Proficiency Testing

Drinking Water Microbiology

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Linnea Blom & Tommy Šlapokas

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

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

Responsible for the report
Linnea Blom, Microbiologist, Department of Biology, 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 **35/36/37 °C**

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

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Proficiency testing
ISO/IEC 17043

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 method data and results

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. As a result 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, in order to obtain the most appropriate evaluation 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 27 under "Processing of numerical results" with further reference to the scheme protocol [1].

Results of the PT round

General outcome

Test items were dispatched to 89 laboratories, 33 in Sweden, 45 in other Nordic countries (Faeroe Islands, Greenland and Åland included), three more from EU, four from the rest of Europe and four from outside Europe. Results were reported from 87 laboratories.

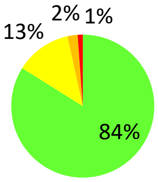
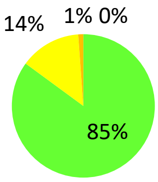
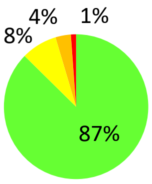
The percentages of false results and outliers are compiled in **table 1**.

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	502			501			498		
No. of deviating results *	18 (4%)			14 (3%)			17 (3%)		
Microorganisms	*Escherichia coli* *Citrobacter freundii* *Enterococcus faecalis* *Pseudomonas aeruginosa* *(Clostridium perfringens)*			*Enterobacter cloacae* *Cronobacter sakazakii* *Enterococcus hirae* *Staphylococcus capitis*			*Escherichia coli,* 2 strains *Pseudomonas aeruginosa* *Burkholderia cepacia* *Staphylococcus saprophyticus*		
Analysis	**Target org.**	**F%**	**X%**	**Target org.**	**F%**	**X%**	**Target org.**	**F%**	**X%**
Coliform bacteria (MF)	*E. coli* *C. freundii*	2	0	*E. cloacae* *C. sakazakii*	3	2	*E. coli,* 2 strains	0	7
Susp. thermotolerant coliform bact. (MF)	*E. coli*	–	–	[*E. cloacae*] [*C. sakazakii*]	–	–	*E. coli,* 2 strains	–	–
E. coli (MF)	*E. coli*	0	0	[*E. cloacae*] [*C. sakazakii*]	2	–	*E. coli* {*E. coli*}	2	0
Coliform bacteria (rapid method)	*E. coli* *C. freundii*	0	2	*E. cloacae* *C. sakazakii*	0	0	*E. coli,* 2 strains	0	2
E. coli (rapid meth.)	*E. coli*	0	2	–	2	–	*E. coli,* 2 strains	2	2
Intestinal enterococci (MF)	*E. faecalis*	2	8	*E. hirae*	3	3	–	2	–
Pseudomonas aeruginosa (MF)	*P. aeruginosa*	2	8	–	0	–	*P. aeruginosa* {*B. cepacia*}	0	0
Culturable micro-organisms (total count), 3 days 22 °C	*E. faecalis* *P. aeruginosa* *E. coli* *C. freundii*	0	2	*E. hirae* *E. cloacae* *C. sakazakii*	0	6	*S. saprophyticus* *(E. coli)* *(P. aeruginosa)* *(B. cepacia)*	0	6
Culturable micro-organisms (total count), 2 days 36 °C	*E. faecalis* *P. aeruginosa* *E. coli* *C. freundii*	2	2	*S. capitis* *(E. hirae)* *(E. cloacae)* *(C. sakazakii)*	0	0	*S. saprophyticus* *(E. coli)* *(P. aeruginosa)* *(B. cepacia)*	0	5

* In total 24 of 89 laboratories (27 %) 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

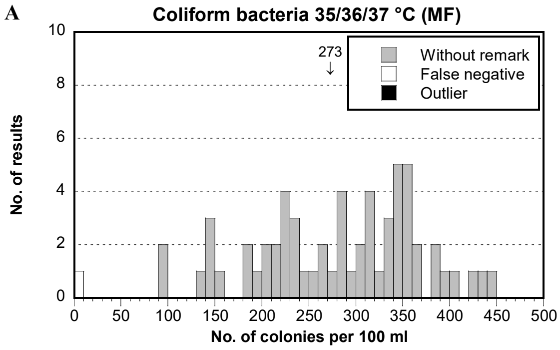
Coliform bacteria (MF)

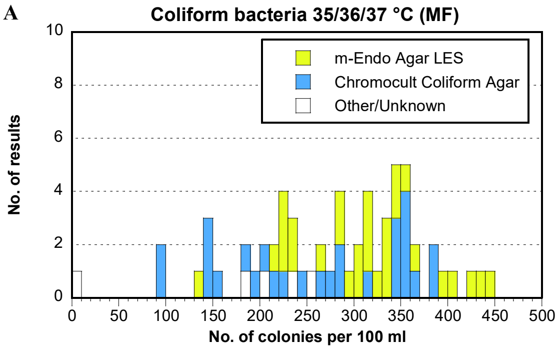
The primary cultivation media for the analysis of coliform bacteria were the enzyme-based chromogenic medium CCA together with LES that is based on lactose fermentation. The group Other/Unknown in the table includes six different media, from both water and food methods, as well as from methods in the medical field.

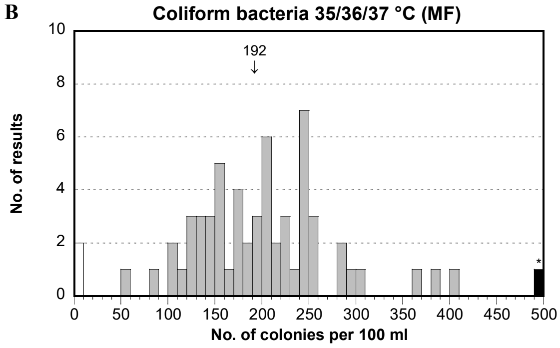
As previous PT rounds, CCA gave lower average result than LES, at least in sample A and B. Furthermore, CCA had a total of four high outliers whereas the other groups had none.

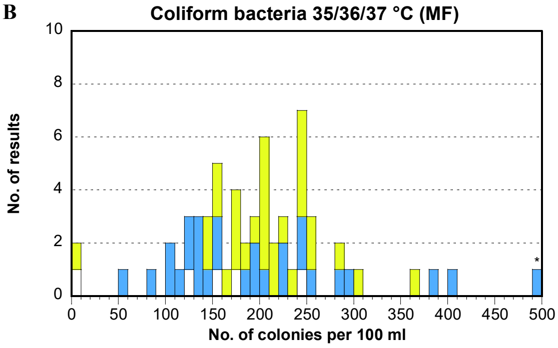
In total six coliform bacteria, including *E. coli*, were present in the samples.

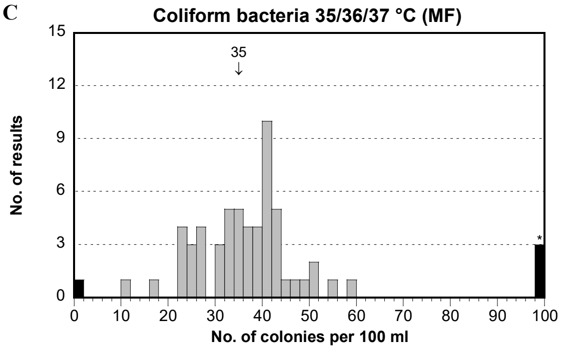
Medium	N	A						B						C					
		n	**Mv**	CV	F	<	>	n	**Mv**	CV	F	<	>	n	**Mv**	CV	F	<	>
Total	61	60	**273**	16	1	0	0	58	**192**	18	2	0	1	56	**35**	14	0	1	3
m-Endo Agar LES	29	29	**304**	13	0	0	0	28	**210**	11	1	0	0	29	**36**	12	0	0	0
Chromocult C. Agar	27	27	**250**	20	0	0	0	26	**178**	23	0	0	1	23	**34**	14	0	0	3
Other/Unknown	5	4	–	–	1	0	0	4	–	–	1	0	0	4	–	–	0	1	0

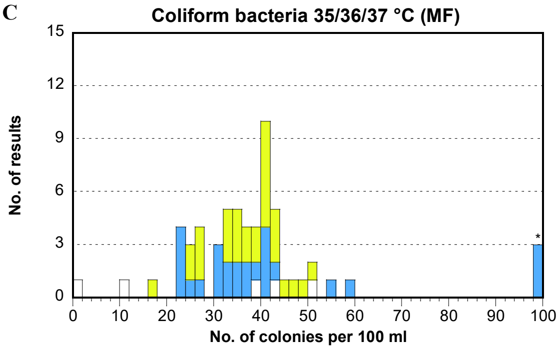












Sample A

- Two strains of coliform bacteria were present in the sample. Both *E. coli* and *C. freundii* grow with typical colonies, with a metallic sheen on LES, and blue and pink, respectively, on CCA at 35/36/37 °C (see annex C).
- The average recovery was lower for the MF methods compared to the rapid methods (273 cfu/100 ml compared to 309 MPN-index/100 ml, see page 11), indicating that the strains were not detected to the full extent by the MF-methods.
- The distribution of the result was somewhat broad with a tendency of two peaks. The dispersion was small in average, CCA however had medium dispersion (CV, see page 27).
- One false negative result were reported.

Sample B

- Two strains of coliform bacteria were present in the sample. Both *E. cloacae* and *C. sakazakii* grow with typical colonies, with a metallic sheen on LES and pink CCA at 35/36/37 °C.
- As for sample A, the average recovery is lower for the MF methods compared to the rapid methods (192 cfu/100 ml compared to 236 MPN/100 ml, see page 11).
- Two laboratories reported a false negative result, one of which also reported a false negative result for sample A.
- One high outlier was present.

Sample C

- Two strains of *E. coli* were present in the sample. One strain forms typical colonies with MF methods at 35/36/37 °C. The other strain is also typical on LES but has weak *β*-glucuronidase activity and forms atypical, non-blue, colonies on CCA. The colonies however usually have a weak violet tint, at least in the colony centre.
- Four deviant results were present. One low outlier which was caused by incorrect reporting of results and three high outliers. The high outliers were all obtained by CCA, which also may indicate that colonies other than coliform bacteria were erroneously included. Atypical small pink colonies of *S. saprophyticus* may appear on CCA, which based on experience should be excluded (see annex C).

Suspected thermotolerant coliform bacteria (MF)

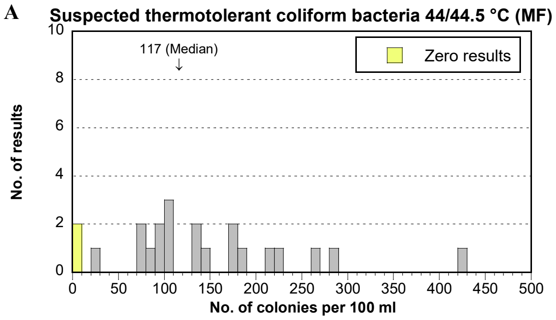
No evaluation in relation to performance is done for what is called suspected (not confirmed) colonies (see page 4). Therefore, no outliers are assessed. The *medians* are then more robust than the means and are given in the table and in histograms. **Thus, the parameter is not included in the performance assessment**.

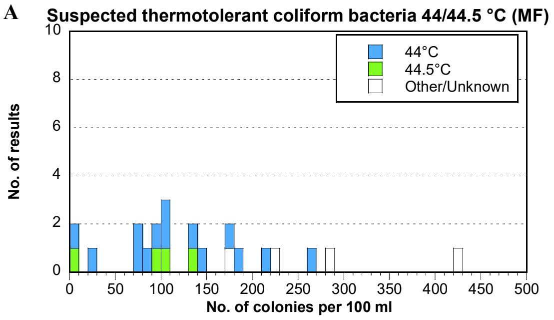
The primary growth media used at 44 or 44.5 °C to identify suspected thermotolerant coliform bacteria is m-FC. The four laboratories in the group Other/Unknown have stated methods where the primary media are incubated at 35/36/37 °C. This is not the intention of the parameter suspected thermotolerant coliform bacteria according to the definition in the instruction and on the website for the program. Instead, it is the typical colonies appearing on the membrane filter at 44/44.5 °C that should be reported. Most likely, the primary incubation at 35/36/37 °C is the cause for the high averages for the group Other/Unknown in sample A and B, since there is no inhibition by high temperature.

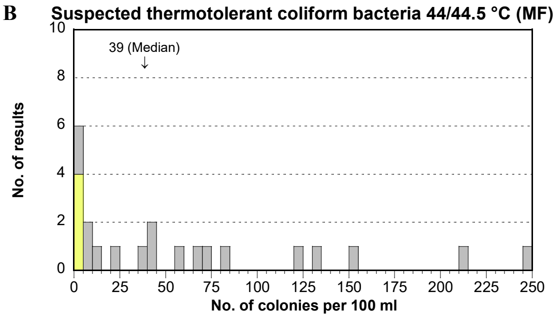
Incubation temp.	N	A						B						C					
		n	**Med**	CV	F	<	>	n	**Med**	CV	F	<	>	N	**Med**	CV	F	<	>
Total	22	22	**117**	–	–	–	–	22	**39**	–	–	–	–	22	**34**	–	–	–	–
44 °C	14	14	**101**	–	–	–	–	14	**31**	–	–	–	–	14	**34**	–	–	–	–
44.5 °C	4	4*	**100**	–	–	–	–	4*	**41**	–	–	–	–	4*	**30**	–	–	–	–
Other/Unknown	4	4*	**252**	–	–	–	–	4*	**62**	–	–	–	–	4*	**35**	–	–	–	–

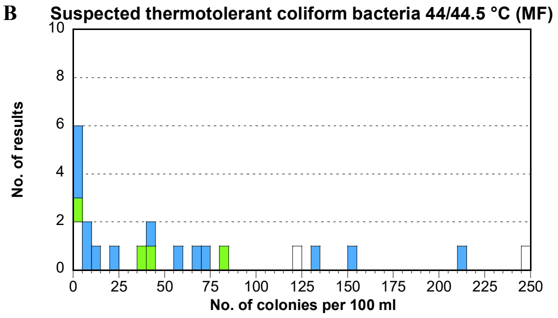
Med = Median; used here instead of mean value because it describes "suspected" colonies

*Median is given for comparison despite few results









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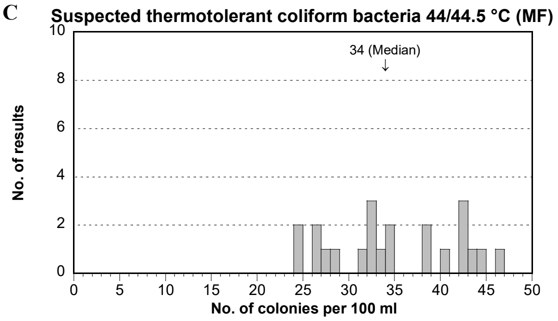
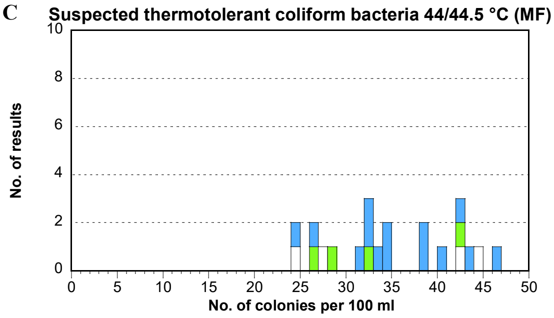

Suspected thermotolerant coliform bacteria 44/44.5 °C (MF)

C


Suspected thermotolerant coliform bacteria 44/44.5 °C (MF)

Sample A

- The strain of *E. coli* appears as a suspected thermotolerant bacterium with blue colonies on m-FC at 44/44.5 °C. The strain of *C. freundii* is usually not seen at 44 °C but may appear with small colonies when the temperature is too low.
- *C. freundii* has been included when the primary media were incubated at 35/36/37 °C. As shown in the table, the median result for the group Other/Unknown was more than double compared to the averages when incubating at 44/44.5 °C.
- Two zero results were obtained.

Sample B

- No genuine thermotolerant coliform bacterium was present. However, the strain of *E. cloacae* may sometimes grow as a (suspected) thermotolerant coliform bacterium on m-FC with small blue colonies. Correspondingly the strain of *C. sakazakii* usually grows at 44 °C with blue-grey to brownish colonies (see annex C).
- Four laboratories have reported zero cfu per 100 ml.

Sample C

- Both *E. coli* strains appears with blue colonies on m-FC at 44/44.5 °C.

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 considered as a confirmed *E. coli*. Corresponding reactions occur on other chromogenic media based on β-glucuronidase activity.

The primary MF growth media CCA and LES are used at 35/36/37 °C and m-FC at 44/44.5 °C. In addition to primary incubation temperature, the results are also grouped by standard. For ISO 9308-1:2014 the incubation is at 35/36/37 °C on CCA. For the standards from the Nordic countries (NS, SS and SFS) the majority of the results are from incubation at 35/36/37 °C on LES but some are also from incubation at 44/44.5 °C on m-FC.

E. coli was included in sample A and C. LES average results were higher than the mean value for other MF methods incubated at 35/36/37 °C.

All results

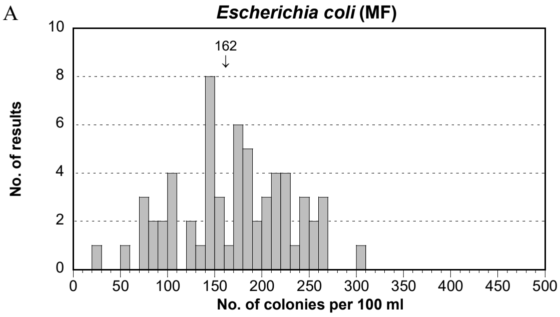
Origin &Standard	N	A						B						C					
		n	**Mv**	CV	F	<	>	n	**Mv**	CV	F	<	>	n	**Mv**	CV	F	<	>
Total	62	62	**162**	20	0	0	0	61	**0**	–	1	–	–	60	**23**	25	1	0	0
Colony origin																			
36 ± 2 °C	42	42	**171**	17	0	0	0	42	**0**	–	0	–	–	41	**22**	27	0	0	0
44/44.5 °C	9	9	**126**	35	0	0	0	9	**0**	–	0	–	–	9	**28**	21	0	0	0
36 ± 2 & 44/44.5 °C	9	9	**166**	11	0	0	0	8	**0**	–	1	–	–	8	**21**	15	1	0	0
Other/Unknown	2	2*	**116**	–	0	0	0	2*	**0**	–	0	–	–	2*	**15**	–	0	0	0
Standard																			
ISO 9308-1:2014	31	31	**162**	17	0	0	0	31	**0**	–	0	–	–	29	**19**	24	1	0	0
SS 028167	10	10	**178**	15	0	0	0	10	**0**	–	0	–	–	10	**33**	12	0	0	0
SFS 3016 (4088)	13	13	**183**	21	0	0	0	13	**0**	–	0	–	–	13	**26**	26	0	0	0
NS 4792	2	2*	**115**	–	0	0	0	2*	**0**	–	0	–	–	2*	**37**	–	0	0	0
”ISO 9308-1:1990”	2	2*	**115**	–	0	0	0	1*	**0**	–	1	–	–	2*	**19**	–	0	0	0
Other/Unknown	4	4*	**108**	–	0	0	0	4*	**0**	–	0	–	–	4*	**13**	–	0	0	0

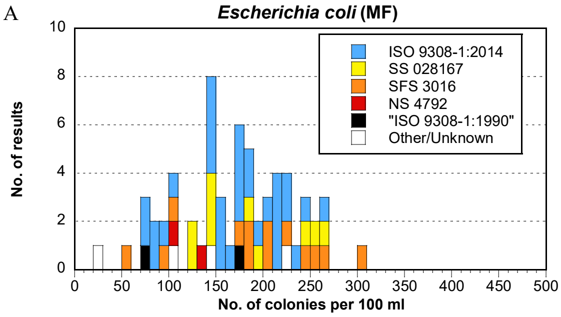
Results for E. coli from the analysis of "coliform bacteria" MF at 35/36/37 °C

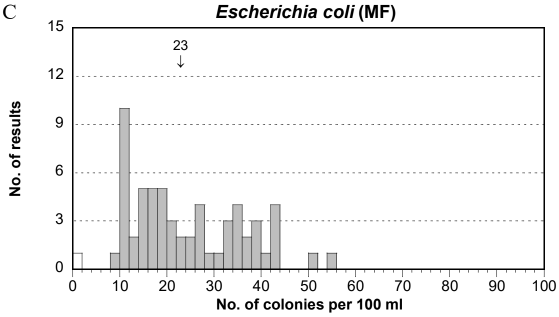
Medium	N	A						B						C					
		n	**Mv**	CV	F	<	>	N	**Mv**	CV	F	<	>	n	**Mv**	CV	F	<	>
Total	45[#]	45	**169**	17	0	0	0	45	**0**	–	0	–	–	44	**22**	27	0	0	0
m-Endo Agar LES	15	15	**186**	15	0	0	0	15	**0**	–	0	–	–	15	**31**	23	0	0	0
Chromocult C Agar	28	28	**165**	17	0	0	0	28	**0**	–	0	–	–	27	**18**	24	0	0	0
CCA, "wrong standard"	1	1*	**95**	–	0	0	0	1*	**0**	–	0	–	–	1*	**10**	–	0	0	0
Other/Unknown	1	1*	**100**	–	0	0	0	1*	**0**	–	0	–	–	1*	**10**	–	0	0	0

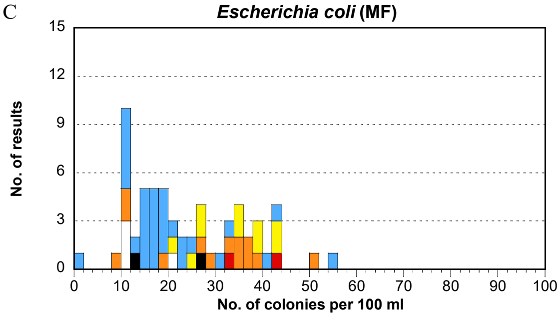
[#] Compare the table above – the total number of results for 36 °C may differ somewhat due to different method information for coliform bacteria and *E. coli*

* Mean value is given for comparison despite few results









Sample A

- One typical *E. coli* strain was included. It grows with typical colonies on the various primary growth media and has activity of β-glucuronidase as well as indole- and gas-production.
- No deviant result was present.

Sample B

- No *E. coli* was included in the sample but one false positive result was obtained.

Sample C

- Two strains of *E. coli* were included in the sample. Both strains of *E. coli* are producing gas in lactose broth at 44 °C, are positive when testing for indole production but one strain shows a weak β-glucuronidase activity.
- The colony appearance of *E. coli* with weak β-glucuronidase activity is typical on LES and m-FC. However, on CCA the colony colour is atypical for *E. coli*. On this medium the colonies are pinkish with a more or less evident violet hue in the middle. In the histogram is a trend of lower results using ISO 9308-1:2014, indicating that these colonies on CCA are often interpreted as originating from other coliform bacteria than *E. coli.*
- One false negative 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. Of the 57 laboratories that reported Colilert some used trays with 51 wells, while others used trays with 97 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*.

Colilert 24 seem to have lower recovery than Colilert 18 since the result average was lower than the average mean, at least in sample A and B. However, the results for Colilert 24 are too few to draw any conclusions.

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.#	57	57	**309**	14	0	0	0	56	**238**	18	0	0	0	56	**38**	9	0	0	1
Colilert-18, 51 wells	8	8	**286**	17	0	0	0	7	**216**	18	0	0	0	8	**39**	9	0	0	0
Colilert-18, 97 wells	44	44	**323**	13	0	0	0	44	**249**	17	0	0	0	43	**39**	10	0	0	1
Colilert-18, ? wells	1	1*	**320**	–	0	0	0	1*	**165**	–	0	0	0	1*	**32**	–	0	0	0
Colilert-24	4	4*	**211**	–	0	0	0	4*	**179**	–	0	0	0	4*	**35**	–	0	0	0
Wrong method##	1	0	–	–	0	0	1	1*	**140**	–	0	0	0	1*	**49**	–	0	0	0

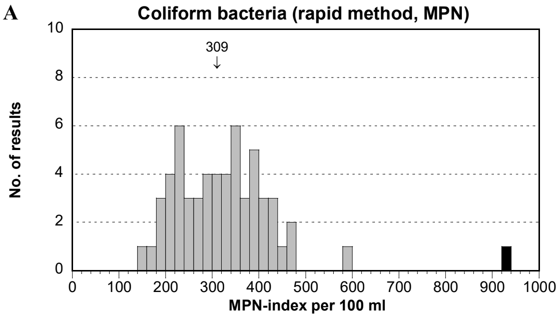
E. coli, Rapid method with MPN

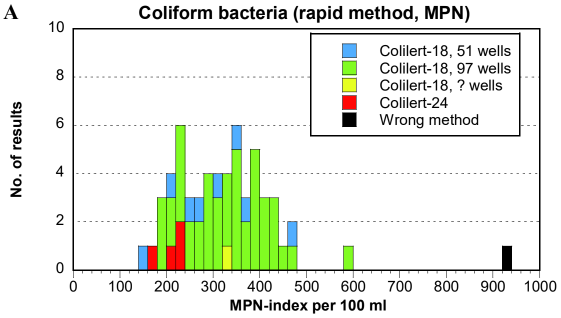
Principle	N	A						B						C					
		n	**Mv**	CV	F	<	>	n	**Mv**	CV	F	<	>	n	**Mv**	CV	F	<	>
Total, Rapid meth[#]	57	56	**184**	14	0	0	1	56	**0**	–	1	–	–	56	**17**	15	1	0	0
Colilert-18, 51 wells	7	7	**151**	17	0	0	0	7	**0**	–	0	–	–	7	**20**	11	0	0	0
Colilert-18, 97 wells	45	44	**194**	12	0	0	1	44	**0**	–	1	–	–	44	**17**	15	1	0	0
Colilert-18, ? wells	2	2*	**202**	–	0	0	0	2*	**0**	–	0	–	–	2*	**11**	–	0	0	0
Colilert-24	3	3*	**112**	–	0	0	0	3*	**0**	–	0	–	–	3*	**17**	–	0	0	0
Wrong method[##]	1	1*	**79**	–	0	0	0	1*	**0**	–	0	–	–	0	–	–	0	0	1

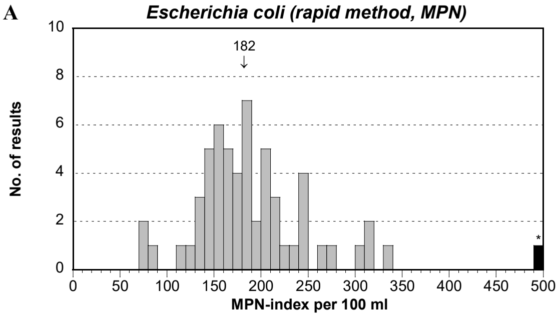
[#] Wrong method is not included in Total, Rapid methods.

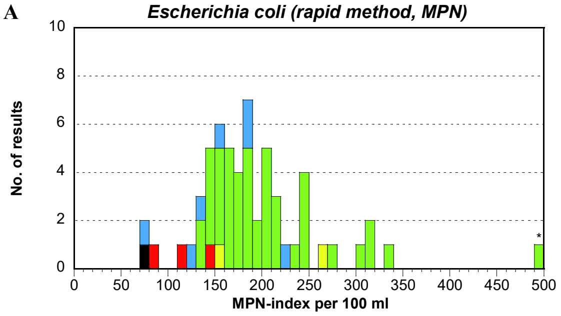
[##] No rapid kit method but a multiple tube method based on lactose fermentation.

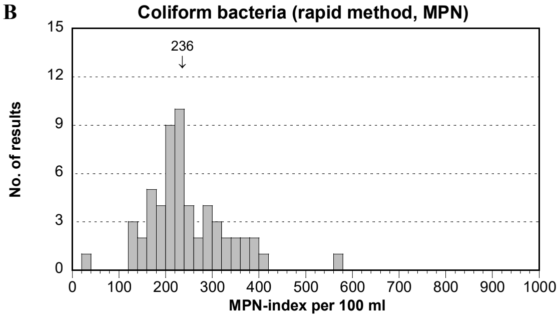
* Mean value is given for comparison despite few results.

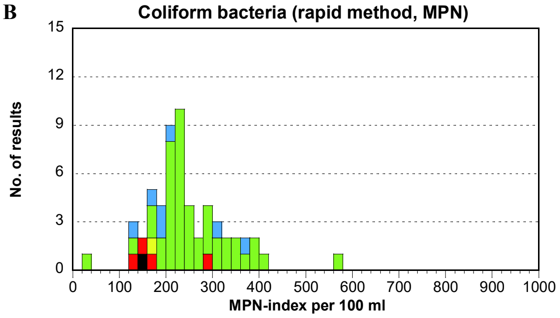


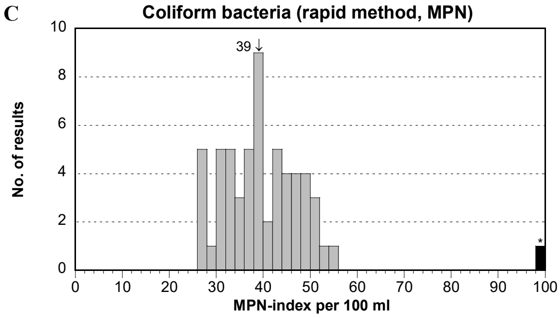


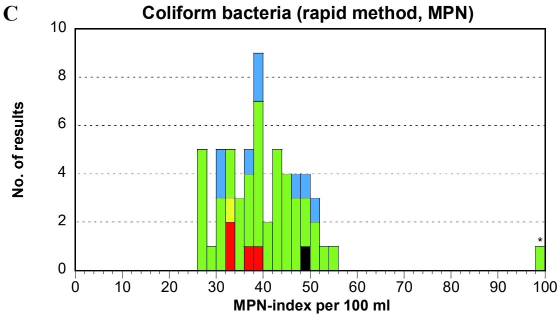


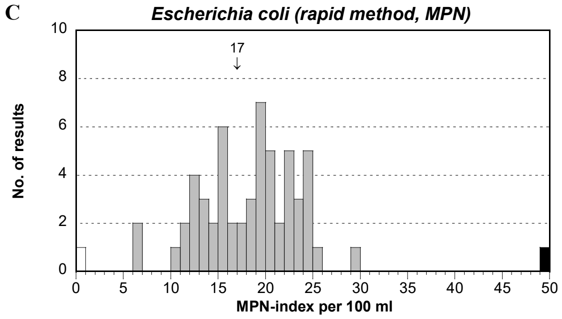


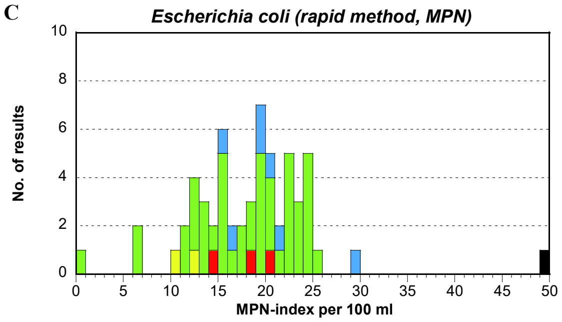












Sample A

- In this sample the coliform bacteria *E. coli* and *C. freundii* were present. Both of them possess the enzyme *β*-galactosidase and are detected as coliform bacteria but only *E. coli* has the enzyme *β*-glucuronidase and is detected as *E. coli*.
- The averages recovery for coliform bacteria was about 12 % higher with the rapid methods compared to the MF methods (see page 6)
- One high outlier was reported for both coliform bacteria and *E. coli*.

Sample B

- In this sample the coliform bacteria *E. cloacae* and *C. sakazakii* were present. Both of them possess *β*-galactosidase but not *β*-glucuronidase. They are thus detected as coliform bacteria but not as *E. coli*.
- The average recovery for coliform bacteria was about 19 % higher with the rapid methods compared to the MF methods (see page 6)
- One false positive result for *E. coli* was present which was probably caused by a mix up between sample B and C.

Sample C

- Two *E. coli* strains were present, both possessing *β*-glucuronidase. However, in one of the strains the activity is so low that the fluorescence is usually interpreted as negative.
- The average result for *E. coli* was, as expected, lower than for the MF methods using LES (17 MPN index/100 ml compared to 31 cfu/100 ml, see page 6). This is because LES is based on lactose fermentation and not *β*-glucuronidase activity.
- A mix up between sample B and C resulted in one false negative result for *E. coli*. Furthermore, one high outlier was reported for both coliform bacteria and *E. coli*.

Intestinal enterococci (MF/MPN)

The MF method used for intestinal enterococci was almost exclusively EN ISO 7899-2:2000. The primary growth medium was m-Enterococcus Agar (Slanetz & Bartley), here designated m-Ent. Six laboratories used the rapid method Enterolert® (Idexx Inc.). Four of these used Enterolert®-E (Idexx Inc.) and the other two used Enterolert®-DW (Idexx Inc.). The group Other/Unknown in the table includes the use of Rapid Enterococcus Agar or Standard Methods [5].

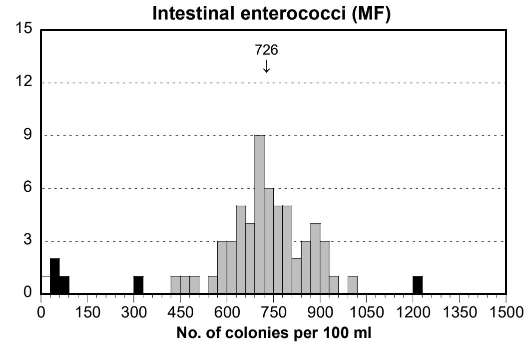
The incubation temperature for m-Ent was 35, 36 or 37 °C, except for one laboratory that incubated at 41 °C. The incubation temperature was 41 °C for Enterolert, 44 °C for the Rapid Enterococcus Agar and 35 °C for the Standard Methods.

Somewhat lower mean values were seen for Enterolert in sample A and B. The dispersions were very small for both m-Ent and Enterolert.

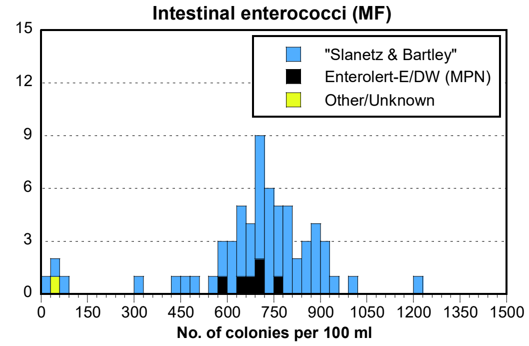
Method/Medium	N	A						B						C					
		n	**Mv**	CV	F	<	>	n	**Mv**	CV	F	<	>	n	**Mv**	CV	F	<	>
Total	65	58	**726**	8	1	4	1	60	**384**	8	2	2	0	63	**0**	–	1	–	–
Slanetz & Bartley	57	52	**732**	9	1	3	1	53	**387**	7	2	2	0	55	**0**	–	1	–	–
Enterolert®#	6	6	**677**	5	0	0	0	6	**370**	15	0	0	0	6	**0**	–	0	–	–
Other/unknown	2	0	–	–	0	1	0	1	–	–	0	0	0	2	–	–	0	–	–

Two variants of Enterolert® are included, E and DW, respectively– no confirmation was performed

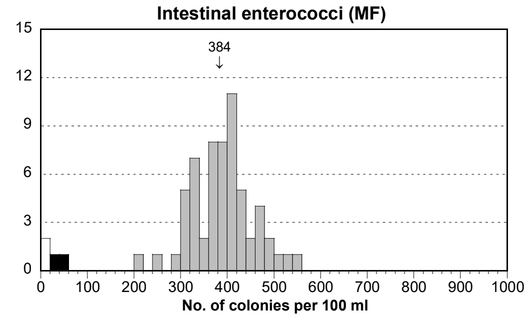
A



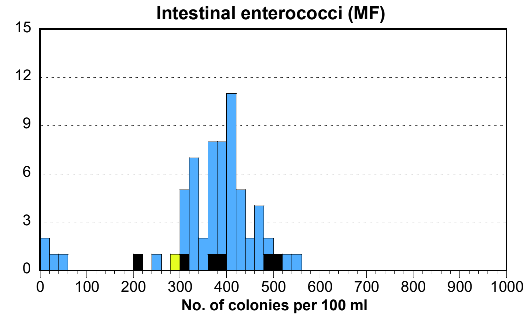
A



B



B



Sample A

- A strain of *E. faecalis* was present. The colonies have a dark brown-red colour on m-Ent and there is normally no problem regarding confirmation.
- Six deviant result were present. One false negative result, one high outlier and four low outliers were reported. Some low outliers may be caused by reporting the results in 10 ml instead of 100 ml.

Sample B

- A strain of *E. hirae* was present in the sample. The colour of the colonies is usually dark brown-red on m-Ent and without any confirmation problems.
- Two false negative results as well as two low outliers were obtained.

Sample C

- No intestinal enterococcus strain was included in the sample.
- One false positive result was reported, that is probably caused by a mix up between sample B and C.

Pseudomonas aeruginosa (MF/MPN)

EN ISO 16266:2008 with or without modification was used by 43 out of the 53 laboratories that reported results. Pseudalert® (Idexx Inc.) was used by eight laboratories.

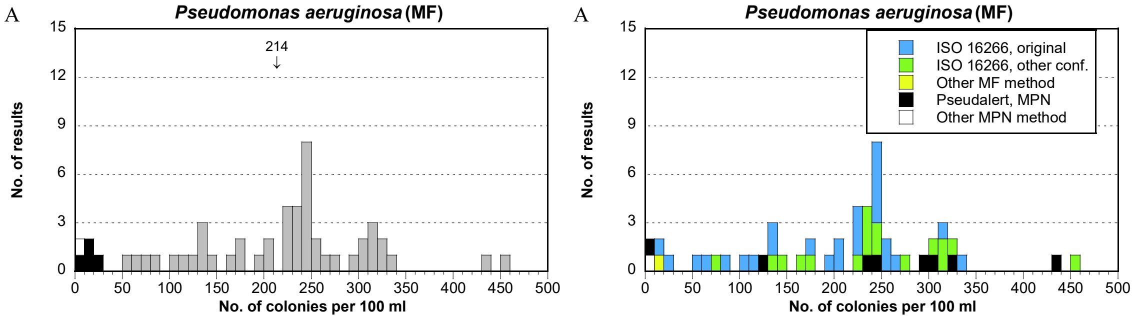
Since unhealthy substances like mercury are included, many laboratories have replaced the confirmation tests in the standard by another method. The major modifications of the method therefore concern the confirmation. When only typical yellow-green to blue-green colonies are present, no confirmation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

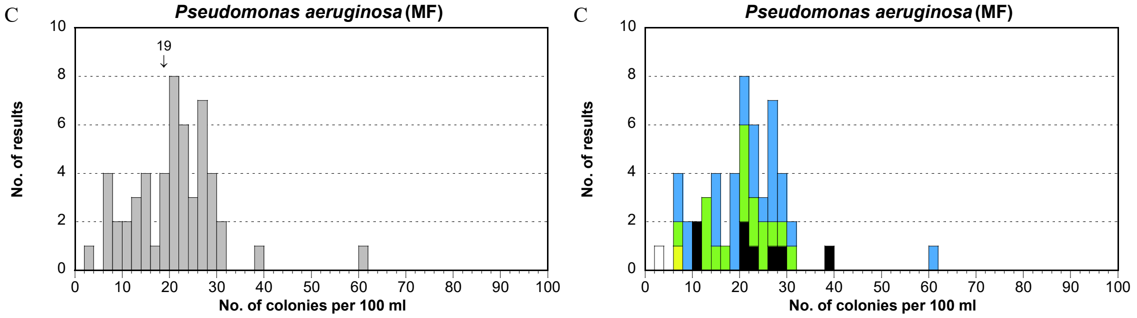
In sample A the average result was higher for Pseudalert® compared to MF-methods.

Standard/Method	**N**	**A**						**B**						**C**					
		n	**Mv**	CV	F	<	>	n	**Mv**	CV	F	<	>	n	**Mv**	CV	F	<	>
Total	53	48	**214**	21	1	4	0	53	**0**	–	0	–	–	53	**19**	25	0	0	0
Membrane filtration	*44*	*41*	***205***	*21*	*0*	*3*	*0*	*44*	***0***	–	*0*	–	–	*44*	***20***	*23*	*0*	*0*	*0*
ISO 16266 [a]	26	24	**189**	22	0	2	0	26	**0**	–	0	–	–	26	**20**	24	0	0	0
ISO 16266, mod.[b]	17	17	**230**	20	0	0	0	17	**0**	–	0	–	–	17	**19**	18	0	0	0
Other, MF	1	0	–	–	0	1	0	1	–	–	0	–	–	1	–	–	0	0	0
MPN methods	*9*	*7*	***271***	*18*	*1*	*1*	*0*	*9*	***0***	–	*0*	–	–	*9*	***18***	*34*	*0*	*0*	*0*
Pseudalert®, MPN	8	7	**271**	18	0	1	0	8	**0**	–	0	–	–	8	**21**	22	0	0	0
Other, MPN	1	0	–	–	1	0	0	1	–	–	0	–	–	1	–	–	0	0	0

a Modification not stated for confirmation

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





Sample A

- One strain of *P. aeruginosa* with typical, blue-green colonies on PACN was included in the sample. The colonies showed clear fluorescence under UV light. No confirmation is necessary according to the standard EN ISO 16266:2008.
- The distribution of the results was unusually scattered leading to a medium-sized dispersion (CV, see page 27).
- One false negative result and four low outliers were present. An explanation for the low outliers may be that some laboratories forgot to convert their count to the reference volume 100 ml.

Sample B

- There was no *P. aeruginosa* in the sample and no false positive result was reported.

Sample C

- One strain of *P. aeruginosa* was present in the sample. On PACN agar, it appears with light yellow-green to blue-green colonies that fluoresce under UV-light. *B. cepacia* was also present in the sample. That strain sometimes forms yellow colonies on PACN that could be suspected as *P. aeruginosa.* However, confirmation will show that the strain is not *P. aeruginosa*.
- The distribution of the results was fairly good with medium dispersion.
- No outliers could be discern but when considering the colony count, the highest result could be caused by inclusion of *B. cepacia.*

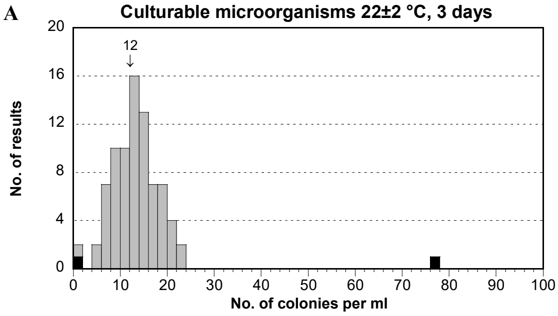
Culturable microorganisms 22 °C, 3 days

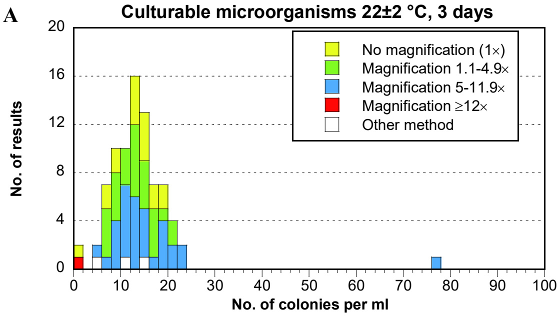
Seventy-eight of the 81 laboratories performing the analysis stated the use of EN ISO 6222:1999, which prescribes Yeast extract Agar (YeA). While still stating the use of EN ISO 6222:1999, nine laboratories used Plate Count Agar (PCA) instead. One laboratory used Petrifilm™ and two laboratories used YeA in conjunction with Standard methods [5]. These laboratories comprises the group "Other method". The majority of the laboratories have claimed counting both bacterial and fungal colonies. Nine laboratories stated that they did not count fungi, and four stated that they counted yeasts but not moulds.

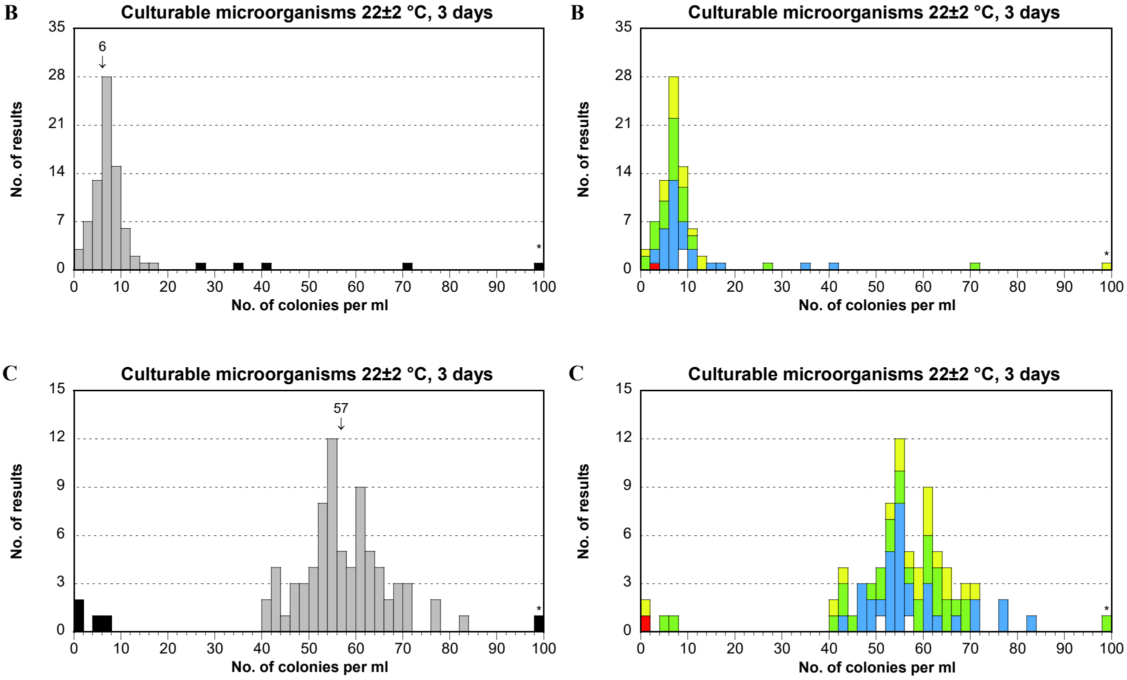
Since all except three laboratories refer to EN ISO 6222:1999, differences among method variants are relevant to discuss only for these. Results are shown for culture media and magnification at reading.

It is difficult to find any consistent difference based on methods or relation to magnification between the samples, except that PCA gave a larger dispersion (CV) than YeA in sample B.

Group of results	N	A						B						C					
		n	**Mv**	CV	F	<	>	n	**Mv**	CV	F	<	>	n	**Mv**	CV	F	<	>
Total, all results	81	79	**12**	19	0	1	1	76	**6**	25	0	0	5	75	**57**	8	0	4	1
EN ISO 6222	*78*	*76*	***12***	*19*	*0*	*1*	*1*	*73*	***6***	*25*	*0*	*0*	*5*	*73*	***57***	*8*	*0*	*4*	*1*
Medium																			
Yeast extract Agar	69	68	**12**	19	0	1	0	67	**6**	23	0	0	2	64	**57**	7	0	4	1
"Plate Count Agar"	9	8	**12**	13	0	0	1	6	**5**	42	0	0	3	9	**55**	9	0	0	0
Magnification																			
None	17	16	**13**	16	0	1	0	16	**7**	28	0	0	1	16	**58**	7	0	1	0
1,1–4,9×	28	28	**12**	17	0	0	0	26	**6**	27	0	0	2	25	**56**	7	0	2	1
5–11,9×	32	31	**13**	18	0	0	1	30	**7**	21	0	0	2	32	**57**	8	0	0	0
≥ 12×	1	1*	**1**	–	0	0	0	1*	**2**	–	0	0	0	0	–	–	0	1	0
Other method	*3*	*3**	***10***	*–*	*0*	*0*	*0*	*3**	***9***	*–*	*0*	*0*	*0*	*2**	***53***	*–*	*0*	*0*	*0*







Sample A

- About 50 % of the colonies belong to *E. faecalis* and the rest are made up of the two coliform bacteria and *P. aeruginosa*.
- The distribution of the results was good except for two outliers.

Sample B

- The rather few colonies are made up of the coliform bacteria and *E. hirae*.
- The distribution was good except for a tail with some high outliers. Due to the low concentration, the relative dispersion was medium despite the good distribution.
- The five high outliers are probably caused by an incubation temperature exceeding 22 °C, where colonies of *S. capitis* might be able to grow.

Sample C

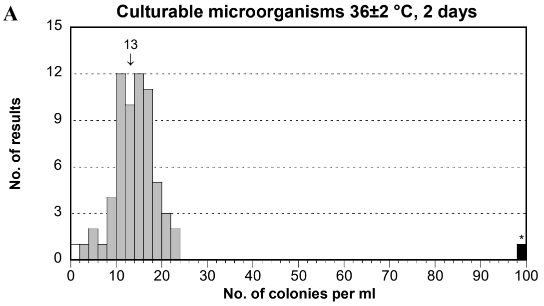
- The colonies consist almost exclusively of *S. saprophyticus*.
- The distribution was good and showed very low dispersion.
- Four low outliers and one high outlier were present. Some of the low outliers were caused by incorrect reporting.

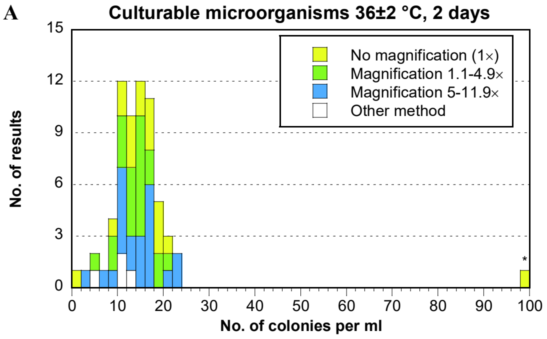
Culturable microorganisms 36 °C, 2 days

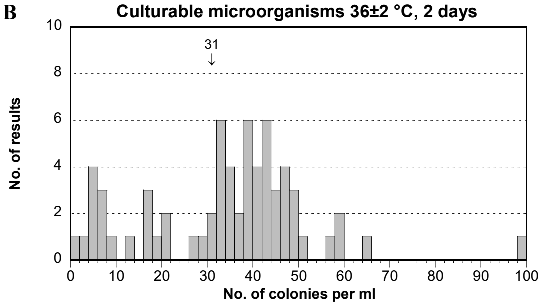
Sixty-one of the 65 laboratories stated that they followed EN ISO 6222:1999. Five of these reported the use of PCA. The values for PCA are for comparison shown in parallel with YeA for EN ISO 6222:1999 in the table below. Two of the four laboratories in the group Other/Unknown stated the use of Standard Methods [5].

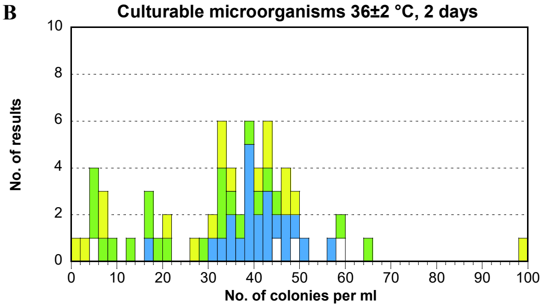
As for the analysis at 22 °C, comparisons of method variants are relevant to discuss only when EN ISO 6222:1999 was used. Here as well, results are shown for both culture media and magnification at reading. PCAs average result was higher for sample B as well as for the laboratories that used higher magnification at reading.

Group of results	N	A						B						C					
		n	**Mv**	CV	F	<	>	n	**Mv**	CV	F	<	>	n	**Mv**	CV	F	<	>
Total, all results	65	63	**13**	17	1	0	1	65	**31**	32	0	0	0	61	**55**	7	0	3	0
EN ISO 6222	*61*	*59*	***13***	*16*	*1*	*0*	*1*	*61*	***31***	*31*	*0*	*0*	*0*	*59*	***55***	*7*	*0*	*2*	*0*
Medium																			
Yeast extract Agar	56	55	**14**	16	1	0	0	56	**29**	31	0	0	0	54	**54**	7	0	2	0
Plate Count Agar	5	4*	**10**	–	0	0	1	5	**44**	32	0	0	0	5	**59**	8	0	0	0
Magnification																			
None	17	15	**14**	13	1	0	1	17	**29**	41	0	0	0	15	**57**	9	0	2	0
1,1–4,9×	22	22	**13**	15	0	0	0	22	**24**	37	0	0	0	22	**51**	8	0	0	0
5–11,9×	22	22	**13**	19	0	0	0	22	**40**	11	0	0	0	22	**56**	5	0	0	0
Other/Unknown	4	4*	**9**	–	0	0	0	4*	**34**	–	0	0	0	2*	**59**	–	0	1	0









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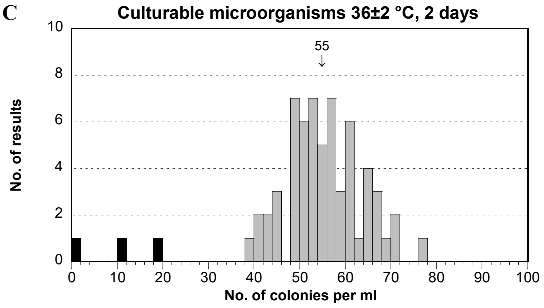

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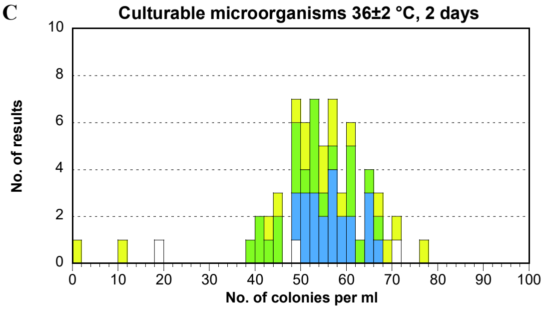

Sample A

- About 50 % of the colonies belong to *E. faecalis* and the rest are made up of the two coliform bacteria and *P. aeruginosa*.
- -The distribution of the results was good and the dispersion small.
- -One high outlier and one false negative result were reported.

Sample B

- All bacteria strains in the sample appear at 35/36/37 °C and contribute to the total number of culturable microorganisms. The considerably higher average here compared to at 22 °C is caused by the strain of *S. capitis* that grows at 35/36/37 °C but not at 22 °C and is present in highest concentration.
- The distribution shows unexpectedly many low results. The reason for these low results is not clear but as shown in the histogram you may suspect that *S. capitis* was difficult to see without appropriate magnification. This time no results could be identified as outliers, leading to the large dispersion that is higher than usual.

Sample C

- The colonies are almost entirely made up of the strain *S. saprophyticus.*
- The distribution of the results was good except for three low outliers.

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

Eight laboratories have more than one deviating result. When whole samples appear to have been mixed up, the corresponding sample numbers are crossed out in annex A. Laboratory 9306 seem to have mixed up sample B and C. Laboratory 1254 may have mixed up the samples for some of the parameters. Two laboratories reported their results as $\log_{10}$ values, which contradicts the instruction for the PT round.

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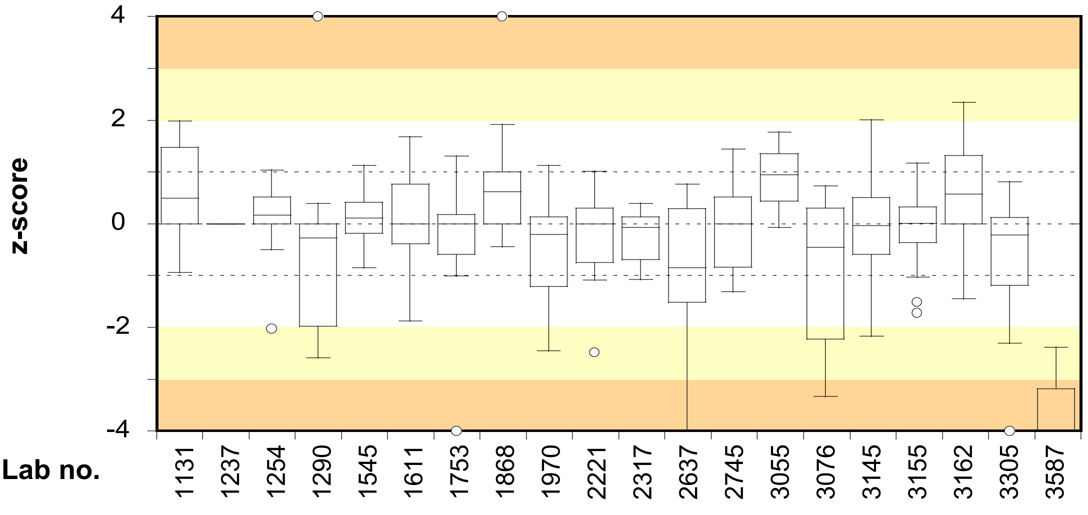
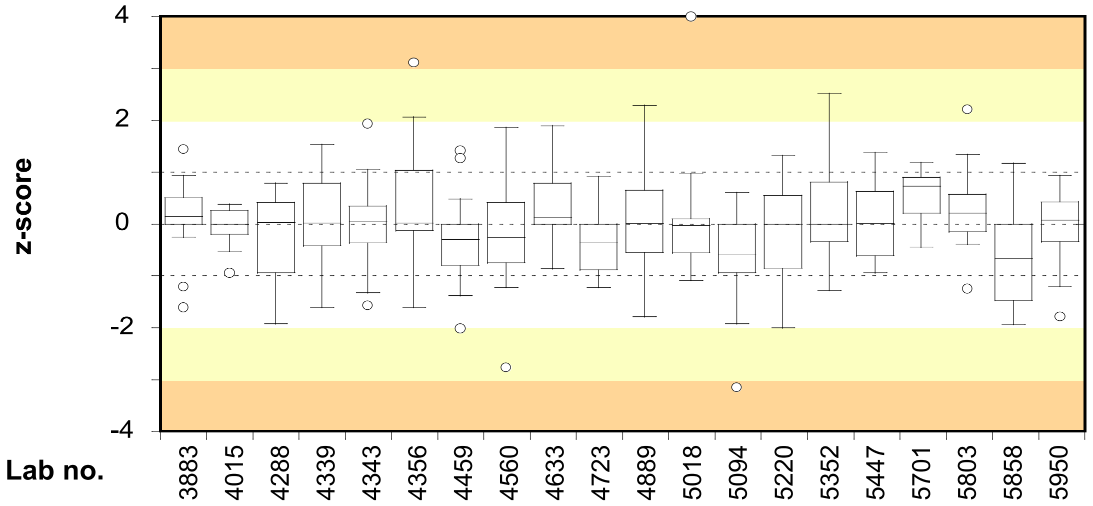
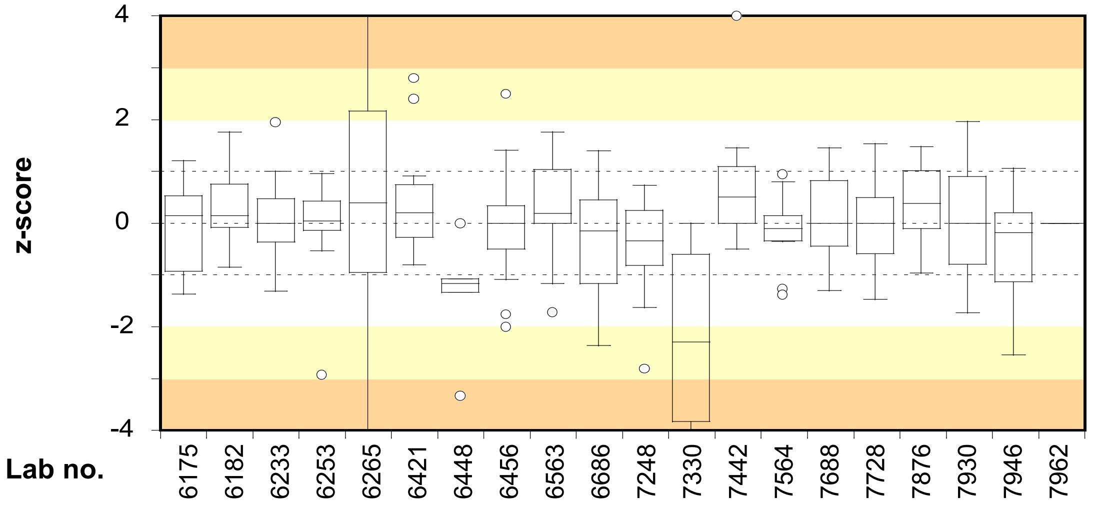
* < [smallest value of the box - 1.5 × (largest value of the box - smallest value of the box)] *or* > [largest value of the box + 1.5 × (largest value of the box - smallest value of the box)]



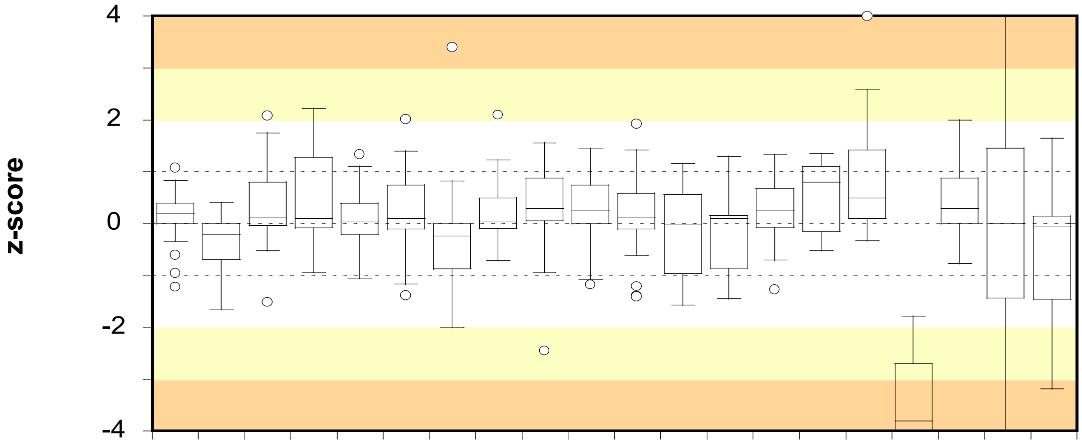
Lab no.	1131	1237	1254	1290	1545	1611	1753	1868	1970	2221	2317	2637	2745	3055	3076	3145	3155	3162	3305	3587
No. of results	9	-	22	12	24	24	18	15	16	12	15	12	9	3	9	18	24	18	23	5
False positive	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
False negative	-	-	1	-	-	-	-	-	2	-	-	-	-	-	-	-	-	-	-	1
Low outliers	-	-	-	-	-	-	1	-	-	-	-	2	-	-	1	-	-	-	2	3
High outliers	-	-	-	1	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-



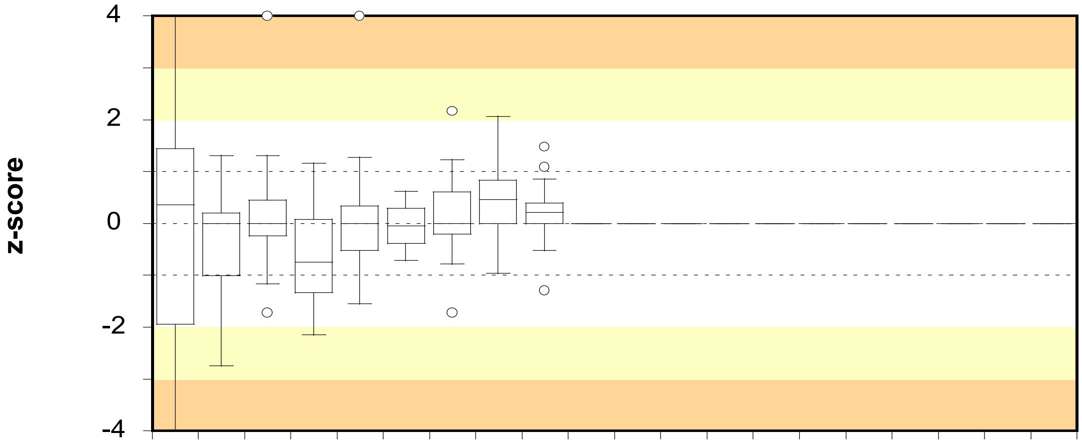
Lab no.	3883	4015	4288	4339	4343	4356	4459	4560	4633	4723	4889	5018	5094	5220	5352	5447	5701	5803	5858	5950
No. of results	24	12	3	24	18	24	21	12	21	12	24	24	14	18	18	18	9	12	18	24
False positive	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
False negative	-	-	-	-	-	-	-	1	-	-	-	-	1	-	-	-	-	-	-	-
Low outliers	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
High outliers	-	-	-	-	-	-	-	-	-	-	-	2	-	-	-	-	-	-	-	-



Lab no.	6175	6182	6233	6253	6265	6421	6448	6456	6563	6686	7248	7330	7442	7564	7688	7728	7876	7930	7946	7962
No. of results	8	18	24	12	23	18	6	21	24	12	24	12	15	12	24	18	24	24	24	-
False positive	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
False negative	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Low outliers	-	-	-	-	1	-	-	-	-	-	-	4	-	-	-	-	-	-	-	-
High outliers	-	-	-	-	4	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-



Lab no.	7968	8019	8068	8260	8329	8380	8435	8569	8626	8628	8663	8742	8751	8766	8829	8862	8891	8898	9002	9051
No. of results	24	24	24	9	18	24	18	18	11	18	24	12	9	24	8	24	4	24	12	24
False positive	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-
False negative	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	-	-	-
Low outliers	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	-	1	1
High outliers	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	1	-	-	2	-



Lab no.	9306	9408	9436	9441	9524	9655	9736	9899	9903
No. of results	10	24	24	12	21	3	18	24	18
False positive	1	-	-	-	-	-	-	-	-
False negative	1	-	-	-	-	-	-	-	-
Low outliers	1	-	-	-	-	-	-	-	-
High outliers	2	-	1	-	1	-	-	-	-

Test material, quality controls and processing of data

Description of the test material

This PT round comprised three test items with different microorganism compositions. The test material was manufactured and freeze-dried in 0.5 ml portions 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 participants were instructed to perform the analyses according to the methods routinely used at their laboratories.

The test material is primarily suited to the EN ISO methods for analyses of drinking water referred to in the current (old) European Drinking water directive [4] and its updates [6]. The new directive [7] has to be implemented by January 2023. Alternative methods and other standards can usually be used without any problem.

Table 2 *Microorganisms present in the samples*

Sample [1]	**Microorganism**	**Strain collection no.**		**cfu/100 ml** [2]
		SLV [3]	Reference [4]	
A	*Escherichia coli*	082	CCUG 45097	200
	Citrobacter freundii	424	–	150
	Enterococcus faecalis	051	CCUG 45101	750
	Pseudomonas aeruginosa	395	CCUG 43596	350
	Clostridium perfringens	442	CCUG 43593	800
B	*Enterobacter cloacae*	451	CCUG 30205	150
	Cronobacter sakazakii	419	–	100
	Enterococcus hirae	536	CCUG 46536	400
	Staphylococcus capitis	463	CCUG 35173	50*
C	*Escherichia coli*	084	–	20
	Escherichia coli	295	–	20
	Pseudomonas aeruginosa	455	CCUG 30209	30
	Burkholderia cepacia	042	–	30
	Staphylococcus saprophyticus	013	CCUG 45100	55 *

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 Internal strain collection number at the Swedish Food Agency (SLV).

4 Origin or typing collection no., CCUG: Culture Collection University of Gothenburg, ATCC: American Type Culture Collection; A dash (–) indicates a strain from the Swedish Food Agency's internal culture collection that has not yet been characterised at another culture collection.

Quality control of the test material

In order to allow comparison of results from the freeze-dried samples, it is essential that the original sample mixture is homogeneous and that a uniform volume is distributed in all vials. The sample volume was monitored during production by weighing 2-3 % of the vials before and after addition of the sample. The largest detected differences between vials were 8, 6 and 5 mg in samples A, B and C, respectively. The largest accepted difference is 15 mg (3 %).

Table 3 *Concentration (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*	38[a]	0.4	1.2	25[a]	0.6	1.4	42	0.4	1.2
Suspected thermotolerant colif. bact. (MF) *m-FC Agar. 44 °C according to SS 028167*	11[a]	1.6	2.3	3[a]	1.6	4.3	38	1.0	1.4
Escherichia coli (MF) *m-Endo Agar LES according to SS 028167*	21[a]	0.3	1.3	–	–	–	42	0.4	1.2
Intestinal enterococci (MF) *m-Enterococcus Agar acc. to SS-EN ISO 7899-2:2000*	74[a]	2.7	1.5	17[a]	1.0	1.6	–	–	–
Pseudomonas aeruginosa (MF) *Pseudomonas Agar base with cetrimide and nalidixic acid according to SS-EN ISO 16266:2008*	34[a]	0.8	1.4	–	–	–	14[b]	0.6	1.5
Culturable microorg. 2d 37 °C (pour plate) *Yeast extract Agar according to SS-EN ISO 6222:1999*	15	2.5[c]	2.1[c]	54	1.1	1.3	55	0.7	1.3
Culturable microorg. 3d 22 °C (pour plate) *Yeast extract Agar according to SS-EN ISO 6222:1999*	14	1.8	2.1	9	1.4	2.2	56	1.1	1.3

1 5 vials analysed in duplicate for sample A and B and 10 vials for sample C, normally 100 ml for MF and 1 ml for pour plate. The samples were analysed 27, 22 and 20 weeks ahead of the testing round for samples A, B and C, respectively.

a Determined for the volume 10 ml

b Determined for the volume 50 ml

c The results suggest inhomogeneity but are assumed to be random because homogeneity at 22 °C

– No target organism and thus no analysis

Table 3 shows 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. The values are from duplicate analyses of 10 vials the first time a sample mixture is used or from duplicate analyses of 5 vials when a sample 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 homogeneous is that I_2 and T *not simultaneously* are higher than 2. According to that criterion and comment in note c to table 3, all sample mixtures were homogeneous with regard to the parameters that were to be analysed.

Processing of numerical results

Most histograms have "tails" in either or both directions, due to values that do not belong to the expected distribution. For drinking water, $\log_{10}$ transformation of the results is normally not routine. Instead, for the low concentrations normally encountered here, square root transformations of the results usually 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 the 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, for example when many zero results are reported and in some borderline cases, subjective adjustments are made based on the knowledge of the sample mixture's content in order to set the correct 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, the measurement uncertainty will also 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. It is here provided as the relative uncertainty (u_{rel}), which is expressed as per cent after division by the mean value *mv* and multiplication by 100.

More information about result processing and recommendations on follow-up analyses are provided 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.
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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)*.
7. Anonymous 2020. Directive (EU) 2020/2184 OF THE EUROPEAN PARLIAMENT AND OF THE COUNCIL of 16 December 2020 on the quality of water intended for human consumption. Official Journal of the European Union, 23.12.2020, L 435/1-62 *(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	-	-	-	-	-	-	-	-	-	-	-	-	345	388	33	210	0	13
1237	1	3	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1254	1	2	3	-	-	-	280	200	40	-	-	-	224	0	36	345	205	41	238	0	15
1290	3	1	2	-	-	-	90	**5000**	22	-	-	-	75	<1	22	-	-	-	-	-	-
1545	1	3	2	290	240	32	290	240	32	182	150	32	182	0	24	416	222	33	207	0	15
1611	2	3	1	445	280	40	445	280	40	260	72	46	260	0	19	387	345	44	249	0	15
1753	1	3	2	-	-	-	-	-	-	-	-	-	-	-	-	320	183	42	218	0	14
1868	1	3	2	347	282	5271	347	282	**5271**	-	-	-	218	0	19	388	292	54	216	0	24
1970	2	3	1	130	0	40	130	**0**	40	70	0	32	70	0	13	-	-	-	-	-	-
2221	1	2	3	-	-	-	-	-	-	-	-	-	200	<1	16	-	-	-	-	-	-
2317	3	1	2	-	-	-	209	152	33	-	-	-	152	0	12	-	-	-	-	-	-
2637	2	3	1	-	-	-	-	-	-	-	-	-	-	-	-	364	306	31	137	<1	21
2745	3	2	1	283	123	42	283	123	42	283	123	42	196	0	42	-	-	-	-	-	-
3055	2	3	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3076	3	1	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3145	2	3	1	-	-	-	-	-	-	-	-	-	-	-	-	236	225	38	145	0	16
3155	1	3	2	-	-	-	382	209	35	-	-	-	172	<1	16	347	163	45	170	<1	24
3162	1	2	3	-	-	-	-	-	-	-	-	-	-	-	-	461	285	52	249	0	24
3305	3	1	2	390	200	19	330	200	16	-	-	-	170	<1	10	250	220	26	170	<1	11
3587	2	3	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3883	1	3	2	323	199	42	323	199	42	-	-	-	146	<1	42	381	237	42	201	<1	20
4015	2	1	3	-	-	-	-	-	-	-	-	-	-	-	-	311	226	41	173	0	19
4288	3	2	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4339	1	3	2	-	-	-	220	163	40	72	59	42	100	0	8	461	365	38	228	0	19
4343	3	1	2	-	-	-	-	-	-	-	-	-	-	-	-	185	308	36	155	0	19
4356	2	3	1	330	300	37	260	300	35	95	67	34	240	0	35	436	579	43	313	0	22
4459	2	1	3	-	-	-	236	152	38	-	-	-	152	0	11	225	133	33	148	0	20
4560	3	2	1	-	-	-	220	152	27	220	0	27	220	0	10.8	-	-	-	-	-	-
4633	1	3	2	-	-	-	340	255	36	102	5	38	306	0	36	238	218	39	185	0	24
4723	3	2	1	-	-	-	-	-	-	-	-	-	-	-	-	210	261	34	133	0	13
4889	2	1	3	-	-	-	380	180	35	-	-	-	210	0	14	410	330	39	330	0	19
5018	1	2	3	-	-	-	280	170	35	-	-	-	200	0	35	236	201	31	150	0	15
5094	2	3	1	-	-	-	197	103	30	-	-	-	176	0	30	-	-	-	-	-	-
5220	3	2	1	-	-	-	-	-	-	-	-	-	-	-	-	194	219	42	138	0	18
5352	3	2	1	-	-	-	180	400	58	-	-	-	90	0	22	-	-	-	-	-	-
5447	3	1	2	-	-	-	-	-	-	-	-	-	-	-	-	310	200	34	140	0	13
5701	3	2	1	-	-	-	390	240	44	-	-	-	240	0	34	-	-	-	-	-	-
5803	2	3	1	-	-	-	-	-	-	-	-	-	-	-	-	276	276	44	194	<1	25
5858	3	2	1	-	-	-	140	105	22	-	-	-	81	<1	10	-	-	-	-	-	-
5950	1	3	2	355	245	31	355	245	31	82	0	33	227	0	11	326	220	31	200	0	20
6175	3	1	2	-	-	-	-	-	-	-	-	-	-	-	-	200	**>200**	48	129	0	19
6182	3	2	1	345	220	37	345	220	37	-	-	-	215	0	14	399	204	38	246	0	17
6233	2	1	3	220	150	31	220	150	31	-	-	-	180	0	19	260	291	37	185	0	23
6253	3	2	1	-	-	-	-	-	-	-	-	-	-	-	-	305	193	46	186	0	20
6265	2	1	3	200	240	50	200	240	50	0	10	43	100	0	**0**	**920**	140	49	79	0	**49**
6421	3	2	1	-	-	-	310	142	32	137	44	32	131	0	32	-	-	-	-	-	-
6448	2	1	3	-	-	-	180	120	10	-	-	-	100	0	10	-	-	-	-	-	-
6456	3	2	1	-	-	-	230	230	47	-	-	-	59	0	39	340	210	31	150	0	15
6563	1	2	3	427	245	44	427	245	35	427	245	44	256	<1	35	259	255	27	184	<1	12
6686	3	2	1	-	-	-	-	-	-	-	-	-	-	-	-	150	124	36.4	75	<1	16.4
7248	1	2	3	220	170	27	220	170	27	140	130	31	140	<1	27	200	190	44	150	<1	6
7330	1	3	2	-	-	-	-	-	-	-	-	-	24	0	11	-	-	-	-	-	-
7442	3	1	2	355	228	5926	355	228	**5926**	-	-	-	243	0	20	452	249	47	242	0	15
7564	3	2	1	-	-	-	250	170	43	-	-	-	140	0	21	-	-	-	-	-	-
7688	3	2	1	210	200	24	210	200	24	-	-	-	140	0	18	410	330	50	160	0	23
7728	1	3	2	-	-	-	310	240	22	-	-	-	140	0	14	-	-	-	-	-	-
7876	1	3	2	400	206	42	400	206	42	20	7	34	120	0	42	435.2	204.6	31.8	272.3	0	19.5
7930	3	1	2	140	110	22	140	110	22	-	-	-	70	0	11	270	180	50	180	0	29
7946	3	1	2	-	-	-	140	59	38	100	41	24	140	0	16	218.5	148.3	38.9	146.7	0	23.3
7962	3	1	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
7968	1	3	2	-	-	-	305	170	24	-	-	-	185	0	28	330	220	47	205	0	22
8019	1	3	2	270	131	36	270	131	36	-	-	-	160	0	14	254	178	38	150	0	10
8068	3	1	2	-	-	-	310	360	33	-	-	-	250	0	33	370	410	39	160	0	18
8260	3	1	2	282	134	55	282	134	55	-	-	-	171	0	55	-	-	-	-	-	-
8329	1	3	2	-	-	-	-	-	-	-	-	-	-	-	-	291	365	36	172	0	21
8380	3	2	1	-	-	-	305	150	27	-	-	-	185	0	27	380	305	35	310	0	12
8435	3	2	1	-	-	-	260	130	33	0	2	26	180	0	33	-	-	-	-	-	-
8569	3	2	1	-	-	-	366	189	36	-	-	-	192	0	21	428	179	39	187	0	17
8626	1	2	3	430	200	38	430	200	38	172	20	26	172	**20**	26	-	-	-	-	-	-
8628	2	3	1	330	210	43	330	210	43	100	37	42	100	0	42	-	-	-	-	-	-
8663	2	3	1	340	250	50	340	250	50	210	210	38	200	0	50	290	250	29	150	0	11
Mean							**273**	**192**	**35**				**162**	**0**	**23**	**309**	**236**	**39**	**182**	**0**	**17**
CV (%)							16	18	14				20	-	25	14	18	10	15	-	15

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. urel,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 (MF)**			**Susp. *Pseudomonas aeruginosa* (MF)**			***Pseudomonas aeruginosa* (MF)**			**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**	
-	-	-	-	-	-	-	-	-	-	-	-	20	14	70	-	-	-	**1131**
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**1237**
-	-	-	500	**0**	**390**	-	-	-	230	0	20	14	7	64	12	47	56	**1254**
-	-	-	460	410	<1	-	-	-	55	<1	15	-	-	-	-	-	-	**1290**
870	390	77	870	390	0	240	0	50	240	0	23	15	8	55	10	39	48	**1545**
710	370	112	710	370	0	160	0	15	160	0	15	11	8	53	9	5	54	**1611**
718	409	0	678	473	0	-	-	-	**1**	0	11	13	6	54	14	50	50	**1753**
-	-	-	-	-	-	-	-	-	-	-	-	14	6	53	-	-	-	**1868**
0	460	0	**0**	460	0	240	0	18	240	0	18	17	1	45	12	17	50	**1970**
-	-	-	600	240	<1	-	-	-	310	<1	12	-	-	-	18	27	55	**2221**
-	-	-	-	-	-	-	-	-	139	0	23	12	7	58	9	33	58	**2317**
72	43	51	**71**	**43**	0	-	-	-	-	-	-	7	4	43	-	-	-	**2637**
-	-	-	-	-	-	-	-	-	-	-	-	7	4	53	-	-	-	**2745**
-	-	-	-	-	-	-	-	-	-	-	-	12	13	65	-	-	-	**3055**
-	-	-	-	-	-	-	-	-	**19**	0	27	16	5	43	4	37	38	**3076**
-	-	-	579	365	0	-	-	-	435	0	23	18	8	63	17	3	50	**3145**
-	-	-	664	373	<1	-	-	-	227	<1	30	8	7	43	15	35	43	**3155**
560	550	545	560	550	0	310	0	16	310	0	16	21	3	62	15	12	66	**3162**
800	320	-	800	320	-	140	<1	13	140	<1	13	13	5	**4**	17	41	**10**	**3305**
-	-	-	-	-	-	-	-	-	-	-	-	**0.3**	0.3	**1.85**	**0**	1.85	**1.78**	**3587**
845	310	3600	845	310	<1	225	<1	27	225	<1	27	6	6	55	14	38	58	**3883**
759	409	6000	700	409	0	-	-	-	-	-	-	10	7	49	-	-	-	**4015**
-	-	-	-	-	-	-	-	-	-	-	-	5	9	57	-	-	-	**4288**
680	387	0	680	387	0	-	-	-	291	0	10	13	9	64	18	18	56	**4339**
769	385	5391	769	385	0	-	-	-	236	0	20	23	10	46	14	40	49	**4343**
730	390	4600	730	390	0	-	-	-	130	0	20	6	6	69	10	16	52	**4356**
964	445	2150	909	373	0	-	-	-	-	-	-	11	6	68	10	4	48	**4459**
-	-	-	**>23**	**>23**	**<1,1**	-	-	-	**<1,8**	**<1,8**	2	-	-	-	11	58	71	**4560**
-	-	-	664	364	0	-	-	-	-	-	-	16	9	58	17	32	60	**4633**
721	445	6091	703	445	0	-	-	-	-	-	-	10	4	56	-	-	-	**4723**
-	-	-	800	440	0	-	-	-	130	0	21	7	2	50	12	7	57	**4889**
-	-	-	740	330	0	-	-	-	205	0	19	**77**	**34**	50	11	47	50	**5018**
650	280	83	650	**0**	0	-	-	-	-	-	-	5	4	49	3	42	52	**5094**
-	-	-	840	420	0	-	-	-	81	0	7	15	8	41	10	43	66	**5220**
-	-	-	610	420	0	-	-	-	310	0	18	18	5	55	17	39	52	**5352**
830	460	93	830	460	0	270	0	12	270	0	12	13	7	69	18	20	60	**5447**
-	-	-	-	-	-	-	-	-	-	-	-	16	7	53	-	-	-	**5701**
-	-	-	770	308	<1	-	-	-	-	-	-	11	7	77	-	-	-	**5803**
-	-	-	650	340	<1	-	-	-	75	<1	7	14	9	57	13	58	45	**5858**
809	409	0	809	409	0	245	0	22	245	0	22	13	2	47	12	47	49	**5950**
-	-	-	-	-	-	-	-	-	-	-	-	15	8	50	-	-	-	**6175**
956	393	243	956	393	0	-	-	-	-	-	-	13	4	61	-	-	-	**6182**
780	520	96	780	520	0	121	0	28	121	0	28	7	8	60	12	42	53	**6233**
-	-	-	700	218	0	-	-	-	-	-	-	17	7	60	-	-	-	**6253**
790	410	4400	**300**	410	0	370	2900	60	100	0	60	8	**78000**	70	**126**	98	71	**6265**
-	-	-	740	410	0	-	-	-	240	0	29	10	16	83	12	47	57	**6421**
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**6448**
-	-	-	700	480	0	-	-	-	-	-	-	8	7	55	14	6	77	**6456**
-	-	-	639	505	<1	325	<1	27	325	<1	27	10	8	60	22	34	66	**6563**
690	440	<1	-	-	-	-	-	-	-	-	-	13	10	50	20	29	61	**6686**
740	360	2700	740	360	<1	130	<1	27	110	<1	27	9	8	47	7	39	58	**7248**
-	-	-	**44**	**20**	0	-	-	-	**11**	0	6	-	-	-	4	5	**19**	**7330**
-	-	-	-	-	-	-	-	-	-	-	-	18	7	54	-	-	-	**7442**
-	-	-	-	-	-	-	-	-	-	-	-	12	3	65	14	33	44	**7564**
600	380	69	600	380	0	330	0	9	330	0	9	10	5	61	13	45	63	**7688**
-	-	-	690	310	0	-	-	-	170	0	26	8	12	61	15	42	50	**7728**
700	415	0	700	415	0	250	0	28	250	0	28	17	9	52	11	56	65	**7876**
820	460	74	820	460	0	-	-	-	240	0	27	14	10	63	22	16	64	**7930**
420	325	0	770	325.5	0	65	0	8	62	0	8	8	7	63	14	4	60	**7946**
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**7962**
-	-	-	655	325	0	-	-	-	235	0	21	14	7	58	16	49	55	**7968**
700	360	82	700	300	0	240	0	14	240	0	14	9	7	55	15	21	53	**8019**
-	-	-	870	400	0	-	-	-	170	0	25	12	9	54	19	33	43	**8068**
-	-	-	-	-	-	-	-	-	-	-	-	19	4	56	-	-	-	**8260**
775	426	5700	775	426	0	-	-	-	326	0	20	13	7	52	9	38	53	**8329**
-	-	-	730	400	0	-	-	-	230	0	29	16	10	55	20	31	44	**8380**
1200	330	0	**1200**	330	0	190	0	14	190	0	14	9	2	41	9	40	52	**8435**
788	428	104	788	428	0	-	-	-	-	-	-	10	5	76	-	-	-	**8569**
920	480	70	920	480	0	-	-	-	-	-	-	14	1	49	-	-	-	**8626**
590	445	4500	590	400	0	260	0	24	260	0	24	13	10	56	17	33	61	**8628**
700	320	120	700	310	0	220	0	20	220	0	20	15	7	60	16	39	64	**8663**
			726	**384**	**0**				**214**	**0**	**19**	**12**	**6**	**57**	**13**	**31**	**55**	**Mean**
			8	8	-				21	-	25	19	25	8	17	32	7	**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**
8742	3	2	1				150	190	40				80	<1	10	-	-	-	-	-	-
8751	1	3	2				-	-	-				-	-	-	238	288	32	111	<1	18
8766	3	2	1	318	148	49	318	148	49	131	4	40	127	0	39	367	224	48	199	0	24
8829	2	3	1	-	-	-	360	290	-	-	-	-	260	0	-	-	-	-	-	-	-
8862	3	1	2	354	190	40	354	190	40	-	-	-	218	0	19	582	391	50	**582**	0	20
8891	1	2	3	-	-	-	**0**	**0**	**1.54**	-	-	-	-	-	-	-	-	-	-	-	-
8898	2	1	3	336	243	48	336	243	39	-	-	-	264	0	39	316	206	47	308	0	22
9002	3	2	1	-	-	-	99	380	**1900**	-	-	-	95	0	10	-	-	-	-	-	-
9051	1	2	3	-	-	-	216	84	24	170	0	24	170	0	24	188	133	26	140	0	6
9306	1	~~2~~	~~3~~	-	-	-	-	-	-	-	-	-	-	-	-	283	36	**274**	162	**18**	**0**
9408	3	2	1	340	126	40	340	126	40	-	-	-	230	<1	14	320	165	32	261	<1	12
9436	3	1	2	236	218	40	236	218	40	99	80	28	155	<1	40	233	230	27	164	<1	12
9441	1	3	2	-	-	-	-	-	-	-	-	-	-	-	-	165	165	36	83	<1	14
9524	1	2	3	246	149	27	246	149	27	-	-	-	140	<1	17	350	251	42	201	<1	22
9655	1	2	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
9736	1	2	3	-	-	-	-	-	-	-	-	-	-	-	-	291	236	27	186	0	19
9899	2	1	3	350	255	40	350	255	40	-	-	-	220	0	16	353	342	49	167	0	22
9903	1	2	3	-	-	-	355	220	41	-	-	-	149	<1	27	-	-	-	-	-	-
n				30	30	30	61	61	60	22	22	22	62	62	61	58	57	58	58	58	58
Min				130	0	19	0	0	1.54	0	0	24	24	0	0	150	36	26	75	0	0
Max				445	300	5926	445	5000	5926	427	245	46	306	20	55	920	579	274	582	18	49
Median				330	203	40	286.5	199.5	36	116.5	39	33.5	171.5	0	21	316	224	39	180	0	19
Mean							**273**	**192**	**35**				**162**	**0**	**23**	**309**	**236**	**39**	**182**	**0**	**17**
CV (%)							16	18	14				20	-	25	14	18	10	15	-	15
False positive							0	0	0				0	1	0	0	0	0	0	1	0
False negative							1	2	0				0	0	1	0	0	0	0	0	1
Outliers, low							0	0	1				0	0	0	0	0	0	0	0	0
Outliers, high							0	1	3				0	0	0	1	0	1	1	0	1
Low limit OK				130	0	19	90	59	10	0	0	24	24	0	10*	150	36	26	75	0	6
High limit OK				445	300	5926	445	400	58	427	245	46	306	0	55	582	579	54	330	0	29
mv *(√Mean)*							16.515	13.870	5.902				12.714	0.000	4.754	17.586	15.369	6.212	13.485	0.000	4.178
s *(CV*mv/100)*							2.721	2.438	0.824				2.518	0.000	1.199	2.528	2.791	0.593	2.041	0.000	0.614
$u_{rel,mv}$ **(%)** *(100*s/ √n_{mv}/mv)*							2.1	2.3	1.9				2.5		3.3	1.9	2.4	1.3	2.0		2.0
x *(√Result)*																					
z *([x-mv]/s)*																					

 # cfu/ml

Susp. intestinal enterococci (MF)			**Intestinal enterococci (MF)**			**Susp. *Pseudomonas aeruginosa* (MF)**			***Pseudomonas aeruginosa* (MF)**			**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**	
			-	-	-				-	-	-	12	7	67	16	44	50	
			-	-	-				-	-	-	13	11	58	-	-	-	
748	432	464	748	432	0	245	0	23	245	0	23	18	3	55	11	37	55	**8766**
-	-	-	-	-	-	-	-	-	-	-	-	11	9	-	11	49	-	**8829**
890	400	5100	890	400	0	-	-	-	305	0	39	23	7	60	20	41	57	**8862**
-	-	-	-	-	-	-	-	-	-	-	-	1.23	2	**1.74**	-	-	-	**8891**
864	364	3514	864	364	0	306	0	25	306	0	25	9	5	53	17	31	56	**8898**
-	-	-	**32**	290	0	-	-	-	-	-	-	14	**27**	62	-	-	-	**9002**
-	-	-	909	414	0	-	-	-	**23**	0	6	15	6	60	10	34	69	**9051**
-	-	-	-	-	-	-	-	-	-	-	-	20	**70**	**7**	18	64	40	**9306**
430	370	-	430	370	<1	240	<1	19	240	<1	19	7	7	42	14	33	40	**9408**
773	391	<1	773	391	<1	200	<1	27	200	<1	27	19	**40**	55	12	43	57	**9436**
-	-	-	-	-	-	-	-	-	-	-	-	13	7	67	10	6	48	**9441**
636	390	73	636	390	<1	-	-	-	-	-	-	19	5	**103**	14	8	49	**9524**
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	13	44	49	**9655**
883	335	3636	883	335	0	455	0	30	455	0	30	9	6	54	16	42	60	**9736**
1000	324	100	1000	324	0	257	0	21	257	0	21	20	6	52	17	49	55	**9899**
-	-	-	577	355	<1	-	-	-	220	<1	23	14	7	70	11	35	64	**9903**
41	41	39	64	64	64	25	25	25	53	53	53	81	81	80	65	65	64	**n**
0	43	0	0	0	0	65	0	8	0	0	2	0.3	0.3	1.74	0	1.85	1.78	**Min**
1200	550	6091	1200	550	390	455	2900	60	455	0	60	77	78000	103	126	98	77	**Max**
759	391	100	730	390	0	240	0	22	235.5	0	21	13	7	56	14	37	55	**Median**
			726	**384**	**0**				**214**	**0**	**19**	**12**	**6**	**57**	**13**	**31**	**55**	**Mean**
			8	8	-				21	-	25	19	25	8	17	32	7	**CV (%)**
			0	0	1				0	0	0	0	0	0	0	0	0	**False pos.**
			1	2	0				1	0	0	0	0	0	1	0	0	**False neg.**
			4	2	0				4	0	0	1	0	4	0	0	3	**Outliers <**
			1	0	0				0	0	0	1	5	1	1	0	0	**Outliers >**
0	43	0	430	218	0	65	0	8	55	0	2	1	0	41	3	1	38	**Low limit**
1200	550	6091	1000	550	0	455	2900	60	455	0	60	23	16	83	22	98	77	**High limit**
			26.942	19.592	0.000				14.636	0.000	4.399	3.511	2.515	7.530	3.631	5.546	7.397	**mv**
			2.261	1.648	0.000				3.091	0.000	1.079	0.663	0.618	0.565	0.603	1.758	0.553	**s**
			1.1	1.1					3.0		3.4	2.1	2.8	0.9	2.1	3.9	1.0	**$u_{rel,mv}$ (%)**
																		x
																		z

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													0.391	1.551	-0.788	0.493	0.000	-0.932
1237	1	3	2																		
1254	1	2	3				0.080	0.112	0.513				0.895	0.000	1.040	0.391	-0.377	0.323	0.952	0.000	-0.496
1290	3	1	2				**-2.583**	**4.000**	-1.471				-1.610	0.000	-0.053						
1545	1	3	2				0.189	0.665	-0.298				0.309	0.000	0.121	1.112	-0.168	-0.788	0.442	0.000	-0.496
1611	2	3	1				1.683	1.174	0.513				1.355	0.000	-0.330	0.825	1.148	0.711	1.125	0.000	-0.496
1753	1	3	2													0.120	-0.660	0.454	0.627	0.000	-0.710
1868	1	3	2				0.777	1.199	**4.000**				0.815	0.000	-0.330	0.835	0.616	1.917	0.594	0.000	1.174
1970	2	3	1				-1.879		0.513				-1.727	0.000	-0.958						
2221	1	2	3										0.567	0.000	-0.629						
2317	3	1	2				-0.757	-0.632	-0.191				-0.153	0.000	-1.076						
2637	2	3	1													0.591	0.761	-1.086	-0.872	0.000	0.659
2745	3	2	1				0.113	-1.140	0.703				0.511	0.000	1.441						
3055	2	3	1																		
3076	3	1	2																		
3145	2	3	1													-0.880	-0.132	-0.080	-0.707	0.000	-0.289
3155	1	3	2				1.114	0.241	0.017				0.159	0.000	-0.629	0.412	-0.932	0.837	-0.219	0.000	1.174
3162	1	2	3													1.537	0.542	1.685	1.125	0.000	1.174
3305	3	1	2				0.607	0.112	**-2.309**				0.129	0.000	-1.328	-0.702	-0.192	-1.877	-0.219	0.000	-1.402
3587	2	3	1																		
3883	1	3	2				0.536	0.097	0.703				-0.250	0.000	1.441	0.765	0.009	0.454	0.340	0.000	0.479
4015	2	1	3													0.020	-0.120	0.323	-0.163	0.000	0.295
4288	3	2	1																		
4339	1	3	2				-0.619	-0.452	0.513				-1.078	0.000	-1.606	1.537	1.339	-0.080	0.791	0.000	0.295
4343	3	1	2													-1.576	0.781	-0.357	-0.507	0.000	0.295
4356	2	3	1				-0.144	1.415	0.017				1.104	0.000	0.970	1.303	**3.115**	0.583	**2.062**	0.000	0.834
4459	2	1	3				-0.424	-0.632	0.319				-0.153	0.000	-1.199	-1.023	-1.375	-0.788	-0.647	0.000	0.479
4560	3	2	1				-0.619	-0.632	-0.857				0.842	0.000	-1.224						
4633	1	3	2				0.707	0.861	0.119				1.898	0.000	1.040	-0.854	-0.217	0.056	0.057	0.000	1.174
4723	3	2	1													-1.224	0.282	-0.642	-0.957	0.000	-0.932
4889	2	1	3				1.095	-0.186	0.017				0.706	0.000	-0.845	1.053	1.002	0.056	**2.294**	0.000	0.295
5018	1	2	3				0.080	-0.341	0.017				0.567	0.000	0.970	-0.880	-0.427	-1.086	-0.606	0.000	-0.496
5094	2	3	1				-0.911	-1.526	-0.516				0.220	0.000	0.603						
5220	3	2	1													-1.447	-0.204	0.454	-0.851	0.000	0.106
5352	3	2	1				-1.139	**2.514**	**2.080**				-1.282	0.000	-0.053						
5447	3	1	2													0.008	-0.440	-0.642	-0.810	0.000	-0.932
5701	3	2	1				1.188	0.665	0.888				1.104	0.000	0.898						
5803	2	3	1													-0.385	0.446	0.711	0.217	0.000	1.338
5858	3	2	1				-1.721	-1.486	-1.471				-1.475	0.000	-1.328						
5950	1	3	2				0.855	0.731	-0.406				0.935	0.000	-1.199	0.186	-0.192	-1.086	0.322	0.000	0.479
6175	3	1	2													-1.362		1.208	-1.042	0.000	0.295
6182	3	2	1				0.757	0.395	0.219				0.774	0.000	-0.845	0.945	-0.389	-0.080	1.078	0.000	-0.089
6233	2	1	3				-0.619	-0.666	-0.406				0.279	0.000	-0.330	-0.578	0.605	-0.218	0.057	0.000	1.006
6253	3	2	1													-0.048	-0.529	0.962	0.075	0.000	0.479
6265	2	1	3				-0.872	0.665	1.419				-1.078	0.000		**4.000**	-1.267	1.329	**-2.253**	0.000	**4.000**
6421	3	2	1				0.401	-0.801	-0.298				-0.504	0.000	0.753						
6448	2	1	3				-1.139	-1.196	**-3.326**				-1.078	0.000	-1.328						
6456	3	2	1				-0.496	0.531	1.158				-1.999	0.000	1.244	0.338	-0.314	-1.086	-0.606	0.000	-0.496
6563	1	2	3				1.525	0.731	0.017				1.305	0.000	0.970	-0.590	0.215	-1.713	0.039	0.000	-1.162
6686	3	2	1													**-2.112**	-1.517	-0.301	**-2.364**	0.000	-0.209
7248	1	2	3				-0.619	-0.341	-0.857				-0.350	0.000	0.369	-1.362	-0.568	0.711	-0.606	0.000	**-2.813**
7330	1	3	2										**-3.104**	0.000	-1.199						
7442	3	1	2				0.855	0.504	**4.000**				1.142	0.000	-0.235	1.453	0.147	1.086	1.015	0.000	-0.496
7564	3	2	1				-0.259	-0.341	0.796				-0.350	0.000	-0.143						
7688	3	2	1				-0.744	0.112	-1.218				-0.350	0.000	-0.427	1.053	1.002	1.449	-0.410	0.000	1.006
7728	1	3	2				0.401	0.665	-1.471				-0.350	0.000	-0.845						
7876	1	3	2				1.281	0.198	0.703				-0.699	0.000	1.441	1.296	-0.382	-0.966	1.478	0.000	0.388
7930	3	1	2				-1.721	-1.387	-1.471				-1.727	0.000	-1.199	-0.457	-0.700	1.449	-0.034	0.000	1.965
7946	3	1	2				-1.721	**-2.538**	0.319				-0.350	0.000	-0.629	-1.109	-1.143	0.043	-0.673	0.000	1.057
7962	3	1	2																		
7968	1	3	2				0.349	-0.341	-1.218				0.353	0.000	0.448	0.230	-0.192	1.086	0.408	0.000	0.834
8019	1	3	2				-0.031	-0.995	0.119				-0.026	0.000	-0.845	-0.652	-0.726	-0.080	-0.606	0.000	-1.653
8068	3	1	2				0.401	**2.093**	-0.191				1.230	0.000	0.826	0.653	1.748	0.056	-0.410	0.000	0.106
8260	3	1	2				0.102	-0.941	1.838				0.144	0.000	**2.221**						
8329	1	3	2													-0.209	1.339	-0.357	-0.181	0.000	0.659
8380	3	2	1				0.349	-0.666	-0.857				0.353	0.000	0.369	0.755	0.751	-0.499	**2.020**	0.000	-1.162
8435	3	2	1				-0.144	-1.012	-0.191				0.279	0.000	0.826						
8569	3	2	1				0.961	-0.050	0.119				0.454	0.000	-0.143	1.227	-0.713	0.056	0.093	0.000	-0.089
8626	1	2	3				1.551	0.112	0.319				0.159		0.288						
8628	2	3	1				0.607	0.255	0.796				-1.078	0.000	1.441						
8663	2	3	1				0.707	0.796	1.419				0.567	0.000	1.933	-0.220	0.159	-1.394	-0.606	0.000	-1.402
8742	3	2	1				-1.569	-0.035	0.513				-1.497	0.000	-1.328						
8751	1	3	2													-0.854	0.574	-0.936	-1.445	0.000	0.106
8766	3	2	1				0.484	-0.699	1.333				-0.574	0.000	1.244	0.622	-0.144	1.208	0.305	0.000	1.174
8829	2	3	1				0.904	1.296					1.355	0.000							
8862	3	1	2				0.845	-0.035	0.513				0.815	0.000	-0.330	**2.586**	1.578	1.449	**4.000**	0.000	0.479
8891	1	2	3						**-4.000**												
8898	2	1	3				0.667	0.705	0.416				1.404	0.000	1.244	0.075	-0.364	1.086	1.992	0.000	0.834
9002	3	2	1				**-2.413**	**2.306**	**4.000**				-1.178	0.000	-1.328						
9051	1	2	3				-0.668	-1.930	-1.218				0.129	0.000	0.121	-1.533	-1.375	-1.877	-0.810	0.000	**-2.813**
9306	1	2	3													-0.302	**-3.357**	**4.000**	-0.371		
9408	3	2	1				0.707	-1.085	0.513				0.974	0.000	-0.845	0.120	-0.904	-0.936	1.309	0.000	-1.162
9436	3	1	2				-0.424	0.367	0.513				-0.105	0.000	1.310	-0.918	-0.073	-1.713	-0.333	0.000	-1.162
9441	1	3	2													-1.875	-0.904	-0.357	**-2.144**	0.000	-0.710

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**	
												1.449	1.986	1.482				**1131**
																		1237
			-2.026						0.171	0.000	0.068	0.348	0.212	0.833	-0.276	0.745	0.156	**1254**
			-2.430	0.398	0.000				**-2.336**	0.000	-0.487							**1290**
			1.129	0.095	0.000				0.277	0.000	0.368	0.546	0.508	-0.201	-0.776	0.398	-0.848	**1545**
			-0.131	-0.217	0.000				-0.643	0.000	-0.487	-0.293	0.508	-0.442	-1.045	-1.882	-0.088	**1611**
			-0.400	1.309	0.000				**-4.000**	0.000	-1.003	0.142	-0.106	-0.321	0.184	0.868	-0.590	**1753**
												0.348	-0.106	-0.442				**1868**
				1.126	0.000				0.277	0.000	-0.145	0.923	**-2.452**	-1.455	-0.276	-0.809	-0.590	**1970**
			-1.083	**-2.489**	0.000				0.961	0.000	-0.866				1.015	-0.199	0.035	**2221**
									-0.921	0.000	0.368	-0.071	0.212	0.152	-1.045	0.113	0.396	**2317**
			-4.000	**-4.000**	0.000							-1.305	-0.833	-1.722				**2637**
												-1.305	-0.833	-0.442				**2745**
												-0.071	1.765	0.943				**3055**
									-3.325	0.000	0.739	0.737	-0.451	-1.722	**-2.703**	0.306	**-2.230**	**3076**
			-1.274	-0.296	0.000				**2.012**	0.000	0.368	1.103	0.508	0.722	0.816	**-2.169**	-0.590	**3145**
			-0.519	-0.169	0.000				0.139	0.000	1.000	-1.029	0.212	-1.722	0.402	0.211	-1.519	**3155**
			-1.450	**2.343**	0.000				0.961	0.000	-0.370	1.615	-1.267	0.610	0.402	-1.184	1.316	**3162**
			0.594	-1.034					-0.907	0.000	-0.735	0.142	-0.451	**-4.000**	0.816	0.488	**-4.000**	**3305**
												-4.000	**-3.184**	**-4.000**		**-2.380**	**-4.000**	**3587**
			0.941	-1.205	0.000				0.118	0.000	0.739	-1.600	-0.106	-0.201	0.184	0.352	0.396	**3883**
			-0.214	0.383	0.000							-0.526	0.212	-0.938				**4015**
												-1.922	0.785	0.035				**4288**
			-0.383	0.049	0.000				0.784	0.000	-1.146	0.142	0.785	0.833	1.015	-0.741	0.156	**4339**
			0.349	0.018	0.000				0.235	0.000	0.068	1.937	1.048	-1.324	0.184	0.443	-0.718	**4343**
			0.034	0.095	0.000				-1.046	0.000	0.068	-1.600	-0.106	1.376	-0.776	-0.879	-0.336	**4356**
			1.419	-0.169	0.000							-0.293	-0.106	1.269	-0.776	**-2.016**	-0.848	**4459**
					0.000					0.000	**-2.766**				-0.521	1.177	1.862	**4560**
			-0.519	-0.312	0.000							0.737	0.785	0.152	0.816	0.063	0.631	**4633**
			-0.189	0.912	0.000							-0.526	-0.833	-0.082				**4723**
			0.594	0.840	0.000				-1.046	0.000	0.170	-1.305	-1.782	-0.813	-0.276	-1.649	0.277	**4889**
			0.115	-0.866	0.000				-0.103	0.000	-0.037	**4.000**	**4.000**	-0.813	-0.521	0.745	-0.590	**5018**
			-0.640		0.000							-1.922	-0.833	-0.938	**-3.147**	0.532	-0.336	**5094**
			0.902	0.547	0.000				-1.823	0.000	-1.625	0.546	0.508	-1.996	-0.776	0.576	1.316	**5220**
			-0.993	0.547	0.000				0.961	0.000	-0.145	1.103	-0.451	-0.201	0.816	0.398	-0.336	**5352**
			0.826	1.126	0.000				0.581	0.000	-0.866	0.142	0.212	1.376	1.015	-0.611	0.631	**5447**
												0.737	0.212	-0.442				**5701**
			0.357	-1.240	0.000							-0.293	0.212	**2.205**				**5803**
			-0.640	-0.700	0.000				-1.933	0.000	-1.625	0.348	0.785	0.035	-0.042	1.177	-1.246	**5858**
			0.664	0.383	0.000				0.329	0.000	0.270	0.142	-1.782	-1.194	-0.276	0.745	-0.718	**5950**
												0.546	0.508	-0.813				**6175**
			1.759	0.141	0.000							0.142	-0.833	0.497				**6182**
			0.436	1.949	0.000				-1.176	0.000	0.828	-1.305	0.508	0.383	-0.276	0.532	-0.212	**6233**
			-0.214	**-2.930**	0.000							0.923	0.212	0.383				**6253**
			-4.000	0.398	0.000				-1.500	0.000	**3.102**	-1.029	**4.000**	1.482	**4.000**	**2.476**	1.862	**6265**
			0.115	0.398	0.000				0.277	0.000	0.914	-0.526	**2.404**	**2.799**	-0.276	0.745	0.277	**6421**
																		6448
			-0.214	1.406	0.000							-1.029	0.212	-0.201	0.184	-1.761	**2.493**	**6456**
			-0.736	1.748	0.000				1.097	0.000	0.739	-0.526	0.508	0.383	1.757	0.162	1.316	**6563**
												0.142	1.048	-0.813	1.395	-0.091	0.748	**6686**
			0.115	-0.375	0.000				-1.342	0.000	0.739	-0.771	0.508	-1.194	-1.633	0.398	0.396	**7248**
			-4.000	**-4.000**	0.000				**-3.662**	0.000	-1.807				**-2.703**	-1.882	**-4.000**	**7330**
												1.103	0.212	-0.321				**7442**
												-0.071	-1.267	0.943	0.184	0.113	-1.382	**7564**
			-1.083	-0.060	0.000				1.142	0.000	-1.296	-0.526	-0.451	0.497	-0.042	0.661	0.978	**7688**
			-0.298	-1.205	0.000				-0.517	0.000	0.649	-1.029	1.536	0.497	0.402	0.532	-0.590	**7728**
			-0.214	0.473	0.000				0.380	0.000	0.828	0.923	0.785	-0.565	-0.521	1.102	1.204	**7876**
			0.749	1.126	0.000				0.277	0.000	0.739	0.348	1.048	0.722	1.757	-0.879	1.091	**7930**
			0.357	-0.941	0.000				**-2.187**	0.000	-1.455	-1.029	0.212	0.722	0.184	**-2.016**	0.631	**7946**
																		7962
			-0.597	-0.950	0.000				0.225	0.000	0.170	0.348	0.212	0.152	0.612	0.827	0.035	**7968**
			-0.214	-1.379	0.000				0.277	0.000	-0.609	-0.771	0.212	-0.201	0.402	-0.548	-0.212	**8019**
			1.129	0.248	0.000				-0.517	0.000	0.557	-0.071	0.785	-0.321	1.207	0.113	-1.519	**8068**
												1.278	-0.833	-0.082				**8260**
			0.397	0.636	0.000				1.106	0.000	0.068	0.142	0.212	-0.565	-1.045	0.352	-0.212	**8329**
			0.034	0.248	0.000				0.171	0.000	0.914	0.737	1.048	-0.201	1.395	0.013	-1.382	**8380**
			3.405	-0.866	0.000				-0.276	0.000	-0.609	-0.771	-1.782	-1.996	-1.045	0.443	-0.336	**8435**
			0.499	0.665	0.000							-0.526	-0.451	**2.104**				**8569**
			1.499	1.406	0.000							0.348	**-2.452**	-0.938				**8626**
			-1.173	0.248	0.000				0.482	0.000	0.464	0.142	1.048	-0.082	0.816	0.113	0.748	**8628**
			-0.214	-1.205	0.000				0.064	0.000	0.068	0.546	0.212	0.383	0.612	0.398	1.091	**8663**
												-0.071	0.212	1.161	0.612	0.619	-0.590	**8742**
												0.142	1.298	0.152				**8751**
			0.180	0.724	0.000				0.329	0.000	0.368	1.103	-1.267	-0.201	-0.521	0.306	0.035	**8766**
												-0.293	0.785		-0.521	0.827		**8829**
			1.278	0.248	0.000				0.915	0.000	1.711	1.937	0.212	0.383	1.395	0.488	0.277	**8862**
												-3.621	-1.782	**-4.000**				**8891**
			1.084	-0.312	0.000				0.924	0.000	0.557	-0.771	-0.451	-0.442	0.816	0.013	0.156	**8898**
			-4.000	-1.556	0.000							0.348	**4.000**	0.610				**9002**
			1.419	0.458	0.000				**-3.183**	0.000	-1.807	0.546	-0.106	0.383	-0.776	0.162	1.646	**9051**
												1.449	**4.000**	**-4.000**	1.015	1.396	-1.941	**9306**
			-2.745	-0.217	0.000				0.277	0.000	-0.037	-1.305	0.212	-1.858	0.184	0.113	-1.941	**9408**
			0.381	0.110	0.000				-0.160	0.000	0.739	1.278	**4.000**	-0.201	-0.276	0.576	0.277	**9436**
												0.142	0.212	1.161	-0.776	-1.761	-0.848	**9441**

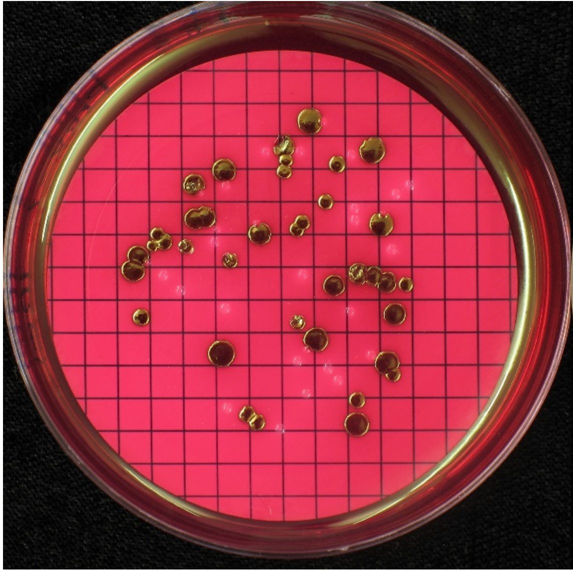
Lab no.	Sample			Suspected coliform bacteria (MF)			Coliform bacteria (MF)			Susp. thermotolerant coliform bact. (MF)			*E. coli* (MF)			Coliform bacteria ("rapid" MPN)			*E. coli* ("rapid" MPN)		
	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C
9524	1	2	3				-0.305	-0.682	-0.857				-0.350	0.000	-0.526	0.444	0.170	0.454	0.340	0.000	0.834
9655	1	2	3																		
9736	1	2	3													-0.209	-0.002	-1.713	0.075	0.000	0.295
9899	2	1	3				0.806	0.861	0.513				0.842	0.000	-0.629	0.476	1.119	1.329	-0.275	0.000	0.834
9903	1	2	3				0.855	0.395	0.608				-0.201	0.000	0.369						
n				0	0	0	60	59	60	0	0	0	62	61	60	58	57	58	58	57	57
Min							-2.583	-2.538	-4.000				-3.104	0.000	-1.606	-2.112	-3.357	-1.877	-2.364	0.000	-2.813
Max							1.683	4.000	4.000				1.898	0.000	2.221	4.000	3.115	4.000	4.000	0.000	4.000
Median							0.151	0.112	0.169				0.152	0.000	-0.143	0.098	-0.144	0.049	0.003	0.000	0.295
Mean							0.000	0.068	0.133				0.000	0.000	0.000	0.069	0.000	0.069	0.069	0.000	0.070
SD							1.000	1.120	1.414				1.000	0.000	1.000	1.122	1.000	1.122	1.122	0.000	1.124
z<-3							0	0	2				1	0	0	0	1	0	0	0	0
-3≤z<-2							2	1	1				0	0	0	1	0	0	3	0	2
2<z≤3							0	3	1				0	0	1	1	0	0	3	0	0
z>3							0	1	3				0	0	0	1	1	1	1	0	1

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**	
			-0.762	0.095	0.000							1.278	-0.451	**4.000**	0.184	-1.545	-0.718	**9524**
															-0.042	0.619	-0.718	**9655**
			1.226	-0.783	0.000				**2.166**	0.000	1.000	-0.771	-0.106	-0.321	0.612	0.532	0.631	**9736**
			2.070	-0.966	0.000				0.451	0.000	0.170	1.449	-0.106	-0.565	0.816	0.827	0.035	**9899**
			-1.292	-0.456	0.000				0.064	0.000	0.368	0.348	0.212	1.482	-0.521	0.211	1.091	**9903**

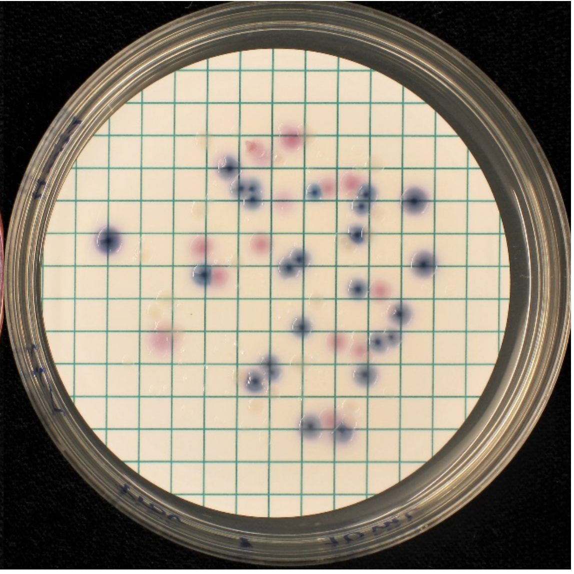
0	0	0	63	62	63	0	0	0	52	53	53	81	81	80	64	65	64	**n**
			-4.000	-4.000	0.000				-4.000	0.000	-2.766	-4.000	-3.184	-4.000	-3.147	-2.380	-4.000	**Min**
			3.405	2.343	0.000				2.166	0.000	3.102	4.000	4.000	4.000	4.000	2.476	2.493	**Max**
			-0.131	0.095	0.000				0.171	0.000	0.170	0.142	0.212	-0.201	0.184	0.306	-0.027	**Median**
			-0.200	-0.129	0.000				-0.272	0.000	0.000	0.000	0.247	-0.150	0.062	0.000	-0.188	**Mean**
			1.448	1.214	0.000				1.356	0.000	1.000	1.173	1.370	1.388	1.111	1.000	1.296	**SD**
																		Summa
			4	2	0				4	0	0	2	1	4	1	0	3	25
			3	2	0				2	0	1	0	2	0	2	4	1	27
			1	1	0				2	0	0	0	1	3	0	1	1	19
			1	0	0				0	0	1	1	5	1	1	0	0	19

Sample A

m-Endo Agar LES, 37 °C



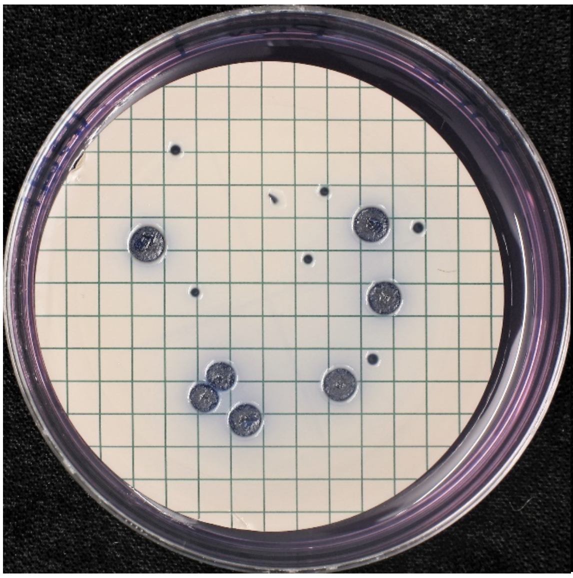
10 ml



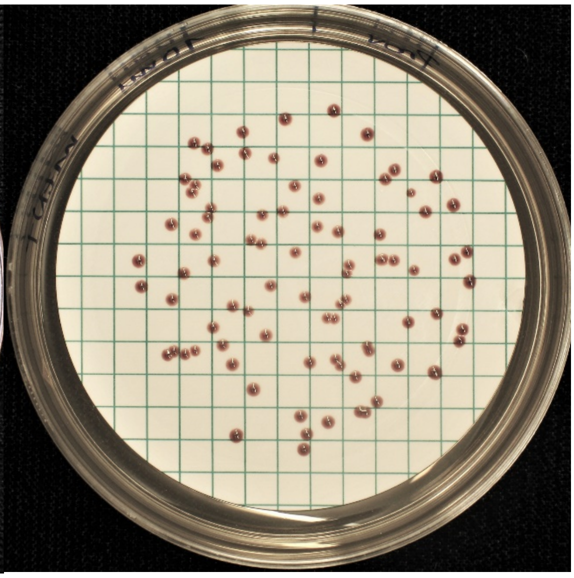
10 ml

Chromocult Coliform Agar, 37 °C

m-FC Agar, 44 °C



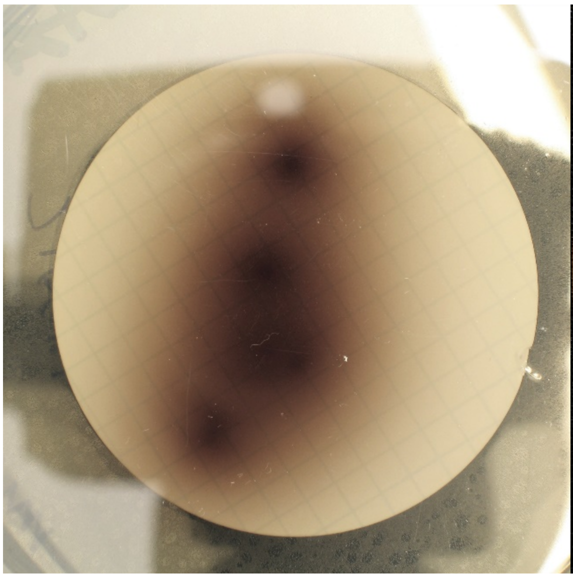
10 ml



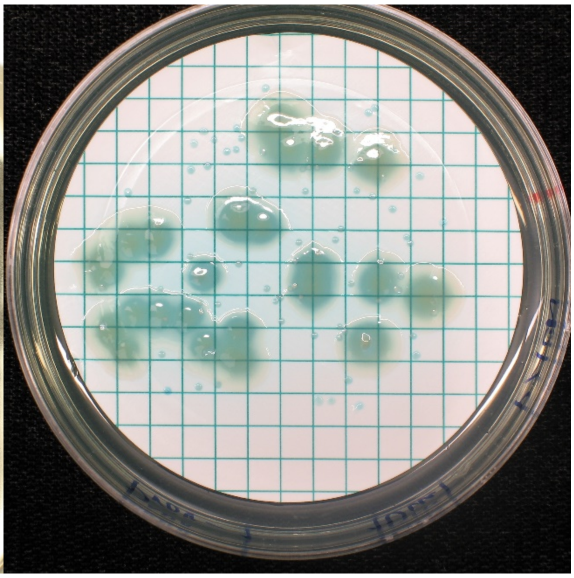
10 ml, 2 days

m-Enterococcus Agar, 37 °C

Bile Esculin Azide Agar, 44 °C



1 ml, 2 days

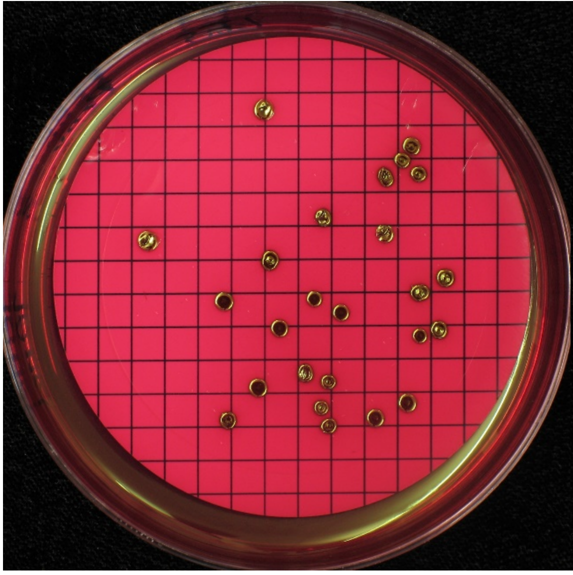


10 ml, 2 days

m-Pseudomonas CN Agar, 37 °C

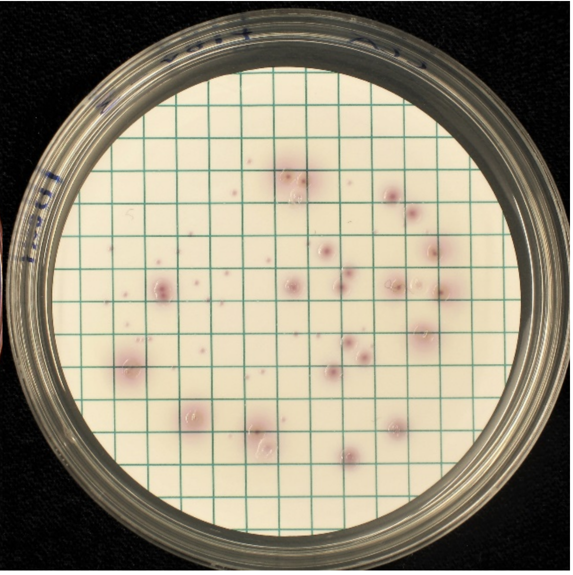
Sample B

m-Endo Agar LES, 37 °C



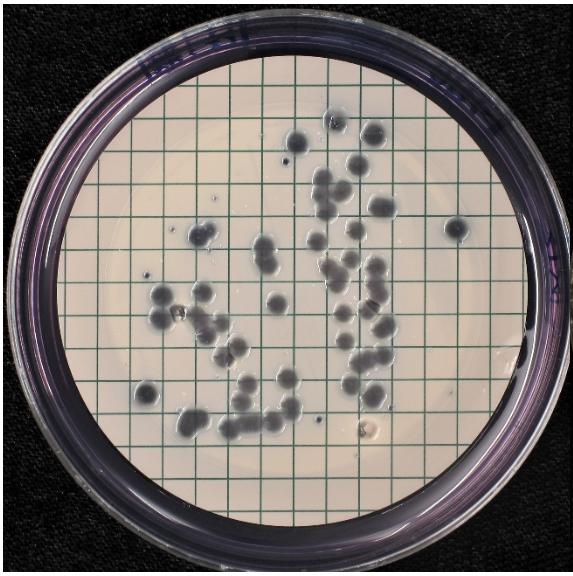
10 ml

Chromocult Coliform Agar, 37 °C



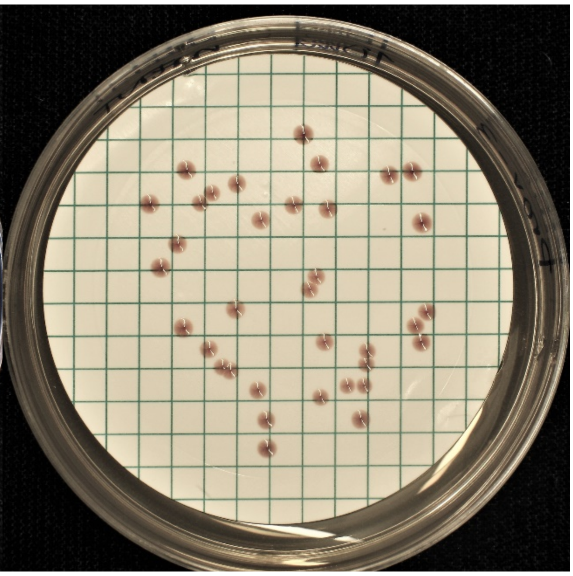
10 ml

m-FC Agar, 44 °C



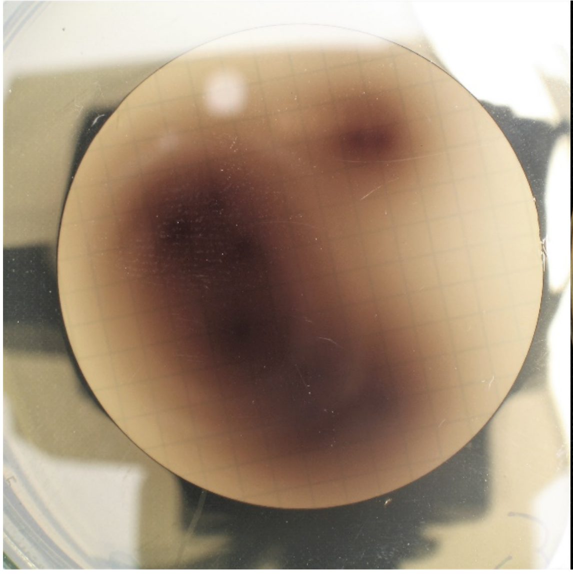
100 ml

m-Enterococcus Agar, 37 °C



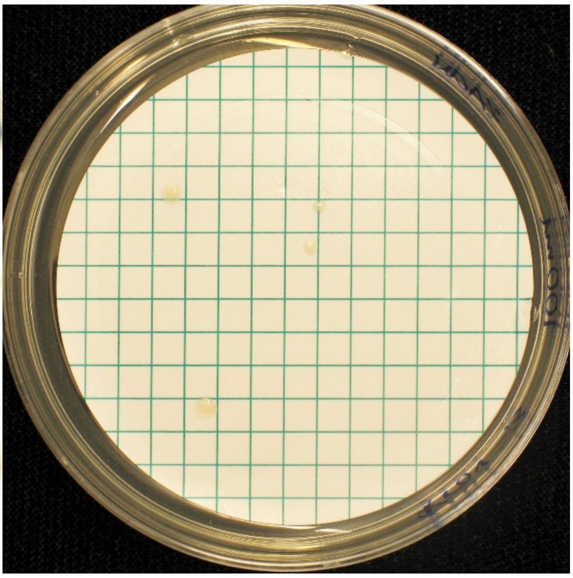
10 ml, 2 days

Bile Esculin Azide Agar, 44 °C



1 ml, 2 days

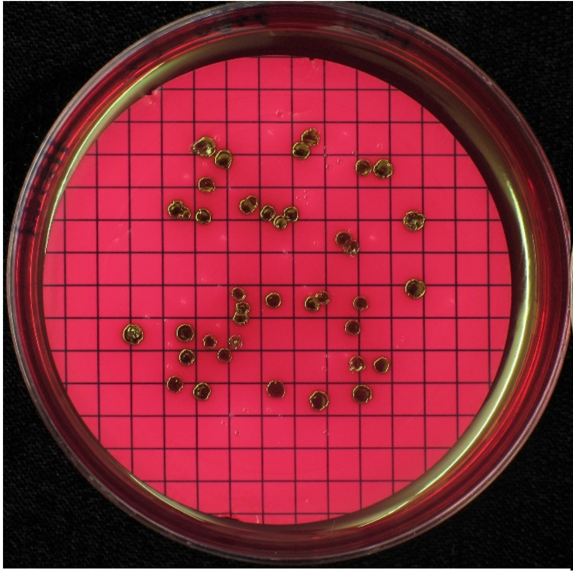
m-Pseudomonas CN Agar, 37 °C



100 ml, 2 days

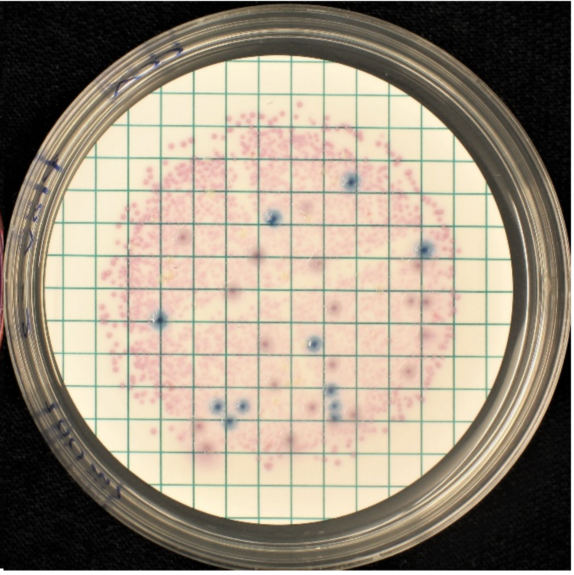
Sample C

m-Endo Agar LES, 37 °C



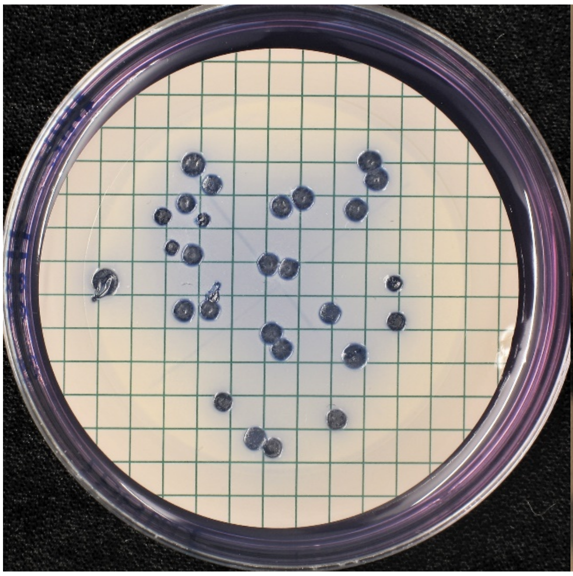
100 ml

Chromocult Coliform Agar, 37 °C



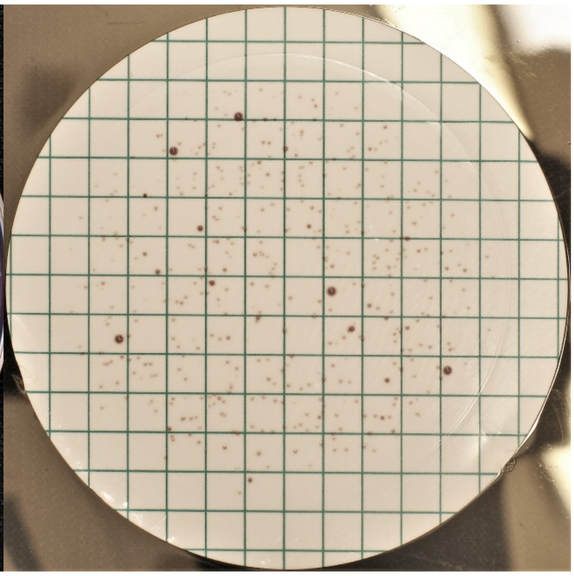
100 ml

m-FC Agar, 44 °C



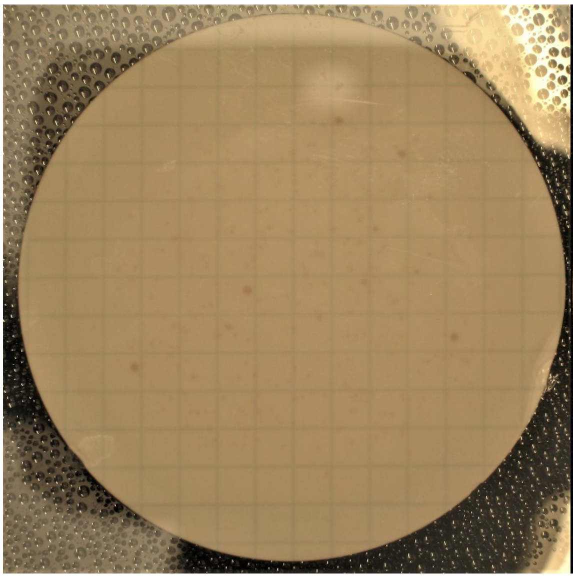
100 ml

m-Enterococcus Agar, 37 °C



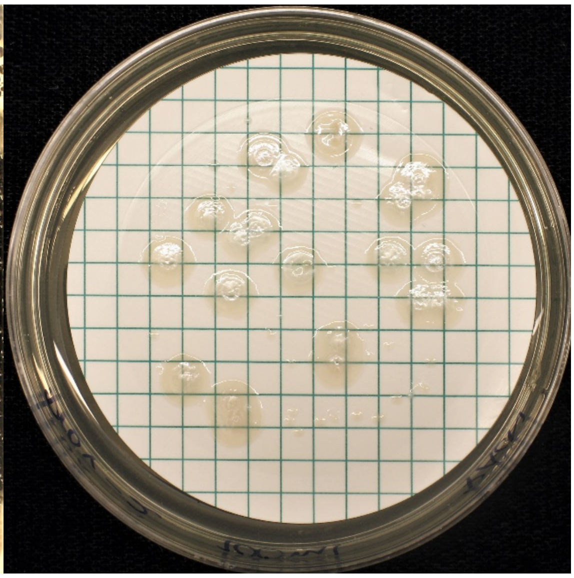
10 ml, 2 days

Bile Esculin Azide Agar, 44 °C



10 ml, 2 days

m-Pseudomonas CN Agar, 37 °C



100 ml, 2 days

PT reports published 2020

Proficiency Testing – Food Microbiology, January 2020, by Jonas Ilbäck

Proficiency Testing – Drinking Water Microbiology, March 2020, by Tommy Šlapokas

Proficiency Testing – Food Microbiology, April 2020, by Jonas Ilbäck

Proficiency Testing – Drinking Water Microbiology, September 2020, by Linnea Blom and Tommy Šlapokas

Proficiency Testing – Food Microbiology, October 2020, by Jonas Ilbäck

PT reports published 2021

Proficiency Testing – Food Microbiology, January 2021, by Jonas Ilbäck

Proficiency Testing – Drinking Water Microbiology, March 2021, by Linnea Blom and Tommy Šlapokas

Proficiency Testing – Food Microbiology, April 2021, 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 Swedish 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 Swedish Food Agency's reference material

As a complement to the proficiency testing but without specific accreditation, Swedish 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