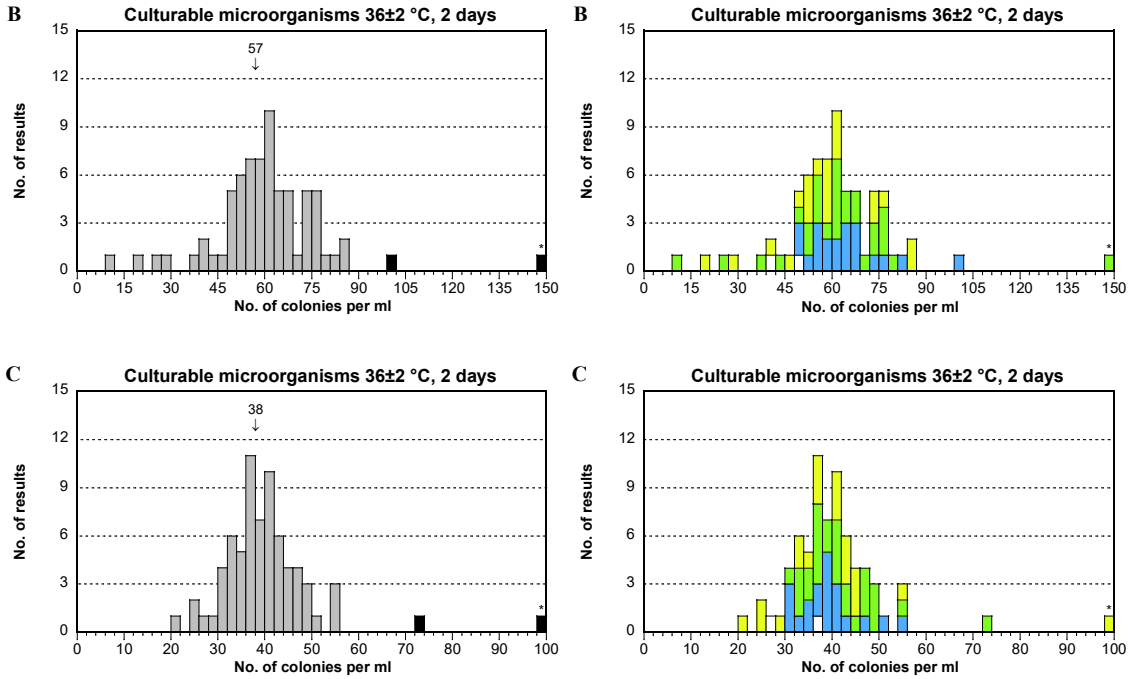
The five laboratories with PCA in sample B show a somewhat lower average result. However, this could be attributed to the way that was used for reading the plates. Three of the laboratories have stated reading without magnification. The average results for "Other method" are somewhat lower than for other groups for all samples.

Group of results	N	A						B						C					
		n	**Mv**	CV	F	<	>	n	**Mv**	CV	F	<	>	n	**Mv**	CV	F	<	>
Total, all results	71	68	**28**	11	0	0	3	69	**57**	14	0	0	2	69	**38**	9	0	0	2
EN ISO 6222	*69*	*66*	***28***	*11*	*0*	*0*	*3*	*67*	***58***	*14*	*0*	*0*	*2*	*67*	***39***	*9*	*0*	*0*	*2*
Medium																			
Yeast extract Agar	64	62	**28**	11	0	0	2	62	**59**	14	0	0	2	63	**39**	9	0	0	1
Plate Count Agar	5	4*	**25**	7	0	0	1	5	**49**	10	0	0	0	4*	**38**	4	0	0	1
Magnification																			
None	21	20	**28**	14	0	0	1	21	**56**	16	0	0	0	20	**37**	11	0	0	1
1.1–4.9×	28	27	**27**	10	0	0	1	27	**57**	16	0	0	1	27	**40**	8	0	0	1
5–11.9×	20	19	**29**	8	0	0	1	19	**62**	7	0	0	1	20	**38**	8	0	0	0
> 12×	0	0	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
Other method	2	2*	**24**	–	0	0	0	2*	**44**	–	0	0	0	2*	**31**	–	0	0	0

* Mean value is given for comparison despite few results







Sample A

- All strains in the sample appeared as culturable microorganisms at 36±2 °C. No particular problems seemed to be present.
- The distribution of the results was good with a very small to small dispersion (CV; see page 29). Three high outliers were present.

Sample B

- All strains in the sample will grow at 36±2 °C. The considerably higher average here compared to at 22 °C is caused by the strain of *S. capitis* that is present in highest concentration and which grows at 36 °C but not at 22 °C.
- The distribution shows, as in previous similar samples (latest September 2018), a small tail of low results. The reason for these is unclear. Possibly, some of the *S. capitis* colonies may not be considered as colonies under the magnification used.
- The lowest results were not objectively identified as deviating ones, although they could be reckoned as such. The relative dispersion of the accepted results was small despite these low results.
- Two high outliers were identified.

Sample C

- All strains in the sample appeared as culturable microorganisms at 36±2 °C. No particular problems seemed to be present.
- The distribution of the results was very good with a very small dispersion.
- Two high outliers were present.

Outcome of the results and laboratory assessment

General information about reported results

The distributions of results for the respective analysis are shown in the histograms. A box plot (see below) gives a summarizing image of all the results of a laboratory, except false results. The number of false results and outliers are given below the plot for each laboratory. These values are highlighted with bold text on yellow background in annex A. The limit values for lowest and highest accepted results are given for each analysis in the summarizing lines at the end of annex A, together with the measurement uncertainty of the mean.

Base for assessment of the performance

The laboratories are not grouped or ranked in relation to their performances. The performance of an individual laboratory can be broadly assessed by the numbers of false results and outliers.

Generally, the laboratories that did not report their results in due time need to evaluate their results themselves. This can be done by comparison with the results of all other laboratories, by looking in tables, figures and annex A.

Mixed up results and other practical errors

Fourteen laboratories have more than one deviating result. When whole samples seem to have been mixed up, the corresponding sample numbers are crossed out in annex A. One laboratory (8663) seems to have mixed up the vials from sample B and C. In one case it seems that two results from a parameter have been mixed up. A number of laboratories seem to have performed individual incorrect calculations from their colony readings to the final concentrations.

Z-scores, box plots and deviating results for each laboratory

The square root transformed results of the laboratories are calculated to standard scores, z-scores, to be comparable between analyses. They are reported in annex B but are not further evaluated here. They are given explicitly to facilitate the follow-up process for laboratories using z-scores in control charts etc. For interpretation and calculation of z-scores, see the explanation to annex A and the scheme protocol [1].

The z-scores are the base for the box plots. The range of the z-scores for each laboratory is shown by a rectangle (box) and lines and/or circles above and beneath the box. The smaller the range from lowest to highest value is in the plot and the more centred around zero the values are, the better the agreement is between the laboratory's results and the means from all laboratories.

Box plots and numbers of deviating results for each participating laboratory

- *z-scores are calculated from the formula z = (x – mv) / s (see annex A).*
- *A correct result "zero" will get z = 0 when there is no target organism present.*
- *False results do not generate z-scores and are not included in 'No. of results'.*
- *The outliers are included in the plots after recalculation to standardised values with the same standard deviation (s) as the rest of the results for each parameter.*
- *z-scores > +4 and < –4 have in the plots been set to +4 and –4, respectively.*
- *The numbers of false positive and false negative results are given in the table under the plots together with the numbers of outliers.*
- *The horizontal line in each box indicates the median for the laboratory.*
- *The box includes 25 % of the results above and below the median. The lines protruding from the box and/or the circles embrace the remaining 50 % of the results, false results excluded.*
- *A circle is for technical reasons shown when a result is to a certain degree deviating* from the rest. This alone does not mean it is an outlier.*
- *The background is divided into coloured fields to simplify localization of the laboratory results.*

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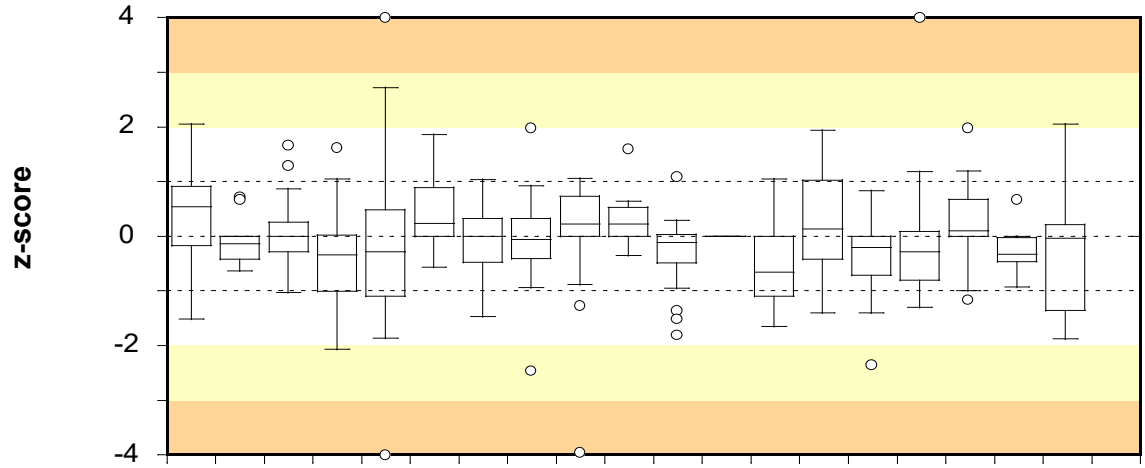
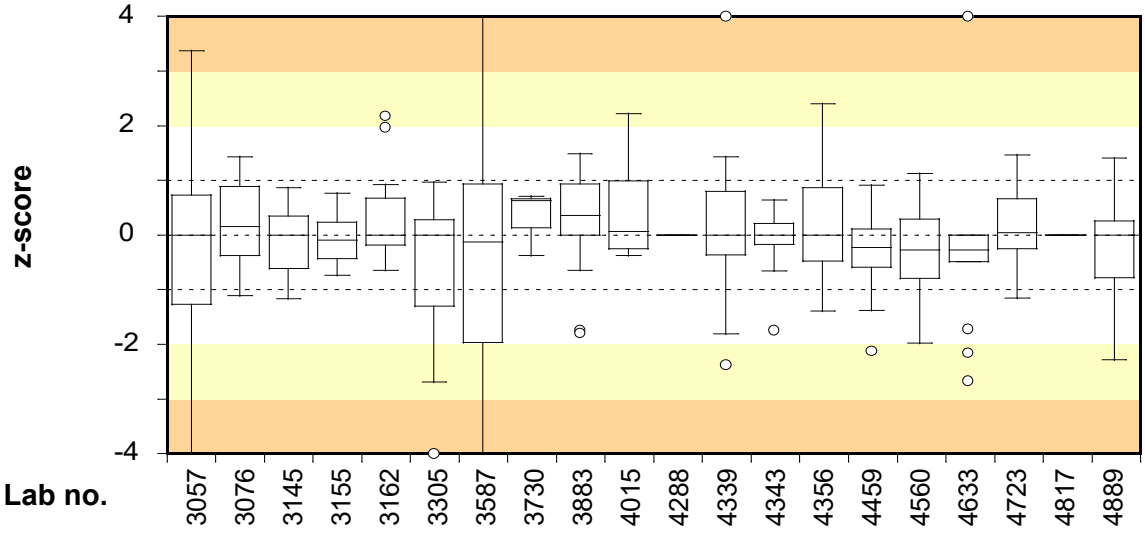
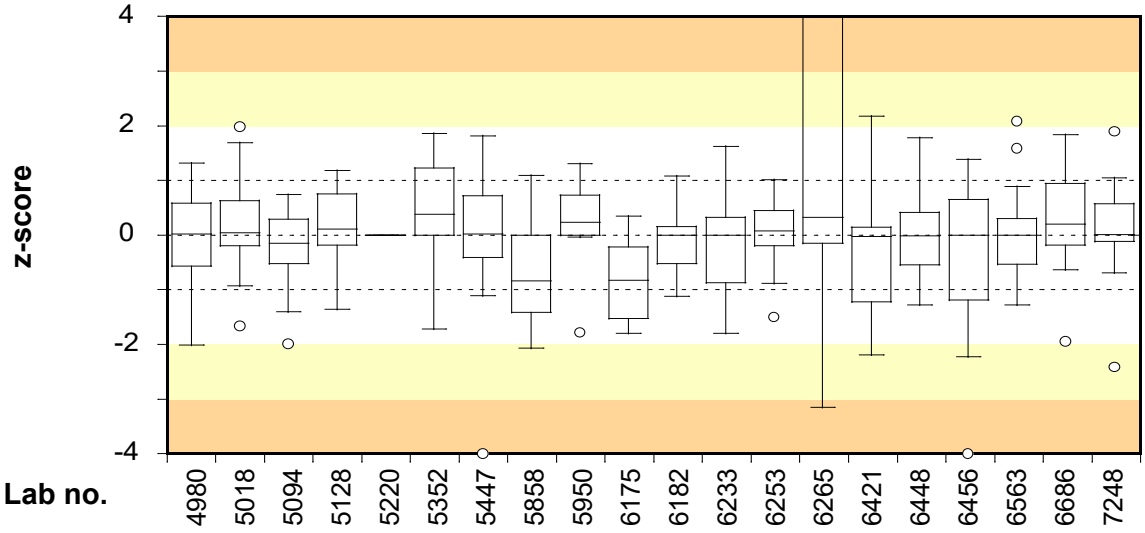
* < [smallest value of the box - 1.5 × (largest value of the box - smallest value of the box)] *or* > [largest value of the box + 1.5 × (largest value of the box - smallest value of the box)]



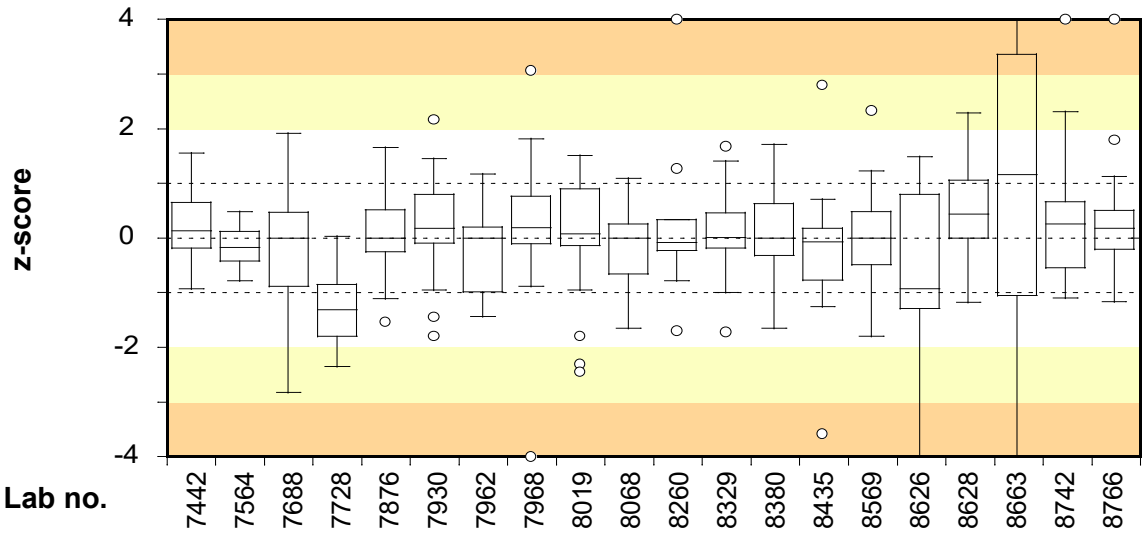
Lab no.	1131	1132	1237	1254	1290	1545	1594	1611	1753	1868	1970	2050	2317	2386	2599	2637	2704	2745	2915	3055
No. of results	9	10	23	24	17	21	24	24	24	15	17	-	18	24	24	15	24	8	10	3
False positive	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
False negative	-	2	1	-	-	-	-	-	-	-	1	-	-	-	-	-	-	1	-	-
Low outliers	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-
High outliers	-	-	-	-	2	-	-	-	-	-	-	-	-	-	-	1	-	-	-	3



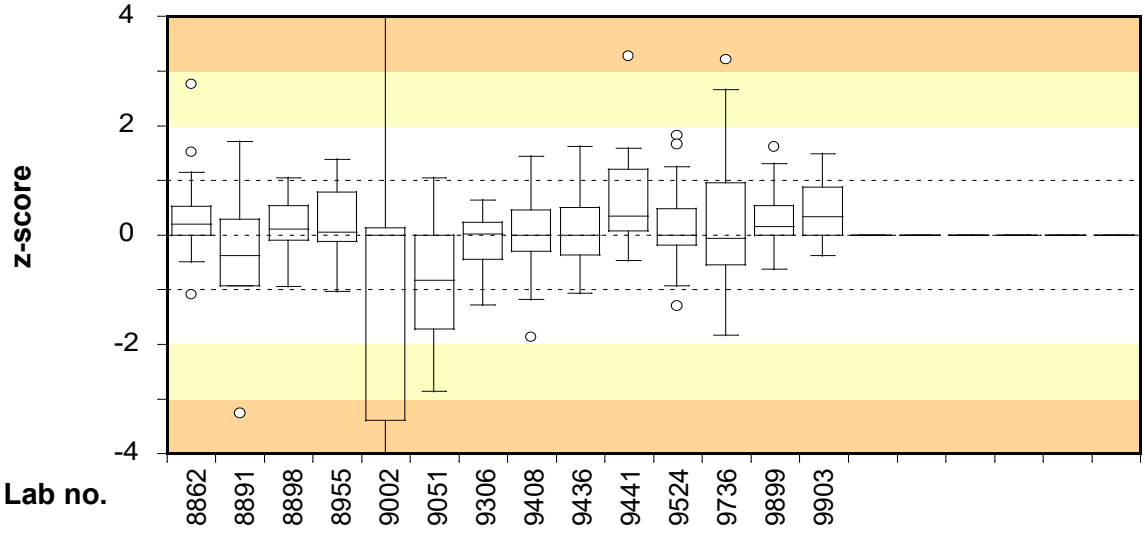
Lab no.	3057	3076	3145	3155	3162	3305	3587	3730	3883	4015	4288	4339	4343	4356	4459	4560	4633	4723	4817	4889
No. of results	19	9	12	8	18	23	7	3	24	12	-	24	18	24	20	11	13	12	-	24
False positive	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
False negative	3	-	-	-	-	1	-	-	-	-	-	-	-	-	1	1	2	-	-	-
Low outliers	1	-	-	-	-	1	1	-	-	-	-	-	-	-	-	-	-	-	-	-
High outliers	-	-	-	-	-	-	1	-	-	-	-	1	-	-	-	-	1	-	-	-



Lab no.	4980	5018	5094	5128	5220	5352	5447	5858	5950	6175	6182	6233	6253	6265	6421	6448	6456	6563	6686	7248
No. of results	24	24	15	18	-	18	24	18	18	9	18	24	12	22	15	12	20	24	12	24
False positive	-	-	-	-	-	-	-	-	-	-	-	-	-	2	-	-	-	-	-	-
False negative	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	-	1	-	-	-
Low outliers	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	1	-	-	-
High outliers	-	-	-	-	-	-	-	-	-	-	-	-	-	7	-	-	-	-	-	-



Lab no.	7442	7564	7688	7728	7876	7930	7962	7968	8019	8068	8260	8329	8380	8435	8569	8626	8628	8663	8742	8766
No. of results	15	12	24	18	24	24	23	24	24	24	9	18	24	18	17	9	15	18	12	23
False positive	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	3	-	1
False negative	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	3	-	-
Low outliers	-	-	-	-	-	-	-	1	-	-	-	-	-	1	-	1	-	2	-	-
High outliers	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	4	2	1



Lab no.	8862	8891	8898	8955	9002	9051	9306	9408	9436	9441	9524	9736	9899	9903
No. of results	20	5	24	24	11	24	12	17	24	12	21	18	24	18
False positive	-	-	-	-	-	-	-	-	-	-	-	-	-	-
False negative	1	1	-	-	1	-	-	1	-	-	-	-	-	-
Low outliers	-	-	-	-	3	-	-	-	-	-	-	-	-	-
High outliers	-	-	-	-	1	-	-	-	-	-	-	-	-	-

Test material, quality controls and processing of data

Description of the test material

This round comprised three test items with different microorganism compositions. The test material was manufactured and freeze-dried in portions of 0.5 ml in small vials, according to the description by Peterz and Steneryd [2]. The simulated water samples were prepared by dissolving the content of the vials in 800 ml of sterile diluent. The composition and approximate concentrations in the samples obtained at the Swedish Food Agency are listed in table 2. The participating laboratories were assigned to perform the analyses according to the methods routinely used by them.

The test material is primarily suited to the EN ISO methods for analyses of drinking water referred to in the European Drinking water directive [4] and its updates [6]. Alternative methods and other standards can usually be used without any problem.

Table 2 *Microorganisms present in the samples*

Sample [1]	**Microorganisms**	**Strain collection no.**		**cfu/100 ml** [2]
		SLV (own)	Reference [3]	
A	*Escherichia coli*	165	CCUG 43600	1000
	Enterobacter cloacae	451	CCUG 30205	1000
	Enterococcus faecalis	051	CCUG 45101	300
	Burkholderia cepacia	042	–	700
B	*Escherichia coli*	082	CCUG 45097	1400
	Hafnia alvei	566	new strain	2800
	Enterococcus faecium	459	CCUG 35172	25
	Pseudomonas aeruginosa	455	CCUG 30209	3
	Staphylococcus capitis	463	CCUG 35173	8
C	*Cronobacter sakazakii*	419	–	50
	Aeromonas hydrophila	533	CCUG 48892	44
	Pseudomonas aeruginosa	395	CCUG 43596	52
	Staphylococcus saprophyticus	013	CCUG 45100	20 *

1 The links between the samples and the randomised sample numbers are shown in annex A; the analyses were performed at the times given in note 1 of table 3

2 cfu = colony forming units; * indicates cfu per ml

3 Origin or typing collection no.; CCUG: Culture Collection University of Gothenburg, Sweden; – indicate a strain from "our own" culture collection that has not yet been typed at another culture collection

Quality control of the test material

It is essential to have a homogeneous sample mixture and a uniform volume in all vials in order to allow comparison of all freeze-dried samples derived from one sample mixture. The volume was checked by weighing 2 to 3 % of the number of vials produced from the sample mixtures. The largest differences between vials were 8, 4 and 8 mg in mixture A, B and C, respectively. The largest accepted difference is 15 mg (3 %).

Table 3 *Contents (cfu) and measures of homogeneity (I_2 and T, see reference 1) in relevant sample volumes for the various parameters in the samples*

Analysis parameter	**Sample** [1]								
Method standard for analysis	**A**			**B**			**C**		
	cfu	**I_2**	**T**	**cfu**	**I_2**	**T**	**cfu**	**I_2**	**T**
Coliform bacteria (MF) *m-Endo Agar LES according to SS 028167*	21 [b]	0.8	1.4	24 [c]	1.4	1.6	65 [a]	0.4	1.2
Suspected thermotolerant colif. bact. (MF) *m-FC Agar. 44 °C according to SS 028167*	8 [b]	0.5	1.7	9	1.1	2.0	–[2]	–	–
Escherichia coli (MF) *m-Endo Agar LES according to SS 028167*	10 [b]	1.4	2.1	7 [c]	0.6	1.7	–	–	–
Intestinal enterococci (MF) *m-Enterococcus Agar acc. to SS-EN ISO 7899-2:2000*	3 [b]	0.5	2.3	43 [c]	0.8	1.3	–	–	–
Pseudomonas aeruginosa (MF) *Pseudomonas Agar base with cetrimide and nalidixic acid according to SS-EN ISO 16266:2008*	–	–	–	34 [c]	0.7	1.4	12 [a]	1.0	1.7
Culturable microorg. 2d 37 °C (pour plate) *Yeast extract Agar according to SS-EN ISO 6222:1999*	22	1.5	1.7	64	0.6	1.2	41	1.1	1.4
Culturable microorg. 3d 22 °C (pour plate) *Yeast extract Agar according to SS-EN ISO 6222:1999*	23	1.3	1.6	1	0.9	5.9	38	1.0	1.4

1 10 vials analysed in duplicate, normally100 ml for MF and 1 ml for pour plate, analysed 22, 13 and 20 weeks ahead of the testing round for the sample A, B and C, respectively

2 Analysis of homogeneity was not performed on m-FC

a Determined for the volume 10 ml

b Determined for the volume 1 ml

c Determined for the volume 50 ml

– No target organism and thus no analysis

Table 3 presents the results from the organizer in the form of concentration means (cfu) and the measures (I_2 and T; see reference 1) used to assess homogeneity from duplicate analyses of 10 vials from each mixture the first time a mixture is used or duplicate analyses from 5 vials in a stability check when a mixture is used a second time. The results relate to the volume that was used for counting the colonies. The

criterion used for a sample mixture to be considered homogenous is that I_2 and T *not simultaneously* are higher than 2. According to that criterion, all mixtures were homogeneous regarding the parameters that were about to be analysed.

Processing of numerical results

Most histograms have "tails" in either or both directions, due to values that do not belong to a normal distribution. For drinking water, ten log transformation of results is seldom routine. With low concentrations as there, calculations are here instead performed after square root transformations of the results, which give the best normal distributions by decreasing the significance of the high deviating results. Very deviating values will still be present in most analyses and are identified as outliers (black bars). False negative results are presented with white bars in the histograms.

Outliers are identified by use of Grubbs' test according to a modification by Kelly [3]. A level of 1 % is set as the risk to incorrectly assess a result as being an outlier. Although the method is objective, there is a prerequisite that the results are normally distributed in order to obtain correct outliers at the 1 % level. A zero result that is a low outlier is considered a false negative result. In special situations, e.g. when many zero results are reported and in some borderline cases, subjective adjustments will be are made based on the knowledge of the sample mixture's content in order to set the right limits. False results and outliers are not included in the calculations of mean values and measures of distribution.

The coefficient of variation (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.

The calculation of uncertainty of measurement of the assigned value is described in the scheme protocol [1]. The assigned value for an analysis is here calculated from the square root transformed results and is the square root of "Mean" in Annex A. It is there denoted as *mv*. Hence, also the measurement uncertainty will be expressed as a square root value. The standard uncertainty of measurement (u) correspond to the standard deviation of the assigned value (s) divided by the number of results squared-root transformed, i.e.: $u = s/\sqrt{n_{mv}}$ where n_{mv} is the number of results in annex A, except the deviating ones. Here is the relative uncertainty (u_{rel}) used and expressed as per cent after division by the mean value *mv* and multiplication by 100.

More about result processing and recommendations on follow-up work are given in the scheme protocol [1]. A PDF of that document is available on the website https://www2.slv.se/absint.

References

1. Anonymous 2018. Scheme protocol, Microbiology, Drinking water & Food, 5th ed. Swedish Food Agency (formerly National Food Agency), Sweden.
2. Peterz, M., Steneryd, A.-C. 1993. Freeze-dried mixed cultures as reference samples in quantitative and qualitative microbiological examinations of food. J. Appl. Bacteriol. 74:143-148.
3. Kelly, K. 1990. Outlier detection in collaborative studies. J. Assoc. Off. Chem. 73:58-64.
4. Anonymous 1998. Council Directive 98/83/EC of 3 November 1998 on the quality of water intended for human consumption. Official Journal of the European Communities. 5.12.98, L 330/32-54 *(national translations available)*.
5. Standard Methods for the Examination of Water and Wastewater, http://www.standardmethods.org/
6. Anonymous 2015. Commission Directive (EU) 2015/1787 of 6 October 2015 amending Annexes II and III to Council Directive 98/83/EC on the quality of water intended for human consumption. Official Journal of the European Union. 7.10.2015, L 260/6-17 *(national translations available)*.

Annex A *Results of the participants, cfu/100 ml (see also the note [#]). Susp. = suspected on membrane filter before confirmation. Results given as < 'value' (e.g. <1, <2, <10 and <100) are treated as zero. The fields with results given as > 'value' are* ***green*** *and are not included in calculations or evaluations. This is also valid for results in* ***shaded columns****. A* ***hyphen*** *indicate that no result has been reported.* ***Figures written in bold in yellow fields*** *indicate outliers, false positive and false negative results.* ***Underlined zero values*** *indicate results characterized as 'False negative ?'.* ***Crossed out sample numbers*** *in a row indicate that the samples probably are mixed up. False positive and false negative values are*

Lab no.	Sample	Suspected coliform bacteria (MF)			Coliform bacteria (MF)			Susp. thermotolerant coliform bact. (MF)			*E. coli* (MF)			Coliform bacteria ("rapid" MPN)			*E. coli* ("rapid" MPN)		
	A B C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C
1131	2 3 1	-	-	-	-	-	-	-	-	-	-	-	-	2014	12	461	866	6	0
1132	1 2 3	-	-	-	-	-	-	-	-	-	-	-	-	1733	16	276	**0**	**0**	0
1237	3 2 1	-	-	-	1400	24	470	-	-	-	830	24	<1	1400	17	440	820	17	<1
1254	3 2 1	1100	7	120	1100	7	24	-	-	-	550	7	0	1600	12	200	730	12	0
1290	2 1 3	-	-	-	1450	7	95	-	-	-	810	7	0	-	-	-	-	-	-
1545	1 2 3	1650	29	335	1650	26	210	1240	18	210	1240	18	0	1680	23	305	1040	23	0
1594	1 3 2	-	-	-	1700	31	300	-	-	-	1100	18	0	1600	17	370	820	14	0
1611	3 1 2	1400	32	310	1400	32	207	570	3	96	800	13	0	1553	19	291	727	19	0
1753	2 1 3	-	-	-	1740	19	420	-	-	-	840	19	0	1986	23	435	921	23	0
1868	3 1 2	1886	16	336	1886	16	182	-	-	-	923	16	0	1962	26	345	957	14	0
1970	2 3 1	1600	24	440	1600	24	270	1600	24	440	1200	11	0	-	-	-	-	-	-
2050	2 1 3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2317	1 3 2	-	-	-	1100	6	100	-	-	-	660	6	0	-	-	-	-	-	-
2386	1 2 3	2300	8	570	2300	8	400	800	5	500	800	5	0	2500	12	450	950	12	<1
2599	3 1 2	1300	17	150	1300	17	150	400	23	0	520	2	0	1700	11	240	650	11	0
2637	2 1 3	-	-	-	-	-	-	-	-	-	-	-	-	1652	9	500	885	9	<1
2704	1 2 3	2700	8	320	2700	8	260	-	-	-	860	8	<1	2070	22	344	945	22	<1
2745	1 3 2	1560	10	280	1560	10	**0**	1560	10	0	760	10	0	-	-	-	-	-	-
2915	3 2 1	-	-	-	1200	-	440	-	-	-	400	-	<1	-	-	-	-	-	-
3055	3 2 1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3057	2 1 3	-	-	-	1700	22	**<10**	-	-	-	1700	22	<10	920	2	**<2**	**240**	2	<2
3076	2 3 1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3145	1 3 2	-	-	-	-	-	-	-	-	-	-	-	-	1553	11	365	1046	11	0
3155	2 1 3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3162	3 2 1	-	-	-	-	-	-	-	-	-	-	-	-	1733	17	435	980	12	0
3305	3 2 1	1100	24	480	1100	24	380	-	-	-	**90**	8	<1	870	6	380	740	6	<1
3587	1 2 3	-	-	-	-	-	-	-	-	-	-	-	-	>1	>1	>1	>1	>1	0
3730	2 3 1	2300	20	500	-	-	-	530	13	270	-	-	-	-	-	-	-	-	-
3883	1 3 2	1830	42	570	1830	42	390	-	-	-	1050	18	< 1	2333	24	468	1185	5	< 1
4015	1 3 2	-	-	-	-	-	-	-	-	-	-	-	-	2203	17	503	923	17	0
4288	1 2 3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4339	3 1 2	2100	34	280	2100	34	170	1070	2	155	**8400**	22	<10	1986	23	488	866	23	0
4343	2 1 3	-	-	-	-	-	-	-	-	-	-	-	-	1553	20	326	866	5	0
4356	2 3 1	2300	42	530	2300	42	424	720	8	320	1687	25	0	1733	20	488	727	20	0
4459	3 2 1	733	0	382	1500	18	**<1**	-	-	-	767	18	<1	2070	8	136	702	8	<1
4560	3 2 1	-	-	-	1650	3	**<1**	-	-	-	990	3	<1	-	-	-	-	-	-
4633	2 3 1	-	-	-	-	-	-	432	>8000	52	432	>8000	0	1603	>24000	311	808	>24000	0
4723	3 2 1	-	-	-	-	-	-	-	-	-	-	-	-	2420	19	387	1203	11	0
4817	2 1 3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4889	2 1 3	-	-	-	1600	30	130	-	-	-	760	12	0	2400	16	460	980	16	0
4980	1 3 2	1300	39	400	1300	39	330	740	9	390	740	9	<1	2005	23.8	144.5	1013	23.8	<1
5018	1 3 2	2100	48	500	2100	48	450	-	-	-	760	15	<1	1990	20	460	730	20	<1
5094	3 1 2	1410	31	350	1410	31	350	-	-	-	670	15	0	-	-	-	-	-	-
5128	1 3 2	-	-	-	-	-	-	-	-	-	-	-	-	1445	18	200	831	18	0
5220	1 3 2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
5352	3 2 1	-	-	-	2500	15	400	1100	15	0	1300	15	0	-	-	-	-	-	-
5447	3 2 1	-	-	-	2000	31	390	-	-	-	1000	15	0	1616	10	432	906	10	0
5858	3 2 1	1020	12	67	1020	12	67	-	-	-	560	12	0	-	-	-	-	-	-
5950	2 3 1	1673	39	536	1673	39	282	536	11	182	945	21	<1	1929	26	453	902	26	<1
6175	2 3 1	-	-	-	-	-	-	-	-	-	-	-	-	>200	18	>200	>200	18	<1
6182	2 1 3	878	<1	233	1613	9	233	-	-	-	735	9	<1	1723	34	273	772	8	<1
6233	3 1 2	980	33	544	980	33	544	-	-	-	630	12	**0**	1418	23	345	727	16	0
6253	3 1 2	-	-	-	-	-	-	-	-	-	-	-	-	1450	19	187	850	19	0
6265	2 1 3	12700	116	10800	1800	**99**	300	700	11	200	700	11	0	**28000**	23	70	1400	5	0
6421	1 2 3	-	-	-	700	**<300**	**<300**	700	<300	<300	700	**<300**	<300	-	-	-	-	-	-
6448	2 1 3	1300	50	200	1300	50	200	-	-	-	700	9	<1	-	-	-	-	-	-
6456	2 3 1	-	-	-	690	25	370	-	-	-	**81**	**<1**	<1	1184	9	288	1184	8	<1
6563	1 2 3	1181	37	645	1181	22	387	1181	22	387	709	15	0	1948	31	367	798	17	0
6686	1 2 3	-	-	-	-	-	-	-	-	-	-	-	-	2005	32.4	150	831	32.4	<1
7248	2 3 1	1800	18	450	1800	18	10	670	10	68	670	10	0	2074	20	390	1300	20	0
7442	2 3 1	1650	10	405	1650	10	200	-	-	-	818	10	0	1873	41	370	1018	23	0
7564	3 2 1	-	-	-	1600	27	310	-	-	-	920	11	<1	-	-	-	-	-	-
7688	2 1 3	2500	10	150	2500	1	150	-	-	-	1500	1	0	2400	10	290	920	10	0
7728	1 3 2	-	-	-	1200	2	120	-	-	-	620	2	0	-	-	-	-	-	-
7876	2 3 1	2400	16	454	2400	16	227	680	1	38	1400	16	<1	1221	16	328	781	16	<1
7930	2 3 1	2000	32	260	2000	32	260	-	-	-	490	13	<1	2400	36	410	1200	36	<1
7962	1 2 3	1400	21	360	1200	18	290	470	5	100	530	6	0	1990	15	410	690	15	0
7968	2 3 1	-	-	-	1700	38	360	-	-	-	**88**	18	0	2000	14	340	800	14	0
8019	2 1 3	1400	18	473	1400	18	218	730	7	150	960	18	0	980	33	548	980	22	0
8068	2 3 1	-	-	-	1700	32	96	-	-	-	1200	14	0	1500	31	280	660	16	0
8260	3 1 2	1119	72	216	1550	40	46	-	-	-	791	14	0	-	-	-	-	-	-
Mean					**1587**	**20**	**232**				**857**	**12**	**0**	**1788**	**20**	**343**	**899**	**15**	**0**
CV (%)					15	32	33				17	25	-	11	27	17	11	25	-

excluded, as well as other outliers, in the summarizing calculated results at the end of the table. The mean value (Mean) is the square of the mean value for the square root transformed results (mv). The coefficient of variation (CV) is the standard deviation (s) in percentage of the mean value for the square root transformed results. As means to calculate the z-values of your own, the appropriate values of mv and s are given at the end of the table. The x-values are obtained as the square roots of the reported result, respectively. z = (x - mv) / s. $u_{rel,mv}$ is the relative standard uncertainty of mv in per cent. For calculation see the scheme protocol (1); also briefly described in the text.

Susp. intestinal enterococci (MF)			Intestinal enterococci			Susp. *Pseudomonas aeruginosa* (MF)			*Pseudomonas aeruginosa*			Total plate count 22 °C, 3 days #			Total plate count 36±2 °C, 2 days #			Lab no.
A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	
-	-	-	-	-	-	-	-	-	-	-	-	43	4	42	-	-	-	1131
-	-	-	350	85	0	-	-	-	-	-	-	22	3	37	-	-	-	1132
-	-	-	350	<1	<1	-	-	-	<1	54	76	24	1	44	27	57	40	1237
290	80	57	290	49	0	0	44	82	0	44	82	31	4	34	28	86	41	1254
-	-	-	290	75	0	-	-	-	180	35	69	130	10	26	130	11	45	1290
420	66	24	420	66	0	0	34	76	0	34	76	32	6	52	-	-	-	1545
-	-	-	270	22	0	-	-	-	0	30	88	19	2	34	25	75	43	1594
500	108	17	500	92	0	0	32	88	0	32	88	25	3	35	15	73	36	1611
430	82	28	430	82	0	-	-	-	0	52	10	32	2	32	31	60	30	1753
-	-	-	-	-	-	0	43	117	-	-	-	39	2	42	-	-	-	1868
300	0	0	300	0	0	0	38	91	0	38	91	15	1	29	27	36	35	1970
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2050
-	-	-	430	41	0	-	-	-	0	22	63	26	4	34	20	45	41	2317
290	77	2950	290	77	0	0	32	120	0	32	120	42	1	40	32	76	48	2386
390	51	0	390	51	0	0	39	82	0	39	82	28	2	44	25	68	33	2599
280	83	2600	280	63	<1	-	-	-	-	-	-	21	187	33	23	53	44	2637
360	90	18	360	90	<1	-	-	-	<1	29	70	28	3	44	28	78	43	2704
-	-	-	-	-	-	-	-	-	-	-	-	24	3	34	-	-	-	2745
410	90	<1	-	-	-	-	-	-	-	-	-	26	2	29	20	57	54	2915
-	-	-	-	-	-	-	-	-	-	-	-	1020	700	1025	-	-	-	3055
-	-	-	400	<1	120	-	-	-	700	100	120	31	1	44	27	51	25	3057
-	-	-	-	-	-	0	60	109	0	60	109	19	1	33	32	60	49	3076
-	-	-	387	67	0	-	-	-	0	54	54	-	-	-	-	-	-	3145
-	-	-	313	42	<1	-	-	-	-	45	105	-	-	-	29	51	37	3155
350	81	4100	350	80	0	0	40	110	0	39	110	26	3	53	24	54	55	3162
400	64	3500	400	<1	<1	<1	20	85	<1	20	85	16	1	45	31	62	34	3305
-	-	-	-	-	-	-	-	-	-	-	-	2	19	37	40	20	32	3587
-	-	-	-	-	-	-	-	-	-	-	-	31	1	43	-	-	-	3730
385	65	2800	385	65	< 1	< 1	63	104	< 1	63	104	27	< 1	49	25	62	34	3883
518	49	90	518	49	0	-	-	-	-	-	-	34	1	36	-	-	-	4015
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4288
390	76	2100	290	69	0	0	48	76	0	34	64	25	3	36	18	26	39	4339
400	99	2791	400	61	0	-	-	-	0	42	66	24	2	42	31	68	38	4343
400	80	13	400	18	0	-	-	-	0	27	59	25	2	30	25	50	43	4356
315	91	>300	315	91	<1	-	-	-	-	-	-	24	3	36	25	61	36	4459
-	-	-	-	-	-	-	-	-	-	-	-	35	3	36	25	41	36	4560
-	-	-	233	0	0	-	-	-	0	0	26	-	-	-	26	13273	37	4633
373	81	3600	373	23	0	-	-	-	-	-	-	27	1	45	-	-	-	4723
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4817
-	-	-	310	16	0	-	-	-	0	48	65	25	0	44	17	27	29	4889
450	79	22	450	24	<1	-	-	-	<1	47.8	59.1	30	3	32	33	58	31	4980
500	92	51	500	13	<1	<1	46	85	<1	46	85	25	3	41	25	52	37	5018
350	71	120	350	8	0	-	-	-	-	-	-	23	3	34	20	54	39	5094
420	93	-	420	93	0	0	54	78	0	54	78	31	2	38	32	70	47	5128
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	5220
-	-	-	490	12	0	-	-	-	0	45	120	29	2	52	31	64	32	5352
-	-	-	100	91	0	-	-	-	0	51	140	28	1	46	26	48	32	5447
356	66	>3000	356	66	0	0	18	43	0	18	43	20	0	41	19	76	32	5858
363	81	3254	363	11	<1	<1	52	82	<1	52	82	-	-	-	-	-	-	5950
-	-	-	-	-	-	-	-	-	-	-	-	17	<1	28	23	48	27	6175
370	96	3257	370	96	<1	-	-	-	-	-	-	25	2	39	-	-	-	6182
304	100	13	304	100	0	0	54	83	0	54	83	16	0	35	36	64	40	6233
-	-	-	370	98	0	-	-	-	-	-	-	33	2	41	-	-	-	6253
0	0	0	360	159	24	0	0	2120	2600	120	75	300	0	8300	200	58	162	6265
-	-	-	410	74	0	-	-	-	0	27	51	18	1	40	19	57	55	6421
-	-	-	-	-	-	-	-	-	<1	44	82	-	-	-	36	39	43	6448
-	-	-	453	74	<1	-	-	-	-	-	-	30	<1	46	33	55	37	6456
309	127	2700	309	127	0	0	43	150	0	43	150	18	2	31	26	50	34	6563
410	74	<1	-	-	-	-	-	-	-	-	-	22	6	40	28	73	39	6686
420	78	3300	420	78	0	340	48	76	0	48	76	23	4	38	33	67	38	7248
-	-	-	-	-	-	-	-	-	-	-	-	21	5	43	-	-	-	7442
-	-	-	-	-	-	-	-	-	-	-	-	21	1	35	24	51	37	7564
470	74	18	470	64	0	0	29	79	0	29	79	29	0	22	35	67	34	7688
-	-	-	300	18	0	-	-	-	0	26	49	14	0	29	20	58	25	7728
391	102	3300	391	102	<1	<1	49	120	<1	49	120	30	1	39	27	55	31	7876
300	89	<1	300	89	<1	-	-	-	<1	45	72	25	<1	35	28	64	41	7930
440	67	3600	440	17	0	0	19	55	0	-	55	19	1	38	28	73	42	7962
-	-	-	310	69	0	-	-	-	0	49	140	39	2	32	49	60	44	7968
300	93	14	300	3	0	400	40	114	0	40	114	33	0	39	35	60	48	8019
-	-	-	260	76	0	-	-	-	0	43	81	21	2	32	26	62	37	8068
-	-	-	-	-	-	-	-	-	-	-	-	21	62	37	-	-	-	8260
			359	**56**	**0**				**0**	**41**	**83**	**26**	**2**	**38**	**28**	**57**	**38**	**Mean**
			9	31	-				-	16	17	14	56	9	11	14	9	**CV (%)**

Lab no.	Sample	Suspected coliform bacteria (MF)			Coliform bacteria (MF)			Susp. thermotolerant coliform bact. (MF)			*E. coli* (MF)			Coliform bacteria ("rapid" MPN)			*E. coli* ("rapid" MPN)		
	A B C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C
8329	1 2 3	-	-	-	-	-	-	-	-	-	-	-	-	1796	43	345	717	19	0
8380	2 1 3	-	-	-	2000	33	310	-	-	-	800	17	0	1600	19	350	610	19	0
8435	2 3 1	-	-	-	1950	13	80	480	13	89	650	13	0	-	-	-	-	-	-
8569	1 3 2	1360	15	330	1360	15	330	-	-	-	640	15	0	1990	36	310	800	12	0
8626	2 3 1	2070	7	370	1150	7	370	-	-	-	1150	7	0	-	-	-	-	-	-
8628	1 2 3	-	-	-	2300	**<300**	**<300**	900	<300	<300	900	**<300**	<300	-	-	-	-	-	-
8663	1 ~~2~~ ~~3~~	2300	540	16	2300	**380**	14	760	250	5	2100	**0**	**8**	2400	**520**	**19**	1100	**0**	**15**
8742	3 1 2	-	-	-	1100	18	130	-	-	-	570	10	<1	-	-	-	-	-	-
8766	3 1 2	1827	25	218	1827	25	218	-	-	-	909	25	0	2012	25	218	745	25	0
8862	1 2 3	1763	26	464	1763	26	264	-	-	-	918	11	0	1379	62	359	1025	29	0
8891	2 1 3	-	-	-	400	10	**<1**	-	-	-	-	-	-	-	-	-	-	-	-
8898	2 1 3	1829	34	486	1829	34	391	-	-	-	1000	10	0	1790	21	365	769	9	0
8955	2 3 1	-	-	-	1200	39	210	700	11	110	900	17	0	1400	30	340	920	22	0
9002	1 2 3	-	-	-	**29**	21	2	-	-	-	**5**	**0**	0	-	-	-	-	-	-
9051	1 2 3	-	-	-	1368	8	79	-	-	-	729	8	**0**	1733	9	119	1046	9	<1
9306	3 1 2	-	-	-	-	-	-	-	-	-	-	-	-	1787	11	425	847	11	0
9408	3 1 2	-	-	-	-	-	-	-	-	-	-	-	-	2419	20	411	687	20	<1
9436	2 1 3	1482	12	485	1482	12	345	618	4	309	809	12	0	1938	19	566	1098	19	0
9441	3 2 1	-	-	-	-	-	-	-	-	-	-	-	-	2380	24	560	1640	14	0
9524	3 2 1	-	-	-	2600	7	280	-	-	-	1000	7	<1	2086	14	313	1248	14	<1
9736	1 2 3	-	-	-	-	-	-	-	-	-	-	-	-	1226	71	330	582	42	0
9899	3 1 2	1648	13	410	1648	13	410	-	-	-	881	13	0	2356	42	423	967	14	0
9903	2 1 3	2045	44	556	2045	44	320	1550	10	272	900	10	0	-	-	-	-	-	-
n		42	42	42	67	66	67	26	25	26	67	65	67	63	63	63	63	63	65
Min		733	0	16	29	0	0	400	0	0	5	0	0	870	2	0	0	0	0
Max		12700	540	10800	2700	380	544	1600	250	500	8400	25	8	28000	520	566	1640	42	15
Median		1650	24	391	1631	21.5	267	710	10	130	809.5	12	0	1793	19.5	359	866	16	0
Mean					**1587**	**20**	**232**				**857**	**12**	**0**	**1788**	**20**	**343**	**899**	**15**	**0**
CV (%)					15	32	33				17	25	-	11	27	17	11	25	-
False positive					0	0	0				0	0	1	0	0	0	0	0	1
False negative					0	2	7				0	5	0	0	0	1	1	2	0
Outliers, low					1	0	0				4	0	0	0	0	1	1	0	0
Outliers, high					0	2	0				1	0	0	1	1	0	0	0	0
Low limit OK		733	0	16	400	1	2	400	0	0	400	1	0	870	2	70	582	2	0
High limit OK		1E+05	540	10800	2700	50	544	1600	250	500	2100	25	0	2500	71	566	1640	42	0
mv *(√Mean)*					39.836	4.498	15.218				29.266	3.449	0.000	42.290	4.510	18.531	29.977	3.912	0.000
s *(CV*mv/100)*					6.102	1.439	4.990				4.924	0.867	0.000	4.767	1.217	3.231	3.205	0.965	0.000
$u_{rel,mv}$ (%) *(100*s/ √n_{mv}/mv)*					1.9	4.1	4.2				2.1	3.2		1.4	3.4	2.2	1.4	3.2	
x *(√Result)*																			
z *([x-mv]/s)*																			

 # cfu/ml

Susp. intestinal enterococci (MF)			Intestinal enterococci			Susp. *Pseudomonas aeruginosa* (MF)			*Pseudomonas aeruginosa*			Total plate count 22 °C, 3 days #			Total plate count 36±2 °C, 2 days #			Lab no.
A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	
367	12	2773	367	12	0	-	-	-	0	31	81	25	1	45	31	82	40	**8329**
-	-	-	290	62	0	-	-	-	0	35	100	40	3	33	26	74	36	**8380**
-	-	-	300	55	0	0	21	74	0	**7**	74	21	2	60	24	56	40	**8435**
310	63	2100	310	63	**2100**	-	-	-	-	-	-	28	0	56	-	-	-	**8569**
-	-	-	-	-	-	-	-	-	-	-	-	38	0	**9**	-	-	-	**8626**
-	-	-	400	73	0	-	-	-	0	27	140	26	3	38	43	84	44	**8628**
510	300	70	510	**0**	**16**	0	77	35	0	77	35	20	**39**	**1**	31	42	**73**	**8663**
-	-	-	-	-	-	-	-	-	-	-	-	31	**520**	42	32	**100**	42	**8742**
350	66	1800	350	43	0	690	33	91	**690**	33	91	28	4	36	**59**	73	36	**8766**
373	73	3900	373	**0**	0	-	-	-	-	-	-	29	4	38	35	50	38	**8862**
-	-	-	-	-	-	-	-	-	-	-	-	40	1	40	-	-	-	**8891**
332	80	0	332	80	0	0	48	78	0	48	78	33	1	39	33	63	46	**8898**
350	91	3700	350	90	0	-	-	-	0	48	93	34	5	34	32	56	32	**8955**
-	-	-	**32**	22	0	-	-	-	-	-	-	50	2	**120**	-	-	-	**9002**
-	-	-	252	90	0	-	-	-	0	20	44	14	4	21	22	52	21	**9051**
-	-	-	-	-	-	-	-	-	-	-	-	18	2	41	28	61	40	**9306**
-	-	-	390	**0**	0	-	-	-	0	48	94	23	1	26	26	75	41	**9408**
327	56	3624	327	25	0	509	41	69	0	41	69	21	2	34	31	77	50	**9436**
344	101	0	-	-	-	-	-	-	-	-	-	29	2	41	25	60	46	**9441**
-	-	-	355	54	<1	-	-	-	-	-	-	36	1	38	28	63	46	**9524**
325	117	0	325	117	0	0	43	111	0	43	111	16	4	37	25	55	30	**9736**
338	71	0	338	71	0	0	43	93	0	43	93	30	3	42	30	57	38	**9899**
342	91	13	342	44	0	0	60	128	0	60	128	33	1	40	35	67	41	**9903**
48	48	45	70	70	70	32	32	32	58	58	59	85	85	85	71	71	71	**n**
0	0	0	32	0	0	0	0	35	0	0	10	2	0	1	15	11	21	**Min**
518	300	4100	518	159	2100	690	77	2120	2600	120	150	1020	700	8300	200	13273	162	**Max**
365	80	70	355.5	66	0	0	43	85	0	43	82	26	2	38	27.5	60	38	**Median**
			359	**56**	**0**				**0**	**41**	**83**	**26**	**2**	**38**	**28**	**57**	**38**	**Mean**
			9	31	-				-	16	17	14	56	9	11	14	9	**CV (%)**
			0	0	4				4	0	0	0	0	0	0	0	0	**False pos.**
			0	8	0				0	1	0	0	0	0	0	0	0	**False neg.**
			2	0	0				0	1	1	1	0	2	0	0	0	**Outliers <**
			0	0	0				0	1	0	3	6	3	3	2	2	**Outliers >**
0	0	0	233	3	0	0	0	35	0	18	26	14	0	21	15	11	21	**Low limit**
518	300	4100	518	159	0	690	77	2120	0	100	150	50	10	60	49	86	55	**High limit**
			18.956	7.512	0.000				0.000	6.435	9.105	5.129	1.261	6.157	5.263	7.579	6.191	**mv**
			1.715	2.354	0.000				0.000	1.058	1.503	0.696	0.701	0.568	0.565	1.045	0.563	**s**
			1.1	4.0						2.2	2.2	1.5	6.3	1.0	1.3	1.7	1.1	**$u_{rel,mv}$ (%)**
																		x
																		z

 # cfu/ml

Annex B *z-scores calculated from the laboratory results. Susp. = Suspected on the membrane filters before confirmation. z = (x - mv) / s. z-scores are calculated also for outliers (excluding false negative results) in the same way as ordinary z-scores. From false*

Lab no.	Sample	Suspected coliform bacteria (MF)			Coliform bacteria (MF)			Susp. thermotolerant coliform bact. (MF)			*E. coli* (MF)			Coliform bacteria ("rapid" MPN)			*E. coli* ("rapid" MPN)		
	A B C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C
1131	2 3 1													0.543	-0.859	0.910	-0.171	-1.515	0.000
1132	1 2 3													-0.139	-0.419	-0.594			0.000
1237	3 2 1				-0.397	0.278	1.295				-0.093	1.673	0.000	-1.022	-0.318	0.757	-0.418	0.219	0.000
1254	3 2 1				-1.093	-1.287	**-2.068**				-1.181	-0.926	0.000	-0.480	-0.859	-1.359	-0.923	-0.464	0.000
1290	2 1 3				-0.288	-1.287	-1.097				-0.164	-0.926	0.000						
1545	1 2 3				0.129	0.417	-0.146				1.208	0.916	0.000	-0.273	0.235	-0.330	0.709	0.916	0.000
1594	1 3 2				0.229	0.743	0.421				0.792	0.916	0.000	-0.480	-0.318	0.218	-0.418	-0.176	0.000
1611	3 1 2				-0.397	0.805	-0.167				-0.199	0.181	0.000	-0.605	-0.124	-0.456	-0.940	0.464	0.000
1753	2 1 3				0.308	-0.097	1.057				-0.058	1.050	0.000	0.477	0.235	0.720	0.116	0.916	0.000
1868	3 1 2				0.589	-0.346	-0.346				0.226	0.636	0.000	0.420	0.484	0.013	0.299	-0.176	0.000
1970	2 3 1				0.027	0.278	0.243				1.092	-0.152	0.000						
2050	2 1 3																		
2317	1 3 2				-1.093	-1.424	-1.046				-0.726	-1.153	0.000						
2386	1 2 3				1.331	-1.160	0.958				-0.199	-1.399	0.000	1.617	-0.859	0.830	0.264	-0.464	0.000
2599	3 1 2				-0.620	-0.261	-0.595				-1.313	**-2.347**	0.000	-0.222	-0.980	-0.941	-1.398	-0.616	0.000
2637	2 1 3													-0.345	-1.241	1.186	-0.071	-0.945	0.000
2704	1 2 3				1.987	-1.160	0.182				0.012	-0.716	0.000	0.673	0.149	0.005	0.238	0.807	0.000
2745	1 3 2				-0.056	-0.928					-0.345	-0.330	0.000						
2915	3 2 1				-0.851		1.154				-1.882		0.000						
3055	3 2 1																		
3057	2 1 3				0.229	0.133					**2.430**	1.432	0.000	**-2.508**	**-2.544**		**-4.000**	**-2.588**	0.000
3076	2 3 1																		
3145	1 3 2													-0.605	-0.980	0.178	0.738	-0.616	0.000
3155	2 1 3																		
3162	3 2 1													-0.139	-0.318	0.720	0.414	-0.464	0.000
3305	3 2 1				-1.093	0.278	0.857				**-4.000**	-0.716	0.000	**-2.684**	-1.693	0.298	-0.865	-1.515	0.000
3587	1 2 3																		0.000
3730	2 3 1																		
3883	1 3 2				0.482	1.377	0.908				0.637	0.916	0.000	1.261	0.320	0.960	1.388	-1.736	0.000
4015	1 3 2													0.975	-0.318	1.206	0.126	0.219	0.000
4288	1 2 3																		
4339	3 1 2				0.982	0.926	-0.437				**4.000**	1.432	0.000	0.477	0.235	1.102	-0.171	0.916	0.000
4343	2 1 3													-0.605	-0.031	-0.147	-0.171	-1.736	0.000
4356	2 3 1				1.331	1.377	1.077				**2.398**	1.789	0.000	-0.139	-0.031	1.102	-0.940	0.581	0.000
4459	3 2 1				-0.181	-0.178					-0.319	0.916	0.000	0.673	-1.382	**-2.126**	-1.086	-1.122	0.000
4560	3 2 1				0.129	-1.922					0.446	-1.980	0.000						
4633	2 3 1										-1.723		0.000	-0.473		-0.277	-0.484		0.000
4723	3 2 1													1.448	-0.124	0.353	1.469	-0.616	0.000
4817	2 1 3																		
4889	2 1 3				0.027	0.680	-0.765				-0.345	0.018	0.000	1.405	-0.419	0.903	0.414	0.092	0.000
4980	1 3 2				-0.620	1.214	0.591				-0.419	-0.518	0.000	0.522	0.303	**-2.015**	0.578	1.002	0.000
5018	1 3 2				0.982	1.688	1.201				-0.345	0.489	0.000	0.487	-0.031	0.903	-0.923	0.581	0.000
5094	3 1 2				-0.375	0.743	0.699				-0.687	0.489	0.000						
5128	1 3 2													-0.897	-0.219	-1.359	-0.359	0.343	0.000
5220	1 3 2																		
5352	3 2 1				1.666	-0.435	0.958				1.379	0.489	0.000						
5447	3 2 1				0.801	0.743	0.908				0.479	0.489	0.000	-0.439	-1.107	0.698	0.038	-0.776	0.000
5858	3 2 1				-1.294	-0.719	-1.410				-1.138	0.018	0.000						
5950	2 3 1				0.175	1.214	0.316				0.300	1.308	0.000	0.342	0.484	0.852	0.018	1.230	0.000
6175	2 3 1														-0.219			0.343	0.000
6182	2 1 3				0.054	-1.041	0.009				-0.438	-0.518	0.000	-0.164	1.086	-0.622	-0.684	-1.122	0.000
6233	3 1 2				-1.398	0.866	1.624				-0.846	0.018	0.000	-0.972	0.235	0.013	-0.940	0.092	0.000
6253	3 1 2													-0.883	-0.124	-1.503	-0.256	0.464	0.000
6265	2 1 3				0.425	**3.788**	0.421				-0.570	-0.152	0.000	**4.000**	0.235	**-3.146**	**2.321**	-1.736	0.000
6421	1 2 3				**-2.193**						-0.570		0.000						
6448	2 1 3				-0.620	1.788	-0.216				-0.570	-0.518	0.000						
6456	2 3 1				**-2.224**	0.349	0.805				**-4.000**		0.000	-1.653	-1.241	-0.483	1.383	-1.122	0.000
6563	1 2 3				-0.897	0.133	0.893				-0.536	0.489	0.000	0.387	0.870	0.194	-0.539	0.219	0.000
6686	1 2 3													0.522	0.972	-1.945	-0.359	1.845	0.000
7248	2 3 1				0.425	-0.178	**-2.416**				-0.687	-0.330	0.000	0.682	-0.031	0.377	1.897	0.581	0.000
7442	2 3 1				0.129	-0.928	-0.216				-0.135	-0.330	0.000	0.207	1.556	0.218	0.602	0.916	0.000
7564	3 2 1				0.027	0.485	0.479				0.216	-0.152	0.000						
7688	2 1 3				1.666	**-2.431**	-0.595				1.922	**-2.824**	0.000	1.405	-1.107	-0.465	0.111	-0.776	0.000
7728	1 3 2				-0.851	**-2.143**	-0.855				-0.887	**-2.347**	0.000						
7876	2 3 1				1.500	-0.346	-0.031				1.655	0.636	0.000	-1.541	-0.419	-0.130	-0.634	0.092	0.000
7930	2 3 1				0.801	0.805	0.182				-1.448	0.181	0.000	1.405	1.225	0.532	1.455	**2.164**	0.000
7962	1 2 3				-0.851	-0.178	0.363				-1.268	-1.153	0.000	0.487	-0.523	0.532	-1.157	-0.040	0.000
7968	2 3 1				0.229	1.158	0.753				**-4.000**	0.916	0.000	0.510	-0.631	-0.029	-0.528	-0.176	0.000
8019	2 1 3				-0.397	-0.178	-0.091				0.349	0.916	0.000	**-2.304**	1.015	1.510	0.414	0.807	0.000
8068	2 3 1				0.229	0.805	-1.086				1.092	0.338	0.000	-0.747	0.870	-0.557	-1.337	0.092	0.000
8260	3 1 2				-0.076	1.269	-1.691				-0.232	0.338	0.000						
8329	1 2 3													0.019	1.683	0.013	-0.998	0.464	0.000
8380	2 1 3				0.801	0.866	0.479				-0.199	0.778	0.000	-0.480	-0.124	0.055	-1.647	0.464	0.000
8435	2 3 1				0.709	-0.620	-1.257				-0.766	0.181	0.000						
8569	1 3 2				-0.485	-0.435	0.591				-0.806	0.489	0.000	0.487	1.225	-0.286	-0.528	-0.464	0.000
8626	2 3 1				-0.971	-1.287	0.805				0.943	-0.926	0.000						
8628	1 2 3				1.331						0.149		0.000						
8663	1 2 3				1.331	**4.000**	**-2.300**				**3.363**			1.405	**4.000**	**-4.000**	0.995		
8742	3 1 2				-1.093	-0.178	-0.765				-1.095	-0.330	0.000						
8766	3 1 2				0.477	0.349	-0.091				0.179	1.789	0.000	0.538	0.403	-1.166	-0.837	1.128	0.000
8862	1 2 3				0.353	0.417	0.206				0.210	-0.152	0.000	-1.081	**2.765**	0.129	0.636	1.527	0.000
8891	2 1 3				**-3.251**	-0.928													
8898	2 1 3				0.480	0.926	0.913				0.479	-0.330	0.000	0.004	0.060	0.178	-0.701	-0.945	0.000
8955	2 3 1				-0.851	1.214	-0.146				0.149	0.778	0.000	-1.022	0.795	-0.029	0.111	0.807	0.000

positive results can no z-scores be calculated. z-scores from outliers are not real z-scores but a practical means to express also the results from the outliers. Very low and high values are here limited to –4 and +4, respectively.

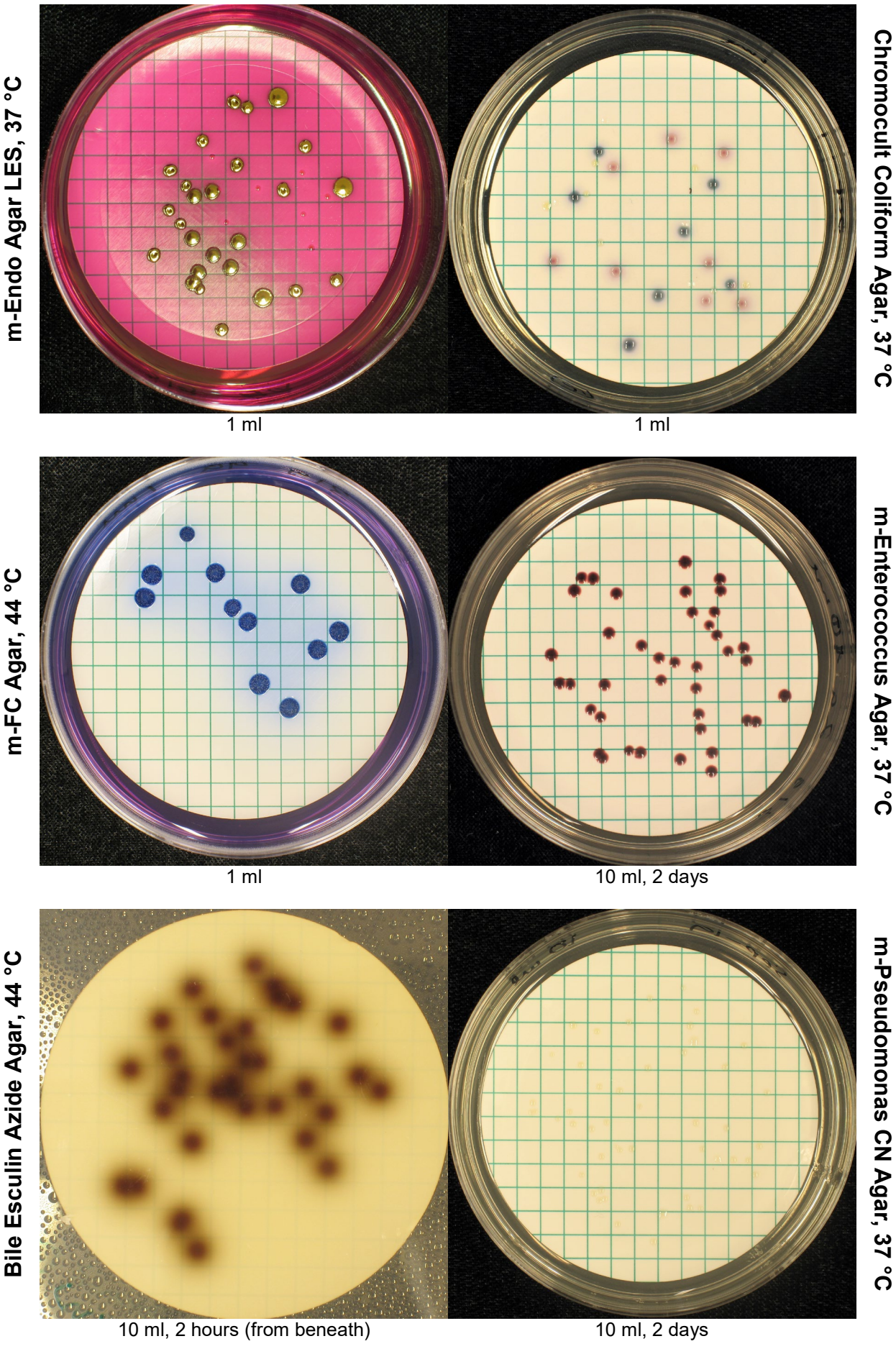
Susp. intestinal enterococci (MF)			Intestinal enterococci			Susp. *Pseudomonas aeruginosa* (MF)			*Pseudomonas aeruginosa*			Total plate count 22 °C, 3 days			Total plate count 36±2 °C, 2 days			Lab no.
A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	
												2.051	1.054	0.570				**1131**
			-0.144	0.725	0.000							-0.631	0.672	-0.130				**1132**
			-0.144		0.000				0.000	0.864	-0.258	-0.331	-0.373	0.839	-0.118	-0.028	0.238	**1237**
			-1.123	-0.218	0.000				0.000	0.188	-0.033	0.630	1.054	-0.574	0.050	1.622	0.377	**1254**
			-1.123	0.488	0.000					-0.490	-0.531	**4.000**	**2.713**	-1.863	**4.000**	**-4.000**	0.919	**1290**
			0.897	0.260	0.000				0.000	-0.571	-0.258	0.758	1.696	1.857				**1545**
			-1.472	-1.199	0.000				0.000	-0.905	0.184	-1.107	0.218	-0.574	-0.465	1.035	0.651	**1594**
			1.986	0.883	0.000				0.000	-0.736	0.184	-0.186	0.672	-0.424	**-2.459**	0.923	-0.339	**1611**
			1.038	0.656	0.000				0.000	0.734	**-3.954**	0.758	0.218	-0.881	0.539	0.160	-1.267	**1753**
												1.603	0.218	0.570				**1868**
			-0.954		0.000				0.000	-0.256	0.289	-1.805	-0.373	-1.359	-0.118	-1.512	-0.488	**1970**
																		2050
			1.038	-0.471	0.000				0.000	-1.649	-0.777	-0.044	1.054	-0.574	-1.399	-0.834	0.377	**2317**
			-1.123	0.536	0.000				0.000	-0.736	1.230	1.941	-0.373	0.295	0.697	1.090	1.310	**2386**
			0.462	-0.158	0.000				0.000	-0.179	-0.033	0.233	0.218	0.839	-0.465	0.638	-0.792	**2599**
			-1.296	0.181	0.000							-0.786	**4.000**	-0.726	-0.827	-0.286	0.786	**2637**
			0.010	0.839	0.000				0.000	-0.992	-0.491	0.233	0.672	0.839	0.050	1.199	0.651	**2704**
												-0.331	0.672	-0.574				**2745**
												-0.044	0.218	-1.359	-1.399	-0.028	**2.056**	**2915**
												4.000	**4.000**	**4.000**				**3055**
			0.609							**3.370**	1.230	0.630	-0.373	0.839	-0.118	-0.419	**-2.114**	**3057**
									0.000	1.240	0.888	-1.107	-0.373	-0.726	0.697	0.160	1.437	**3076**
			0.418	0.286	0.000				0.000	0.864	-1.169							**3145**
			-0.737	-0.438	0.000					0.258	0.760				0.216	-0.419	-0.192	**3155**
			-0.144	0.608	0.000				0.000	-0.179	0.920	-0.044	0.672	1.978	-0.644	-0.221	**2.176**	**3162**
			0.609		0.000				0.000	-1.855	0.076	-1.623	-0.373	0.971	0.539	0.282	-0.639	**3305**
												-4.000	**4.000**	-0.130	1.878	**-2.974**	-0.948	**3587**
												0.630	-0.373	0.706				**3730**
			0.388	0.234	0.000				0.000	1.420	0.727	0.096	-1.800	1.485	-0.465	0.282	-0.639	**3883**
			2.218	-0.218	0.000							1.008	-0.373	-0.276				**4015**
																		4288
			-1.123	0.337	0.000				0.000	-0.571	-0.735	-0.186	0.672	-0.276	-1.805	**-2.374**	0.096	**4339**
			0.609	0.127	0.000				0.000	0.043	-0.653	-0.331	0.218	0.570	0.539	0.638	-0.047	**4343**
			0.609	-1.389	0.000				0.000	-1.171	-0.947	-0.186	0.218	-1.197	-0.465	-0.487	0.651	**4356**
			-0.704	0.861	0.000							-0.331	0.672	-0.276	-0.465	0.221	-0.339	**4459**
												1.130	0.672	-0.276	-0.465	-1.126	-0.339	**4560**
			-2.153		0.000				0.000		**-2.665**				-0.290	**4.000**	-0.192	**4633**
			0.208	-1.154	0.000							0.096	-0.373	0.971				**4723**
																		4817
			-0.787	-1.492	0.000				0.000	0.466	-0.694	-0.186	-1.800	0.839	**-2.017**	**-2.281**	-1.431	**4889**
			1.316	-1.110	0.000				0.000	0.453	-0.943	0.500	0.672	-0.881	0.852	0.035	-1.106	**4980**
			1.986	-1.660	0.000				0.000	0.329	0.076	-0.186	0.672	0.434	-0.465	-0.353	-0.192	**5018**
			-0.144	-1.990	0.000							-0.479	0.672	-0.574	-1.399	-0.221	0.096	**5094**
			0.897	0.905	0.000				0.000	0.864	-0.182	0.630	0.218	0.013	0.697	0.754	1.181	**5128**
																		5220
			1.854	-1.720	0.000				0.000	0.258	1.230	0.367	0.218	1.857	0.539	0.403	-0.948	**5352**
			-4.000	0.861	0.000				0.000	0.668	1.814	0.233	-0.373	1.102	-0.290	-0.623	-0.948	**5447**
			-0.051	0.260	0.000				0.000	**-2.072**	-1.695	-0.944	-1.800	0.434	-1.600	1.090	-0.948	**5858**
			0.056	-1.783	0.000				0.000	0.734	-0.033							**5950**
												-1.446	-1.800	-1.524	-0.827	-0.623	-1.766	**6175**
			0.163	0.971	0.000							-0.186	0.218	0.155				**6182**
			-0.887	1.057	0.000				0.000	0.864	0.004	-1.623	-1.800	-0.424	1.304	0.403	0.238	**6233**
			0.163	1.014	0.000							0.884	0.218	0.434				**6253**
			0.010	**2.165**						**4.000**	-0.296	**4.000**	-1.800	**4.000**	**4.000**	0.035	**4.000**	**6265**
			0.754	0.463	0.000				0.000	-1.171	-1.306	-1.274	-0.373	0.295	-1.600	-0.028	**2.176**	**6421**
									0.000	0.188	-0.033				1.304	-1.277	0.651	**6448**
			1.358	0.463	0.000							0.500	-1.800	1.102	0.852	-0.156	-0.192	**6456**
			-0.803	1.596	0.000				0.000	0.116	**2.091**	-1.274	0.218	-1.037	-0.290	-0.487	-0.639	**6563**
												-0.631	1.696	0.295	0.050	0.923	0.096	**6686**
			0.897	0.561	0.000				0.000	0.466	-0.258	-0.479	1.054	0.013	0.852	0.580	-0.047	**7248**
												-0.786	1.391	0.706				**7442**
												-0.786	-0.373	-0.424	-0.644	-0.419	-0.192	**7564**
			1.588	0.207	0.000				0.000	-0.992	-0.144	0.367	-1.800	**-2.583**	1.155	0.580	-0.639	**7688**
			-0.954	-1.389	0.000				0.000	-1.263	-1.400	-1.994	-1.800	-1.359	-1.399	0.035	**-2.114**	**7728**
			0.477	1.099	0.000				0.000	0.534	1.230	0.500	-0.373	0.155	-0.118	-0.156	-1.106	**7876**
			-0.954	0.816	0.000				0.000	0.258	-0.412	-0.186	-1.800	-0.424	0.050	0.403	0.377	**7930**
			1.178	-1.440	0.000				0.000		-1.124	-1.107	-0.373	0.013	0.050	0.923	0.515	**7962**
			-0.787	0.337	0.000				0.000	0.534	1.814	1.603	0.218	-0.881	**3.073**	0.160	0.786	**7968**
			-0.954	**-2.456**	0.000				0.000	-0.104	1.046	0.884	-1.800	0.155	1.155	0.160	1.310	**8019**
			-1.651	0.512	0.000				0.000	0.116	-0.070	-0.786	0.218	-0.881	-0.290	0.282	-0.192	**8068**
												-0.786	**4.000**	-0.130				**8260**
			0.118	-1.720	0.000				0.000	-0.820	-0.070	-0.186	-0.373	0.971	0.539	1.413	0.238	**8329**
			-1.123	0.154	0.000				0.000	-0.490	0.595	1.717	0.672	-0.726	-0.290	0.979	-0.339	**8380**
			-0.954	-0.041	0.000				0.000	**-3.582**	-0.334	-0.786	0.218	**2.799**	-0.644	-0.092	0.238	**8435**
			-0.787	0.181								0.233	-1.800	**2.336**				**8569**
												1.487	-1.800	**-4.000**				**8626**
			0.609	0.438	0.000				0.000	-1.171	1.814	-0.044	0.672	0.013	**2.290**	1.518	0.786	**8628**
			2.115						0.000	**2.212**	**-2.122**	-0.944	**4.000**	**-4.000**	0.539	-1.052	**4.000**	**8663**
												0.630	**4.000**	0.570	0.697	**2.317**	0.515	**8742**
			-0.144	-0.406	0.000					-0.653	0.289	0.233	1.054	-0.276	**4.000**	0.923	-0.339	**8766**
			0.208		0.000							0.367	1.054	0.013	1.155	-0.487	-0.047	**8862**
												1.717	-0.373	0.295				**8891**
			-0.429	0.608	0.000				0.000	0.466	-0.182	0.884	-0.373	0.155	0.852	0.343	1.051	**8898**
			-0.144	0.839	0.000				0.000	0.466	0.358	1.008	1.391	-0.574	0.697	-0.092	-0.948	**8955**

Lab no.	Sample			Suspected coliform bacteria (MF)			Coliform bacteria (MF)			Susp. thermotolerant coliform bact. (MF)			*E. coli* (MF)			Coliform bacteria ("rapid" MPN)			*E. coli* ("rapid" MPN)		
	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C
9002	1	2	3				**-4.000**	0.058	**-2.767**				**-4.000**		0.000						
9051	1	2	3				-0.467	-1.160	-1.269				-0.460	-0.716	0.000	-0.139	-1.241	**-2.360**	0.738	-0.945	0.000
9306	3	1	2													-0.004	-0.980	0.645	-0.273	-0.616	0.000
9408	3	1	2													1.446	-0.031	0.539	-1.175	0.581	0.000
9436	2	1	3				-0.220	-0.719	0.673				-0.167	0.018	0.000	0.363	-0.124	1.628	0.986	0.464	0.000
9441	3	2	1													1.362	0.320	1.589	**3.282**	-0.176	0.000
9524	3	2	1				1.828	-1.287	0.304				0.479	-0.926	0.000	0.710	-0.631	-0.260	1.669	-0.176	0.000
9736	1	2	3													-1.526	**3.219**	-0.113	-1.826	**2.662**	0.000
9899	3	1	2				0.125	-0.620	1.008				0.084	0.181	0.000	1.311	1.620	0.630	0.349	-0.176	0.000
9903	2	1	3				0.883	1.483	0.535				0.149	-0.330	0.000						
n				0	0	0	67	64	60	0	0	0	67	60	66	63	63	62	62	61	64
Min							-4.000	-2.431	-2.767				-4.000	-2.824	0.000	-2.684	-2.544	-4.000	-4.000	-2.588	0.000
Max							1.987	4.000	1.624				4.000	1.789	0.000	4.000	4.000	1.628	3.282	2.662	0.000
Median							0.054	0.133	0.225				-0.199	0.018	0.000	0.019	-0.031	0.092	-0.171	0.092	0.000
Mean							-0.060	0.122	0.000				-0.179	0.000	0.000	0.063	0.063	-0.065	-0.065	0.000	0.000
SD							1.106	1.198	1.000				1.450	1.000	0.000	1.113	1.113	1.114	1.114	1.000	0.000
z<-3							2	0	0				4	0	0	0	0	2	1	0	0
-3≤z<-2							2	2	4				0	3	0	3	1	3	0	1	0
2<z≤3							0	0	0				2	0	0	0	1	0	1	2	0
z>3							0	2	0				2	0	0	1	2	0	1	0	0

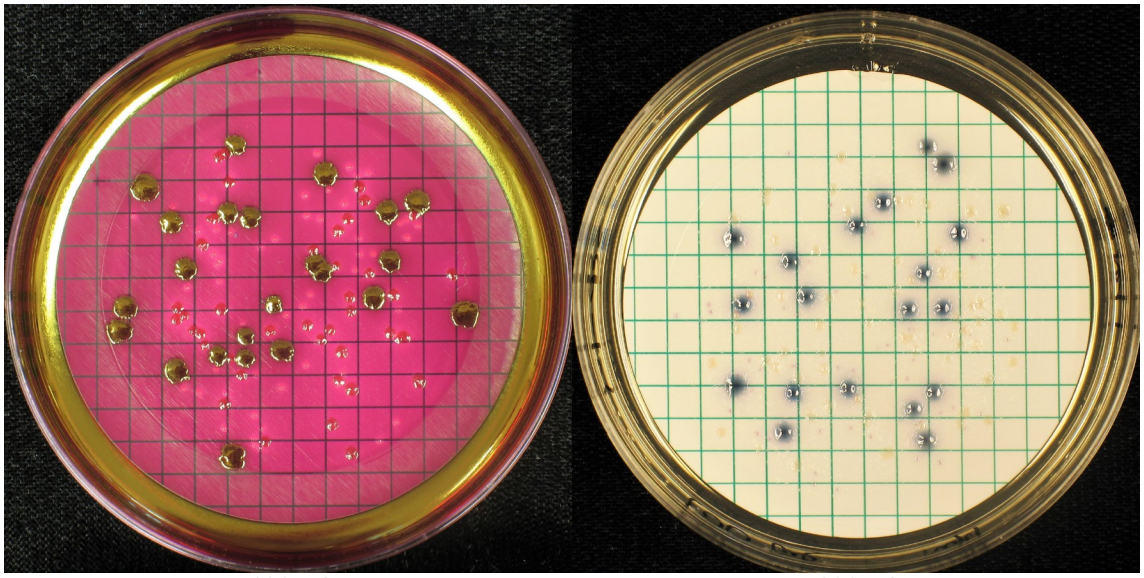
Susp. intestinal enterococci (MF)			Intestinal enterococci			Susp. *Pseudomonas aeruginosa* (MF)			*Pseudomonas aeruginosa*			Total plate count 22 °C, 3 days			Total plate count 36±2 °C, 2 days			Lab no.
A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	
			-4.000	-1.199	0.000							**2.789**	0.218	**4.000**				**9002**
			-1.797	0.839	0.000				0.000	-1.855	-1.644	-1.994	1.054	**-2.772**	-1.013	-0.353	**-2.856**	**9051**
												-1.274	0.218	0.434	0.050	0.221	0.238	**9306**
			0.462		0.000				0.000	0.466	0.393	-0.479	-0.373	-1.863	-0.290	1.035	0.377	**9408**
			-0.509	-1.067	0.000				0.000	-0.030	-0.531	-0.786	0.218	-0.574	0.539	1.145	1.563	**9436**
												0.367	0.218	0.434	-0.465	0.160	1.051	**9441**
			-0.067	-0.070	0.000							1.251	-0.373	0.013	0.050	0.343	1.051	**9524**
			-0.541	1.404	0.000				0.000	0.116	0.952	-1.623	1.054	-0.130	-0.465	-0.156	-1.267	**9736**
			-0.333	0.388	0.000				0.000	0.116	0.358	0.500	0.672	0.570	0.379	-0.028	-0.047	**9899**
			-0.270	-0.374	0.000				0.000	1.240	1.469	0.884	-0.373	0.295	1.155	0.580	0.377	**9903**

0	0	0	70	62	66	0	0	0	54	57	59	85	85	85	71	71	71	**n**
			-4.000	-2.456	0.000				0.000	-3.582	-3.954	-4.000	-1.800	-4.000	-2.459	-4.000	-2.856	**Min**
			2.218	2.165	0.000				0.000	4.000	2.091	4.000	4.000	4.000	4.000	4.000	4.000	**Max**
			-0.106	0.260	0.000				0.000	0.116	-0.033	-0.044	0.218	0.013	0.050	0.160	0.096	**Median**
			-0.114	0.000	0.000				0.000	0.007	-0.067	0.094	0.282	0.047	0.169	0.090	0.113	**Mean**
			1.192	1.000	0.000				0.000	1.216	1.117	1.306	1.411	1.375	1.270	1.122	1.190	**SD**
																		Summa
			2	0	0				0	1	1	1	0	2	0	1	0	17
			1	1	0				0	1	2	0	0	2	2	3	3	34
			2	1	0				0	1	1	2	1	2	1	1	3	21
			0	0	0				0	2	0	3	6	3	4	1	2	29

Mixture A

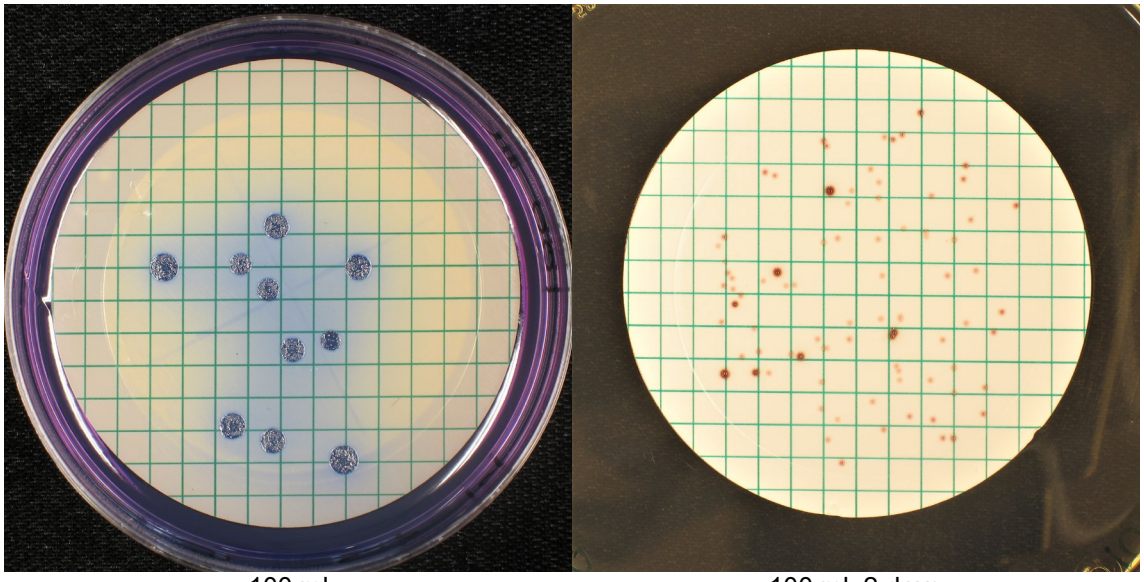

m-Endo Agar LES, 37 °C
Chromocult Coliform Agar, 37 °C
1 ml
1 ml
m-FC Agar, 44 °C
m-Enterococcus Agar, 37 °C
1 ml
10 ml, 2 days
Bile Esculin Azide Agar, 44 °C
m-Pseudomonas CN Agar, 37 °C
10 ml, 2 hours (from beneath)
10 ml, 2 days

Mixture B



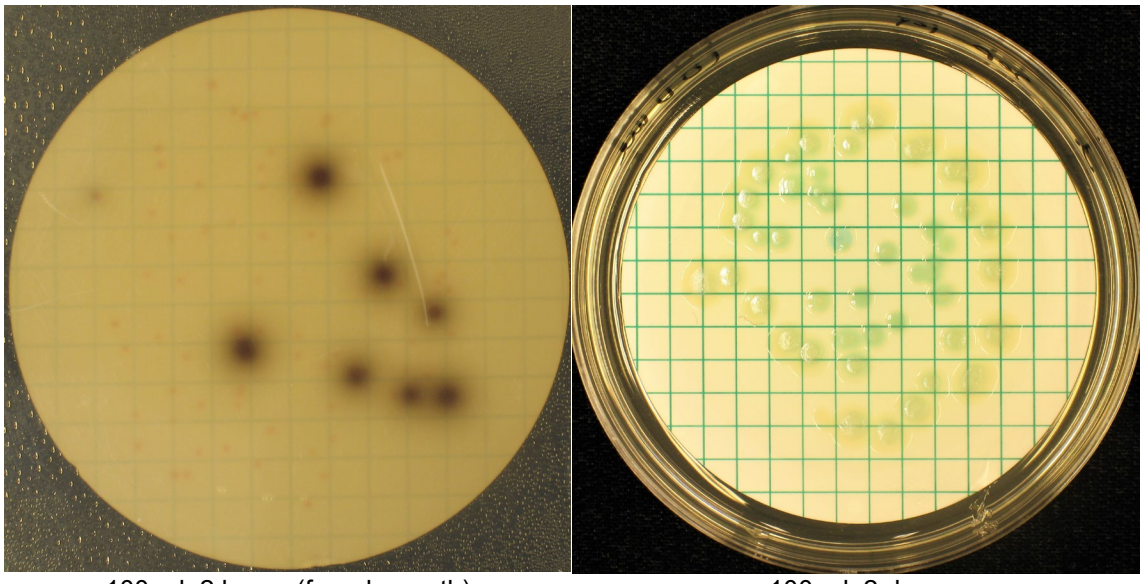
m-Endo Agar LES, 37 °C — 100 ml

Chromocult Coliform Agar, 37 °C — 100 ml



m-FC Agar, 44 °C — 100 ml

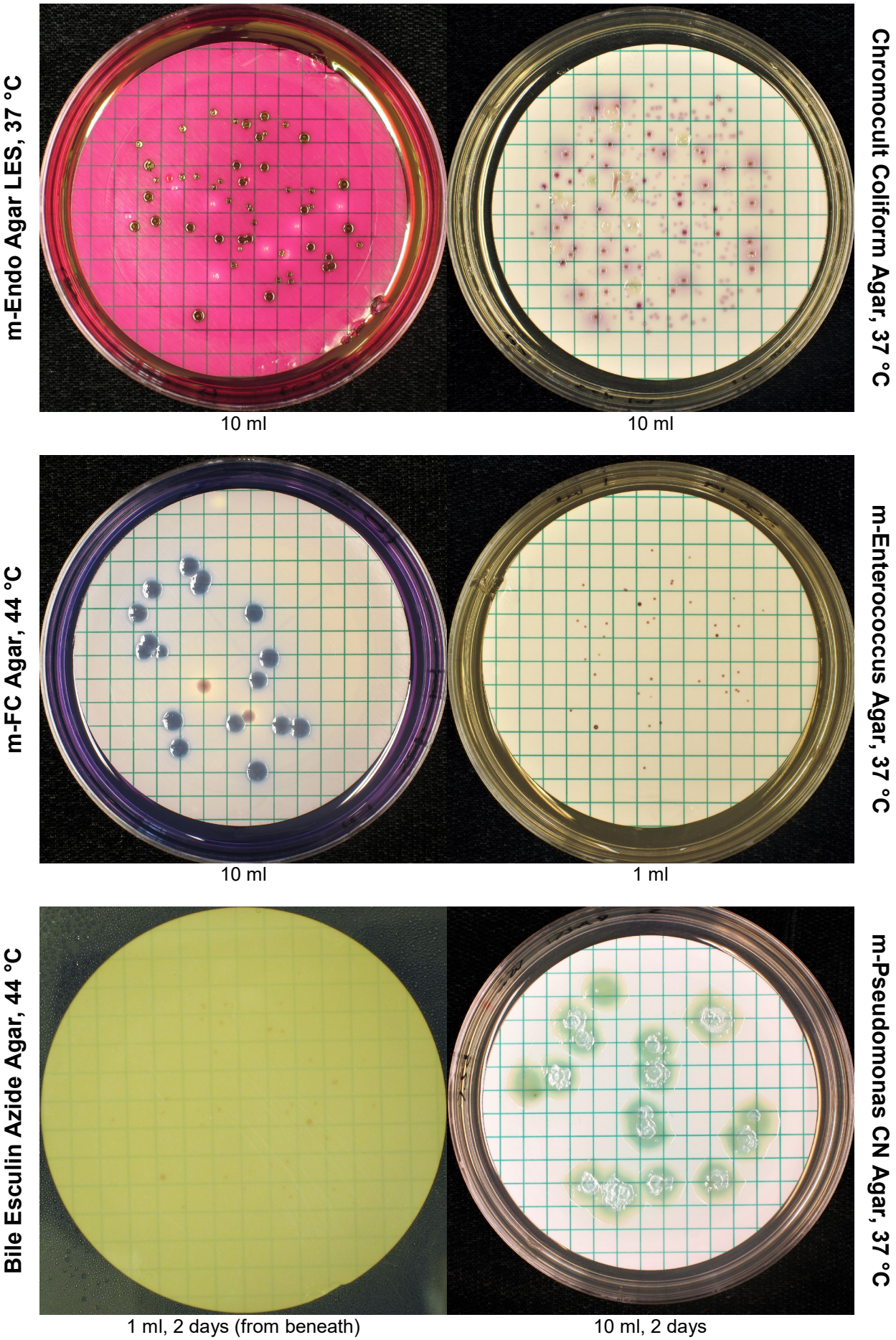
m-Enterococcus Agar, 37 °C — 100 ml, 2 days



Bile Esculin Azide Agar, 44 °C — 100 ml, 2 hours (from beneath)

m-Pseudomonas CN Agar, 37 °C — 100 ml, 2 days

Mixture C


m-Endo Agar LES, 37 °C
Chromocult Coliform Agar, 37 °C
10 ml
10 ml
m-FC Agar, 44 °C
m-Enterococcus Agar, 37 °C
10 ml
1 ml
Bile Esculin Azide Agar, 44 °C
m-Pseudomonas CN Agar, 37 °C
1 ml, 2 days (from beneath)
10 ml, 2 days

PT reports published 2018

Proficiency Testing – Food Microbiology, January 2018, by Jonas Ilbäck

Proficiency Testing – Drinking Water Microbiology, March 2018, by Tommy Šlapokas

Proficiency Testing – Food Microbiology, April 2018, by Jonas Ilbäck

Proficiency Testing – Drinking Water Microbiology, September 2018, by Tommy Šlapokas

Proficiency Testing – Food Microbiology, October 2018, by Jonas Ilbäck

PT reports published 2019

Proficiency Testing – Food Microbiology, January 2019, by Jonas Ilbäck

Proficiency Testing – Drinking Water Microbiology, March 2019, by Tommy Šlapokas

Proficiency Testing – Food Microbiology, April 2019, by Jonas Ilbäck

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 laboratories carry out some form of internal quality assurance, but their analytical work also has 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 proficiency test, identical test material is analysed by a number of laboratories using their routine methods. The laboratories report their results to the organiser that evaluates them and compiles them in a report.

The National Food Agency's PT program offers

- External and independent evaluation of laboratories analytical competence.
- Improved knowledge of analytical methods with respect to various types of organisms.
- Expert support.
- Tool for inspections regarding accreditation.
- Free extra material for follow-up analyses

For more information, visit our website: https://www2.slv.se/absint

The National Food Agency's reference material

As a complement to the proficiency testing but without specific accreditation, National Food Agency also produces reference material (RM) for internal quality control: a total of 8 RM for food and drinking water microbiological analyses, including pathogens, are available.

Information available on our website: https://www.livsmedelsverket.se/en/RM-micro