

Drinking Water Microbiology

September 2016

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Edition

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ISO/IEC 17043

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

Pseudomonas aeruginosa with MF

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

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

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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)
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; according to EN ISO 8799-2:2000)
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)
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 <i>excluded</i>)
Med	median value (with outliers and false results <i>included</i>)
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
	remarkably low result
	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

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General information on results evaluation

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

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

The method information gathered is sometimes difficult to interpret. Sometimes there is no consistency between the standard referred to and the information given 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. To obtain an as appropriate evaluation as possible, it is important that correct information 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 measure of dispersion and mean value are not shown for groups with 4 or fewer results, more than exceptionally where this is mentioned. However, when possible all results are shown in the method histograms.

Results of the PT round

General outcome

Test items were sent to 107 laboratories, 37 in Sweden, 58 in other Nordic countries (Faeroe Islands, Greenland and Åland included), 4 more from EU, 3 from the rest of Europe and 5 from countries outside Europe. Results were reported from 106 laboratories.

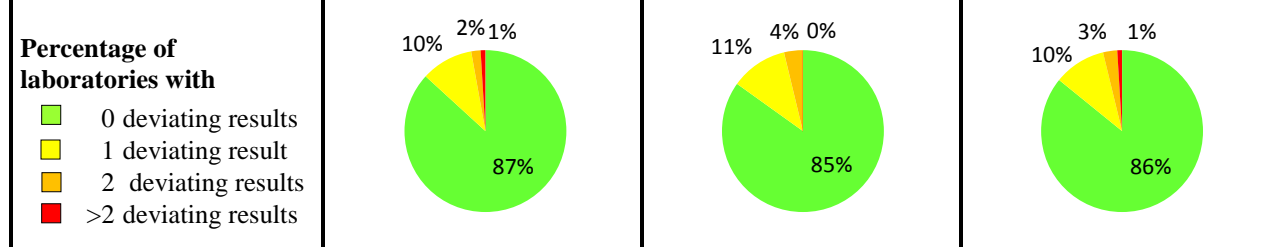
The percentages of false results and outliers are compiled in **table 1**. These deviating results are excluded in most calculations.

Microorganisms and parameters of analyses are also compiled in **table 1**. For the MF analyses the parameters *suspected* coliform bacteria and thermotolerant coliform bacteria (shaded in table 1 and table 3), as well as *suspected* intestinal enterococci and *Pseudomonas aeruginosa* on primary media could be reported as well. The results from suspected colonies are only used for interpretations and discussions.

All reported results are compiled in **annex A** and results for each laboratory are also shown on our website after logging in (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 mixture and percentages of deviating results (F%: false positive or false negative, X%: outliers); parameters with grey rows are not assessed

Mixture	A			B			C		
Percentage of laboratories with  <ul style="list-style-type: none"> ■ 0 deviating results ■ 1 deviating result ■ 2 deviating results ■ >2 deviating results 	<p>10% 2% 1% 87%</p>			<p>11% 4% 0% 85%</p>			<p>10% 3% 1% 86%</p>		
No. of evaluable results	588			591			589		
No. of deviating results *	27 (5 %)			26 (4 %)			12 (2 %)		
Microorganisms	<i>Escherichia coli</i> <i>Klebsiella oxytoca</i> <i>Enterococcus faecium</i> <i>Pseudomonas aeruginosa</i> <i>Stenotrophomonas maltophilia</i>			<i>Enterobacter cloacae</i> <i>Cronobacter sakazakii</i> <i>Enterococcus hirae</i> <i>Staphylococcus capitis</i>			<i>Escherichia coli</i> (weak β -glu) <i>Aeromonas hydrophila</i> <i>Pseudomonas aeruginosa</i> <i>Pseudomonas fluorescens</i>		
Analysis	Target org.	F%	X%	Target org.	F%	X%	Target org.	F%	X%
Coliform bacteria (MF)	<i>E. coli</i> <i>K. oxytoca</i>	1	0	<i>E. cloacae</i> <i>C. sakazakii</i>	3	0	<i>E. coli</i> [<i>A. hydrophila</i>]	1	3
Susp. thermotolerant coliform bact. (MF)	<i>E. coli</i>	–	–	[<i>E. cloacae</i>] [<i>C. sakazakii</i>]	–	–	<i>E. coli</i>	–	–
<i>E. coli</i> (MF)	<i>E. coli</i>	4	0	[<i>E. cloacae</i>] [<i>C. sakazakii</i>]	2	–	{ <i>E. coli</i> }	0 [#]	4
Coliform bacteria (rapid method)	<i>E. coli</i> <i>K. oxytoca</i>	0	0	<i>E. cloacae</i> <i>C. sakazakii</i>	0	0	<i>E. coli</i>	0	0
<i>E. coli</i> (rapid meth.)	<i>E. coli</i>	1	0	–	1	–	–	3	–
Intestinal enterococci (MF)	<i>E. faecium</i>	5	0	<i>E. hirae</i>	0	3	–	0	–
<i>Pseudomonas aeruginosa</i> (MF)	<i>P. aeruginosa</i>	0	9	–	0	–	<i>P. aeruginosa</i>	0	4
Culturable micro-organisms (total count), 3 days 22 °C	<i>S. maltophilia</i> (<i>E. faecium</i>) (<i>E. coli</i>) (<i>K. oxytoca</i>) (<i>P. aeruginosa</i>)	0	2	<i>E. hirae</i> <i>E. cloacae</i> <i>C. sakazakii</i>	2	6	<i>P. fluorescens</i> (<i>P. aeruginosa</i>) (<i>A. hydrophila</i>) (<i>E. coli</i>)	6	0
Culturable micro-organisms (total count), 2 days 36 °C	<i>S. maltophilia</i> (<i>E. faecium</i>) (<i>E. coli</i>) (<i>K. oxytoca</i>) (<i>P. aeruginosa</i>)	0	2	<i>S. capitis</i> (<i>E. hirae</i>) (<i>E. cloacae</i>) (<i>C. sakazakii</i>)	0	1	(<i>P. aeruginosa</i>) (<i>A. hydrophila</i>) (<i>E. coli</i>)	0	5

* In total 31 of 106 laboratories (29 %) reported at least one deviating result

– Organism missing or numerical result irrelevant

() The organism contributes with only very few colonies

[] The organism is false positive on the primary growth medium

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

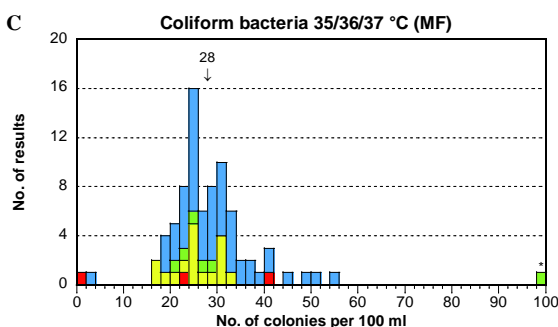
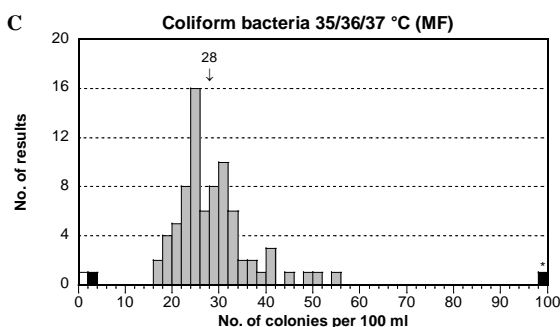
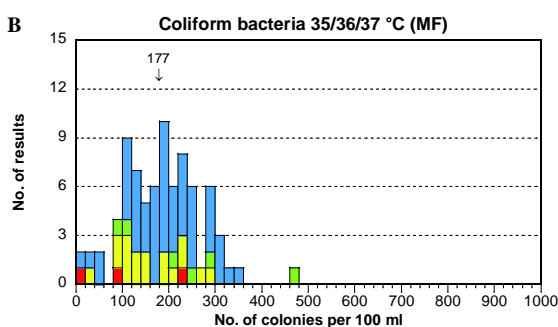
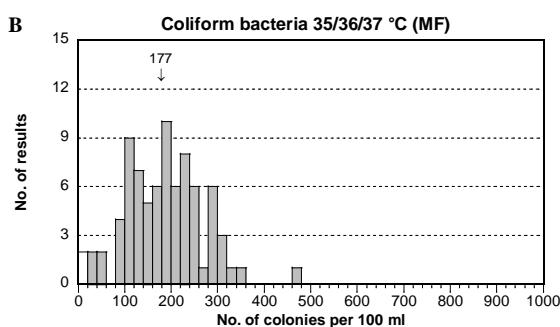
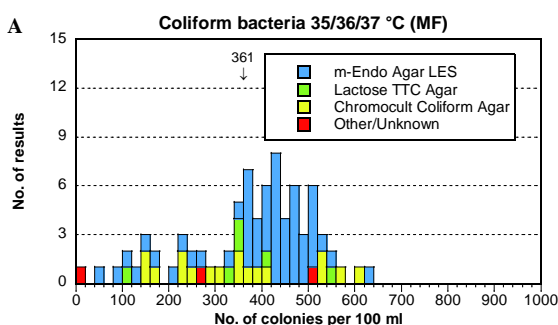
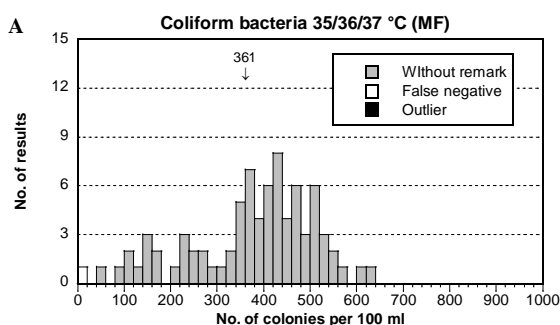
There were 21 zero results (26 %) not treated as erroneous results

Coliform bacteria (MF)

In three cases the primary medium reported was not the one prescribed in the standard referred to. In these cases the reported medium is assumed to be correct. The medium Endo Agar reported by some participants is here included in m-Endo Agar LES (LES).

CCA are used in a higher degree than in the previous rounds, due to the fact that the standard EN ISO 9308-1:2014 has been more used. Fewer laboratories have used

Medium	N	A						B						C					
		n	Mv	CV	F	<	>	n	Mv	CV	F	<	>	n	Mv	CV	F	<	>
Total	81	79	361	20	1	0	0	78	177	23	2	0	0	77	28	13	1	1	1
m-Endo Agar LES	55	54	374	20	0	0	0	53	183	21	1	0	0	53	29	13	0	1	0
Lactose TTC Agar	6	6	329	24	0	0	0	6	215	31	0	0	0	5	24	7	0	0	1
Chromocult C Agar	17	17	329	22	0	0	0	17	148	25	0	0	0	17	25	10	0	0	0
Other/Unknown	3	2	-	-	-	0	0	2	-	-	1	0	0	2	-	-	1	0	0



LTTC while the use of LES has about the same frequency as before. There is an indication that LES gave somewhat higher mean result than average in all mixtures. CCA is low in all the mixtures while there is a variation for LTTC. The relative dispersion (CV) varies between both media and mixtures, but is clearly the lowest for all media in mixture C.

Mixture A

- Two strains of coliform bacteria were included in the mixture. Both *E. coli* and *K. oxytoca* grow with typical colonies, with a metallic sheen on LES, light to dark yellow on LTTC and bluish and pink, respectively, on CCA at 37 °C (see annex C). There was no general problem with this analysis.
- Due to the unexplained tail of results lower than the main peak in the histogram, the average is quite a bit lower than for coliform bacteria with the rapid methods (see page 14). However, the main peak has about the same location and distribution. The methods histogram indicates that the lower results predominantly are from LTTC and CCA.

Mixture B

- Two strains of coliform bacteria were included in the mixture. Both *E. cloacae* and *C. sakazakii* grow with typical colonies, with a metallic sheen on LES and light yellow to yellow on LTTC and pink or pink with a pink zone on CCA at 37 °C. The analysis was without problem.
- The average recovery is somewhat lower for the MF methods compared to the rapid methods (see page 14).

Mixture C

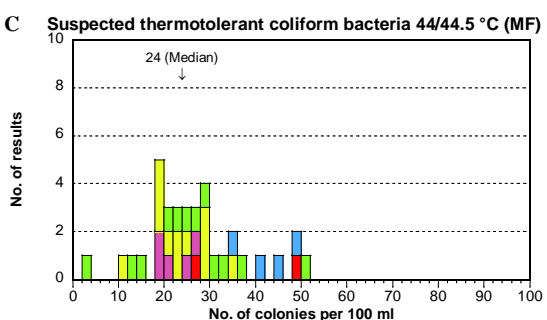
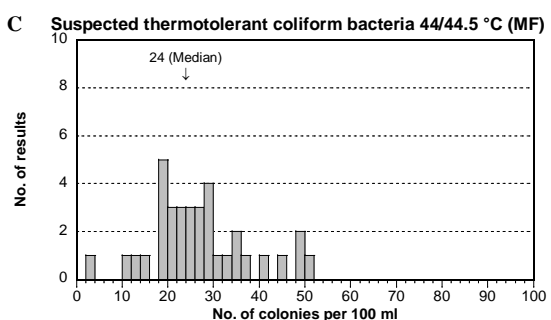
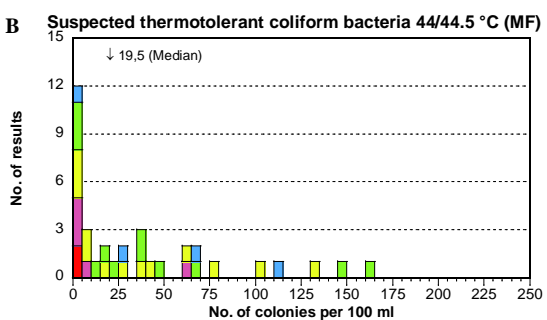
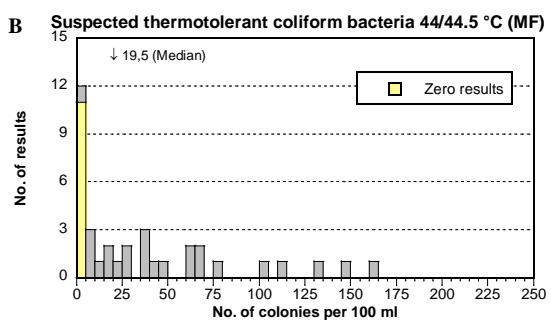
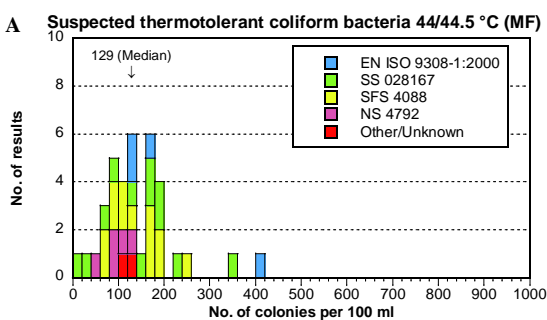
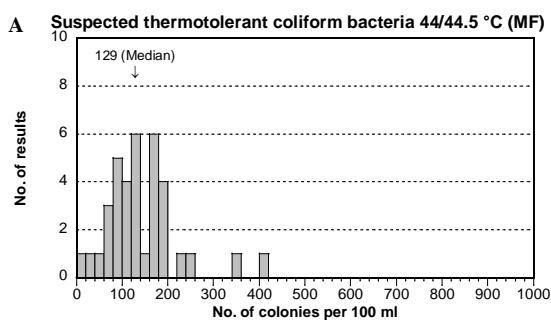
- A strain of *E. coli* was the only coliform bacterium. It grows with for coliform bacteria typical colonies on the MF media, a metallic sheen on LES, yellow on LTTC and dark pink to violet on CCA at 37 °C. There was no problem with this analysis.
- One false negative result and one low and one high outlier were present. The rest of the results were well distributed.
- A strain of *A. hydrophila* was also included in the mixture. It usually grows with for coliform bacteria more or less typical colonies on the used media. *A. hydrophila* is oxidase positive and the colonies can be excluded as coliform bacteria after confirmation by the oxidase test (see below).
- The average number of coliform bacteria in this analysis was identical to that for the rapid methods (page 14). This might seem unexpected as the MF methods usually give somewhat lower average. A probable explanation is that some laboratories have included *A. hydrophila* in the results for the MF method, thus compensating for the expected difference between the methods.
- The results for suspected coliform bacteria and coliform bacteria are equal for 30 out of the 57 laboratories. For the remaining 27 cases, the results for suspected coliform bacteria are higher, indicating that *A. hydrophila* has been excluded there after confirmation.

Suspected thermotolerant coliform bacteria (MF)

N.B.! By a mistake this parameter was given as *Thermotolerant coliform bacteria* on the website before and during this round, but the results will still be treated as usual; i.e. confirmation is not a prerequisite (suspected colonies are enough).

The growth medium mainly used is m-FC and only partly LTTC. The incubation temperature was 44 or 44.5 °C. Here, results were separated based on the method

Standard, Method	N	A					B					C							
		n	Med	CV	F	<	>	n	Med	CV	F	<	>	n	Med	CV	F	<	>
Total	36	36	128	-	-	-	-	36	21	-	-	-	-	35	24	-	-	-	-
EN ISO 9308-1	4	4	145	-	-	-	-	4	47	-	-	-	-	4	43	-	-	-	-
SS 028167	12	12	161	-	-	-	-	12	28	-	-	-	-	12	26	-	-	-	-
SFS 4088	13	13	133	-	-	-	-	13	29	-	-	-	-	12	23	-	-	-	-
NS 4792	5	5	90	-	-	-	-	5	0	-	-	-	-	5	20	-	-	-	-
Other/Unknown	2	2	-	-	-	-	-	2	0	-	-	-	-	2	-	-	-	-	-



standards most commonly used, to get a further division beyond the media. They are EN ISO 9308-1:2000 with LTTC and three standards with m-FC from the Nordic countries, namely SS 028167 from Sweden, SFS 4088 from Finland and NS 4792 from Norway. The methods were sometimes used slightly modified. The average from EN ISO 9308-1:2000 is given as comparison, although only 4 results were present.

The table shows the *medians* instead of mean values because no outliers have been identified. The reason is that *the analysis is not included in performance assessment*.

The Swedish standard states incubation at 44 °C but one laboratory reported 44.5 °C. The temperature 44 °C is also stated in EN ISO 9308-1:2000. The Norwegian standard, NS 4792, states 44.5 °C for incubation. Two of six laboratories using that standard have this time incubated at 44 °C, the rest at 44.5 °C. All laboratories using Finnish standard has incubated at 44 °C, according to the standard.

Among the groups compared, the one for NS 4792, and thus perhaps indirectly the temperature 44.5 °C, has lowest average in all mixtures. In mixture B, three of five results for that standard were zero.

Mixture A

- The strain of *E. coli* appears with blue colonies on m-FC at 44/44.5 °C. The corresponding colonies are yellow on LTTC. Only 4 results were present for LTTC, making it difficult to compare them with m-FC.

Mixture B

- No genuine thermotolerant coliform bacterium was present. However, there was a strain of *E. cloacae* that sometimes grow as a (suspected) thermotolerant coliform bacterium on both m-FC and LTTC. Correspondingly the strain of *C. sakazakii* usually grows at 44 °C with blue-grey to brownish colonies. These colonies are light yellow on LTTC.
- Eleven laboratories have reported zero cfu per 100 ml.

Mixture C

- The strain of *E. coli* appears with blue colonies on m-FC at 44/44.5 °C. The corresponding colonies are dark yellow on LTTC.
- No zero results were obtained.

***Escherichia coli* (MF)**

No confirmation is necessary to identify and quantify *E. coli* from CCA but from the other media, either incubated at 36±2 °C or at 44/44.5 °C, confirmation must be done. Depending on the method, test of either indole production or β-glucuronidase activity or both is used as necessary confirmation.

The primary growth media LTTC, LES and CCA are used at 36±2 °C and LTTC or m-FC at 44/44.5 °C. Each result for *E. coli* can only come from one of these media-temperature combinations. However, for about half of the laboratories it is not clear

what the primary temperature for the given results has been. Figures for where the temperature is unambiguous are given in two separate tables. The 42 results with unclear incubation temperature are not shown separately but are included only in the table "All results".

Depending on the low number of total results, several groups contain less than 5 results. Just as indication, the averages are given also for these. Such averages should, however, not be compared or discussed individually.

Since almost half of the results could not be connected to method – although they belong to either temperature – evaluation of differences between method groups within the respective temperature is of limited value. A tendency could, however, be that LES gives higher average than LTTC and CCA at 36±2 °C. At the high temperature there is no such tendency.

Mixture A

- One typical *E. coli* strain was included together with another coliform bacterium (*K. oxytoca*). With CCA β -glucuronidase activity is checked directly on the plate, no more confirmation is needed. For the other media confirmation is necessary.
- Three false negative results were present.

All results

Medium	N	A					B					C							
		n	Mv	CV	F	<	>	n	Mv	CV	F	<	>	n	Mv	CV	F	<	>
Total	83	79	184	28	3	0	0	80	0	-	2	-	-	58	28 [#]	15 [#]	- [#]	2	1

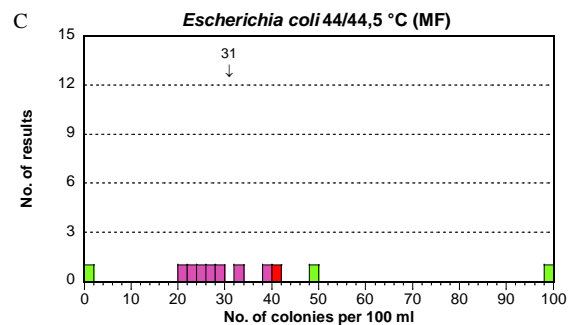
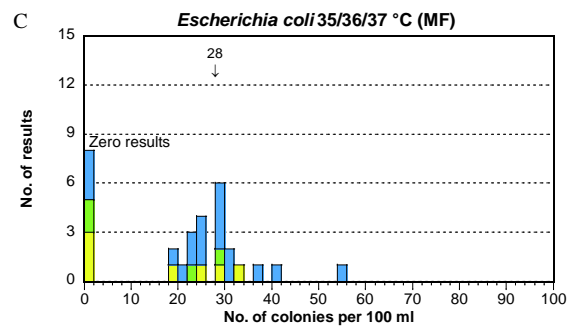
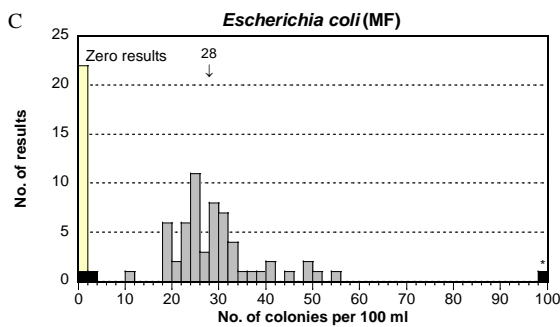
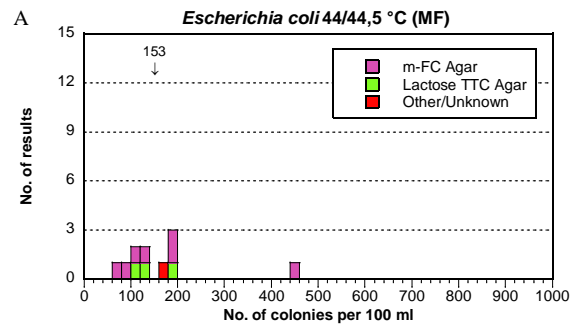
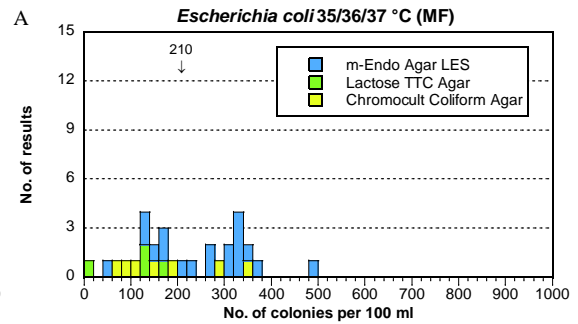
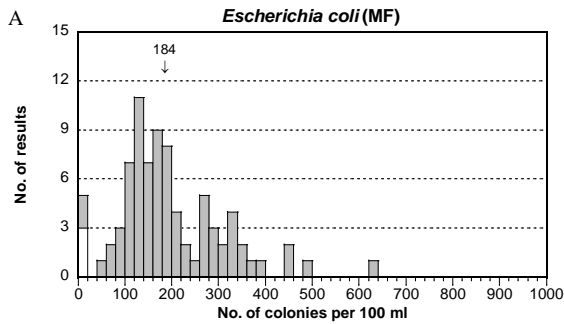
36±2 °C

Medium	N	A					B					C							
		n	Mv	CV	F	<	>	n	Mv	CV	F	<	>	n	Mv	CV	F	<	>
Total	30	29	210	26	1	0	0	30	0	-	0	-	-	22	28 [#]	14 [#]	- [#]	0	0
m-Endo Agar LES	19	19	243	23	0	0	0	19	0	-	0	-	-	16	28	14	-	0	0
Lactose TTC Agar	4	3	136	-	1	0	0	4	0	-	0	-	-	2	25	-	-	0	0
Chromocult C Agar	7	7	164	30	0	0	0	7	0	-	0	-	-	4	26	-	-	-	-
Other/Unknown	0	0	-	-	-	-	-	0	-	-	-	-	-	0	-	-	-	-	-

44/44.5 °C

Medium/Standard	N	A					B					C							
		n	Mv	CV	F	<	>	n	Mv	CV	F	<	>	n	Mv	CV	F	<	>
Total	11	11	153	28	0	0	0	11	0	-	0	-	-	9	31	15	-	1	1
<i>Medium</i>																			
m-FC Agar	7	7	159	34	0	0	0	7	0	-	0	-	-	7	27	11	-	0	0
Lactose TTC Agar	3	3	138	-	0	0	0	3	0	-	0	-	-	1	48	-	-	1	1
Other/Unknown	1	1	160	-	0	0	0	1	0	-	0	-	-	1	41	-	-	0	0
<i>Standard</i>																			
EN ISO 9308-1	3	3	128	-	0	0	0	3	0	-	0	-	-	2	44	-	-	0	1
SS 028167	0	0	-	-	-	-	-	0	-	-	-	-	-	0	-	-	-	-	-
SFS 4088	2	2	302	-	0	0	0	2	0	-	0	-	-	2	35	-	-	0	0
NS 4792	3	3	107	-	0	0	0	3	0	-	0	-	-	3	24	-	-	0	0
Other/Unknown	3	3	148	-	0	0	0	3	0	-	0	-	-	2	25	-	-	1	0

Calculated without the 21 zero results



Mixture B

- No *E. coli* was included in the mixture but two false positive results were obtained.

Mixture C

- One strain of *E. coli* with weak β -glucuronidase activity was present in the mixture, resulting in varying outcome on different primary media.

- Twenty one zero results were reported together with 61 results where presence of *E. coli* were reported. The zero results probably originate from media where test of β -glucuronidase activity has been decisive, since the strain is indole positive. Of the 15 laboratories that have used XX-EN ISO 9308-1:2014 and the medium CCA or corresponding 10 reported a zero result (only pink colonies), while 5 reported higher results (blue to violet colonies present).
- The other 11 zero results are from different methods from different countries. The most probable is that test of β -glucuronidase activity has been used as confirmation, e.g. test in broth with MUG reagent, and that the fluorescence has been interpreted as negative. A weak enzyme activity is present and the incubation time before reading is crucial for the interpretation of the outcome. In our tests with the strain, the outcome is weakly positive but it is necessary to compare with a clearly positive and negative strain to state the result.
- The same average result was obtained as with the rapid method, 28 cfu per 100 ml, with the zero results excluded.
- The low result 1 and 2 cfu per 100 ml, respectively, are outliers when the zero results are separately handled. One high outlier was also present. The distribution of accepted results looks good and has small dispersion.

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

The rapid methods used for both these parameters were almost exclusively Colilert[®] Quanti-Tray[®] from the manufacturer IDEXX Inc. with incubation at either 35, 36 or 37 °C. Out of the about 67 laboratories that reported Colilert some used trays with 51 wells, while others used trays with 97 wells (a few of which, probably incorrectly, have reported 96 wells). The laboratories often analysed both diluted and undiluted samples. Three laboratories stated the use of "Colilert 24 hours". One laboratory, has wrongly reported coliform bacteria from an ordinary fermentation MPN technique.

Coliform bacteria, Rapid method with MPN

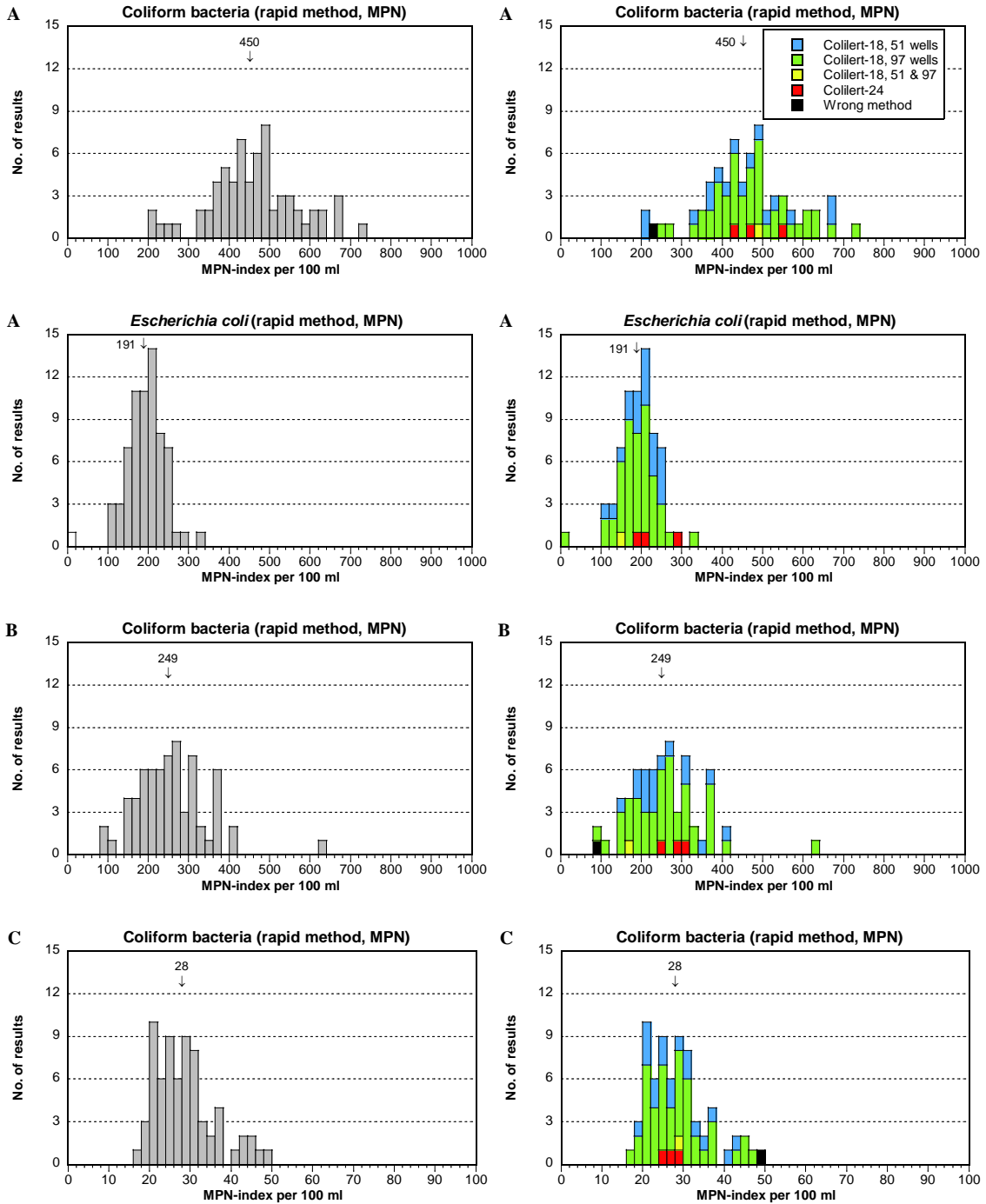
Principle	N	A					B					C							
		n	Mv	CV	F	<	>	n	Mv	CV	F	<	>	n	Mv	CV	F	<	>
Total, Rapid meth.	68	66	450	13	0	0	0	66	249	17	0	0	0	68	28	13	0	0	0
Colilert-18, 51 wells	18	16	426	16	0	0	0	16	249	14	0	0	0	18	27	13	0	0	0
Colilert-18, 97 wells	45	45	462	11	0	0	0	45	253	18	0	0	0	45	27	13	0	0	0
Colilert-18, 51 & 97	1	1	-	-	0	0	0	1	-	-	0	0	0	1	-	-	0	0	0
Colilert-24, ? wells	3	3	-	-	0	0	0	3	-	-	0	0	0	3	-	-	0	0	0
Wrong method	1	1	230	-	0	0	0	1	95	-	0	0	0	1	49	-	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.	68	67	191	11	1	0	0	67	0	-	1	-	-	65	0	-	2	-	-
Colilert-18, 51 wells	19	19	192	11	0	0	0	19	0	-	0	-	-	19	0	-	0	-	-
Colilert-18, 97 wells	45	44	189	11	1	0	0	44	0	-	1	-	-	42	0	-	2	-	-
Colilert-18, 51 & 97	1	1	-	-	0	0	0	1	0	-	0	-	-	1	0	-	0	-	-
Colilert-24, ? wells	3	3	-	-	0	0	0	3	0	-	0	-	-	3	0	-	0	-	-

For coliform bacteria in all mixtures and *E. coli* in mixture A there was this time, in contrast to in many previous rounds, no clear tendency that the trays with 51 wells give somewhat lower average recovery than trays with 97 wells. Only for coliform bacteria in mixture A such a difference could be assumed.

No outliers are seen in any of the analyses for coliform bacteria. Individual false results were obtained in the mixtures for the analyses of *E. coli*.



Mixture A

- The strains of *E. coli* and *K. oxytoca* grow and possess β -galactosidase. They are thus detected as coliform bacteria by methods based on the activity of this enzyme (ONPG positive), e.g. Colilert[®]-18/24 Quanti-Tray[®] where ONPG is a substrate.
- The strain of *E. coli* possesses the enzyme β -glucuronidase and is also detected as *E. coli*. One false negative result was present.
- The averages are here somewhat higher than for the MF methods in general.

Mixture B

- In this mixture the coliform bacteria *E. cloacae* and *C. sakazakii* were present. Both of them possess β -galactosidase but not β -glucuronidase and are thus detected as coliform bacteria but not as *E. coli*.
- The average result is somewhat higher than for the MF methods for coliform bacteria. One false positive result was present.

Mixture C

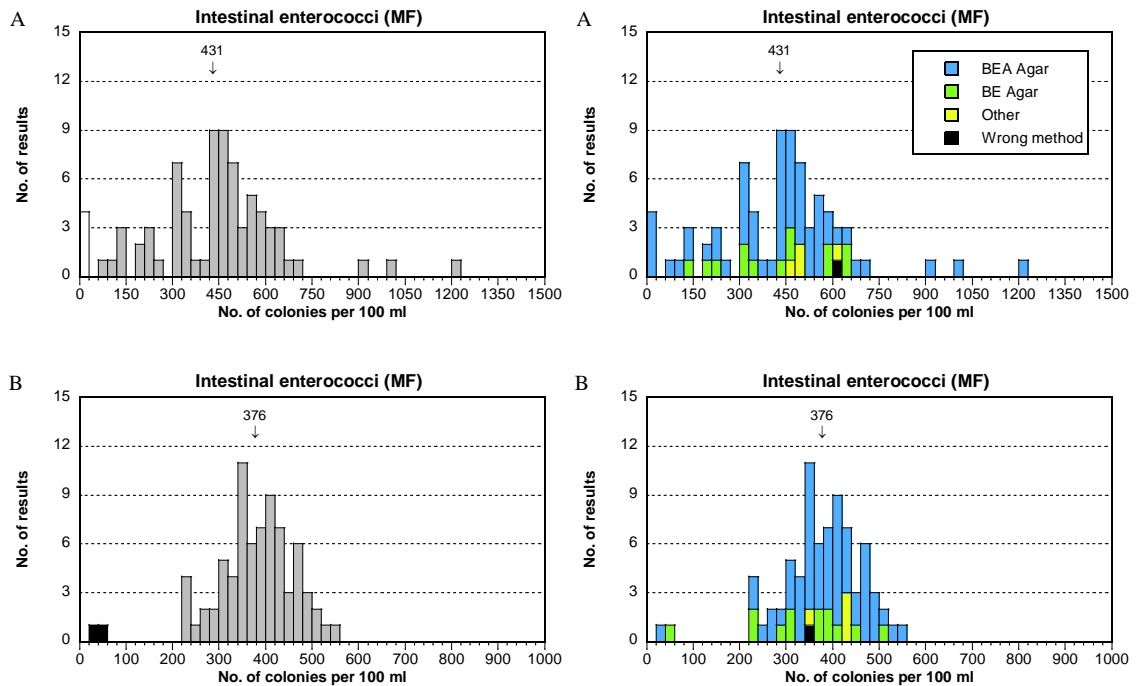
- The strain of *E. coli* is here detected as coliform bacterium only. It possesses β -galactosidase but has only very weak activity of the enzyme β -glucuronidase, leading to negative outcome for *E. coli* within the stated incubation time.
- The zero results for *E. coli* are here regarded as correct. The two none zero results are here instead regarded as false positives in relation to the others, based on an assumption of equivalent methods.
- The average for coliform bacteria is the same as for the MF methods.

Intestinal enterococci (MF)

The method used for intestinal enterococci is almost exclusively EN ISO 7899-2:2000. Only in 4 cases have another method reference, like national standards, been stated, but in all cases m-Enterococcus Agar (m-Ent) has been used as primary medium. Fairly often, even when EN ISO 7899-2:2000 is stated, this medium is referred to as Slanetz & Bartley Agar in the comments field. In one laboratory Enterolert[®]-DW has been used, in spite of not being an MF method.

The reported temperature for incubation was always 35, 36 or 37 °C and confirmation was in all cases performed for the MF methods. It was in 78 % of the cases performed with Bile-esculin-azide agar (BEA Agar) as is stated in EN ISO 7899-2:2000 and in 17 % performed on Bile-esculin agar (BE Agar; without azide).

Confirmation medium	N	A					B					C							
		n	Mv	CV	F	<	>	n	Mv	CV	F	<	>	n	Mv	CV	F	<	>
Total	77	72	431	22	4	0	0	74	376	10	0	2	0	76	0	-	0	-	-
BEA Agar	59	54	432	23	4	0	0	57	381	10	0	1	0	58	0	-	0	-	-
BE Agar	13	13	386	23	0	0	0	12	346	12	0	1	0	13	0	-	0	-	-
Other/Unknown	4	4	-	-	0	0	0	4	-	-	0	0	0	4	0	-	0	-	-
Wrong method	1	1	602	-	0	0	0	1	350	-	0	0	0	1	0	-	0	-	-



The temperature for confirmation was in 93 % of the laboratories 44 °C, in 3 % less than 44 °C and in 4 % 44.5 °C.

The method for intestinal enterococci is not different for the vast majority of the 77 results obtained. Differences in the method are, therefore, most seen in the confirmation step. Both for mixture A and B the average recovery are somewhat lower when BE Agar was used compared to when BEA Agar were used. The "Wrong method" mentioned in the table is Enterolert[®]-DW and is given for information.

Mixture A

- A strain of *E. faecium* was present in the mixture. The colonies of this strain are often light brown-red on m-Ent and may give poor blackening in the confirmation step, in particular in the centre when there are plenty of colonies. A partly negative interpretation of results is the probable reason for the quite scattered distribution of the values with an over representation of low results. The dispersion of the results was medium, in this case the double of that in mixture B.
- Four false negative results were present, but the other low results were not discerned as low outliers, because they were too many.
- This strain has been found to give a low recovery on certain membrane filter batches. If this is experienced, the filters used should be compared with filter of another brand or batch.

Mixture B

- A strain of *E. hirae* was present in the mixture. The distribution of the results was good with low dispersion. The colour of the colonies is usually dark brown-red on m-Ent and without any confirmation problems.

- Two low deviating results were obtained.

Mixture C

- No enterococcus strain was included and no false positive result was reported.

Pseudomonas aeruginosa (MF)

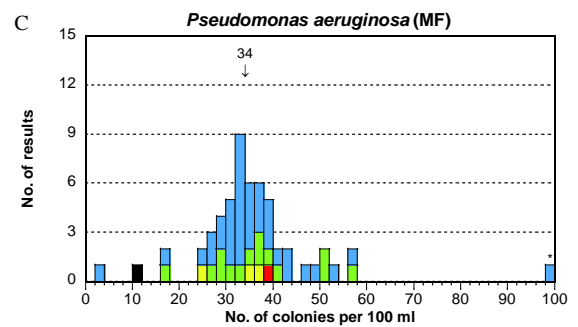
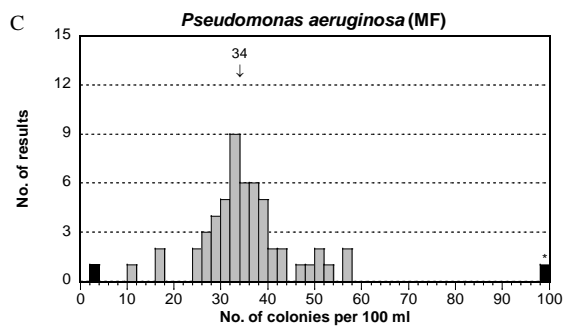
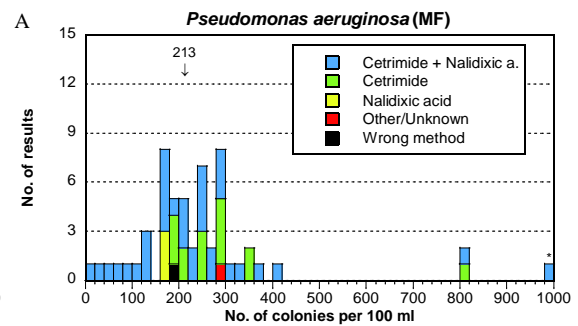
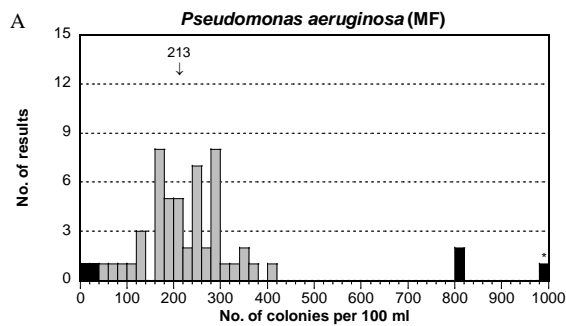
The method used by the 57 laboratories reporting results was for 54 of them EN ISO 16266:2008 with or without modification. Some of the laboratories have reported the method by reference to the identical, since long time withdrawn, CEN standard EN 12780:2002, with or without modification. Incubation of the plates has in all cases been done at 35, 36 or 37 °C. In one case Pseudalert[®] has been used.

A medium consists usually of a base medium and one or more selective substances (supplements), like cetrimide (C) nalidixic acid (N) or Irgasan[®]. The primary cultivation medium for *P. aeruginosa* is the same for the vast majority of the results, viz. Pseudomonas Agar base/CN-agar. In 3 of 4 cases Pseudomonas Isolation agar was reported as primary medium together with OXOID, CM 559, which is Pseudomonas Agar base. Irgasan[®], that is a constituent of Pseudomonas Isolation agar, has not been stated but instead cetrimide, alone or in combination. Therefore, in these 3 cases the medium used is assumed to be Pseudomonas Agar base/CN-agar. The medium Pseudomonas Cetrimide Agar with cetrimide only, reported in 3 cases, is normally used with methods for other matrices than drinking water. Methods are usually stating 50 % higher concentration of cetrimide when used alone compared to when used together with nalidixic acid. Media with both substances has been claimed to give higher recovery of *P. aeruginosa* than with higher cetrimide content alone.

The various selective substances used are normally correlated to the medium stated but other combinations also seem to be used. For example, sometimes cetrimid or nalidixic acid alone is stated together with Pseudomonas Agar base/CN-agar even though the standard prescribes both. In the table results are compared based on selective substances irrespectively of which base medium that is used.

At least for mixture A the laboratories using only cetrimide seem to have obtained the highest average, opposite to what could be expected. In mixture C the tendency is not equally clear. The average for the group of only 3 results with nalidixic acid is also given as it supports the general picture of lower results when this substance was included. The "Wrong method" in the table is Pseudalert[®] and is given for information.

Method variant, supplement	N	A						B						C					
		n	Mv	CV	F	<	>	n	Mv	CV	F	<	>	n	Mv	CV	F	<	>
Total	57	50	213	19	0	2	3	56	0	-	0	-	-	54	34	13	0	1	1
Cetrimide + Nalidixic acid	37	31	202	22	0	2	2	36	0	-	0	-	-	35	34	11	0	1	1
Cetrimide	15	14	247	11	0	0	1	15	0	-	0	-	-	14	35	15	0	0	0
Nalidixic acid	3	3	167	-	0	0	0	3	0	-	0	-	-	3	31	-	0	0	0
Other/Unknown	1	1	-	-	0	0	0	1	0	-	0	-	-	1	-	-	0	0	0
Wrong method	1	1	186	-	0	0	0	1	0	-	0	-	-	1	11	-	0	0	0



Mixture A

- One strain of *P. aeruginosa* with typical, blue-green colonies on PACN was included in the mixture. The colonies there also showed clear fluorescence under UV light.
- The distribution of the results was somewhat scattered, but still had a small dispersion (CV). Two low and three high outliers were present.

Mixture B

- There was no *P. aeruginosa* in the mixture. No false positive result was reported.

Mixture C

- One strain of *P. aeruginosa* was included in the mixture. The colonies were not typical by having both a blue-green and a red-brown pigment on PACN, but they still showed clear fluorescence under UV light. The brownish colour was best visible from the reverse side of the plate, as well as in colonies transferred to an unselective medium.
- Because of the blue green pigmentation and fluorescence on PACN, no confirmation of the colonies was needed according to the standard.
- The distribution of the results was good and the dispersion small. One false negative result was present also here.

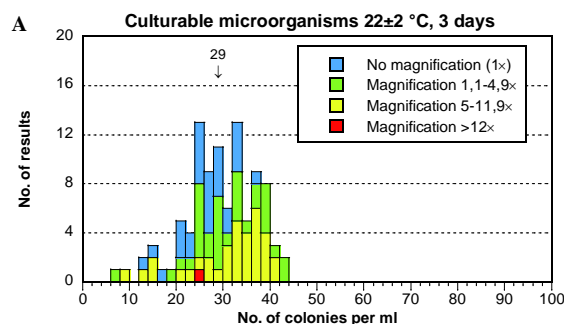
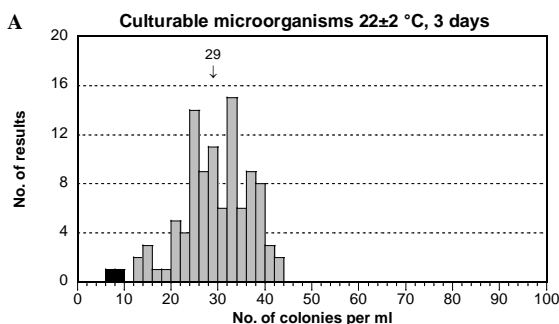
Culturable microorganisms 22 °C, 3 days

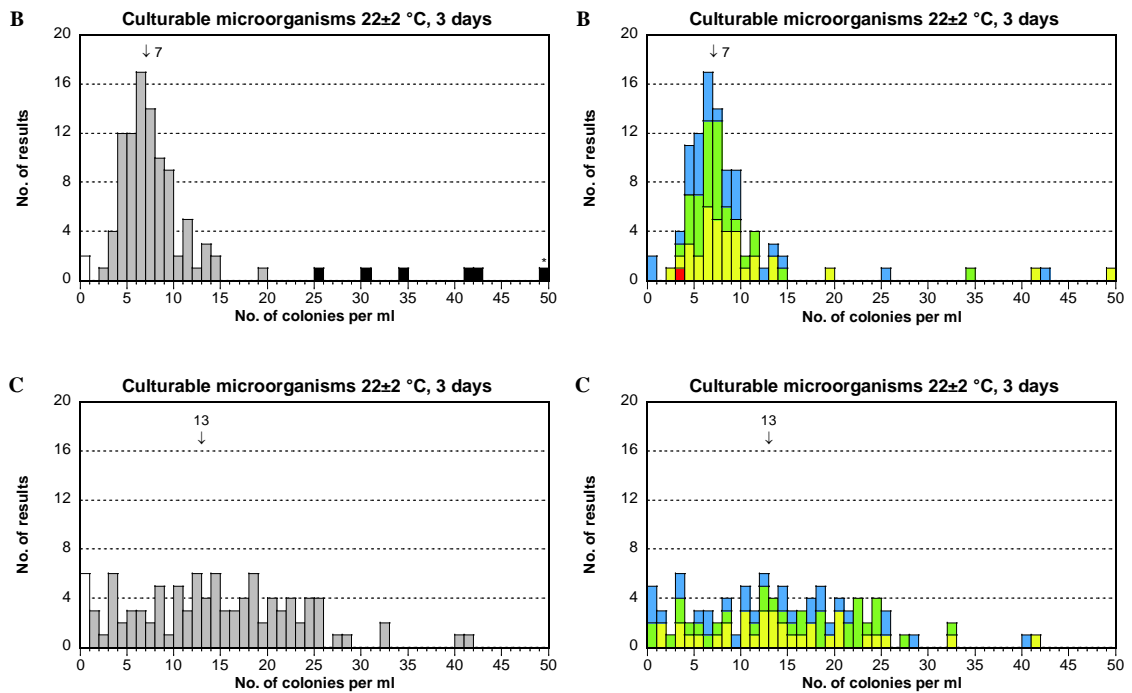
Ninety seven of the 101 laboratories performing the analysis reported EN ISO 6222:1999 as method, which prescribes the use of Yeast extract Agar. Six laboratories used Plate Count Agar (whereof one as Standard Methods Agar) together with EN ISO 6222:1999. Some others used Plate Count Agar together with national standards or "Standard methods" (5). Two laboratories used Nutrient Agar, of which one used spread plating together with EN ISO 6222:1999 and the other membrane filtration and "Nutrient pads". Seven more laboratories reported spread plating in combination with EN ISO 6222:1999.

Comparisons of method variants are relevant to discuss only in connection to EN ISO 6222:1999. Results are given for culture media and magnification for reading. Thus, the 4 results for "Other method" are not shown in the method histograms.

For mixture B the group averages are too low to see any differences. For mixture C there are no differences. For mixture A somewhat lower results were obtained without magnification than when magnification were used. Lower results in average were also obtained when PCA (erroneously?) was used on the basis of the standard EN ISO 6222:1999. In 3 of these 6 cases no magnification was used. Thus, it is not easy to state whether the magnification or the medium is the cause.

Group of results	N	A						B						C					
		n	Mv	CV	F	<	>	n	Mv	CV	F	<	>	n	Mv	CV	F	<	>
Total, all results	101	99	29	13	0	2	0	93	5	20	2	-	6	95	13	32	6	0	0
<i>EN ISO 6222</i>	97	95	29	13	0	2	0	90	7	20	2	0	5	92	13	32	5	0	0
<i>Medium</i>																			
Yeast extract Agar	90	88	29	12	0	2	0	84	7	20	2	0	4	85	13	31	5	0	0
Plate Count Agar	6	6	25	13	0	0	0	5	6	33	0	0	1	6	11	41	0	0	0
Other/Unknown	1	1	-	-	0	0	0	1	-	-	0	0	0	1	-	-	0	0	0
<i>Magnification</i>																			
None	29	29	25	12	0	0	0	25	7	21	2	0	2	26	13	34	3	0	0
1,1-4,9×	33	32	30	11	0	1	0	32	6	17	0	0	1	31	14	30	2	0	0
5-11,9×	34	33	31	13	0	1	0	32	7	22	0	0	2	34	12	34	0	0	0
> 12×	1	1	-	-	0	0	0	1	-	-	0	0	0	1	-	-	0	0	0
<i>Other method</i>	4	4	-	-	0	0	0	3	-	-	-	0	1	3	-	-	1	0	0





Mixture A

- Mainly the strain of *Stenotrophomonas maltophilia* constitutes the culturable microorganisms. The other four bacteria can also grow but appear with very low numbers, viz. <1 cfu per ml.
- The distribution was good except for 2 low outliers. The dispersion (CV) was small.

Mixture 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 and 2 false negative results. Due to the low concentration, the relative dispersion was medium in spite of the good distribution.
- The six high outliers are probably caused by use of a higher temperature than 22 °C. Colonies of the fourth bacteria, *Staphylococcus capitis*, might then be visible. This is what happens in the corresponding analysis at 36±2 °C. No other particular circumstance prevails for these high results.

Mixture C

- The colonies are almost entirely made up of *Pseudomonas fluorescens*. All other strains will also grow but only with low numbers.
- The distribution is bad with unusually many low results. The strain of *P. fluorescens* is known to sometimes give quite scattered distribution, even though the colonies are not particularly small.
- Due to the many low results it was impossible to discern any outliers. However, 6 zero results were present, which here are judged as false negatives.

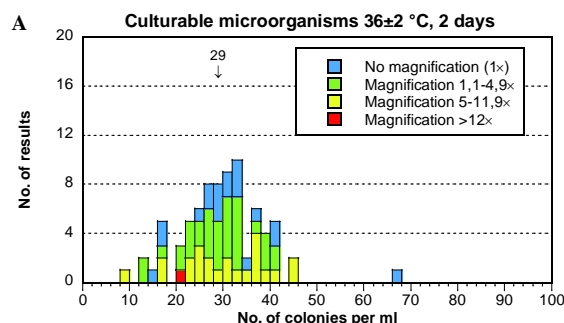
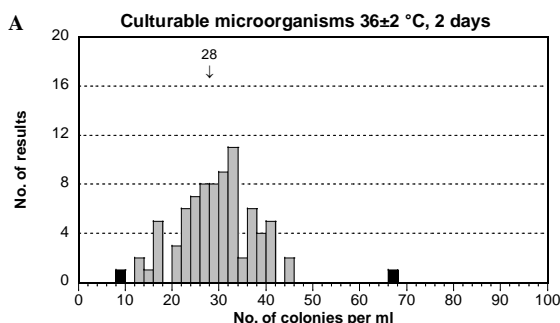
Culturable microorganisms 36 °C, 2 days

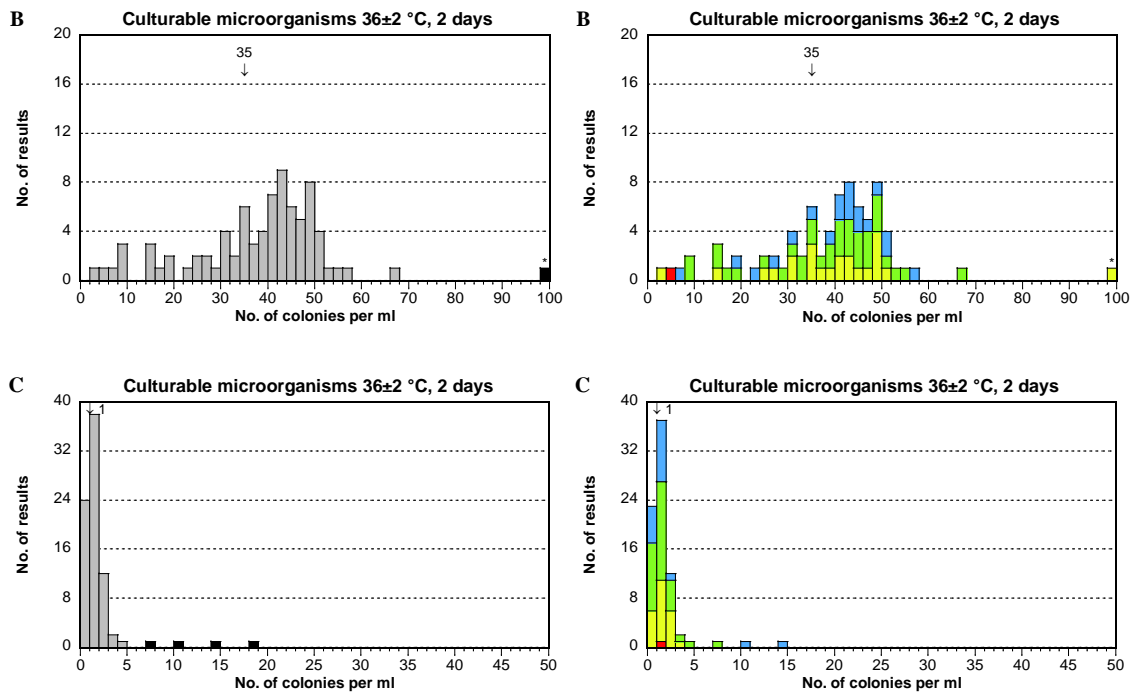
Almost all laboratories have stated the use of EN ISO 6222:1999. Two of the laboratories in the group "Other method" in the table have stated national standards and the third one Standard Methods (5). Seven laboratories have reported Plate Count Agar (whereof one as Standard Methods Agar) together with EN ISO 6222:1999, even though that standard states the use of Yeast extract Agar. One laboratory has reported Nutrient Agar together with EN ISO 6222:1999 (= "Other/Unknown").

As for the analysis at 22 °C, comparisons of method variants are relevant to discuss only when EN ISO 6222:1999 was used. Also here, the results are presented in relation to culture media and magnification for reading. *The 3 results with "Other method" are not shown in the method histograms.*

For mixture C with very few colonies, no tendencies can be seen. As for mixture A at 22 °C, the average result for mixture B seems to be somewhat lower when Plate Count Agar were used compared to Yeast extract Agar. However, the same is here not valid for mixture A. No differences can be seen regarding the magnification.

Group of results	N	A						B						C					
		n	Mv	CV	F	<	>	n	Mv	CV	F	<	>	n	Mv	CV	F	<	>
Total, all results	81	79	28	13	0	1	1	80	35	22	0	0	1	77	1	72	-	-	4
<i>EN ISO 6222</i>	78	76	29	13	0	1	1	77	35	22	0	0	1	75	1	72	-	-	3
<i>Medium</i>																			
Yeast extract Agar	70	68	29	14	0	1	1	69	36	20	0	0	1	67	1	73	-	-	3
Plate Count Agar	7	7	28	8	0	0	0	7	27	37	0	0	0	7	1	75	-	-	0
Other/Unknown	1	1	-	-	0	0	0	1	-	-	0	0	0	1	-	-	-	-	0
<i>Magnification</i>																			
None	19	18	28	14	0	0	1	19	37	20	0	0	0	17	0	78	-	-	2
1,1-4,9×	35	35	28	13	0	0	0	35	36	21	0	0	0	34	1	76	-	-	1
5-11,9×	23	22	30	14	0	1	0	22	35	22	0	0	1	23	1	65	-	-	0
> 12×	1	1	-	-	0	0	0	1	-	-	0	0	0	1	-	-	-	-	0
<i>Other method</i>	3	3	-	-	0	0	0	3	-	-	0	0	0	2	-	-	-	-	1





Mixture A

- Mainly the strain of *Stenotrophomonas maltophilia* constitutes the culturable microorganisms. The other four bacteria can also grow but appear with very low numbers, viz. <1 cfu per ml.
- The distribution was good and the dispersion small and the same as for the corresponding analysis at 22 °C. One low and 1 high outlier were present.

Mixture B

- All bacteria strains in the mixture appear at 36±2 °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 36 but not at 22 °C and is present in highest concentration.
- The distribution shows, as in the September round 2015, unexpectedly many low results, which is unusual when *S. capitis* is used. The reason for these low results is not clear. This time no low results could be identified as outliers, leading to medium dispersion which is higher than usually.

Mixture C

- The few colonies originate from the other three strains except the strain of *P. fluorescens* that doesn't grow at 36±2 °C.
- Due to the very low average, also a zero result is appropriate and acceptable.
- The distribution was good except for 4 high outliers. The relative dispersion is very large due to the very low average concentration.

Outcome of the results and laboratory assessment

General information about reported results

The distributions of results for the respective analysis are shown in 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 analyse 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 assessment is basically a clear indication of the numbers of false results and outliers given beneath the box plots.

Generally, the laboratories that did not report their results in due time, have to compare their results themselves with all other laboratory's by looking in tables, figures and annex A.

Mixed up results and other practical errors

When whole samples seem to have been mixed up, the corresponding sample numbers are hatched in annex A. One laboratory (1131) seems to have mixed up the vials for mixture A and B but no laboratory seems to have mixed up sample/results for individual analyses. No laboratory seems to have calculated the results for another volume than asked for.

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

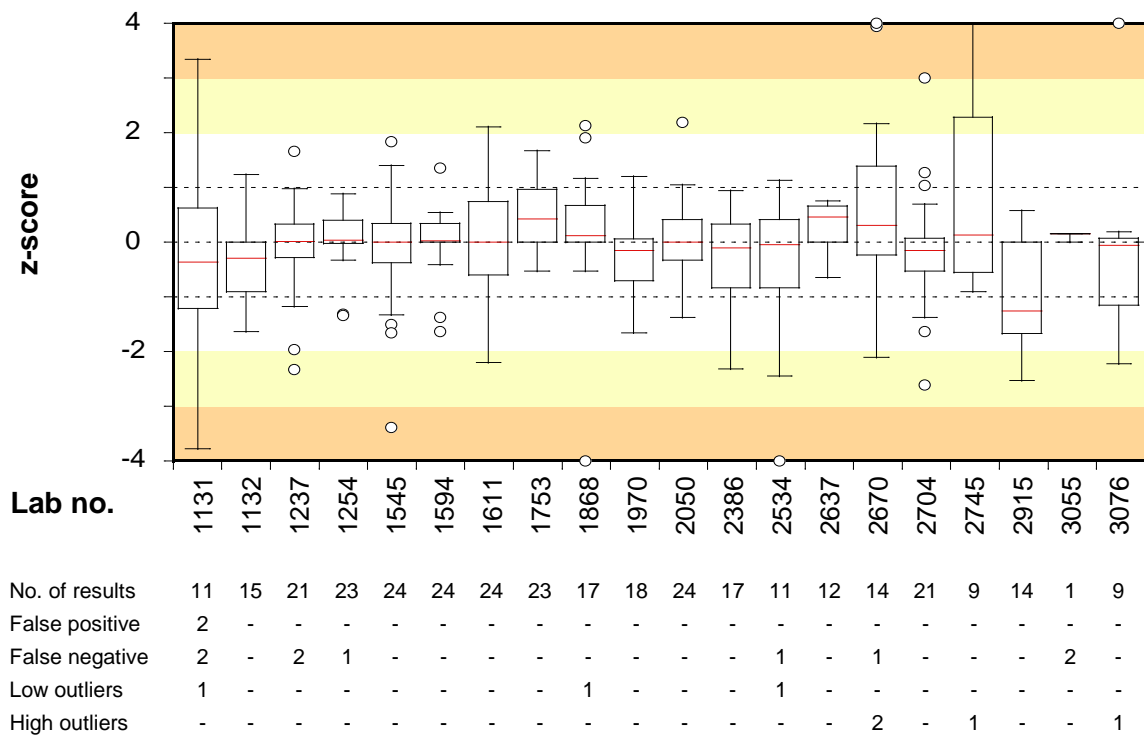
The square-root transformed results of the laboratories are calculated to standard scores, z-scores, to be comparable between analyses. They are shown in annex B but not further evaluated. They are given explicitly to facilitate the follow-up process for laboratories using z-scores in control charts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

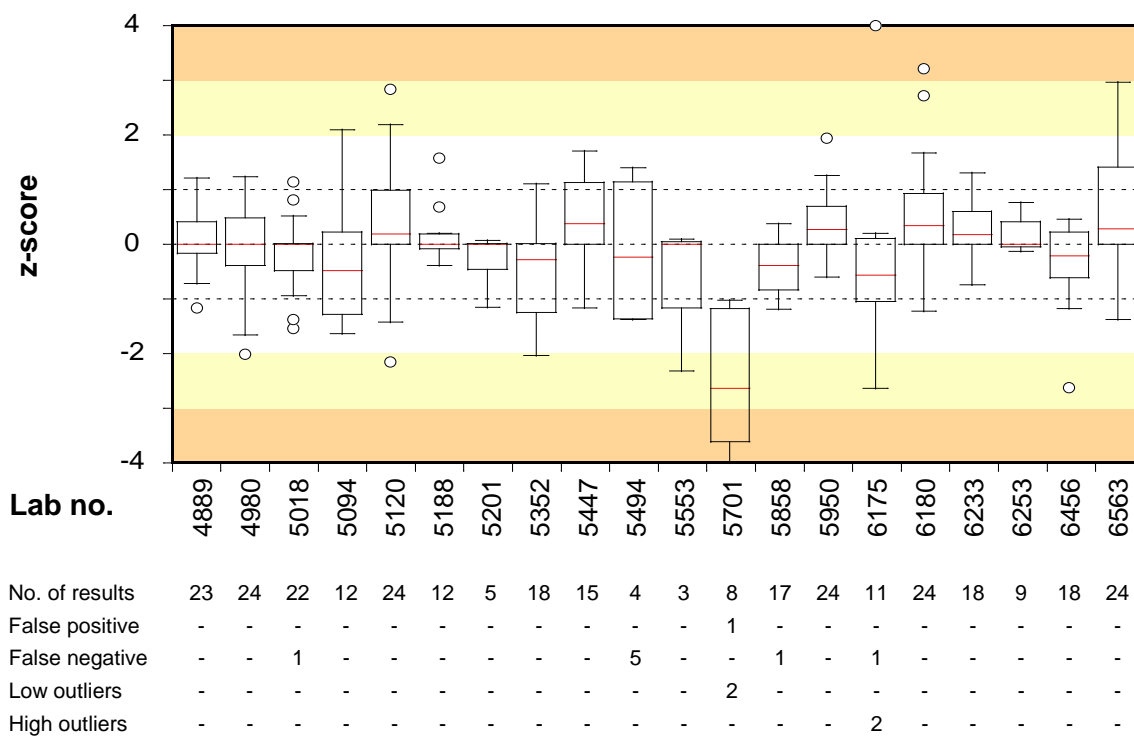
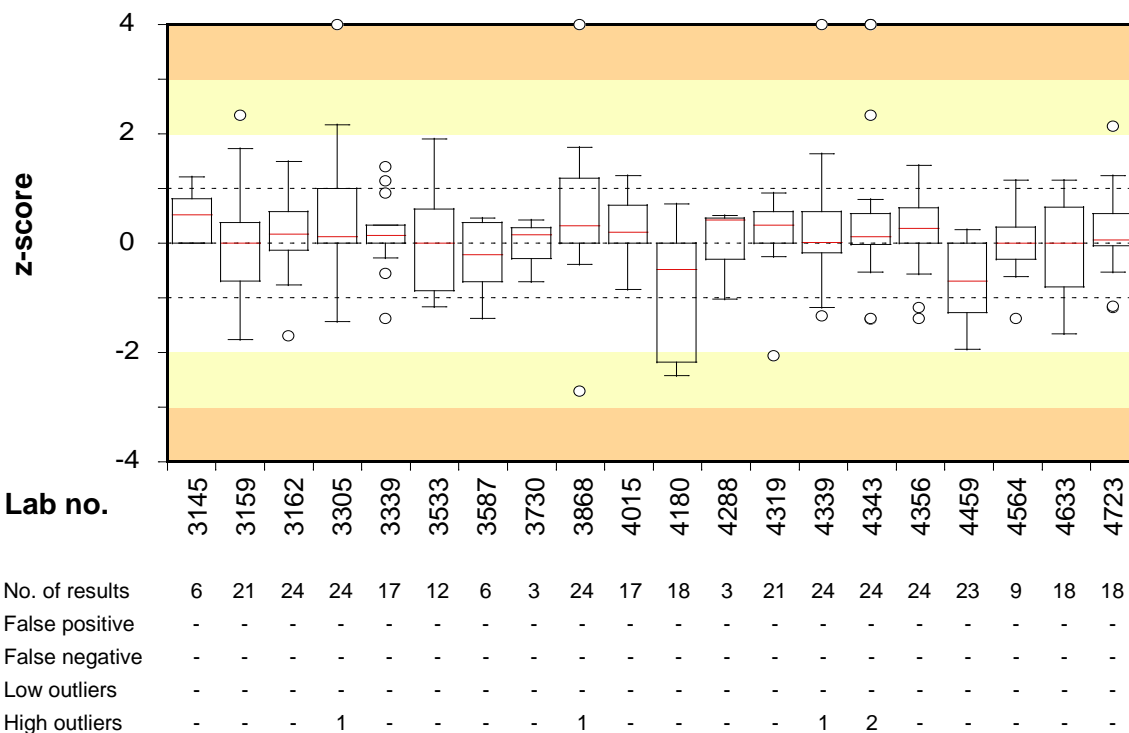
The z-scores are the base for the box plots. The range of the z-scores for each laboratory is shown by a rectangle (box) and lines and/or circles above and beneath the box. The smaller the range from lowest to highest value is in the plot and the more centred around zero the values are, the better is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

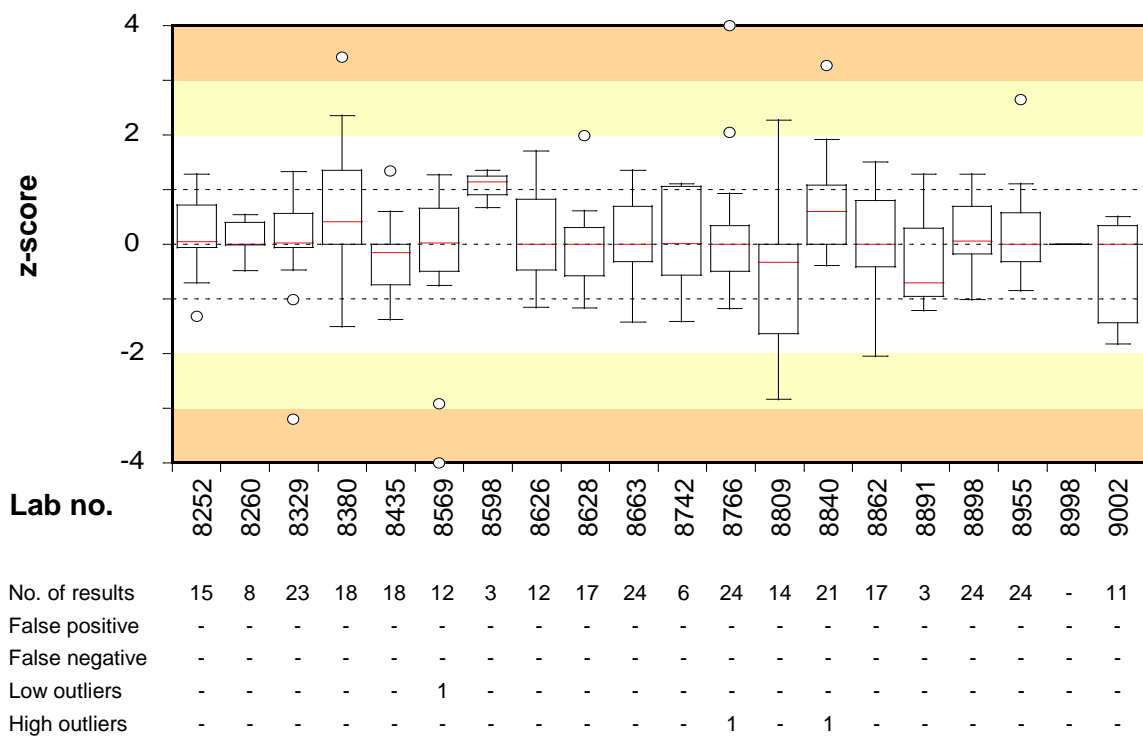
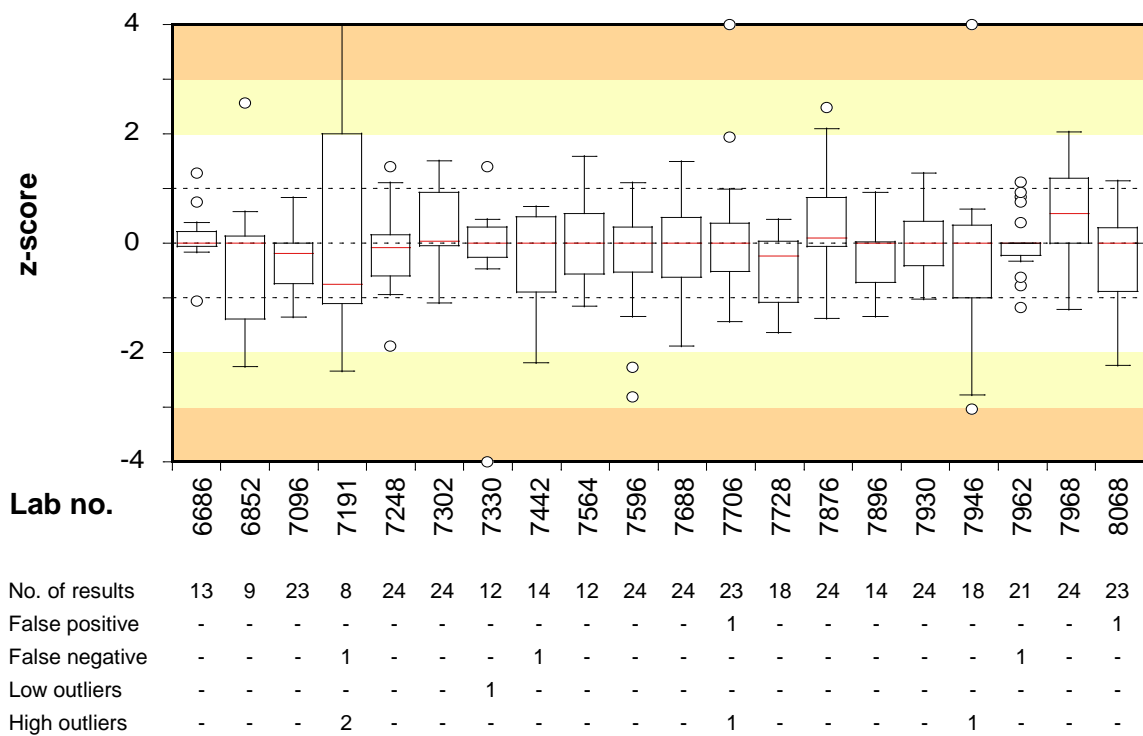
Box plots and numbers of deviating results for each participating laboratory

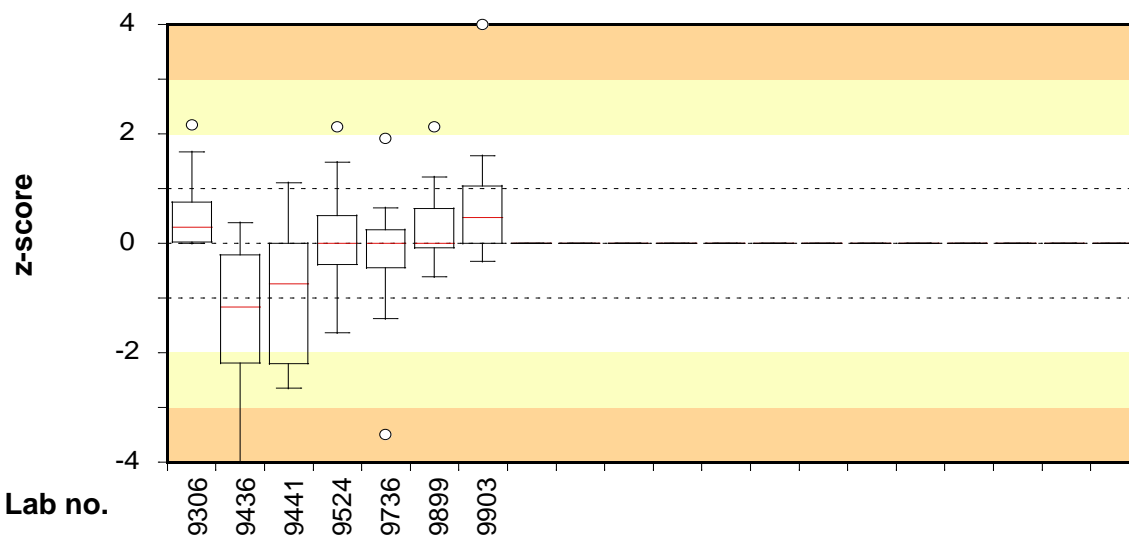
- z-scores are calculated from the formula $z = (x - mv) / s$ (see annex A).
- False results do not generate z-scores and are not included in 'No. of results'.
- The outliers are included in the plots after recalculation to standardised values with the same standard deviation (s) as the rest of the results.
- z-scores > +4 and < -4 have in the plots been set to +4 and -4, respectively.
- The numbers of false positives and false negatives are given in the table under the plots together with the numbers of outliers.
- The horizontal red 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.
- A circle is pure technically 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 in order to simplify localization of the laboratory results.

* < [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)]









No. of results	12	24	10	20	24	23	18
False positive	-	-	-	-	-	-	-
False negative	-	-	-	-	-	-	-
Low outliers	-	3	-	-	1	-	-
High outliers	-	-	-	-	-	-	1

Test material, quality controls and processing of data

Description of the test material

This round comprised three test items with different microorganism mixtures. The test material was manufactured and freeze-dried in portions of 0.5 ml in small vials, according to the description by Peterz and Steneryd (2). The simulated water samples were prepared by dissolving the content of the vials in 800 ml of sterile diluent. The composition and approximate concentrations in each mixture is listed in table 2. The participating laboratories were assigned to perform the analyses according to the methods routinely used by them.

The test material is primarily adapted to the EN ISO methods for analyses of drinking water referred to in the European Drinking water directive (4) and its updates (6). Alternative methods and other standards may usually also be used without any problem.

Table 2 *Microorganisms present in the mixtures*

Mixture ¹	Microorganisms	Strain collection no.		cfu/100 ml ²
		SLV (own)	Reference ³	
A	<i>Escherichia coli</i>	165	CCUG 43600	210
	<i>Klebsiella oxytoca</i>	089	CCUG 43602	320
	<i>Enterococcus faecium</i>	459	CCUG 35172	580
	<i>Pseudomonas aeruginosa</i>	453	CCUG 551	440
	<i>Stenotrophomonas maltophilia</i>	041	CCUG 46537	26 *
B	<i>Enterobacter cloacae</i>	451	CCUG 30205	170
	<i>Cronobacter sakazakii</i>	419	Från vatten	35
	<i>Enterococcus hirae</i>	536	CCUG 46536	390
	<i>Staphylococcus capitis</i>	463	CCUG 35173	40 *
C	<i>Escherichia coli</i>	295	Från vatten	26
	<i>Aeromonas hydrophila</i>	081	CCUG 45103	12
	<i>Pseudomonas aeruginosa</i>	xxx ⁴	–	47
	<i>Pseudomonas fluorescens</i>	535	CCUG 45106	25 *

1 The links between the mixtures 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

3 Origin or culture collection number; CCUG: Culture Collection University of Gothenburg, Sweden

4 Not yet included in the collection

* Indicates cfu per ml

Quality control of the test material

It is essential to have a homogeneous mixture and a uniform volume in all vials in order to allow comparison of all freeze-dried samples derived from one mixture. The volume was checked by weighing 13 to 20 dispensed aliquots in vials of each mixture. The largest differences between vials were between 6 and 9 mg in the mixtures. The largest accepted difference is 15 mg (3 %).

Table 3 presents the results from the organizer in the form of concentration means (cfu) and the measures (I_2 and T; see reference 1) used to assess homogeneity from duplicate analyses of 10 vials from each mixture. The results relate to the volume that was used for counting the colonies. The criterion used for a mixture to be considered homogenous is that I_2 and T are not simultaneously higher than 2. According to that criterion, all mixtures were homogeneous regarding the assessed parameters that were about to be analysed.

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

Analysis parameter <i>Method standard for analysis</i>	Mixture								
	A			B			C ²		
	cfu	I_2	T	cfu	I_2	T	cfu	I_2	T
Coliform bacteria (MF) <i>m-Endo Agar LES according to SS 028167</i>	53 ^a	0.9	1.3	21 ^a	0.9	1.5	38	4.1	1.9
Suspected thermotolerant colif. bact. (MF) [*] <i>m-FC Agar, 44 °C according to SS 028167</i>	17 ^a	1.2	1.7	15	6.8	3.8	24	0.7	1.4
<i>Escherichia coli</i> (MF) <i>m-Endo Agar LES according to SS 028167</i>	21 ^a	1.4	1.6	–	–	–	26	1.3	1.5
Intestinal enterococci (MF) <i>m-Enterococcus Agar acc. to SS-EN ISO 7899-2:2000</i>	58 ^a	0.7	1.2	39 ^a	1.2	1.4	–	–	–
<i>Pseudomonas aeruginosa</i> (MF) <i>Pseudomonas Agar base with cetrimide and nalidixic acid according to SS-EN ISO 16288:2008</i>	44 ^a	1.1	1.4	–	–	–	47	1.2	1.4
Culturable microorg., 2d 37 °C (pour plate) <i>Yeast extract Agar according to SS-EN ISO 6222:1999</i>	44	1.3	1.4	46	0.7	1.3	<1	– ^b	– ^b
Culturable microorg., 3d 22 °C (pour plate) <i>Yeast extract Agar according to SS-EN ISO 6222:1999</i>	42	1.4	1.5	6	0.8	2.2	26	0.4	1.2

1 n=10 vials analysed in duplicate, normally 100 ml for MF and 1 ml for pour plate, 22 and 14 weeks ahead of the testing round start for the mixtures A and B, respectively (for C, see note 2)

2 n=5 vials analysed in duplicate (stability test; 16 weeks before the start of testing for mixture C)

a Determined for the volume 10 ml

b Zero result in 4 of the 5 vials from the two analyses implies that no T or I_2 value can be calculated.

* This parameter is not assessed; no genuine thermotolerant bacteria but only "false positives" were included this time, leading to the high I_2 and T values in mixture B

– No target organism and thus no analysis

Processing of numerical results

Most histograms have "tails" in either or both directions, due to values that do not belong to a normal distribution. Calculations are performed after square root transformations of the results that give better normal distributions by decreasing the significance of the high end "tails". Very deviating values are still present in most analyses and are identified as outliers (black bars). False negative results are presented with white bars in the histograms.

Outliers are identified by use of Grubbs' test according to a modification by Kelly (3). A level of 1 % is set as the risk to incorrectly assess a result as being an outlier. Although the method is objective, there is a prerequisite that the results are normally distributed in order to obtain correct outliers at the 1 % level. A zero result that is a low outlier is considered a false negative result. In special situations, e.g. when many zero results are reported and in some borderline cases, a few subjective adjustments are made in order to set the right limits based on the knowledge of the mixture's content. 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 calculated from the square root transformed results and is the square root of "Mean" in Annex A. It is there denoted as mv . Hence, also the measurement uncertainty will be expressed as a square root value. The standard uncertainty of measurement (u) correspond to the standard deviation of the assigned value (s) divided by the number of results squared-root transformed, i.e.: $u = s/\sqrt{n_{mv}}$ where n_{mv} is the number of results in annex A, except the deviating ones. Here is the relative uncertainty (u_{rel}) used and expressed as per cent after division by the mean value mv and multiplication by 100.

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

References

1. Anonymous 2014. Scheme protocol, Microbiology, Drinking water & Food, 3rd ed. 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*).

Annex A Results of the participants. Susp. = suspected on membrane filter before confirmation. Results given as <1, <2, <10 and <100 are treated as zero. The fields with other results given as < 'value' and results given as > 'value' are yellow, and those results 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

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
1131	1 1	80	310	37	80	310	25	-	-	-	<1	260	25	248	365	25	<1	172	<1
1132	3 2 1	-	-	-	-	-	-	111	9	20	111	0	20	387	365	20	179	0	0
1237	2 3 1	-	-	-	410	255	28	-	-	-	<1	<1	28	390	110	20	210	<1	-
1254	1 3 2	460	180	32	460	180	32	-	-	-	180	0	32	440	150	19	200	0	0
1545	1 3 2	400	160	30	400	160	18	220	160	24	220	0	18	425	262	25	208	0	0
1594	2 1 3	435	220	28	435	220	28	103	8	24	210	0	28	454	250	30	184	0	0
1611	2 3 1	480	190	40	480	190	23	96	15	23	320	0	23	387	228	24	236	0	0
1753	1 2 3	570	210	51	570	210	24	-	-	-	189	0	0	660	411	29	230	0	0
1868	2 3 1	463	190	24	463	190	24	-	-	-	150	0	0	486	256	45	244	0	0
1970	3 1 2	410	160	45	370	160	25	410	68	45	330	0	25	-	-	-	-	-	-
2050	2 1 3	-	-	-	360	216	35	-	-	-	120	0	35	361	185	30	176	0	0
2386	3 1 2	250	110	30	250	110	30	-	-	-	147	0	0	-	-	-	-	-	-
2534	2 1 3	545	173	31	545	173	31	-	-	-	280	<1	31	-	-	-	-	-	-
2637	2 3 1	-	-	-	-	-	-	-	-	-	-	-	-	380	210	32	220	<1	<1
2670	1 2 3	119	0	26	119	0	26	119	0	26	119	0	26	-	-	-	-	-	-
2704	1 3 2	-	-	-	340	100	24	-	-	-	340	0	24	504	344	24	222	<1	<1
2745	3 1 2	380	110	50	380	110	50	190	0	50	380	0	50	-	-	-	-	-	-
2915	1 2 3	-	-	-	144	30	17	-	-	-	77	<1	<u>1</u>	-	-	-	-	-	-
3055	2 1 3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3076	3 2 1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3145	3 1 2	-	-	-	-	-	-	-	-	-	-	-	-	548	313	37	205	0	0
3159	1 3 2	-	-	-	270	90	23	-	-	-	120	0	22	453	306	40.6	124	<1	<1
3162	2 1 3	400	290	29	400	290	29	-	-	-	160	0	29	517	276	17	166	0	0
3305	1 2 3	-	-	-	390	280	28	-	-	-	156	0	28	478	220	36	192	0	0
3339	2 3 1	410	260	30	410	260	30	-	-	-	170	0	0	-	-	-	-	-	-
3533	1 2 3	-	-	-	450	150	20	-	-	-	360	0	20	-	-	-	-	-	-
3587	1 3 2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3730	1 2 3	270	0	33	-	-	-	167	0	33	-	-	-	-	-	-	-	-	-
3868	3 2 1	400	250	25	400	250	25	60	7	10	200	0	10	660	410	31	190	0	0
4015	3 2 1	500	230	42	429	230	22	-	-	-	211	0	0	596	365	25	195	0	0
4180	2 3 1	-	-	-	280	94	25	-	-	-	110	0	25	-	-	-	-	-	-
4288	1 3 2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4319	2 3 1	475	245	58	426	245	31	190	102	28	262	0	27	492	300	26	221	0	0
4339	1 3 2	-	-	-	430	240	19	250	<1	18	220	<1	19	488	166	28	145	<1	<1
4343	3 2 1	464	136	33	464	136	30	-	-	-	182	0	30	488	145	33	201	0	0
4356	1 3 2	530	330	32	471	312	32	170	3	29	265	0	32	488	249	33	201	0	0
4459	2 3 1	-	-	-	152	141	17	-	-	-	152	0	0	260	160	21	118	0	0
4564	3 1 2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4633	1 3 2	-	-	-	436	191	-	170	0	-	260	0	-	535	191	22	243	0	0
4723	2 3 1	436	136	29	436	136	29	-	-	-	301	0	29	727	365	20	228	0	0
4889	2 3 1	-	-	-	350	290	20	-	-	-	130	0	0	490	310	26	190	0	0
4980	1 2 3	440	50	38	160	50	29	90	62	24	90	0	24	429	364	19.2	192	<1	<1
5018	2 1 3	460	180	34	368	108	27	-	-	-	322	0	0	548	194	28	214	0	0
5094	3 2 1	-	-	-	540	210	25	128	26	48	128	0	48	-	-	-	-	-	-
5120	3 2 1	480	190	29	480	190	29	110	79	28	480	0	29	610	370	22	330	0	0
5188	2 1 3	-	-	-	-	-	-	-	-	-	-	-	-	420	310	25	200	0	0
5201	3 2 1	250	114	26	-	-	-	-	-	-	140	0	0	-	-	-	-	-	-
5352	3 1 2	260	162	45	210	162	36	78	21	23	78	<1	23	-	-	-	-	-	-
5447	3 2 1	-	-	-	527	336	41	-	-	-	304	0	41	-	-	-	-	-	-
5494	2 1 3	-	-	-	<10	<10	<10	-	-	-	-	-	-	-	-	-	-	-	-
5553	3 1 2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
5701	2 3 1	44	21	5	44	21	3	-	-	-	18	1	1	-	-	-	-	-	-
5858	2 3 1	-	-	-	-	-	-	-	-	-	-	-	-	400	183	20	155	0	0
5950	2 3 1	436	164	27	436	164	27	128	35	30	128	<1	30	461	261	29	248	<1	<1
6175	1 2 3	-	-	-	-	-	-	-	-	-	-	-	-	200	200	20	200	0	0
6180	2 1 3	460	240	55	460	240	55	170	60	20	322	0	55	660	310	29	250	0	0
6233	2 1 3	-	-	-	-	-	-	-	-	-	-	-	-	473	218	31	161	<1	<1
6253	1 2 3	-	-	-	-	-	-	-	-	-	-	-	-	541	245	27	186	0	0
6456	2 1 3	-	-	-	425	165	24	-	-	-	126	0	19	201	207	25	201	0	0
6563	3 2 1	620	206	45	620	206	45	-	-	-	620	0	45	606	298	22	250	0	0
6686	2 1 3	-	-	-	-	-	-	-	-	-	-	-	-	>200	>200	20.7	200.5	<1	<1
6852	1 3 2	-	-	-	-	-	-	130	<1	49	-	-	-	230	94.5	49	137	<1	<1
7096	2 1 3	-	-	-	340	83	26	-	-	-	160	0	0	360	220	34	165	0	0
7191	3 1 2	>250	137	250	100	100	100	-	-	-	100	0	100	-	-	-	-	-	-
7248	1 3 2	441	109	22	441	109	22	155	48	13	100	0	22	450	178	30	185	0	0
7302	3 1 2	445	300	37	445	300	25	168	69	27	297	<1	25	464	331	36	148	<1	<1
7330	3 1 2	-	-	-	-	-	-	-	-	-	168	0	25	-	-	-	-	-	-
7442	3 2 1	424	233	48	242	233	32	-	-	-	0	0	32	365	177	21	110	0	0
7564	3 1 2	-	-	-	500	220	40	-	-	-	170	<1	25	-	-	-	-	-	-
7596	2 3 1	510	140	32	510	140	32	120	0	27	120	0	27	461	276	19	199	0	0
7688	3 1 2	-	-	-	230	200	36	-	-	-	120	0	36	490	240	31	260	0	0
Mean					361	177	28				184	0	28	450	249	28	191	0	0
CV (%)					20	23	13				28	-	15	13	17	13	11	-	-

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

Susp. intestinal enterococci (MF)			Intestinal enterococci (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	
-	-	-	-	-	-	-	-	-	-	-	-	8	19	12	-	-	-	1131
590	350	0	590	350	0	-	-	-	-	-	-	22	7	3	-	-	-	1132
-	-	-	<1	380	<1	-	-	-	192	<1	16	25	7	23	30	48	3	1237
540	370	0	0	370	0	240	0	38	240	0	38	30	7	22	26	47	1	1254
500	350	0	500	350	0	280	0	29	280	0	29	40	3	11	44	2	1	1545
425	405	0	355	405	0	230	0	34	230	0	34	33	11	3	32	38	0	1594
580	510	0	580	510	0	400	0	56	400	0	56	24	4	12	17	9	1	1611
660	430	0	660	430	0	280	0	51	280	0	51	41	6	18	32	46	1	1753
604	45	0	571	45	0	267	0	30	-	-	-	36	13	19	-	-	-	1868
210	370	0	210	370	0	130	0	28	130	0	28	24	3	14	30	14	1	1970
-	-	-	490	405	0	-	-	-	240	0	57	37	6	23	23	34	0	2050
250	220	0	250	220	0	180	1	32	180	0	32	23	6	21	36	49	1	2386
-	-	-	-	-	-	37	<1	<1	-	-	-	7	6	<1	13	31	<1	2534
400	370	<1	-	-	-	-	-	-	-	-	-	32	9	18	34	46	1	2637
470	490	0	470	490	0	-	-	-	-	-	-	32	14	25	66	42	14	2670
-	-	-	1200	340	<1	-	-	-	-	-	-	26	6	3	29	6	0	2704
-	-	-	-	-	-	-	-	-	-	-	-	25	25	9	-	-	-	2745
-	-	-	440	280	<1	-	-	-	-	-	-	26	3	1	33	44	0	2915
-	-	-	-	-	-	-	-	-	-	-	-	30	0	0	-	-	-	3055
-	-	-	-	-	-	160	0	100	160	0	100	15	4	15	29	34	0	3076
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3145
1000	520	0	1000	520	<1	-	-	-	-	-	-	36	5	4	29	38	1	3159
690	320	0	310	320	0	290	0	49	290	0	49	33	9	24	33	27	1	3162
420	300	0	630	300	0	810	0	43	810	0	43	38	14	24	32	16	1	3305
430	400	0	330	400	0	230	0	36	230	0	36	27	7	16	40	55	0	3339
-	-	-	500	430	0	-	-	-	-	-	-	24	13	6	-	-	-	3533
-	-	-	-	-	-	-	-	-	-	-	-	28	5	11	32	41	<1	3587
-	-	-	-	-	-	-	-	-	-	-	-	30	8	8	-	-	-	3730
500	400	0	500	400	0	300	0	52	300	0	52	36	12	28	36	35	10	3868
664	450	0	600	450	0	-	-	-	-	-	-	30	8	20	-	-	-	4015
-	-	-	580	285	0	-	-	-	73	0	17	14	6	1	14	38	1	4180
-	-	-	-	-	-	-	-	-	-	-	-	22	8	18	-	-	-	4288
126	450	0	126	450	0	-	-	-	-	-	-	29	7	14	31	48	1	4319
450	350	<1	310	350	<1	810	0	34	810	0	34	42	7	24	38	40	2	4339
427	363	0	427	363	0	118	0	38	118	0	38	35	56	41	27	291	1	4343
470	470	0	470	470	0	130	0	37	130	0	37	25	7	21	32	42	0	4356
-	-	-	309	396	0	-	-	-	200	0	26	24	4	2	23	34	0	4459
-	-	-	430	470	0	-	-	-	-	-	-	28	6	16	24	45	0	4564
-	-	-	-	318	-	-	-	-	-	-	-	19	3	21	28	46	0	4633
482	436	0	391	409	0	-	-	-	-	-	-	33	4	13	-	-	-	4723
-	-	-	420	340	0	-	-	-	160	0	36	25	9	20	31	43	2	4889
540	430	0	540	430	<1	290	0	43	290	0	38	33	6	22	27	19	1	4980
550	350	0	0	350	0	168	0	34	168	0	34	28	7	8	27	15	0	5018
520	480	0	-	-	-	-	-	-	-	-	-	20	5	3	20	36	0	5094
200	230	0	200	230	0	280	0	26	280	0	26	33	8	15	40	56	1	5120
-	-	-	450	390	0	-	-	-	200	0	50	-	-	-	-	-	-	5188
-	-	-	-	-	-	-	-	-	-	-	-	29	4	14	-	-	-	5201
360	260	0	360	260	<1	250	0	29	250	<1	29	16	9	14	16	35	<1	5352
-	-	-	700	390	0	-	-	-	-	-	-	26	5	19	29	19	1	5447
-	-	-	-	-	-	-	-	-	-	-	-	20	<10	<10	40	50	<10	5494
-	-	-	450	220	0	-	-	-	-	-	-	-	-	-	-	-	-	5553
-	-	-	-	-	-	-	-	-	-	-	-	22	4	5	-	-	-	5701
479	370	0	479	370	0	185	0	24	173	0	24	24	6	0	22	29	1	5858
636	464	<1	636	464	<1	245	<1	40	245	<1	40	34	9	16	45	47	1	5950
-	-	-	-	-	-	-	-	-	-	-	-	25	30	0	22	8	18	6175
560	320	0	560	320	0	340	0	31	340	0	31	32	6	13	20	40	1	6180
460	425	0	460	425	0	270	0	32	270	0	32	34	7	27	32	45	1	6233
-	-	-	-	-	-	-	-	-	-	-	-	32	8	17	-	-	-	6253
-	-	-	-	-	-	-	-	-	-	-	-	27	5	17	32	26	1	6456
460	450	0	460	450	0	180	0	36	180	0	36	36	13	32	24	37	0	6563
-	-	-	440	300	<1	-	-	-	-	-	-	29	9	12	39	34	1	6686
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	33	37	<1	6852
-	-	-	480	310	0	-	-	-	120	0	34	31	6	5	25	23	1	7096
-	-	-	-	-	-	-	-	-	-	-	-	25	4	0	-	-	-	7191
464	404	0	350	346	0	292	2	31	292	0	31	40	9	10	16	30	2	7248
536	373	<1	445	373	<1	336	<1	29	336	<1	29	39	6	13	41	48	1	7302
-	-	-	460	28	0	-	-	-	340	0	36	-	-	-	25	42	1	7330
-	-	-	-	-	-	-	-	-	-	-	-	34	7	14	-	-	-	7442
-	-	-	-	-	-	-	-	-	-	-	-	29	4	7	33	24	1	7564
590	460	0	60	460	0	170	0	32	170	0	32	31	2	12	23	49	2	7596
-	-	-	330	260	0	-	-	-	90	0	34	39	5	22	30	43	0	7688
			431	376	0				213	0	34	29	7	13	28	35	1	Mean
			22	10	-				19	-	13	13	20	32	13	22	72	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
7706	3 2 1	-	-	-	340	100	33	-	-	-	150	0	33	435.2	142.1	29.2	146.7	0	29.2
7728	3 1 2	-	-	-	220	180	18	-	-	-	80	0	18	-	-	-	-	-	-
7876	2 3 1	382	127	64	382	127	48	89	18	21	173	<1	48	520	293	34	163	<1	<1
7896	3 2 1	510	180	20	510	180	20	-	-	-	150	<1	<1	410	190	29	210	<1	<1
7930	3 1 2	390	235	24	390	235	24	-	-	-	180	0	24	360	222	22	210	0	0
7946	1 3 2	278	120	33	230	120	30	130	110	35	120	0	30	-	-	-	-	-	-
7962	2 1 3	330	280	38	330	280	34	79	29	18	170	0	0	326	249	26	160	0	0
7968	2 3 1	505	340	38	455	340	38	133	133	34	455	0	38	521	271	26	235	0	0
8068	2 1 3	-	-	-	369	220	30	-	-	-	273	0	30	387	187	22	155	0	22
8252	3 2 1	-	-	-	-	-	-	-	-	-	-	-	-	570	150	27	240	<1	<1
8260	3 2 1	360	139	27	360	139	27	-	-	-	193	<1	<1	-	-	-	-	-	-
8329	2 3 1	517	140	25	517	140	25	-	-	-	250	0	0	579	239	21	222	0	0
8380	3 1 2	-	-	31	-	-	31	-	-	-	-	-	31	623	624	47	133	0	0
8435	3 1 2	-	-	-	350	101	29	83	0	18	350	0	29	-	-	-	-	-	-
8569	1 3 2	370	180	41	260	180	26	6	0	2	6	0	2	-	-	-	-	-	-
8598	3 1 2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
8626	3 1 2	400	230	41	360	100	41	160	0	41	160	0	41	-	-	-	-	-	-
8628	1 2 3	-	-	-	310	230	20	50	<1	19	120	<1	<1	-	-	-	-	-	-
8663	3 2 1	400	190	22	400	190	22	190	41	19	160	0	22	410	210	23	180	0	0
8742	3 1 2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
8766	3 1 2	509	136	32	509	136	22	355	39	37	458	0	19	350	276	30	166	0	0
8809	3 2 1	170	82	30	170	82	30	-	-	-	112	0	0	-	-	-	-	-	-
8840	2 1 3	460	280	25	460	280	25	-	-	-	276	0	25	480	270	43	240	0	0
8862	2 1 3	536	145	35	536	145	22	-	-	-	209	0	0	638	243	36	144	0	0
8891	2 3 1	34	14	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
8898	3 1 2	480	239	25	480	239	25	-	-	-	190	0	25	356	214	21	160	0	0
8955	3 1 2	-	-	-	330	460	22	99	38	23	120	0	22	410	330	28	170	0	0
8998	2 3 1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
9002	1 3 2	-	-	-	150	200	20	-	-	-	50	0	0	-	-	-	-	-	-
9306	2 1 3	-	-	-	-	-	-	-	-	-	-	-	-	463	289	28	294	0	0
9436	1 2 3	139	46	18	139	46	18	25	11	15	111	<1	18	325	90	24	140	<1	<1
9441	3 2 1	-	-	-	-	-	-	-	-	-	-	-	-	>201	>201	31	109	<1	<1
9524	1 2 3	610	190	30	610	190	25	-	-	-	290	<1	<1	435	272	24	219	<1	<1
9736	2 3 1	364	127	31	364	127	30	-	-	-	91	0	30	429	237	43	163	0	0
9899	2 1 3	536	626	42	536	290	24	-	-	-	185	0	0	434	300	45	185	0	0
9903	1 3 2	512	258	55	512	258	32	188	149	28	188	0	28	-	-	-	-	-	-

n	56	57	57	80	80	80	36	36	35	82	82	82	66	66	68	68	68	67
Min	34	0	5	0	0	0	6	0	2	0	0	0	200	90	17	0	0	0
Max	620	626	250	620	460	100	410	160	50	620	260	100	727	624	49	330	172	29.2
Median	436	180	32	400	185	27	129	19.5	24	170	0	27.5	457.5	249	27	195	0	0
Mean				361	177	28				184	0	28	450	249	28	191	0	0
CV (%)				20	23	13				28	-	15	13	17	13	11	-	-
False positive				0	0	0				0	2	0	0	0	0	0	1	2
False negative				1	2	1				3	0	0	0	0	0	0	1	0
Outliers, low				0	0	1				0	0	2	0	0	0	0	0	0
Outliers, high				0	0	1				0	0	1	0	0	0	0	0	0
Low limit OK	34	0	5	44	21	17	6	0	2	6	0	10*	200	90	17	109	0	0
High limit OK	620	626	250	620	460	55	410	160	50	620	0	55	727	624	49	330	0	0

mv				18.995	13.287	5.256				13.575	0.000	5.282	21.215	15.772	5.265	13.827	0.000	0.000
($\sqrt{\text{Mean}}$)																		
s				3.843	3.082	0.674				3.814	0.000	0.784	2.683	2.687	0.675	1.529	0.000	0.000
($CV \cdot mv/100$)																		
$u_{rel,mv}$ (%)				2.3	2.6	1.5				3.2		1.7	1.6	2.1	1.6	1.4		
($100 \cdot s / \sqrt{n_{mv}/mv}$)																		
x																		
($\sqrt{\text{Result}}$)																		
z																		
($[x-mv]/s$)																		

* The calculated results and acceptance limits are calculated without the 21 zero results. However, these zero results are judged as acceptable and not false negatives.

Susp. intestinal enterococci (MF)			Intestinal enterococci (MF)			Susp. <i>Pseudomonas aeruginosa</i> (MF)			<i>Pseudomonas aeruginosa</i> (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	
-	-	-	540	540	0	-	-	-	170	0	30	26	34	15	23	52	0	7706
-	-	-	450	340	0	-	-	-	240	0	31	28	5	3	26	42	1	7728
518	336	<1	518	336	<1	475	<1	36	218	<1	36	38	11	7	37	49	<1	7876
-	-	-	-	-	-	-	-	-	-	-	-	20	5	6	-	-	-	7896
500	430	0	500	430	0	250	0	38	250	0	38	39	5	6	28	32	1	7930
488	416	0	480	410	0	46	60	40	40	0	40	14	42	10	20	5	1	7946
55	330	0	0	330	0	200	0	27	200	0	-	28	9	12	26	51	1	7962
540	515	0	230	515	0	240	0	46	240	0	46	42	8	11	38	43	2	7968
-	-	0	108	345	0	-	-	-	280	0	25	20	7	25	17	48	0	8068
-	-	-	440	400	<1	230	<1	33	-	-	-	39	5	18	26	51	1	8252
-	-	-	-	-	-	-	-	-	-	-	-	33	8	17	-	-	-	8260
440	485	0	440	485	0	-	-	-	186	0	11	33	7	17	30	49	1	8329
600	-	0	305	-	0	-	0	33	-	0	33	37	11	13	38	51	3	8380
-	-	-	300	300	0	-	-	-	180	0	32	24	4	8	28	45	0	8435
560	480	0	560	480	0	-	-	-	-	-	-	36	8	20	-	-	-	8569
-	-	-	-	-	-	-	-	-	-	-	-	34	11	25	-	-	-	8598
-	-	-	-	-	-	-	-	-	-	-	-	33	4	8	28	40	2	8626
-	-	-	900	400	<1	-	-	-	170	<1	26	26	4	10	30	41	1	8628
580	460	0	200	460	0	260	0	42	260	0	42	36	11	22	30	32	2	8663
-	-	-	-	-	-	-	-	-	-	-	-	25	6	4	37	40	2	8742
514	391	0	234	391	0	1045	0	30	1045	0	30	27	7	10	34	42	1	8766
140	230	0	140	230	0	0	0	0	-	-	-	12	6	40	17	30	1	8809
420	430	0	420	430	0	-	-	-	-	-	-	33	10	32	40	45	7	8840
482	473	0	127	473	0	-	-	-	-	-	-	35	6	8	-	-	-	8862
-	-	-	-	-	-	-	-	-	-	-	-	39	5	5	-	-	-	8891
530	390	0	530	390	0	297	0	38	297	0	38	39	7	20	36	42	2	8898
640	370	0	640	360	0	-	-	-	160	0	33	27	10	14	36	39	2	8955
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8998
-	-	-	300	250	0	-	-	-	-	-	-	32	8	18	-	-	-	9002
-	-	-	-	-	-	-	-	-	-	-	-	29	8	24	30	66	1	9306
482	345	<1	318	345	<1	24	3	5	8	<1	2	12	4	1	8	24	1	9436
-	-	-	-	-	-	-	-	-	-	-	-	21	6	3	12	9	2	9441
602	350	<1	602	350	<1	-	-	-	-	-	-	25	5	18	25	14	4	9524
564	396	0	564	396	0	26	0	32	26	0	32	32	6	10	25	41	0	9736
629	429	0	629	429	0	2200	0	33	210	0	33	29	9	12	24	45	1	9899
586	409	0	539	409	0	360	0	35	360	0	35	37	41	25	27	30	2	9903

55	54	56	76	76	76	43	44	44	55	56	56	101	101	101	81	81	81	n
55	45	0	0	28	0	0	0	0	8	0	2	7	0	0	8	2	0	Min
1000	520	0	1200	540	0	2200	60	100	1045	0	100	42	56	41	66	291	18	Max
500	400	0	455	390	0	250	0	34	224	0	34	29	7	14	29	40	1	Median
			431	376	0				213	0	34	29	7	13	28	35	1	Mean
			22	10	-				19	-	13	13	20	32	13	22	72	CV (%)
			0	0	0				0	0	0	0	0	0	0	0	0	False pos.
			4	0	0				0	0	0	0	2	6	0	0	0	False neg.
			0	2	0				2	0	1	2	0	0	1	0	0	Outliers <
			0	0	0				3	0	1	0	6	0	1	1	4	Outliers >
55	45	0	60	220	0	0	0	0	40	0	11	12	2	1	12	2	0	Low limit
1000	520	0	1200	540	0	2200	60	100	400	0	57	42	19	41	45	66	4	High limit

	20.749	19.403	0.000			14.611	0.000	5.830	5.377	2.604	3.654	5.334	5.905	0.785				mv
	4.635	1.970	0.000			2.728	0.000	0.785	0.675	0.525	1.175	0.708	1.325	0.569				s
	2.6	1.2				2.6		1.8	1.3	2.1	3.3	1.5	2.5	8.3				U _{rel,mv} (%)
																		x
																		z

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.

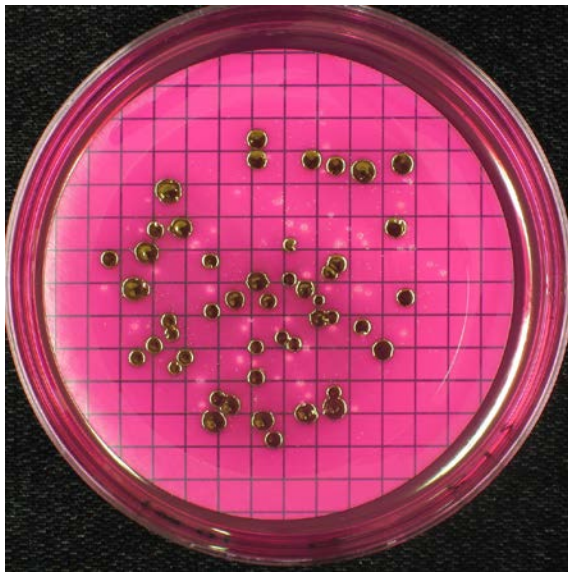
Susp. intestinal enterococci (MF)			Intestinal enterococci (MF)			Susp. Pseudomonas aeruginosa (MF)			Pseudomonas aeruginosa (MF)			Total plate count 22 °C, 3 days			Total plate count 36±2 °C, 2 days			Lab no.	
A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C		
			0.764	-0.353	0.000							-3.776	3.341	-0.162				1131	
				0.046	0.000				-0.276	0.000	-2.332	-1.017	0.080	-1.636				1132	
				-0.085	0.000				0.323	0.000	0.426	0.148	0.080	0.883	-0.202	0.773	1.666	1237	
			0.348	-0.353	0.000				0.778	0.000	-0.567	1.404	-1.660	-0.287	1.835	-3.390	0.378	1254	
			-0.412	0.366	0.000				0.204	0.000	0.001	0.545	1.357	-1.636	0.456	0.196	-1.381	1594	
			0.719	1.615	0.000				1.976	0.000	2.107	-0.708	-1.150	-0.162	-1.710	-2.193	0.378	1611	
			1.066	0.677	0.000				0.778	0.000	1.671	1.520	-0.294	0.501	0.456	0.662	0.378	1753	
			0.679	-4.000	0.000							0.923	1.907	0.600				1868	
			-1.350	-0.085	0.000				-1.176	0.000	-0.686	-0.708	-1.660	0.075	0.202	-1.633	0.378	1970	
			0.299	0.366	0.000				0.323	0.000	2.192	1.046	-0.294	0.972	-0.760	-0.056	-1.381	2050	
			-1.065	-2.321	0.000				-0.438	0.000	-0.221	-0.861	-0.294	0.791	0.940	0.827	0.378	2386	
												-4.000	-0.294		-2.441	-0.255	-1.381	2534	
												0.415	0.754	0.501	0.701	0.662	0.378	2637	
			0.201	1.387	0.000							0.415	2.166	1.146	3.940	0.435	4.000	2670	
			2.997	-0.490	0.000							-0.412	-0.294	-1.636	0.072	-2.609	-1.381	2704	
												-0.559	4.000	-0.557				2745	
			0.049	-1.356	0.000							-0.412	-1.660	-2.259	0.579	0.550	-1.381	2915	
												0.148						3055	
									-0.719	0.000	4.000	-2.228	-1.150	0.187	0.072	-0.056	-1.381	3076	
												0.923	-0.701	-1.408	0.072	0.196	0.378	3145	
			2.346	1.726	0.000							0.887	0.000	1.491	0.545	0.754	1.060	3159	
			-0.678	-0.769	0.000							4.000	0.000	0.927	1.166	2.166	1.060	3162	
			0.939	-1.057	0.000							0.204	0.000	0.217	-0.268	0.080	0.295	3305	
			-0.557	0.303	0.000										-0.708	1.907	-1.025	3339	
			0.348	0.677	0.000										-0.127	-0.701	-0.287	3533	
															0.148	0.427	-0.703	3587	
									0.993	0.000	1.760	0.923	1.637	1.394	0.456	0.376	-1.381	3730	
			0.348	0.303	0.000							0.148	0.427	0.697	0.940	0.009	4.000	3868	
			0.808	0.919	0.000							-2.224	0.000	-2.175	-2.423	-0.294	-2.259	4015	
			0.719	-1.280	0.000							-1.017	0.427	0.501	-2.249	0.196	0.378	4288	
												0.012	0.080	0.075	0.330	0.773	0.378	4319	
			-2.055	0.919	0.000							4.000	0.000	0.001	1.635	0.080	1.060	4339	
			-0.678	-0.353	0.000							-1.374	0.000	0.426	0.799	4.000	2.341	4399	
			-0.018	-0.178	0.000							-1.176	0.000	0.322	-0.559	0.080	0.791	4434	
			0.201	1.156	0.000							-0.172	0.000	-0.932	-0.708	-1.150	-1.907	4356	
			-0.684	0.252	0.000										-0.127	-0.294	0.295	4459	
			-0.003	1.156	0.000										-0.615	0.607	-1.381	4564	
				-0.797								-0.221	-1.508	-1.660	0.791	-0.060	0.662	-1.381	4633
			-0.210	0.417	0.000							0.545	-1.150	-0.041				4723	
			-0.055	-0.490	0.000							-0.719	0.000	0.217	-0.559	0.754	0.697	4889	
			0.537	0.677	0.000							0.887	0.000	0.426	0.545	-0.294	0.883	4980	
				-0.353	0.000							-0.605	0.000	0.001	-0.127	0.080	-0.703	5018	
															-1.341	-0.701	-1.636	5094	
			-1.425	-2.151	0.000							0.778	0.000	-0.932	0.545	0.427	0.187	5120	
			0.100	0.175	0.000							-0.172	0.000	1.582				5188	
															0.012	-1.150	0.075	5201	
															-2.040	0.754	0.075	5352	
			-0.383	-1.665	0.000										-0.412	-0.701	0.600	5447	
			1.232	0.175	0.000										-1.341			5494	
															1.399	0.880	-1.381	5553	
			0.100	-2.321	0.000													5701	
															-1.017	-1.150	-1.207	5858	
			0.245	-0.085	0.000										-0.708	-0.294		5950	
			0.964	1.085	0.000										0.672	0.754	0.295	6175	
															-0.559	4.000	4.000	6180	
			0.629	-0.769	0.000										1.404	0.000	-0.334	6233	
			0.151	0.616	0.000										0.668	0.000	-0.221	6253	
															0.415	0.427	0.400	6456	
															-0.268	-0.701	0.400	6563	
			0.151	0.919	0.000										0.923	1.907	1.705	6686	
			0.049	-1.057	0.000										0.012	0.754	-0.162	6852	
															1.286	-0.056	0.378	7096	
			0.250	-0.912	0.000										0.579	0.134	-1.381	7191	
															-0.472	-0.837	0.378	7248	
			-0.440	-0.407	0.000										-0.559	-1.150		7302	
			0.075	-0.046	0.000										1.404	0.754	-0.419	7330	
			0.151	-4.000	0.000										1.286	-0.294	-0.041	7442	
															-0.472	0.435	0.378	7564	
															0.672	0.080	0.075	7596	
			-2.805	1.038	0.000										0.012	-1.150	-0.858	7688	
			-0.557	-1.665	0.000										0.283	-2.265	-0.162	7706	
			0.537	1.947	0.000										-0.760	-0.701	0.883	7728	
			0.100	-0.490	0.000										-0.576	0.000	-0.450	7876	
			0.434	-0.545	0.000										0.323	0.000	-0.334	7896	
															0.057	0.000	0.217	7930	
															1.166	1.357	-0.858	7946	
															-1.341	-0.701	-1.025	7962	
			0.348	0.677	0.000										0.440	0.000	0.426	7968	
			0.250	0.429	0.000										1.286	-0.701	-1.025	8068	
				-0.628	0.000										-3.038	0.000	0.630	8252	
			-1.205	1.671	0.000										-0.172	0.000		8260	
			-2.234	-0.421	0.000										-0.127	0.754	-0.162	8329	
			0.049	0.303	0.000										0.323	0.000	1.214	8380	
															0.778	0.000	-1.058		
			0.049	1.330	0.000										1.635	0.427	-0.287		
			-0.709		0.000										-1.341	0.080	1.146		
															1.286	-0.701	0.501		
															0.545	0.427	0.400		
															-0.356	0.000	-3.203		
															0.000	-0.109	1.046		
															1.046	1.357	-0.041		

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			
8435					-0.075	-1.050	0.191				1.346	0.000	0.132									
8569					-0.747	0.042	-0.234				-2.917	0.000	-4.000									
8598																						
8626					-0.006	-1.066	1.703				-0.243	0.000	1.430									
8628					-0.361	0.610	-1.165				-0.687	0.000	0.000									
8663					0.261	0.161	-0.840				-0.243	0.000	-0.754	-0.360	-0.477	-0.695	-0.269	0.000	0.000			
8742																						
8766					0.928	-0.527	-0.840				2.052	0.000	-1.177	-0.934	0.313	0.314	-0.617	0.000	0.000			
8809					-1.550	-1.373	0.328				-0.785	0.000	0.000									
8840					0.638	1.118	-0.381				0.797	0.000	-0.359	0.259	0.246	1.913	1.089	0.000	0.000			
8862					1.081	-0.404	-0.840				0.231	0.000	0.000	1.507	-0.068	1.088	-1.195	0.000	0.000			
8891																						
8898					0.758	0.705	-0.381				0.055	0.000	-0.359	-0.875	-0.425	-1.011	-0.770	0.000	0.000			
8955					-0.216	2.648	-0.840				-0.687	0.000	-0.754	-0.360	0.891	0.039	-0.516	0.000	0.000			
8998																						
9002					-1.756	0.278	-1.165				-1.705	0.000	0.000									
9306														0.113	0.457	0.039	2.171	0.000	0.000			
9436					-1.875	-2.110	-1.505				-0.797	0.000	-1.325	-1.188	-2.339	-0.542	-1.305	0.000	0.000			
9441															0.448		-2.215	0.000	0.000			
9524					1.484	0.161	-0.381				0.906	0.000	0.000	-0.134	0.268	-0.542	0.635	0.000	0.000			
9736					0.022	-0.655	0.328				-1.058	0.000	0.249	-0.187	-0.140	1.913	-0.693	0.000	0.000			
9899					1.081	1.214	-0.531				0.007	0.000	0.000	-0.142	0.576	2.137	-0.148	0.000	0.000			
9903					0.945	0.901	0.595				0.036	0.000	0.013									
n					0	0	0	79	78	79	0	0	0	79	80	82	66	66	68	67	67	65
Min					-3.216	-2.824	-4.000				-2.917	0.000	-4.000	-2.636	-2.339	-1.691	-2.215	0.000	0.000			
Max					1.536	2.648	4.000				2.969	0.000	4.000	2.143	3.427	2.569	2.837	0.000	0.000			
Median					0.261	0.102	-0.090				-0.141	0.000	0.000	0.065	0.003	-0.102	0.090	0.000	0.000			
Mean					0.000	0.000	0.000				0.000	0.000	-0.049	0.000	0.000	0.000	0.000	0.000	0.000			
SD					1.000	1.000	1.177				1.000	0.000	1.137	1.000	1.000	1.000	1.000	0.000	0.000			
z<-3					1	0	1				0	0	2	0	0	0	0	0	0			
-3≤z<-2					3	4	0				2	0	1	4	2	0	2	0	0			
-2<z≤3					0	1	3				4	0	4	1	0	4	2	0	0			
z>3					0	0	2				0	0	1	0	1	0	0	0	0			

Susp. intestinal enterococci (MF)			Intestinal enterococci (MF)			Susp. <i>Pseudomonas aeruginosa</i> (MF)			<i>Pseudomonas aeruginosa</i> (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	
			-0.740	-1.057	0.000				-0.438	0.000	-0.221	-0.708	-1.150	-0.703	-0.060	0.607	-1.381	8435
			0.629	1.272	0.000							0.923	0.427	0.697				8569
												0.672	1.357	1.146				8598
												0.545	-1.150	-0.703	-0.060	0.317	1.107	8626
			1.996	0.303	0.000				-0.576	0.000	-0.932	-0.412	-1.150	-0.419	0.202	0.376	0.378	8628
			-1.425	1.038	0.000				0.555	0.000	0.829	0.923	1.357	0.883	0.202	-0.187	1.107	8663
												-0.559	-0.294	-1.408	1.057	0.317	1.107	8742
			-1.176	0.188	0.000				4.000	0.000	-0.450	-0.268	0.080	-0.419	0.701	0.435	0.378	8766
			-1.924	-2.151	0.000							-2.834	-0.294	2.274	-1.710	-0.323	0.378	8809
			-0.055	0.677	0.000							0.545	1.063	1.705	1.399	0.607	3.273	8840
			-2.045	1.191	0.000							0.799	-0.294	-0.703				8862
												1.286	-0.701	-1.207				8891
			0.490	0.175	0.000				0.962	0.000	0.426	1.286	0.080	0.697	0.940	0.435	1.107	8898
			0.981	-0.218	0.000				-0.719	0.000	-0.109	-0.268	1.063	0.075	0.940	0.257	1.107	8955
																		8998
			-0.740	-1.824	0.000							0.415	0.427	0.501				9002
												0.012	0.427	1.060	0.202	1.675	0.378	9306
			-0.629	-0.421	0.000				-4.000	0.000	-4.000	-2.834	-1.150	-2.259	-3.539	-0.759	0.378	9436
												-1.177	-0.294	-1.636	-2.641	-2.193	1.107	9441
			0.817	-0.353	0.000							-0.559	-0.701	0.501	-0.472	-1.633	2.137	9524
			0.647	0.252	0.000				-3.487	0.000	-0.221	0.415	-0.294	-0.419	-0.472	0.376	-1.381	9736
			0.934	0.665	0.000				-0.044	0.000	-0.109	0.012	0.754	-0.162	-0.615	0.607	0.378	9899
			0.532	0.417	0.000				1.599	0.000	0.110	1.046	4.000	1.146	-0.195	-0.323	1.107	9903
0	0	0	72	76	76	0	0	0	55	56	56	101	99	95	81	81	81	n
			-2.805	-4.000	0.000				-4.000	0.000	-4.000	-4.000	-2.265	-2.259	-3.539	-3.390	-1.381	Min
			2.997	1.947	0.000				4.000	0.000	4.000	1.635	4.000	2.341	3.940	4.000	4.000	Max
			0.125	0.111	0.000				0.204	0.000	0.001	0.012	0.080	0.075	0.072	0.317	0.378	Median
			0.000	-0.105	0.000				0.082	0.000	0.000	-0.077	0.242	0.000	0.005	0.049	0.189	Mean
			1.000	1.178	0.000				1.520	0.000	1.243	1.130	1.363	1.000	1.151	1.089	1.284	SD
			0	2	0				3	0	2	2	0	0	1	1	0	Summa
			4	4	0				1	0	2	6	1	3	3	5	0	15
			2	0	0				0	0	2	0	2	2	0	0	1	47
			0	0	0				3	0	1	0	7	0	1	1	4	28
																		21

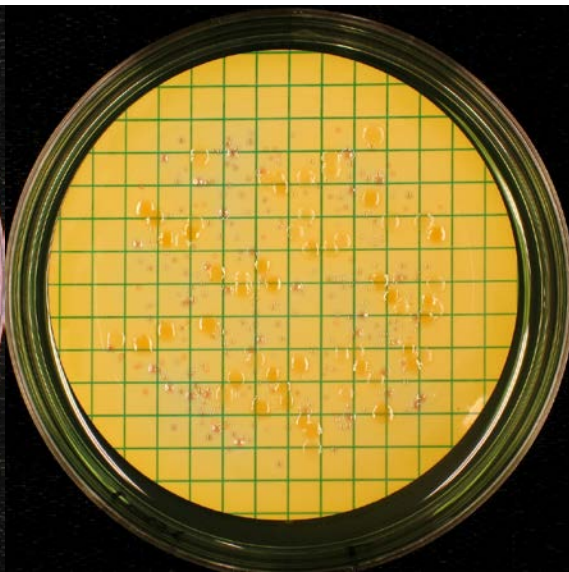
Mixture A

m-Endo Agar LES, 37 °C



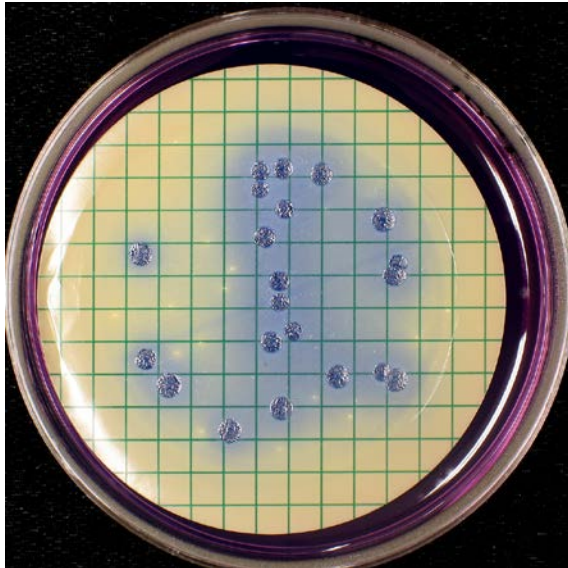
10 ml

m-Lactose TTC Agar, 37 °C



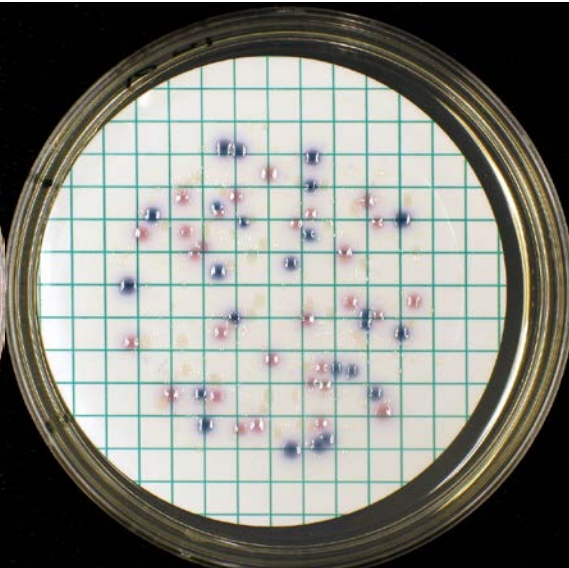
10 ml

m-FC Agar, 44 °C



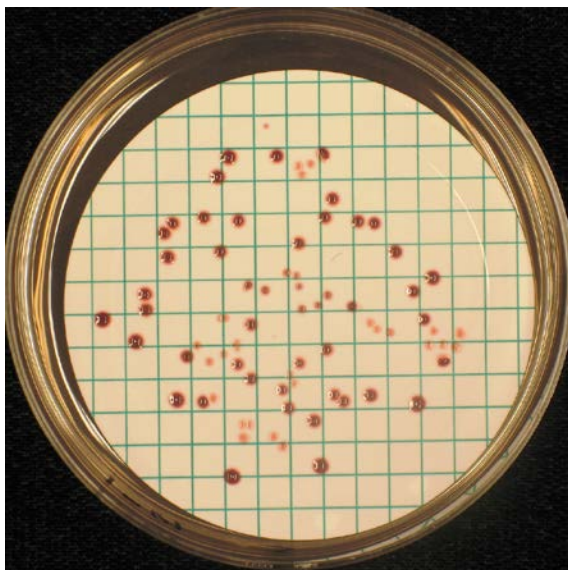
10 ml

Chromocult Coliform Agar, 37 °C



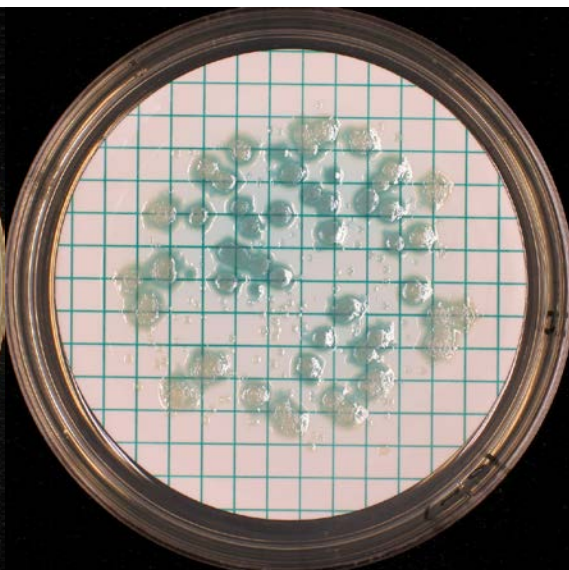
10 ml

m-Enterococcus Agar, 37 °C



10 ml, 2 days

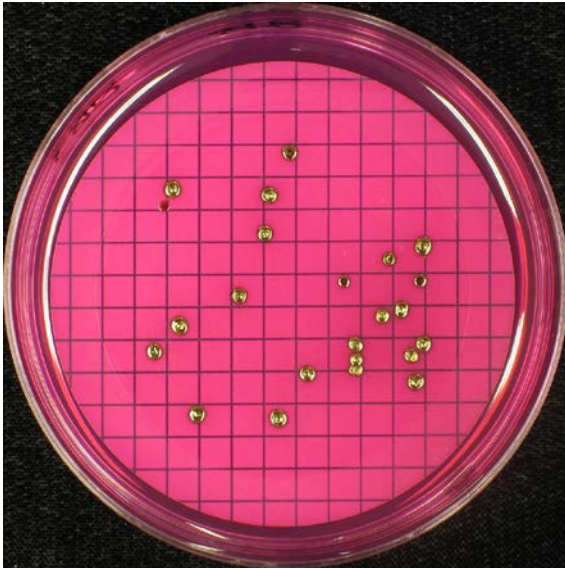
m-Pseudomonas CN Agar, 37 °C



10 ml, 2 days

Mixture B

m-Endo Agar LES, 37 °C

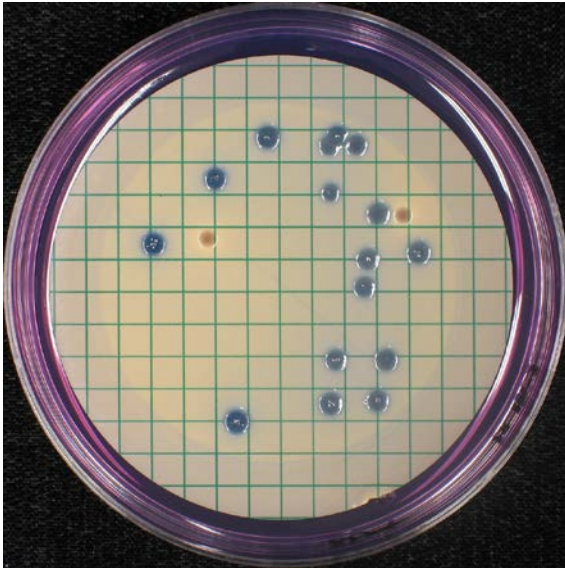


10 ml

m-Lactose TTC Agar, 37 °C

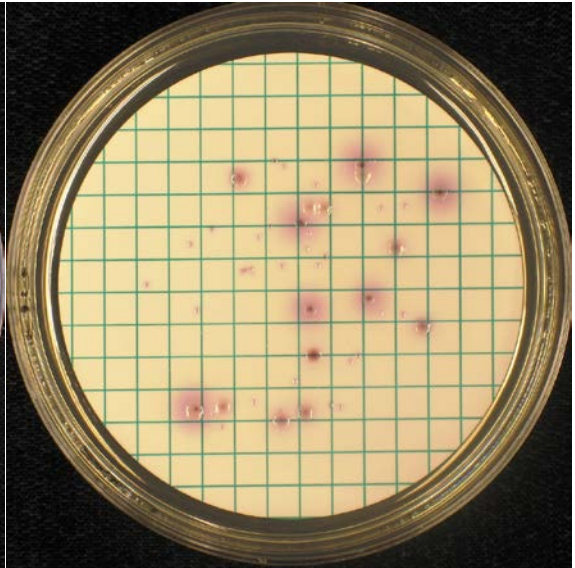
100 ml

m-FC Agar, 44 °C



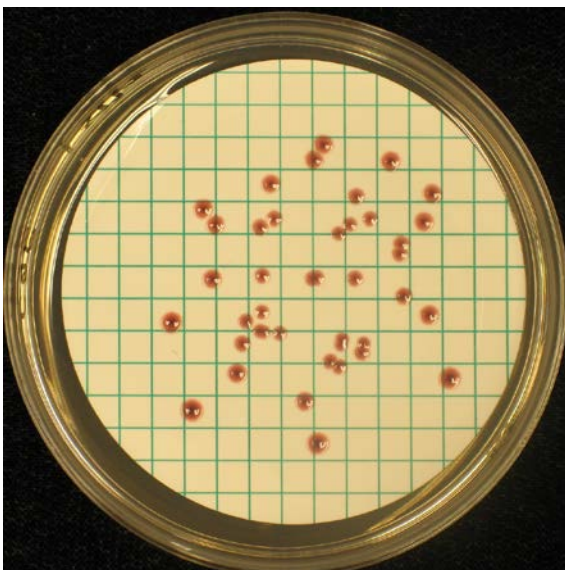
100 ml

Chromocult Coliform Agar, 37 °C



10 ml

m-Enterococcus Agar, 37 °C



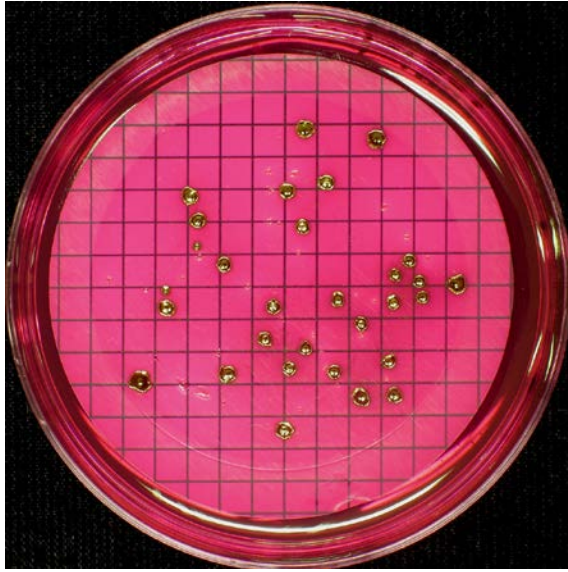
10 ml, 2 days on BEAA

m-Pseudomonas CN Agar, 37 °C

100 ml, 2 days

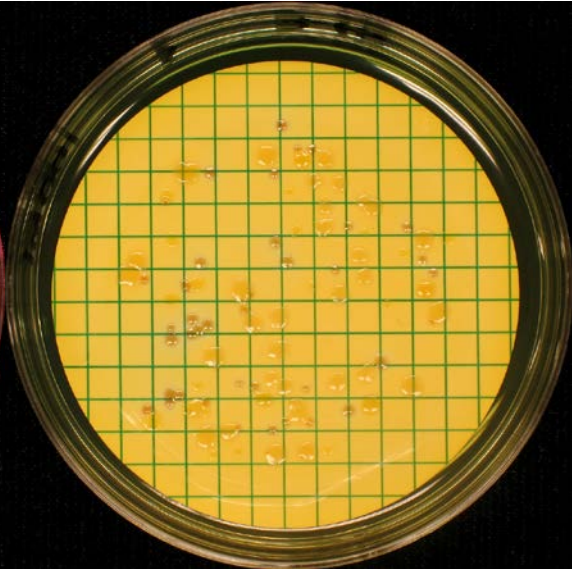
Mixture C

m-Endo Agar LES, 37 °C



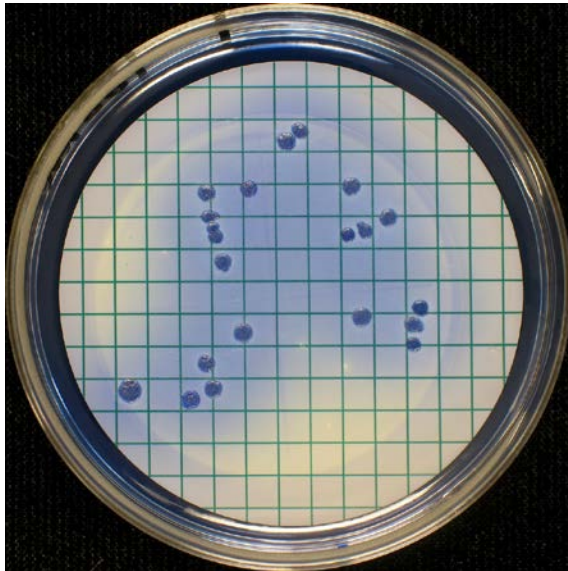
100 ml

m-Lactose TTC Agar, 37 °C



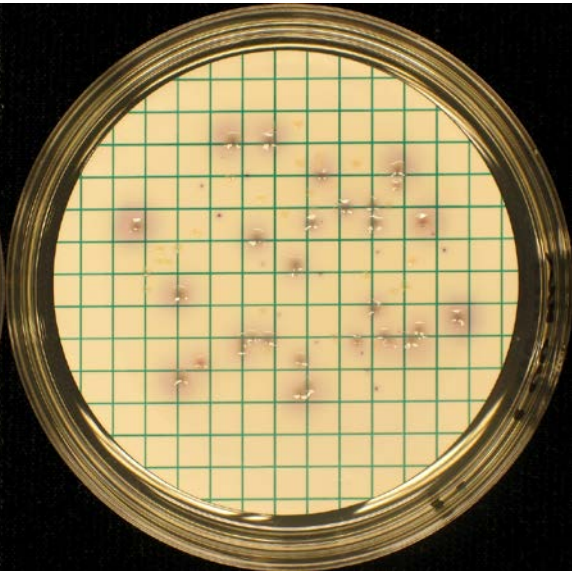
100 ml

m-FC Agar, 44 °C



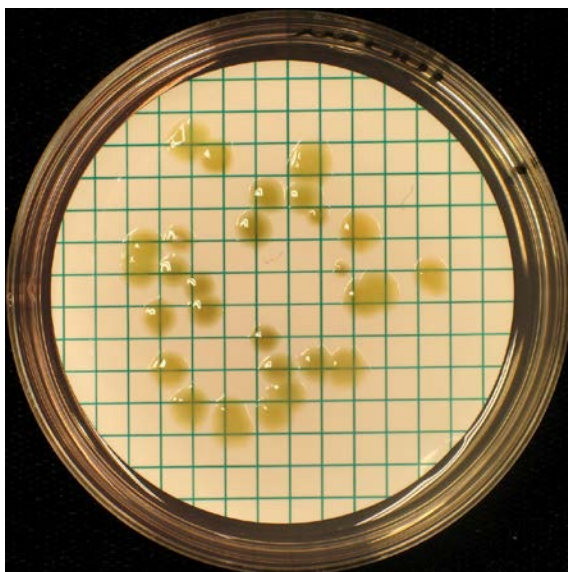
100 ml

Chromocult Coliform Agar, 37 °C



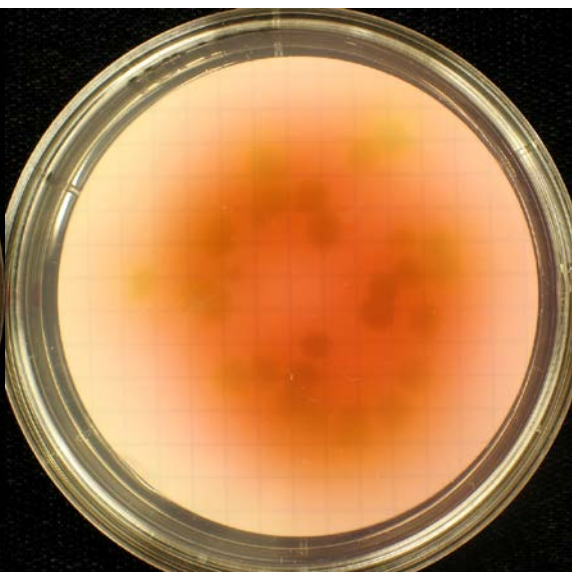
100 ml

m-Pseudomonas CN Agar, 37 °C



100 ml, 2 days

m-Pseudomonas CN Agar, 37 °C



100 ml, 2 days, from back side

PT reports published 2015

Proficiency Testing – Food Microbiology, January 2015

Proficiency Testing – Drinking Water Microbiology, March 2015, by Tommy Šlapokas

Proficiency Testing – Food Microbiology, April 2015

Proficiency Testing – Drinking Water Microbiology, September 2015, by Tommy Šlapokas

Proficiency Testing – Food Microbiology, October 2015

PT reports published 2016

Proficiency Testing – Food Microbiology, January 2016, by Kirsi Mykkänen

Proficiency Testing – Drinking Water Microbiology, March 2016, by Tommy Šlapokas

Proficiency Testing – Food Microbiology, April 2016, by Jonas Ilbäck

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

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

In a proficiency test, identical test material is analysed by a number of laboratories using their routine methods. The laboratories report their results to the organiser that evaluates them and compiles them in a report.

The National Food Agency's PT program offers

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

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

The National Food Agency's reference material

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

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