Proficiency Testing

Drinking Water Microbiology

September 2017

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Livsmedelsverket
National Food Agency

NFA PT
Since 1981

Edition
Version 1 (2017-11-30)

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PT March 2016 is registered as no. 2016/02715 at the National Food Agency, Uppsala

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Accred. no. 1457
Proficiency testing
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 *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
*	result beyond the nearest x-axis limit

Contents

General information on results evaluation

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. Parts of the 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. Although attempts have been made to get rid of it, there are sometimes still inconsistency between the standard referred to and the information given regarding various method details. Results from laboratories with unclear information are usually 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 of the results, it is important that used standards and correct method details are reported.

Outliers and false results for an analysis are not included in the calculation of mean value and measure of dispersion, neither totally or 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 4 or fewer results, more than exceptionally when it is specifically mentioned. However, all results are shown in the method histograms when possible.

The histograms and calculation of outliers are described on page 28 under "Processing of numerical results" with further reference to the scheme protocol (1).

Results of the PT round

General outcome

Test items were sent to 98 laboratories, 36 in Sweden, 54 in other Nordic countries (Faeroe Islands, Greenland and Åland included), 2 more from EU, 2 from the rest of Europe and 4 from countries outside Europe. Results were reported from 91 laboratories.

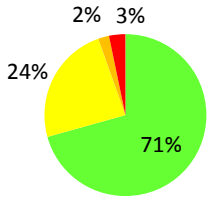
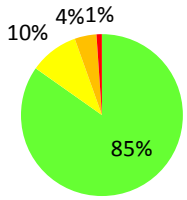
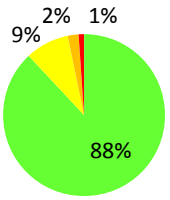
The percentages of false results and outliers are compiled in **table 1**. These deviating results are excluded in most calculations.

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 0 deviating results 1 deviating result 2 deviating results >2 deviating results									
No. of evaluable results	540			534			535		
No. of deviating results *	35 (6 %)			20 (4 %)			16 (3 %)		
Microorganisms	*Escherichia coli (gas-neg.)* *Enterobacter cloacae* *Enterococcus durans* *Burkholderia cepacia* *Staphylococcus capitis*			*Klebsiella pneumoniae* *Serratia marcescens* *Lactobacillus plantarum* *Pseudomonas aeruginosa* *Staphylococcus cohnii*			*Escherichia coli* *Citrobacter freundii* *Enterococcus faecalis* *Pseudomonas aeruginosa*		
Analysis	**Target org.**	**F%**	**X%**	**Target org.**	**F%**	**X%**	**Target org.**	**F%**	**X%**
Coliform bacteria (MF)	*E. coli* *E. cloacae*	1	4	*K. pneumoniae* *{S. marcescens}*	1	3	*E. coli* *C. freundii*	0	4
Susp. thermotolerant coliform bact. (MF)	*E. coli* *[E. cloacae]*	–	–	*K. pneumoniae*	–	–	*E. coli*	–	–
E. coli (MF)	*E. coli*	20#	3	*[K. pneumoniae]*	3	–	*E. coli*	0	1
Coliform bacteria (rapid method)	*E. coli* *E. cloacae*	0	2	*K. pneumoniae* *S. marcescens*	0	0	*E. coli* *C. freundii*	0	0
E. coli (rapid meth.)	*E. coli*	2	2	–	0	–	*E. coli*	0	0
Intestinal enterococci (MF)	*E. durans*	2	2	*[L. plantarum]*	8	–	*E. faecalis*	0	5
Pseudomonas aeruginosa (MF)	*[B. cepacia]*	4	–	*P. aeruginosa*	4	4	*P. aeruginosa*	0	4
Culturable micro-organisms (total count), 3 days 22 °C	*(E. cloacae)* *(B. cepacia)* *(E. durans)* *(E. coli)*	0	1	*S. cohnii* *(S. marcescens)* *(K. pneumoniae)* *(L. plantarum)* *(P. aeruginosa)*	0	5	*E. faecalis* *P. aeruginosa* *E. coli* *C. freundii*	4	4
Culturable micro-organisms (total count), 2 days 36 °C	*S. capitis* *(E. cloacae)* *(B. cepacia)* *(E. durans)* *(E. coli)*	1	7	*S. cohnii* *(S. marcescens)* *(K. pneumoniae)* *(L. plantarum)* *(P. aeruginosa)*	1	1	*E. faecalis* *P. aeruginosa* *E. coli* *C. freundii*	0	1

* In total 36 of 91 laboratories (40 %) reported at least one deviating result; see also the last note below

– 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 are 15 zero results (20 %) that are reckoned as false negative or accepted results dependent on the method used

Coliform bacteria (MF)

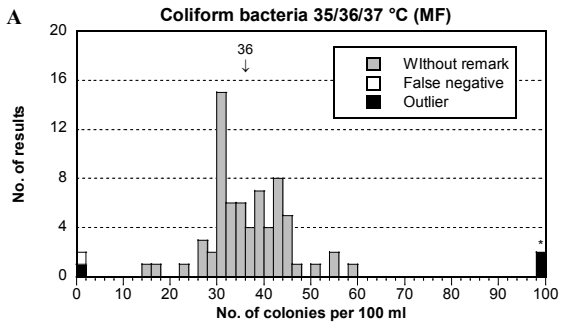
In some cases m-Endo Agar LES (LES) has been used although not prescribed in the standard referred to (ISO 9308-1:2000 or ISO 9308-1:2014). These results have been placed in a separate group, "LES, wrong standard".

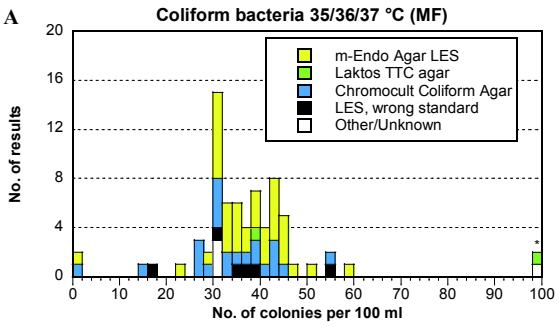
From the table it is clear that LES was used by far more laboratories than other media. The proportion that used CCA is now, as in last spring, considerably higher than in previous years, while the use of LTTC has almost ended. This is logical since CCA has replaced LTTC in the latest edition of EN ISO 9308-1 from 2014.

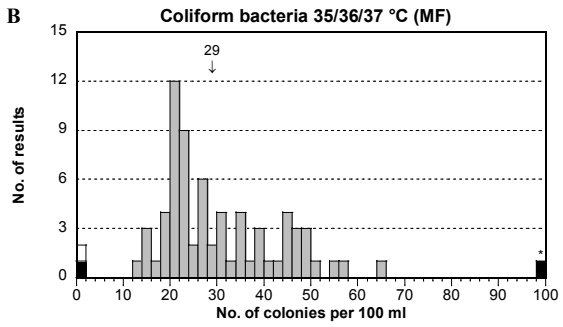
There is an indication that LES gave a somewhat higher mean result compared to CCA, in particular in mixture C. This tendency has been seen in several rounds before. The implication is that CCA has given lower results with many different coliform bacteria that have been present in the samples for some years.

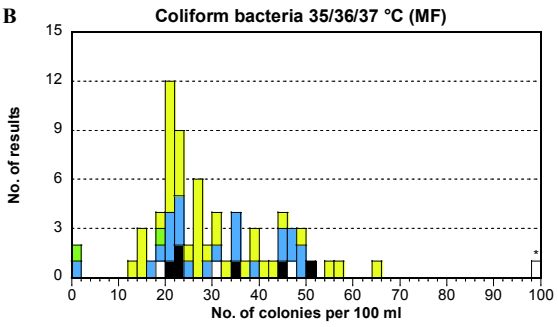
The relative dispersion (CV) varies between both media and mixtures.

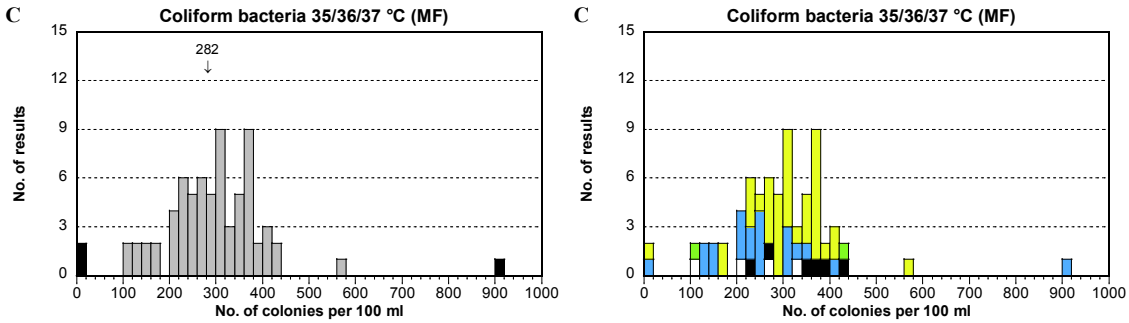
Medium	N	A						B						C					
		n	Mv	CV	F	<	>	n	Mv	CV	F	<	>	n	Mv	CV	F	<	>
Total	72	68	**36**	11	1	1	2	69	**29**	20	1	1	1	68	**282**	16	0	2	1
m-Endo Agar LES	38	37	**37**	9	1	0	0	38	**28**	21	0	0	0	37	**310**	12	0	1	0
LES, wrong standard	6	6	**34**	19	0	0	0	6	**31**	20	0	0	0	6	**334**	12	0	0	0
Lactose TTC Agar	2	1	–	–	0	0	1	1	–	–	1	0	0	2	–	–	0	0	0
Chromocult C Agar	22	21	**34**	13	0	1	0	21	**31**	18	0	1	0	19	**235**	16	0	1	1
Other/Unknown	4	3	–	–	–	0	1	3	–	–	0	0	1	4	–	–	0	0	0











Mixture A

- Two strains of coliform bacteria were included in the mixture. Both *E. coli* and *E. cloacae* 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). The background growth was weak and the analysis was without problem.
- The distribution was good but with four deviating results.

Mixture B

- Two strains of coliform bacteria were included in the mixture. Only *K. pneumoniae* appears with typical colonies with a metallic sheen on LES, yellow on LTTC and pink on CCA at 37 °C. The other strain, *S. marcescens*, appears with small red colonies on LES that would normally not be considered as coming from a coliform bacterium. On CCA the colonies are fairly small but with a light pink tone, indicating that they might come from a coliform bacterium.
- Hence, it is reasonable that laboratories using LES obtained lower results than those using CCA. However, this is not perfectly obvious but there is a tendency. Two phenomena seem to counteract each other. There are results for LES that seem to include *S. marcescens* (the rightmost, small histogram peak) and there are laboratories using CCA that seem not to have included *S. marcescens* among the coliform bacteria, but rather have reported results that correspond to *K. pneumoniae* alone (the large, leftmost peak).
- As most laboratories, however, seem to have excluded *S. marcescens*, the average count should be lower with MF compared to the rapid method used (Colilert®; page 14). This is also the case, 29 versus 50 cfu per 100 ml.
- The result outcome with two peaks and the varied interpretations resulted in a broad distribution. However, 2 low and 1 high result were obvious outliers.

Mixture C

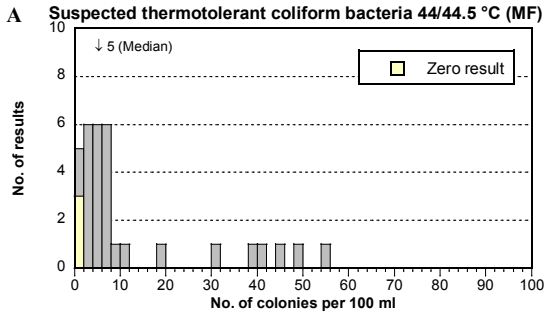
- Two strains of coliform bacteria were present in the mixture. Both *E. coli* and *C. freundii* grow with typical colonies, with a metallic sheen on LES, yellow on LTTC and bluish and pink, respectively, on CCA at 37 °C (see annex C). Some background flora was present but the analysis was in principle without problem.
- The distribution was fairly good but three deviating results were seen.

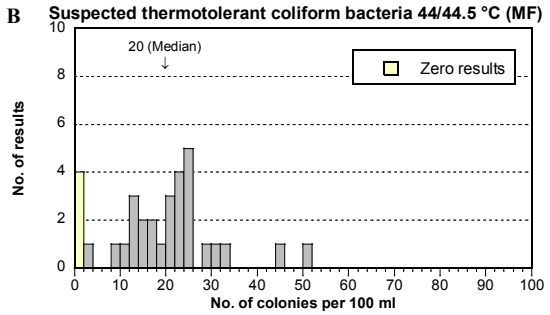
Suspected thermotolerant coliform bacteria (MF)

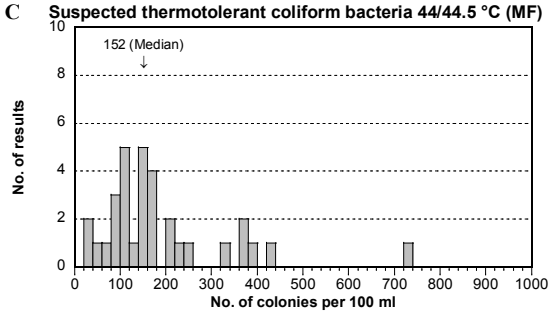
The parameter is not included in performance assessment since only suspected (not confirmed) colonies are asked for. Therefore, no identification of outliers excluded in calculations is done. The *medians* are then more robust than the means and are given in the table and histograms.

The only growth medium that for sure has been used this time is m-FC agar. The incubation temperature is 44 or 44.5 °C. Because all old method details were removed from the dataset as a preparation for the March round and since it was not mandatory to report method details for this parameter, only 12 laboratories using m-FC have done this. Two of them used 44.5 °C. Thus, any method evaluation by grouping is meaningless.

No grouping	N	A						B						C					
		n	Med	CV	F	<	>	n	Med	CV	F	<	>	n	Med	CV	F	<	>
Total	32	32	**5**	–	–	–	–	32	**20**	–	–	–	–	32	**152**	–	–	–	–







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 but no such results were recorded. A strain of *E. cloacae*, which may appear as a (suspected) thermotolerant coliform bacterium with small blue colonies on m-FC, was also included.
- The median was only 5 cfu per 100 ml resulting in a distribution close to zero, where also the zero results are reasonable. There were further 7 higher results probably indicating the growth and inclusion also of *E. cloacae*.

Mixture B

- *K. pneumoniae* was the only thermotolerant coliform bacterium in the mixture. Many unexpected low results were seen compared even to the leftmost peak for coliform bacteria MF (page 6). One reason may be that incubation of m-FC at 44/44.5 °C often gives lower results for a strain than incubation at 37 °C on media for coliform bacteria.
- However, this is not the complete truth as 4 laboratories even recorded zero results. Most likely some kind of confirmation has been performed, e.g. test for gas production, as a criterion as to state whether the colonies are from a thermotolerant coliform bacterium or not. However, such a characterization should not be done for suspected thermotolerant coliform bacteria, but only when the results should be characterized as (confirmed) thermotolerant coliform bacteria, according to some standards (but not the Swedish one).

Mixture C

- The strain of *E. coli* appears as a suspected thermotolerant bacterium with blue colonies on m-FC at 44/44.5 °C. The corresponding colonies are dark yellow on LTTC but no such results were recorded. The strain of *C. freundii* is usually not seen at 44 °C but may appear with small colonies when the temperature is too low. The small histogram peak to the right may originate from inclusion of *C. freundii*.
- No zero results were obtained.

Escherichia coli (MF)

To identify and quantify *E. coli* from the primary media LES, LTTC and m-FC, confirmation must be done, irrespectively if the plates are incubated at 36±2 °C or at 44/44.5 °C. Depending on the method, test of either indole production or *β*-glucuronidase activity of oxidase negative presumptive colonies is used as necessary confirmation. Violet to blue colonies on CCA means positive *β*-glucuronidase activity and is registered as confirmed *E. coli*.

The primary growth media CCA, LES as well as LTTC are used at 36±2 °C and LTTC or m-FC at 44/44.5 °C. The results are here separated in groups based on the used standard. For the standards from the Nordic countries (SS, SFS, NS) the majority of the results are from 36±2 °C but some also from 44/44.5 °C. The results are additionally grouped based on reported incubation temperature.

Groups based on media with the incubation stated to 36±2 °C are shown in a separate table.

There is a small indication that the concentrations in mixture A and C are the highest when incubation temperature was 36±2 °C. The few results with Norwegian standard (NS 4792) indicate a somewhat lower recovery. The reason for this may be incubation in some laboratories at 44.5 °C, which is an option in the standard but will lead to a higher selective pressure than at 44 °C. It is stated in the table that 15 false negative results were present in mixture A. Some of these may, however, be acceptable, see below under Mixture A.

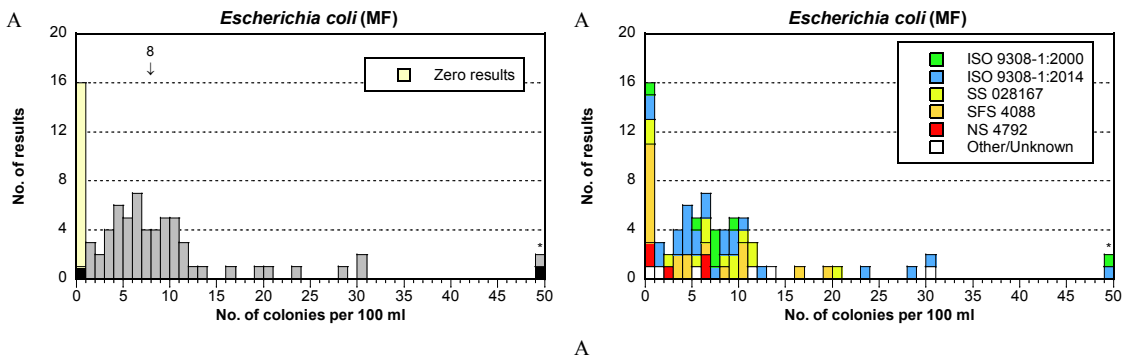
All results

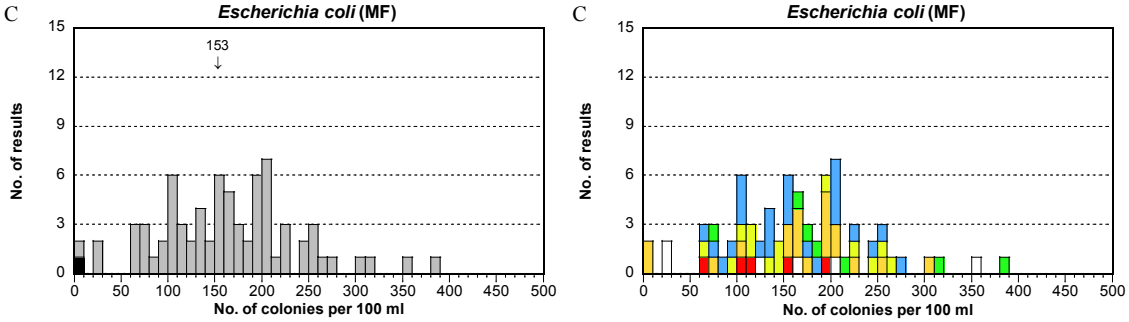
Origin &Standard	N	A						B						C					
		n	Mv	CV	F	<	>	n	Mv	CV	F	<	>	n	Mv	CV	F	<	>
Total	75	58	**8**	41	15	1	1	73	**0**	–	2	–	–	73	**153**	25	0	1	0
Colony origin																			
36 ± 2 °C	40	32	**9**	37	8	0	0	39	**0**	–	1	–	–	39	**166**	24	0	0	0
44/44.5 °C	14	10	**8**	53	4	0	0	13	**0**	–	1	–	–	14	**125**	30	0	0	0
36 ± 2 & 44/44.5 °C	12	8	**5**	37	3	0	1	12	**0**	–	0	–	–	12	**141**	24	0	0	0
Other/Unknown	9	8	**7**	44	0	1	0	9	**0**	–	0	–	–	8	**161**	22	0	1	0
Standard																			
ISO 9308-1:2000	7	6	**11**	53	1	0	0	7	–	–	0	–	–	7	**201**	25	0	0	0
ISO 9308-1:2014	25	22	**7**	44	2	0	1	23	**0**	–	2	–	–	24	**149**	20	0	0	0
SS 028167	13	11	**8**	27	2	0	0	13	**0**	–	0	–	–	13	**155**	21	0	0	0
SFS 4088	19	11	**8**	32	7	1	0	19	**0**	–	0	–	–	18	**162**	25	0	1	0
NS 4792	5	3	**4**	28	2	0	0	5	**0**	–	0	–	–	5	**119**	20	0	0	0
Other/Unknown	6	5	**10**	53	1	0	0	6	–	–	0	–	–	6	**122**	49	0	0	0

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

Medium	N	A						B						C					
		n	Mv	CV	F	<	>	n	Mv	CV	F	<	>	n	Mv	CV	F	<	>
Total	***39#***	***31***	***9***	***35***	***8***	***0***	***0***	***38***	***0***	***–***	***1***	***–***	***–***	***38***	***166***	***24***	***0***	***0***	***0***
m-Endo Agar LES	27	21	**10**	37	6	0	0	27	**0**	–	0	–	–	27	**174**	25	0	0	0
Lactose TTC Agar	0	0	–	–	0	–	–	0	**0**	–	0	–	–	0	–	–	–	–	–
Chromocult C Agar	12	10	**7**	21	2	0	0	11	**0**	–	1	–	–	11	**146**	20	0	0	0
Other/Unknown	0	0	–	–	–	–	–	0	–	–	–	–	–	0	–	–	–	–	–

Compare table above – one more laboratory performed the analysis of *E. coli* at 36±2 °C but not of coliform bacteria





Mixture A

- One strain of *E. coli* with normal *β*-glucuronidase activity and indole production but no gas production from lactose fermentation was present in the mixture. It appears with typical colonies on the various primary growth media, see annex C.
- Fifteen zero results were recorded among the 75 results. Even though the average without the zero results was so low (8 cfu/100 ml) that an individual zero result would be possible by chance, the large numbers of zero results are not explained. Only 2 zero results were obtained by CCA. All other zero results were from methods based on lactose fermentation. **If gas production is a crucial criterion to be judged as *E. coli*, these zero results have to be reckoned as acceptable although they are here stated as false negative results.** In many countries, e.g. Sweden, there is no requirement for gas test. Zero results under such circumstances, as well as from CCA, must be seen as strict false negative values. Only 9 of the laboratories with zero results have stated the use of a gas test.
- The dispersion was good except the 15 zero results that is handled separately. Beside these zero results there were one low and one high outlier.

Mixture B

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

Mixture C

- One typical *E. coli* strain was included. It possesses *β*-glucuronidase activity, indole production and also gas production. It grows with typical colonies on the various primary growth media,
- The average concentration of 153 cfu/100 ml is much lower than the corresponding one from the rapid method, 190 cfu/100 ml. The distribution of the results is also very broad with quite many low results. The average was here for *E. coli* as low as for suspected thermotolerant coliform bacteria, despite that the majority of the laboratories got their *E. coli* results from plates incubated at 35/36/37 °C, where a higher average recovery is expected. This indicates bad recovery of this *E. coli* strain in many laboratories irrespectively of the method used. But in particular, the group NS 4792 and the group Other/Unknown are giving low results.
- One low outlier was present. The dispersion of the broad distribution is medium, which is not unusual when various methods are used for analysis of *E. coli*.

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

The rapid methods used for both these parameters were exclusively Colilert® Quanti-Tray® from the manufacturer Idexx Inc. with incubation at 35, 36 or 37 °C. Out of the 62 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, which not are "Quanti-Trays"). The laboratories often analysed both diluted and undiluted samples. Yellow wells (ONPG positive; with *β*-galactosidase activity) will be interpreted as coliform bacteria and yellow wells also exhibiting fluorescence (MUG positive; with *β*-glucuronidase activity) will be interpreted as *E. coli*.

The maximum incubation time is a bit vague for some laboratories. Only 3 of them have incubated 23-24 hours, out of which 2 stated the use of "Colilert 24 hours". The average for this group was due to that (see below) lower than for the groups that incubated up to 20 or 22 hours. No difference was seen between those two groups.

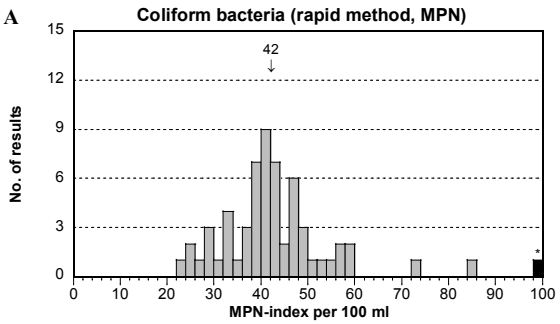
Neither for coliform bacteria nor for *E. coli* there is a tendency for trays with 51 wells to give lower average recovery than for trays with 97 wells. Such a tendency has sometimes been seen. Despite only 2 results, the averages for "Colilert 24 hours" are shown as they were lower than the results for other groups in all mixtures.

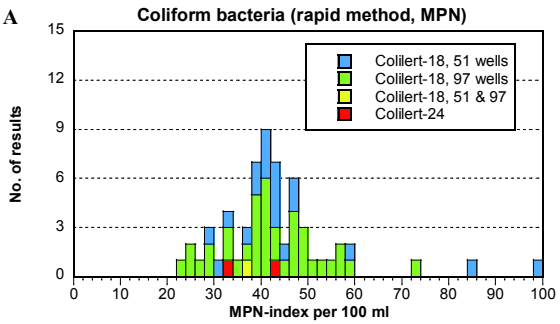
Coliform bacteria, Rapid method with MPN

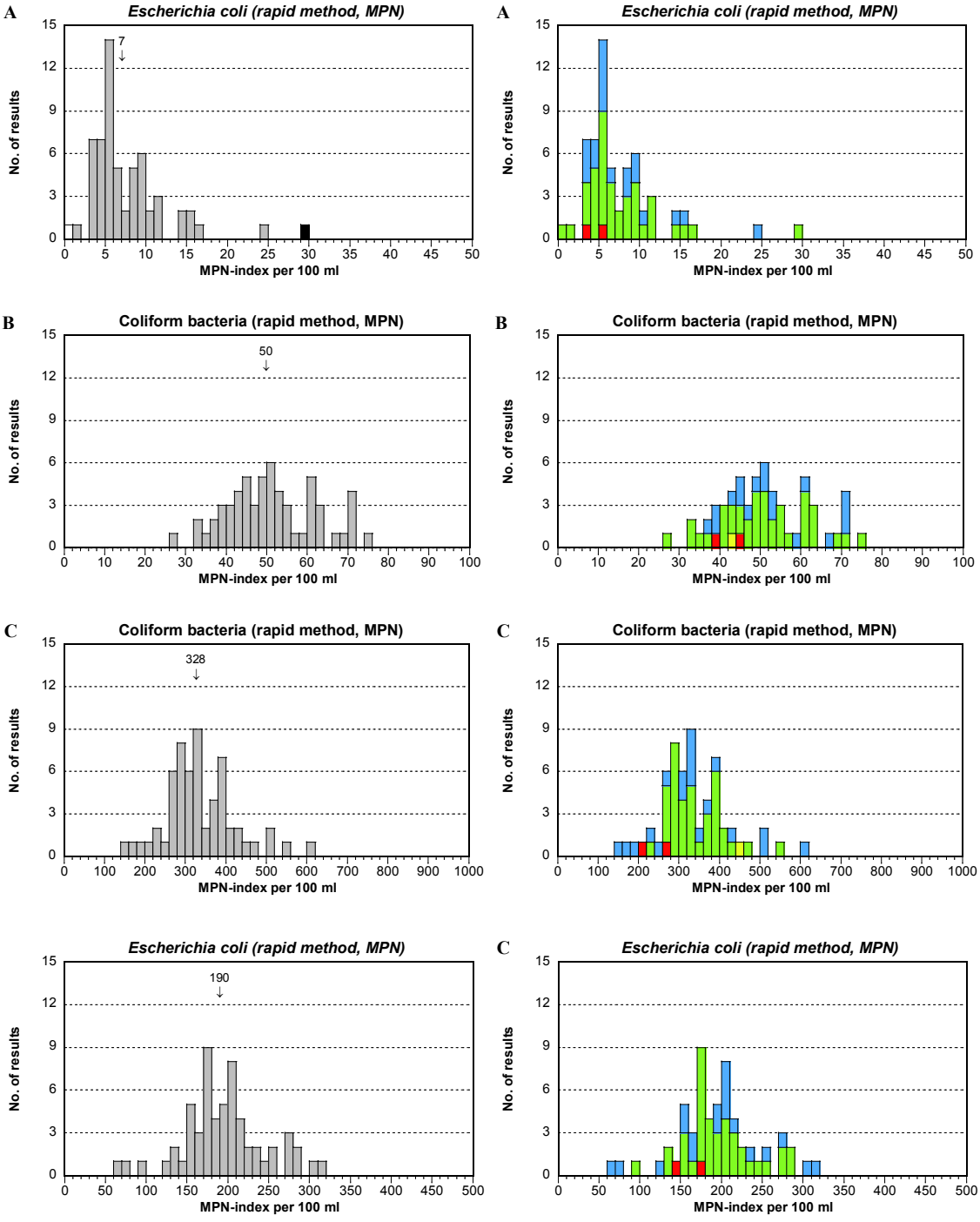
Principle	N	A						B						C					
		n	Mv	CV	F	<	>	n	Mv	CV	F	<	>	n	Mv	CV	F	<	>
Total, Rapid meth.	60	59	**42**	13	0	0	1	59	**50**	11	0	0	0	59	**328**	13	0	0	0
Colilert-18, 51 wells	19	18	**43**	13	0	0	1	18	**52**	11	0	0	0	19	**321**	18	0	0	0
Colilert-18, 97 wells	38	38	**41**	13	0	0	0	38	**50**	11	0	0	0	37	**334**	9	0	0	0
Colilert-18, 51 & 97	1	1	–	–	0	0	0	1	–	–	0	0	0	1	–	–	0	0	0
Colilert-24, ? wells	2	2	**38**	–	0	0	0	2	**42**	–	0	0	0	2	**242**	–	0	0	0
Wrong method	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.	60	58	**7**	28	1	0	1	59	**0**	–	0	–	–	59	**190**	14	0	0	0
Colilert-18, 51 wells	19	19	**7**	32	0	0	0	18	**0**	–	0	–	–	19	**187**	19	0	0	0
Colilert-18, 97 wells	39	37	**7**	25	1	0	1	39	**0**	–	0	–	–	38	**194**	11	0	0	0
Colilert-18, 51 & 97	0	0	–	–	–	–	–	0	–	–	–	–	–	0	–	–	–	–	–
Colilert-24, ? wells	2	2	**4**	–	0	0	0	2	**0**	–	0	–	–	2	**157**	–	0	0	0







Mixture A

- The strains of *E. coli* and *E. cloacae* 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 high outlier was present both for coliform bacteria and *E. coli*, as well as one false negative result for *E. coli*.
- The averages are as usual in general somewhat higher than for the MF methods.

Mixture B
- There was no *E. coli* in the mixture. Instead there were two other members present of the group coliform bacteria, *K. pneumoniae* and *S. marcescens*. They possess *β*-galactosidase but not *β*-glucuronidase and are thus detected as coliform bacteria.
- *S. marcescens* is detected as a coliform bacterium by this method but not by all MF methods. The strain possesses *β*-galactosidase but is bad at producing aldehyde and acid from lactose fermentation. Therefore, the average result is here much higher than by use of the MF methods based on lactose fermentation.
- No deviating results were present for coliform bacteria and no false positive ones for *E. coli*.

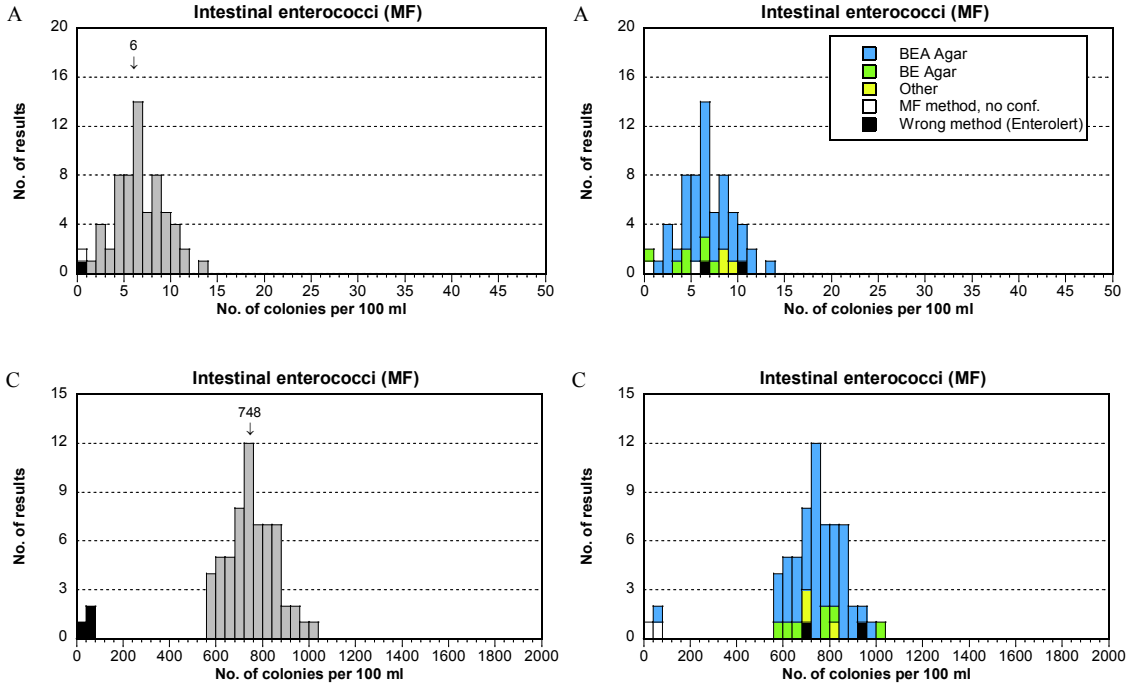
Mixture C
- In this mixture the coliform bacteria *E. coli* and *C. freundii* were present. Both of them possess the enzyme *β*-galactosidase and are detected as coliform bacteria but only *E. coli* has the enzyme *β*-glucuronidase and is detected as *E. coli*.
- No deviating results were present.
- The averages were also for this mixture higher than for the MF methods.

Intestinal enterococci (MF)

The method used for intestinal enterococci is almost exclusively EN ISO 7899-2:2000. Only in 3 cases has another method reference, like national standards or manufacturers instruction been stated. m-Enterococcus Agar (Slanetz & Bartley), here designated m-Ent, has been used as primary medium except in 5 cases. Out of these five, the method Enterolert®-DW (Idexx Inc.) has been used in one case and Enterolert®-E (Idexx Inc.) in another, in spite of not being MF methods.

The incubation temperature for the MF methods was always 35, 36 or 37 °C, except in one case with Rapid Enterococcus Agar where it was 44 °C. Thus, the method for presumptive intestinal enterococci is not different for the vast majority of the 64 results obtained. Method differences are, therefore, most seen in the confirmation step. Confirmation was performed in all cases except 2 where ISO 7899-2:2000

Confirmation medium	N	A						B						C					
		n	**Mv**	CV	F	<	>	n	**Mv**	CV	F	<	>	n	**Mv**	CV	F	<	>
Total	64	62	**6**	22	1	1	0	58	**0**	–	5	–	–	61	**748**	7	0	3	0
Acc. to ISO 7899-2	*62*	*60*	***6***	*22*	*1*	*1*	*0*	*56*	***0***	–	*5*	–	–	*59*	***746***	*7*	*0*	*1*	*0*
BEA Agar	50	50	**6**	23	0	0	0	45	**0**	–	4	–	–	49	**746**	7	0	1	0
BE Agar	7	6	**5**	16	1	0	0	7	**0**	–	0	–	–	7	**744**	9	0	0	0
Other/Unknown	3	3	–	–	0	0	0	3	**0**	–	0	–	–	3	–	5	0	0	0
No confirmation	2	1	–	–	0	1	0	1	**0**	–	1	–	–	0	–	–	0	2	0
Wrong method	*2*	*2*	–	–	*0*	*0*	*0*	*2*	***0***	–	*0*	–	–	*2*	–	–	*0*	*0*	*0*



was stated. In 83 % it was performed with Bile-esculin-azide agar (BEA Agar) as stated in EN ISO 7899-2:2000, in 12 % performed on Bile-esculin agar (BE Agar; without azide) and in 5 % by other means. The temperature for confirmation was in 90 % of the laboratories 44 °C, in 2 % less than 44 °C and in 8 % it was 44.5 °C. No difference can be seen for BE Agar compared to BEA Agar. The two "wrong" methods in the table are the two types of Enterolert® used.

Mixture A

- A strain of *E. durans* was present in the mixture. The distribution of the results was good but with medium dispersion as the average concentration was low, 6 cfu per 100 ml. The colonies are brown-red on m-Ent and are normally confirmed without problem.
- Two low deviating results were obtained, one of which was false negative.

Mixture B

- No enterococcus strain was included but a strain of *Lactobacillus plantarum* grew on m-Ent with small light coloured colonies.
- Five false positive results were reported even though the appearance of the colonies was unlike that of intestinal enterococci.

Mixture C

- A strain of *E. faecalis* was present and the result distribution was good. The dispersion was very low. The colonies have a dark brown-red colour on m-Ent and there is normally no confirmation problem.
- Three low outliers were present. An explanation may be that some laboratories forgot to convert their count to the proper reference volume, 100 ml.

Pseudomonas aeruginosa (MF)

EN ISO 16266:2008 with or without modification was used by 46 out of the 53 laboratories reporting results Some laboratories have as reference stated the identical, but since long time withdrawn CEN standard EN 12780:2002, with or without modification. Pseudalert® (Idexx Inc.) has been used in five cases. Incubation has in two cases with Pseudalert® been done at 38 °C, but in all other cases at 35, 36 or 37 °C for both the MF method and Pseudalert®.

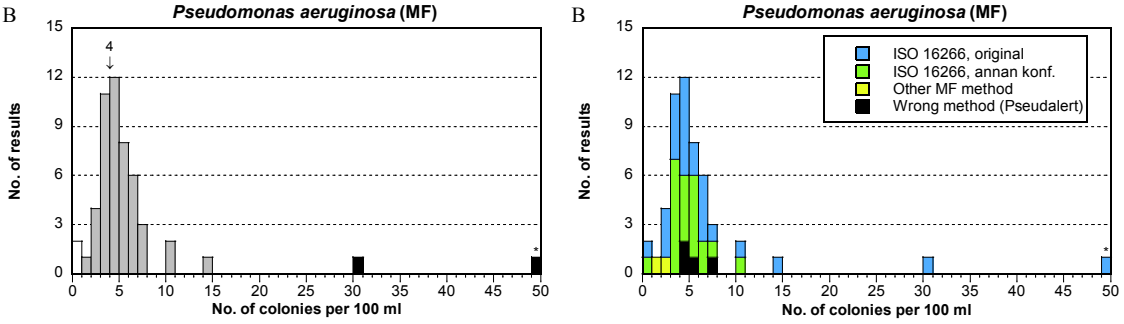
Because unhealthy substances like mercury are included, many laboratories have replaced the confirmation tests in the standard, by some other method. The major modification of the method, therefore, concerns the confirmation. When only typical yellow-green to blue-green colonies are present, no confirmation need to be done. In those cases there is no principal difference between what is counted whether "mod." is stated for the method or not. The colonies in both mixtures B and C were quite typical without any demand for confirmation. This may explain that no difference was seen between "modified" or "original" in the table.

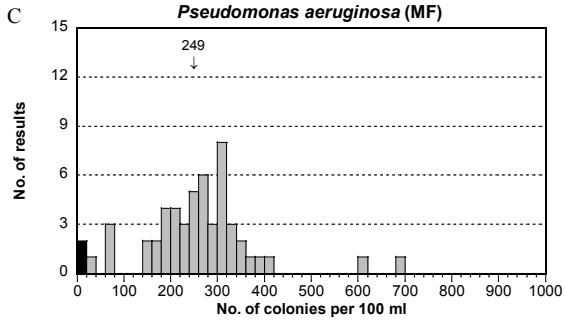
The five laboratories with "wrong" method in the table used Pseudalert® and those results are given as information. In mixture C the average by that method was much lower than by the MF methods.

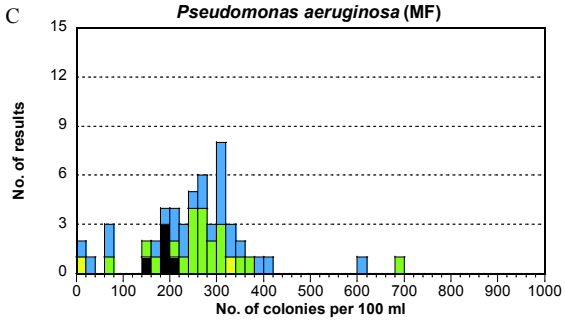
Standard/Method	N	A						B						C					
		n	Mv	CV	F	<	>	n	Mv	CV	F	<	>	n	Mv	CV	F	<	>
Total	53	51	**0**	–	2	–	–	48	**4**	24	2	0	2	51	**249**	23	0	2	0
Membrane filtration	*48*	*46*	***0***	–	*2*	–	–	*44*	***4***	*24*	*2*	*0*	*2*	*46*	***256***	*23*	*0*	*2*	*0*
ISO 16266 [a]	25	23	**0**	–	2	–	–	22	**5**	26	1	0	2	24	**248**	26	0	1	0
ISO 16266, mod. [b]	21	21	**0**	–	0	–	–	20	**4**	18	1	0	0	21	**263**	20	0	0	0
Other	2	2	**0**	–	0	–	–	2	–	–	0	0	0	1	–	–	0	1	0
Wrong method, Pseudalert®, MPN	*5*	*5*	***0***	–	*0*	–	–	*4*	***5***	*14*	*0*	*0*	*0*	*5*	***185***	*6*	*0*	*0*	*0*

a Includes also EN 12780:2002; confirmation performed according to the original standard description

b Includes also EN 12780:2002; alternative confirmation performed, e.g. Maldi-TOF, API







Mixture A

- There was no *P. aeruginosa* in the mixture but yet two false positive results were reported.

Mixture B

- One strain of *P. aeruginosa* with quite typical but pale yellow-green colonies on PACN was included. The colonies showed a clear fluorescence under UV light. Usually, confirmation is not necessary.
- The distribution of the results was good despite the low average concentration. However, it caused a medium-sized relative dispersion (CV).
- Two false negative results and two high outliers were present. The false negative results were identified as low outliers but could possibly as an individual case have been obtained by pure chance.

Mixture C

- One strain of *P. aeruginosa* with typical, blue-green colonies on PACN was included in the mixture. The colonies showed clear fluorescence under UV light. No confirmation was necessary according to the standard.
- The distribution of the results was fairly broad, especially on the lower side where an unexpected tail with low results was seen. An explanation to some of them may be that some laboratories forgot to convert their count to the proper reference volume, 100 ml. In this mixture, the broad distribution leads to a medium-sized dispersion.
- One low and on high outlier was present.

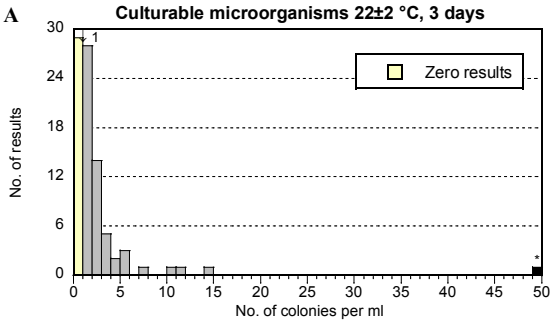
Culturable microorganisms 22 °C, 3 days

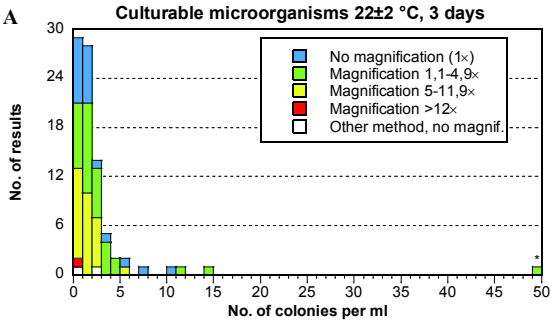
Eighty four of the 86 laboratories performing the analysis reported EN ISO 6222:1999 as method, which prescribes the use of Yeast extract Agar. Six laboratories used Plate Count Agar in combination with this standard. Two laboratories used Standard Methods Agar (5) together with Yeast extract Agar, and in one of these cases by the spread plate technique. They are included in the group "Other standard" in the table. Another laboratory has reported the use of spread plate technique together with EN ISO 6222:1999.

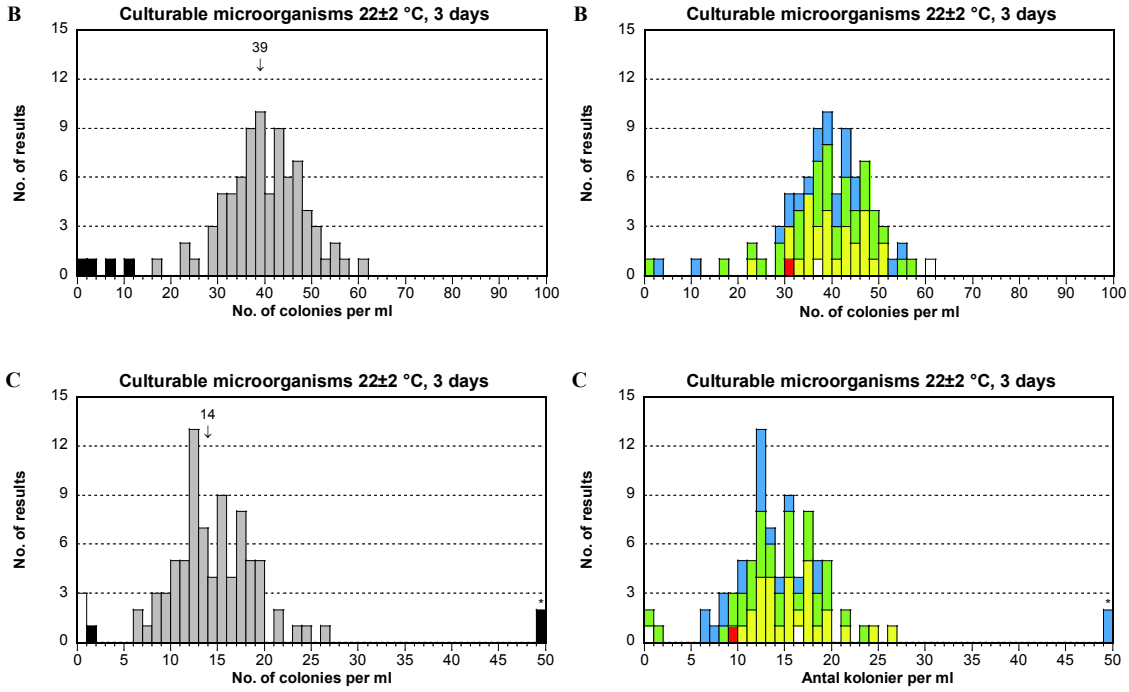
Comparisons of method variants are relevant to discuss only in connection to EN ISO 6222:1999. Results are given for culture media and magnification for reading.

For mixture A the group averages are too low to see any differences. For mixture B there are no differences. For mixture C perhaps somewhat lower results were obtained without magnification compared to when magnification was used.

Group of results	N	A						B						C					
		n	Mv	CV	F	<	>	n	Mv	CV	F	<	>	n	Mv	CV	F	<	>
Total, all results	86	85	**1**	90	0	0	1	81	**39**	11	0	4	0	79	**14**	15	3	1	2
EN ISO 6222	*84*	*83*	***1***	*90*	*0*	*0*	*1*	*79*	***39***	*10*	*0*	*4*	*0*	*78*	***14***	*15*	*2*	*1*	*2*
Medium																			
Yeast extract Agar	78	77	**1**	88	0	0	1	74	**39**	11	0	3	0	73	**14**	14	2	0	2
Plate Count Agar	6	6	**0**	113	0	0	0	5	**40**	5	0	1	0	5	**12**	20	0	1	0
Other/Unknown	0	0	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
Magnification																			
None	20	20	**1**	105	0	0	0	18	**39**	9	0	2	0	18	**11**	17	0	0	2
1,1–4,9×	34	33	**1**	79	0	0	1	32	**39**	13	0	1	0	31	**14**	13	1	1	0
5–11,9×	28	28	**1**	89	0	0	0	28	**39**	9	0	0	0	28	**15**	12	0	0	0
> 12×	1	1	–	–	0	0	0	1	–	–	0	0	0	1	–	–	0	0	0
Other/unknown	1	1	–	–	0	0	0	0	–	–	0	1	0	0	–	–	1	0	0
Other method	*2*	*2*	–	–	*0*	*0*	*0*	*2*	–	–	*0*	*0*	*0*	*1*	–	–	*1*	*0*	*0*







Mixture A

- The rather few colonies are made up of all the strains except *S. capitis*.
- The distribution of the results was good. Zero is here an acceptable result. Due to the low concentration, the relative dispersion (CV) was very large.
- One high outlier was present. This indicates that the incubation temperature in all other cases has been low enough not to cause *Staphylococcus capitis* to grow. It grows well in the corresponding analysis at 36±2 °C. At what temperature it starts to become visible is not checked.

Mixture B

- The colonies of culturable microorganisms are mainly made up of *Staphylococcus cohnii*. The other four strains will also grow but each with <1 cfu per ml.
- The distribution was good except for a tail with some low results. Four of these were low outliers. This resulted in keeping a small relative dispersion. There is no clear reason for the low results.

Mixture C

- The colonies are almost entirely made up of *Enterococcus faecalis* but also some colonies of the coliform bacteria and *P. aeruginosa* will be seen.
- The distribution of the results was good except for the 6 deviating results. Tree of these were false negative results and 1 was low and two were high outliers. There are no obvious reasons for the deviating results.

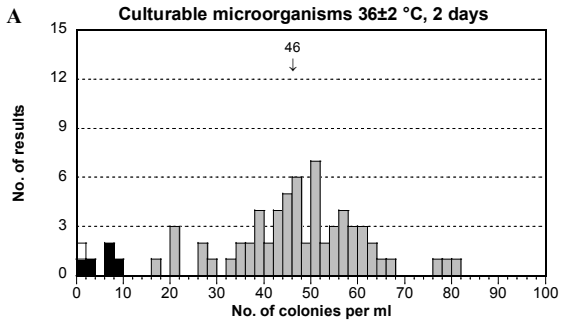
Culturable microorganisms 36 °C, 2 days

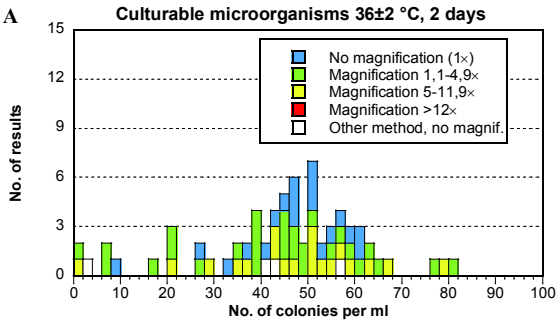
Sixty six of the 70 laboratories have stated the use of EN ISO 6222:1999. Two of the laboratories in the group "Other method" in the table have stated Standard Methods (5) while the other two have not stated any standard. Four laboratories have reported Plate Count Agar, out of which three in combination with EN ISO 6222:1999 and one with Standard Methods Agar.

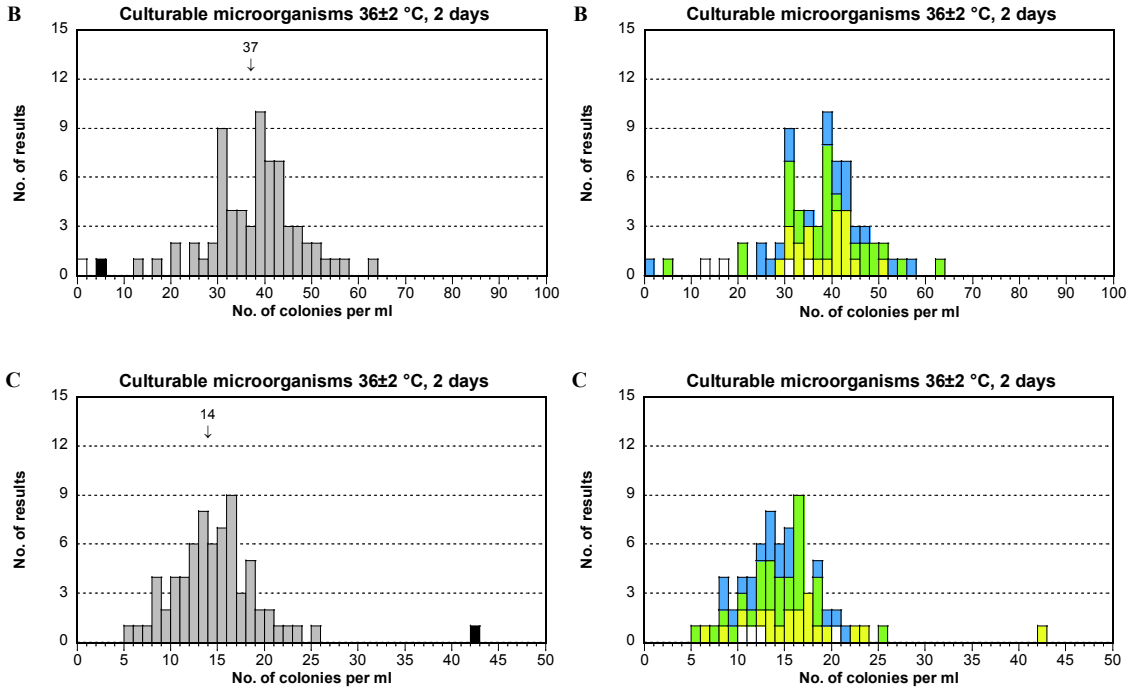
As for the analysis at 22 °C, comparisons of method variants are relevant to discuss only when EN ISO 6222:1999 was used. Also here, the results are presented in relation to culture media and magnification for reading.

For both mixture A and B the average results seem to be somewhat lower when Plate Count Agar was used compared to Yeast extract Agar. This has sometimes been seen before both at 22 and 36 °C. However, here the same is not valid for mixture C where the concentration is lower. No differences can be seen regarding the magnification used.

Group of results	N	A						B						C					
		n	**Mv**	CV	F	<	>	n	**Mv**	CV	F	<	>	n	**Mv**	CV	F	<	>
Total, all results	70	64	**46**	15	1	5	0	67	**37**	13	1	1	0	69	**14**	15	0	0	1
EN ISO 6222	*66*	*61*	***46***	*15*	*1*	*4*	*0*	*63*	***38***	*11*	*1*	*1*	*0*	*65*	***14***	*15*	*0*	*0*	*1*
Medium																			
Yeast extract Agar	63	58	**47**	15	1	4	0	60	**38**	11	1	1	0	62	**14**	15	0	0	1
Plate Count Agar	3	3	**37**	–	0	0	0	3	**31**	–	0	0	0	3	**15**	–	0	0	0
Other/Unknown	0	0	–	–	–	–	–	0	–	–	–	–	-	0	–	–	–	–	–
Magnification																			
None	19	18	**47**	10	0	1	0	18	**37**	13	1	0	0	19	**13**	14	0	0	0
1,1–4,9×	28	25	**45**	19	1	2	0	26	**38**	13	0	1	0	28	**14**	15	0	0	0
5–11,9×	19	18	**48**	15	0	1	0	19	**38**	7	0	0	0	18	**15**	16	0	0	1
> 12×	0	0	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
Other/Unknown	0	0	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
Other method	4	3	–	–	0	1	0	4	–	–	0	0	0	4	–	–	0	0	0







Mixture A

- All bacteria strains in the mixture appear at 36±2 °C. 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 other four bacteria can also grow but appear with very low numbers, viz. <1 cfu/ml.
- The distribution shows, as in the September round 2015 and September round 2016, unexpectedly many low results. The reason for these low results is not clear. It may be caused by laboratories not obtaining the full number of *S. capitis* colonies or not reckon all of them as colonies. Many of the low results could be identified as outliers, causing a small dispersion for the accepted results.
- One false negative result and 5 low outliers were identified.

Mixture B

- The colonies of culturable microorganisms are mainly made up of *Staphylococcus cohnii* like at 22 °C. The other four strains will also grow but each with <1 cfu/ml.
- The distribution was somewhat spread out but still fairly good. Fewer low results were present here than at 22 °C. The dispersion of the accepted results was small.
- One false negative result and one low outlier were identified.

Mixture C

- The colonies are almost entirely made up of *Enterococcus faecalis* but also some colonies of the coliform bacteria and *P. aeruginosa* will be seen.
- The distribution of the results was good and the dispersion small.
- One high outlier was reported.

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 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 assessment is basically a clear indication of the numbers of false results and outliers.

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

Fifteen laboratories obtained more than one deviating result. When whole samples seem to have been mixed up, the corresponding sample numbers are hatched in annex A. No laboratory seems to have mixed up neither samples nor sample/results for individual analyses. A couple of laboratories can be suspected to have forgotten to recalculate some counts to the volume asked for. One laboratory has reported their results as $\log_{10}$ values, contrary to the instruction for the 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 become comparable between analyses. They are given in annex B and used for the box plots. 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).*
- *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 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.*

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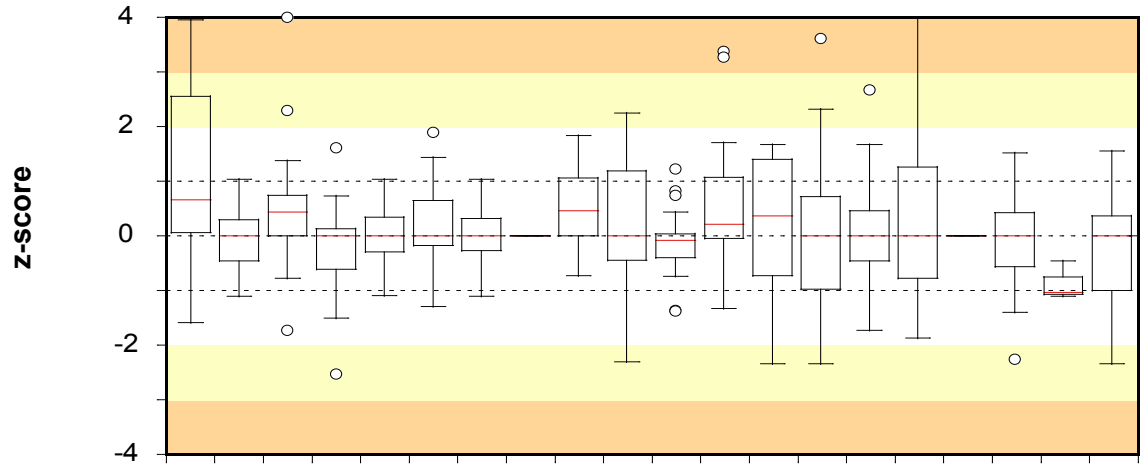
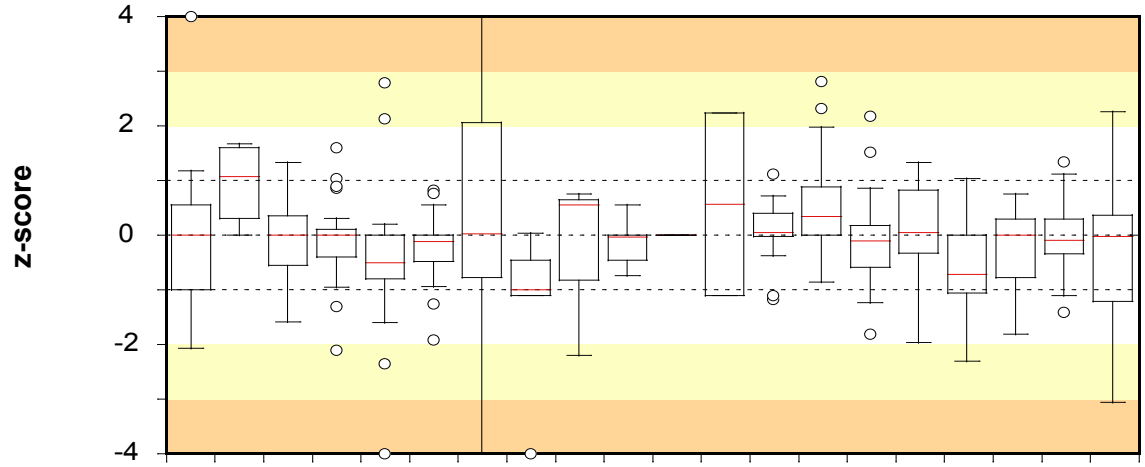
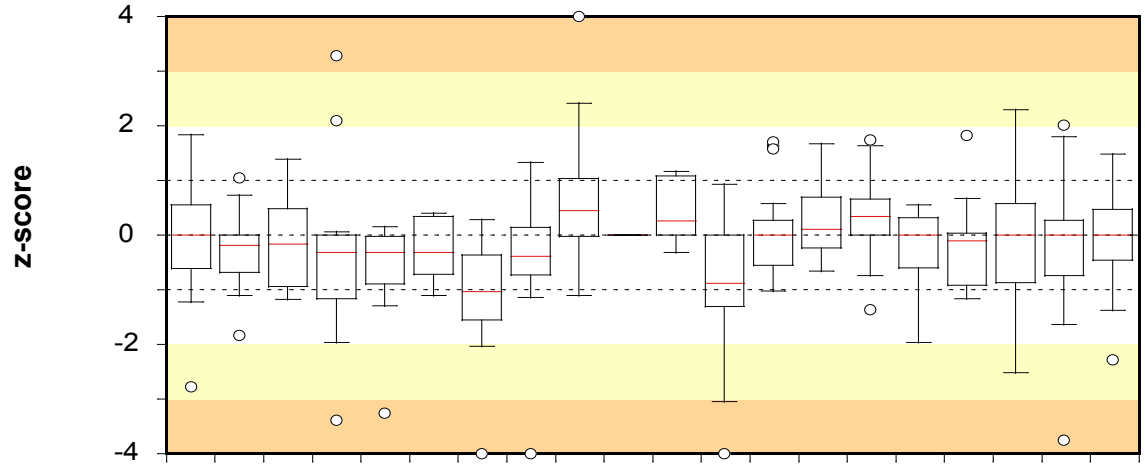
* < [smallest value of the box - 1.5 × (largest value of the box - smallest value of the box)] *or* > [largest value of the box + 1.5 × (largest value of the box - smallest value of the box)]



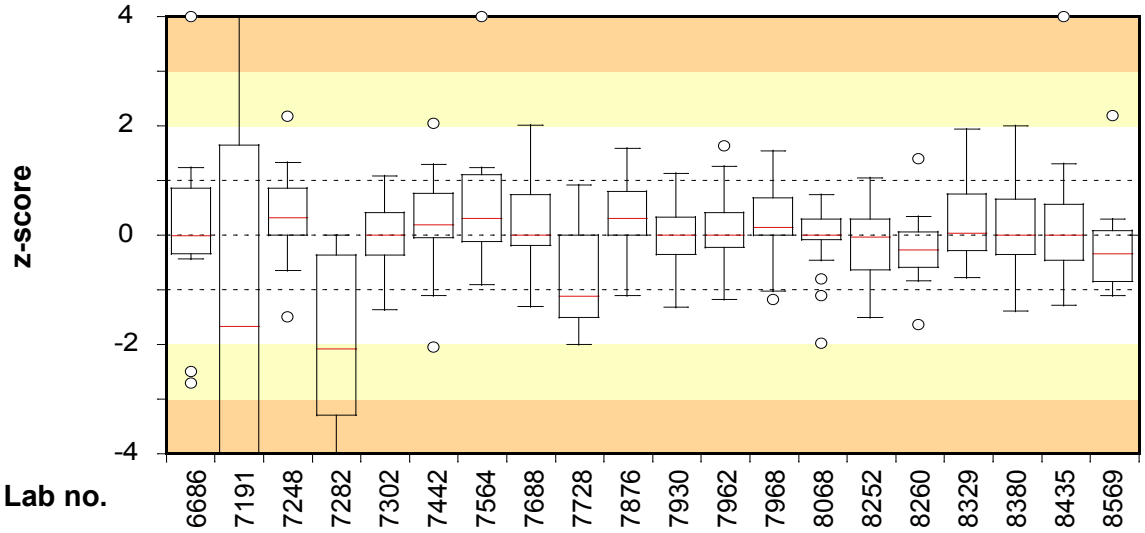
Lab no.	1131	1132	1237	1254	1545	1594	1611	1753	1868	1970	2050	2386	2637	2670	2704	2745	2915	2944	3055	3057
No. of results	6	11	17	20	21	21	20	-	12	18	20	21	9	12	18	9	-	12	3	16
False positive	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-
False negative	-	1	1	1	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	2
Low outliers	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
High outliers	1	-	1	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-



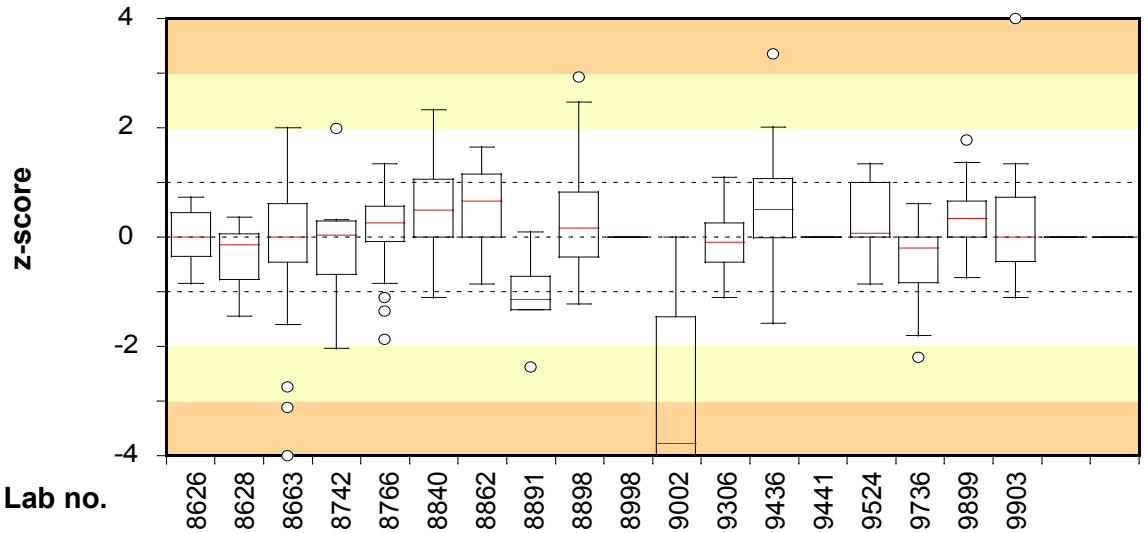
Lab no.	3076	3145	3159	3162	3164	3305	3533	3587	3730	3868	4015	4288	4319	4339	4343	4356	4459	4633	4723	4889
No. of results	9	2	21	21	15	21	14	5	3	21	-	2	18	21	21	20	18	15	15	21
False positive	-	-	-	-	2	-	1	-	-	-	-	-	-	-	-	1	-	-	-	-
False negative	-	-	-	-	1	-	-	1	-	-	-	1	-	-	-	-	-	-	-	-
Low outliers	-	-	-	-	1	-	1	1	-	-	-	-	-	-	-	-	-	-	-	-
High outliers	1	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-



Lab no.	4980	5018	5094	5128	5188	5201	5220	5352	5447	5494	5553	5858	5950	6175	6180	6233	6253	6448	6456	6563
No. of results	21	21	12	18	8	6	7	15	14	-	6	15	21	9	21	21	9	9	14	20
False positive	-	-	-	-	1	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-
False negative	-	-	-	-	-	-	1	-	1	-	-	-	-	-	-	-	-	-	1	1
Low outliers	-	-	-	-	-	-	1	1	-	-	-	1	-	-	-	-	-	-	1	-
High outliers	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-



Lab no.	6686	7191	7248	7282	7302	7442	7564	7688	7728	7876	7930	7962	7968	8068	8252	8260	8329	8380	8435	8569
No. of results	9	10	20	12	21	12	12	21	18	21	21	18	21	19	10	9	21	20	18	12
False positive	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
False negative	-	2	1	-	-	-	-	-	-	-	-	-	-	2	-	-	-	1	-	-
Low outliers	-	3	-	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
High outliers	-	2	-	-	-	-	2	-	-	-	-	-	-	-	-	-	-	-	1	-



Lab no.	8626	8628	8663	8742	8766	8840	8862	8891	8898	8998	9002	9306	9436	9441	9524	9736	9899	9903
No. of results	11	17	19	12	20	17	15	6	21	-	12	9	21	-	15	21	21	18
False positive	-	-	-	-	1	1	-	-	-	-	-	-	-	-	-	-	-	-
False negative	1	1	2	-	-	-	-	-	-	-	-	-	-	-	3	-	-	-
Low outliers	-	-	1	-	-	-	-	-	-	-	9	-	-	-	-	-	-	-
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 obtained at the National Food Agency are listed in table 2. The participating laboratories were assigned to perform the analyses according to the methods routinely used by them.

The test material is primarily suited to the EN ISO methods for analyses of drinking water referred to in the European Drinking water directive (4) and its updates (6). Alternative methods and other standards 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	*Escherichia coli*	532	CCUG 48891	6
	Enterobacter cloacae	451	CCUG 30205	35
	Enterococcus durans	078	CCUG 44816	7
	Burkholderia cepacia	042	–	23
	Staphylococcus capitis	463	CCUG 35173	50 *
B	*Klebsiella pneumoniae*	537	–	24
	Serratia marcescens	040	ATCC 13880	34
	Lactobacillus plantarum	475	CCUG 30503	12
	Pseudomonas aeruginosa	455	CCUG 30209	6
	Staphylococcus cohnii	462	CCUG 35411	27 *
C [4]	*Escherichia coli*	082	CCUG 45097	31
	Citrobacter freundii	424	From water	21
	Enterococcus faecalis	051	CCUG 45101	107
	Pseudomonas aeruginosa	395	CCUG 43596	36
	Clostridium perfringens [5]	442	CCUG 43593	39

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; ATCC: American Type Culture Collection; CCUG: Culture Collection University of Gothenburg, Sweden

4 The results are per 5 ml from a sample reconstituted in 300 ml of diluent

5 Not evaluated since the parameter *Clostridium perfringens* is not included in this round

* 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 14, 24 and 43 dispensed aliquots in vials for mixture A, B and C, respectively. The largest differences between vials were 3, 10 and 8 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 ***Method standard for analysis***	**Mixture**								
	A			**B**			**C** [2]		
	cfu	**I_2**	**T**	**cfu**	**I_2**	**T**	**cfu**	**I_2**	**T**
Coliform bacteria (MF) *m-Endo Agar LES according to SS 028167*	41	0.8	1.3	59	0.6	1.2	52	1.4	1.4
Suspected thermotolerant colif. bact. (MF) * *m-FC Agar, 44 °C according to SS 028167*	5	1.3	2.6	21	1.1	1.6	17	1.2	1.7
Escherichia coli (MF) *m-Endo Agar LES according to SS 028167*	6	1.2	2.3	–	–	–	31	1.0	1.4
Intestinal enterococci (MF) *m-Enterococcus Agar acc. to SS-EN ISO 7899-2:2000*	7	1.1	2.1	–	–	–	107	2.7	1.4
Pseudomonas aeruginosa (MF) *Pseudomonas Agar base with cetrimide and nalidixic acid according to SS-EN ISO 16288:2008*	–	–	–	6	1.1	2.2	36	0.6	1.3
Culturable microorg., 2d 37 °C (pour plate) *Yeast extract Agar according to SS-EN ISO 6222:1999*	50	0.9	1.3	29	0.6	1.3	37	1.0	1.4
Culturable microorg., 3d 22 °C (pour plate) *Yeast extract Agar according to SS-EN ISO 6222:1999*	<1	0.6	– [a]	27	0.5	1.3	44 [b]	1.7 [b]	1.5 [b]

1 n=10 vials analysed in duplicate, normally100 ml for MF and 1 ml for pour plate, 22 and 15 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; 27 months after manufacturing of an old RM); sample volume 300 ml and analytical portions for MF 5 ml and for pour plate 1 ml)

a Zero result in the duplicate for 2 of the 10 vials due to low concentration implies that the T value cannot be calculated.

b Values from the original homogeneity test – no check for this parameter was done after 27 months

– 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 deviating results. 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 square-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 2017. Scheme protocol, Microbiology, Drinking water & Food, 5th ed. National Food Agency, Sweden.
2. Peterz, M., Steneryd, A.-C. 1993. Freeze-dried mixed cultures as reference samples in quantitative and qualitative microbiological examinations of food. J. Appl. Bacteriol. 74:143-148.
3. Kelly, K. 1990. Outlier detection in collaborative studies. J. Assoc. Off. Chem. 73:58-64.
4. Anonymous 1998. Council Directive 98/83/EC of 3 November 1998 on the quality of water intended for human consumption. Official Journal of the European Communities. 5.12.98, L 330/32-54 *(national translations available)*.
5. Standard Methods for the Examination of Water and Wastewater, http://www.standardmethods.org/
6. Anonymous 2015. Commission Directive (EU) 2015/1787 of 6 October 2015 amending Annexes II and III to Council Directive 98/83/EC on the quality of water intended for human consumption. Official Journal of the European Union. 7.10.2015, L 260/6-17 *(national translations available)*.

Annex A *Results of the participants. 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	A	B	C
1131	1 2 3	-	-	-	-	-	-	-	-	-	-	-	-	73	34	387	**29**	0	206
1132	1 3 2	-	-	-	-	-	-	10	15	170	**0**	0	110	33	62	365	5	0	185
1237	3 1 2	-	-	-	42	28	**900**	-	-	-	30	<1	200	-	-	-	-	-	-
1254	3 2 1	31	22	300	31	22	300	-	-	-	**0**	0	300	46	26	290	8	0	150
1545	2 1 3	34	29	350	34	29	260	6	22	240	6	0	240	41	41	291	6	0	210
1594	1 3 2	30	50	280	30	22	280	6	25	51	3	0	100	41	60	380	6	0	229
1611	1 2 3	33	22	300	33	22	300	3	23	168	**0**	0	200	41	62	291	8	0	179
1753	1 2 3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1868	2 1 3	45	42	276	45	42	276	-	-	-	20	0	190	49	63	269	15	0	190
1970	3 1 2	30	50	430	30	50	430	30	50	430	5	0	310	-	-	-	-	-	-
2050	3 2 1	-	-	-	33	39	273	-	-	-	8	0	131	41	49	285	7	0	156
2386	2 3 1	35	49	250	35	49	250	-	-	-	23	0	170	84	60	384	24	<1	254
2637	1 3 2	-	-	-	-	-	-	-	-	-	-	-	-	38	70	364	14	<1	207
2670	2 1 3	49	34	380	39	34	380	49	0	380	49	0	380	-	-	-	-	-	-
2704	2 1 3	-	-	-	31	14	570	-	-	-	6	0	190	59	70	324	5	<1	192
2745	3 2 1	54	45	140	54	45	140	54	45	140	4	0	100	-	-	-	-	-	-
2915	1 2 3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
2944	3 2 1	-	-	-	-	-	-	-	-	-	-	-	-	42.9	50.4	164	3.1	<1	124
3055	2 3 1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3057	1 2 3	-	-	-	42	14	160	-	-	-	**< 1**	< 1	27	-	-	-	-	-	-
3076	1 3 2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3145	2 3 1	-	-	-	-	-	-	-	-	-	-	-	-	59	70	**>200,5**	9	0	**>200,5**
3159	3 1 2	-	-	-	31	46	210	-	-	-	5	<1	120	36.4	42.9	238	9.9	<1	207
3162	2 3 1	43	20	310	43	20	310	-	-	-	7	0	70	39	40	301	5	0	96
3164	3 2 1	28	18	175	34	22	232	-	-	-	28	**18**	102	40	50	308	4	0	201
3305	2 1 3	-	-	-	31	39	310	-	-	-	3	<1	150	24	45	288	4	<1	130
3533	3 2 1	-	-	-	16	22	350	-	-	-	11	0	350	-	-	-	-	-	-
3587	3 2 1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3730	1 3 2	19	27	220	-	-	-	9	24	110	-	-	-	-	-	-	-	-	-
3868	2 3 1	31	26	320	31	26	290	4	20	160	4	0	160	41	45	320	5	0	160
4015	1 2 3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4288	1 3 2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4319	3 2 1	39	26	310	39	26	280	19	13	200	8	0	190	42	53	340	3	0	200
4339	1 3 2	38	30	350	38	30	350	4	20	360	6	0	190	46	67	613	6	0	308
4343	3 2 1	34	20	300	34	20	300	-	-	-	9	0	145	38	32	260	8	0	131
4356	2 1 3	45	20	380	45	20	380	2	17	82	19	0	190	51	51	260	5	0	180
4459	2 1 3	-	-	-	30	19	320	-	-	-	4	<1	130	33	39	210	3	<1	142
4633	1 3 2	-	-	-	-	-	-	-	-	-	-	-	-	29	32	271	4	0	176
4723	3 2 1	42	26	227	42	26	227	-	-	-	6	0	65	54	43	326	6	0	173
4889	1 3 2	-	-	-	37	45	220	-	-	-	1	0	150	25	55	550	1	0	250
4980	1 3 2	-	-	-	31	22	280	2	21	100	2	<1	100	47.8	50.4	429	15	<1	271
5018	1 2 3	41	53	220	37	18	220	-	-	-	4	<1	154	39	48	350	11	<1	210
5094	1 3 2	39	18	930	39	18	420	7	17	720	7	0	120	-	-	-	-	-	-
5128	2 3 1	-	-	-	-	-	-	6	32	150	6	0	150	38	38	250	3	0	160
5188	3 1 2	-	-	-	14	16	240	-	-	-	9	0	150	-	-	-	-	-	-
5201	1 2 3	39	22	-	39	22	-	-	-	-	4	<1	-	-	-	-	-	-	-
5220	2 1 3	-	-	-	38	18	130	-	-	-	**0**	**2**	85	-	-	-	-	-	-
5352	3 2 1	-	-	-	27	46	234	-	-	-	4	0	135	-	-	-	-	-	-
5447	1 3 2	-	-	-	58	26	410	-	-	-	**0**	0	160	-	-	-	-	-	-
5494	1 3 2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
5553	3 1 2	-	-	-	45	35	255	-	-	-	8	0	255	-	-	-	-	-	-
5858	2 3 1	-	-	-	-	-	-	-	-	-	-	-		32	59	180	4	<1	64
5950	1 3 2	31	21	309	31	21	309	5	22	134	5	0	200	32	51	326	5	0	186
6175	1 3 2	-	-	-	-	-	-	-	-	-	-	-	-	41	70	310	10	0	201
6180	2 3 1	40	21	360	40	21	320	3	12	100	10	0	250	45	36	320	9	0	210
6233	1 3 2	32	35	320	32	35	320	-	-	-	3	0	180	26	44	308	5	0	201
6253	1 2 3	-	-	-	-	-	-	-	-	-	-	-	-	31	38	310	5	0	150
6448	3 2 1	40	60	350	-	-	-	-	-	-	30	0	200	-	-	-	-	-	-
6456	1 3 2	-	-	-	28	21	360	-	-	-	**<1**	<1	71	43	53	500	5	<1	310
6563	1 2 3	45	30	370	45	30	370	45	30	370	**<1**	<1	148	37	42	440	5	<1	276
6686	2 3 1	-	-	-	-	-	-	-	-	-	-	-	-	**306**	47.8	150	8.7	<1	75
7191	3 1 2	300	0	159	**100**	**0**	100	40	0	100	**100**	0	100	-	-	-	-	-	-
7248	3 1 2	40	40	360	40	40	360	5	18	154	**0**	0	108	43	61	387	7	0	201
7282	2 1 3	-	-	-	-	-	-	-	-	-	1	0	21	-	-	-	-	-	-
7302	1 2 3	45	26	264	45	26	264	5	24	95	9	0	118	45	36	387	3	0	236
7442	2 3 1	35	57	368	35	57	368	-	-	-	11	<1	268	23	52	385	4	<1	218
7564	3 1 2	-	-	-	**120**	**160**	270	-	-	-	13	<1	160	-	-	-	-	-	-
7688	1 2 3	43	35	240	43	35	210	-	-	-	8	0	70	47	57	310	16	0	180
7728	1 2 3	-	-	-	32	24	140	-	-	-	3	0	60	-	-	-	-	-	-
7876	3 2 1	38	49	360	38	49	360	2	24	30	7	<1	180	36	69	430	6	<1	179
7930	1 3 2	40	21	300	40	21	300	6	<1	220	6	<1	220	29	48	320	8	<1	150
Mean					**36**	**29**	**282**				**8**	**0**	**153**	**42**	**50**	**328**	**7**	**0**	**190**
CV (%)					11	20	16				41	-	25	13	11	13	28	-	14

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	
-	-	-	-	-	-	-	-	-	-	-	-	1	47	26	-	-	-	**1131**
6	0	780	6	0	780	-	-	-	-	-	-	0	38	15	-	-	-	**1132**
-	-	-	**<1**	<1	580	-	-	-	<1	6	300	1	45	15	60	30	20	**1237**
5	0	600	5	0	600	0	3	250	0	3	250	1	33	12	57	42	13	**1254**
9	0	830	9	0	830	0	3	140	0	3	140	1	40	12	55	40	17	**1545**
6	0	800	6	0	800	0	4	280	0	4	280	3	52	18	46	57	9	**1594**
5	0	860	5	0	860	0	4	280	0	4	280	0	45	16	47	39	12	**1611**
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**1753**
6	0	1180	-	-	-	0	5	300	-	-	-	1	48	13	-	-	-	**1868**
6	0	1000	6	0	1000	0	4	310	0	4	310	1	42	19	20	31	12	**1970**
-	-	-	3	**82**	673	-	-	-	0	2	300	1	50	12	42	35	17	**2050**
5	0	770	5	0	770	0	3	340	0	3	340	0	39	9	64	47	18	**2386**
11	<1	400	-	-	-	-	-	-	-	-	-	<1	54	6	27	41	19	**2637**
4	0	620	4	0	620	-	-	-	-	-	-	0	36	6	-	-	-	**2670**
-	-	-	5	<1	580	-	-	-	-	-	-	1	41	10	59	30	16	**2704**
-	-	-	-	-	-	-	-	-	-	-	-	0	42	**60**	-	-	-	**2745**
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**2915**
5	<1	870	5	<1	870	-	-	-	-	-	-	5	36	16	51	47	11	**2944**
-	-	-	-	-	-	-	-	-	-	-	-	0	31	12	-	-	-	**3055**
-	-	-	6	< 1	730	< 1	< 1	66	< 1	**< 1**	66	2	43	12	42	53	15	**3057**
-	-	-	-	-	-	0	30	400	0	**30**	400	2	24	15	35	20	10	**3076**
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**3145**
-	-	-	8	<1	790	-	-	-	<1	4	150	1	49	13	27	40	16	**3159**
6	0	860	6	0	860	0	4	260	0	4	260	1	47	21	38	38	13	**3162**
-	-	-	5	**61**	**73**	-	-	-	-	-	-	11	22	**0**	37	26	8	**3164**
6	<1	830	6	<1	830	<1	4	250	<1	4	250	2	36	13	40	38	13	**3305**
-	-	-	4	0	670	-	-	-	**500**	**100**	600	10	**10**	14	-	-	-	**3533**
-	-	-	-	-	-	-	-	-	-	-	-	<1	**2**	12	47	**<1**	10	**3587**
-	-	-	-	-	-	-	-	-	-	-	-	2	23	17	-	-	-	**3730**
6	0	720	6	0	720	0	5	250	0	5	250	2	39	11	39	39	12	**3868**
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**4015**
-	-	-	-	-	-	-	-	-	-	-	-	<10	60	**<10**	-	-	-	**4288**
8	0	710	8	0	710	-	-	-	-	-	-	0	49	14	45	44	16	**4319**
4	0	790	4	0	790	0	4	440	0	4	380	1	57	15	54	62	16	**4339**
13	0	800	13	0	800	-	-	-	0	4	201	5	30	11	59	36	13	**4343**
2	62	730	2	**62**	730	0	3	370	0	3	370	1	46	14	39	39	18	**4356**
9	<1	755	9	<1	755	-	-	-	-	-	-	1	28	9	20	38	13	**4459**
-	-	-	7	0	600	-	-	-	0	5	309	1	37	17	49	30	15	**4633**
11	0	730	10	0	730	-	-	-	-	-	-	0	42	15	-	-	-	**4723**
-	-	-	4	0	560	-	-	-	0	4	23	3	32	12	55	24	15	**4889**
-	-	-	7	<1	700	-	-	-	<1	7	192	3	33	11	16	36	16	**4980**
5	<1	570	5	<1	570	16	14	230	<1	6	230	<1	37	12	36	31	13	**5018**
4	0	790	-	-	-	-	-	-	-	-	-	2	30	17	44	29	10	**5094**
2	0	740	2	0	740	0	2	220	0	2	220	14	16	12	80	21	14	**5128**
-	-	-	-	-	-	-	-	-	**9**	4	200	-	-	-	-	-	-	**5188**
-	-	-	-	-	-	-	-	-	-	-	-	<1	42	-	-	-	-	**5201**
-	-	-	-	-	-	-	-	-	0	3	**2**	-	-	-	-	-	-	**5220**
4	0	720	-	-	-	-	-	-	0	6	170	2	36	11	**1**	32	15	**5352**
9	0	850	9	0	850	-	-	-	-	-	-	0	39	**160**	33	45	18	**5447**
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**5494**
8	0	735	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**5553**
6	<1	640	6	<1	640	<1	17	75	<1	3	75	3	29	10	**7**	30	9	**5858**
11	0	936	11	0	936	0	3	270	0	3	270	2	35	10	50	28	21	**5950**
-	-	-	-	-	-	-	-	-	-	-	-	2	37	16	43	31	20	**6175**
8	0	790	8	0	790	0	7	340	0	7	340	2	55	12	51	54	14	**6180**
2	0	800	2	0	800	0	5	300	0	5	300	2	39	11	38	38	7	**6233**
-	-	-	6	0	950	-	-	-	-	-	-	1	45	10	-	-	-	**6253**
-	-	-	-	-	-	-	-	-	0	10	160	-	-	-	40	17	10	**6448**
-	-	-	-	-	-	-	-	-	-	-	-	1	38	8	**9**	40	11	**6456**
7	<1	760	7	<1	760	<1	2	320	<1	2	320	<1	38	12	46	50	6	**6563**
<1	<1	74	-	-	-	-	-	-	-	-	-	4	37	19	46	33	14	**6686**
-	-	-	-	-	-	-	-	-	-	-	-	5.5	**6**	**0**	**6.3**	**5.1**	5	**7191**
9	0	810	9	0	810	0	10	190	0	10	190	2	51	19	28	40	15	**7248**
-	-	-	2	0	**41**	-	-	-	0	1	**13**	-	-	-	**3**	13	11	**7282**
8	0	700	8	0	700	0	5	309	0	5	309	1	32	17	43	32	14	**7302**
-	-	-	-	-	-	-	-	-	-	-	-	0	39	18	-	-	-	**7442**
-	-	-	-	-	-	-	-	-	-	-	-	4	32	18	45	33	16	**7564**
6	0	710	6	0	710	0	4	280	0	4	280	3	37	19	77	50	16	**7688**
-	-	-	3	0	620	-	-	-	0	2	74	1	28	8	60	39	8	**7728**
9	<1	809	9	<1	809	21	6	273	<1	6	273	<1	46	16	50	42	19	**7876**
8	<1	710	8	<1	710	<1	7	240	<1	7	240	1	35	15	35	39	16	**7930**
			6	**0**	**748**				**0**	**4**	**249**	**1**	**39**	**14**	**46**	**37**	**14**	**Mean**
			22	-	7				-	24	23	90	11	15	15	13	15	**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
7962	1 3 2	33	45	360	33	45	360	1	8	97	10	0	190	46	42	291	5	0	179
7968	1 3 2	41	69	360	41	32	360	1	23	156	10	0	225	39	49	409	3	0	280
8068	1 3 2	-	-	-	42	37	310	-	-	-	**0**	0	166	41	49	330	4	0	167
8252	3 1 2	-	-	-	-	-	-	-	-	-	-	-	-	41	-	270	5	-	190
8260	1 2 3	31	47	213	31	47	213	-	-	-	6	<1	134	-	-	-	-	-	-
8329	3 1 2	51	21	345	51	21	345	-	-	-	11	0	223	34	46	365	10	0	276
8380	2 1 3	42	58	410	42	26	410	-	-	-	**0**	0	200	29	61	465	3	0	284
8435	3 2 1	-	-	-	26	22	300	2	11	22	9	0	150	-	-	-	-	-	-
8569	1 3 2	37	21	314	37	21	236	-	-	-	10	0	96	-	-	-	-	-	-
8626	2 3 1	36	20	260	36	20	260	0	0	210	**0**	0	210	-	-	-	-	-	-
8628	3 1 2	-	-	-	27	23	200	0	13	63	**0**	0	63	-	-	-	-	-	-
8663	1 2 3	45	15	380	**0**	15	**11**	39	28	320	**0**	0	8	53	74	320	9	0	170
8742	3 1 2	-	-	-	30	30	130	-	-	-	10	0	90	-	-	-	-	-	-
8766	2 1 3	27	20	291	22	20	174	<1	15	113	7	<1	174	47	60	365	9	<1	228
8840	2 1 3	32	54	290	32	54	290	-	-	-	16	0	**174**	43	45	504	4	0	238
8862	2 1 3	42	48	403	42	48	403	-	-	-	5	0	273	43	54	403	14	0	242
8891	2 3 1	-	-	-	30	30	110	-	-	-	-	-	-	-	-	-	-	-	-
8898	1 3 2	31	64	373	31	64	373	-	-	-	2	0	254	48	46	298	11	0	176
8998	2 3 1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
9002	1 2 3	-	-	-	**1.34**	**1.24**	**1.92**	-	-	-	**0.54**	0	**2.23**	-	-	-	-	-	-
9306	2 3 1	-	-	-	-	-	-	-	-	-	-	-	-	43	45	277	5	0	173
9436	1 3 2	54	44	373	54	44	373	7	2	174	1	0	200	48	55	328	5	0	176
9441	1 2 3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
9524	2 3 1	29	39	310	29	39	240	-	-	-	**0**	0	240	56	50	288	**0**	0	194
9736	3 1 2	34	12	243	34	12	243	-	-	-	9	0	162	39	40	222	9	0	155
9899	3 1 2	31	21	345	31	21	345	-	-	-	12	0	205	57	52	380	11	0	192
9903	2 3 1	47	24	341	47	24	341	5	25	148	5	0	111	-	-	-	-	-	-
n		50	50	49	72	72	71	32	32	32	75	75	74	60	59	59	60	59	59
Min		19	0	140	0	0	1.92	0	0	22	0	0	2.23	23	26	150	0	0	64
Max		300	69	930	120	160	900	54	50	720	100	18	380	306	74	613	29	0	310
Median		38.5	28	314	35	26	295	5	20	152	7	0	160	41	50	320	5.5	0	190
Mean					**36**	**29**	**282**				**8**	**0**	**153**	**42**	**50**	**328**	**7**	**0**	**190**
CV (%)					11	20	16				41	-	25	13	11	13	28	-	14
False positive					0	0	0				0	2	0	0	0	0	0	0	0
False negative					1	1	0				15	0	0	0	0	0	1	0	0
Outliers, low					1	1	2				1	0	1	0	0	0	0	0	0
Outliers, high					2	1	1				1	0	0	1	0	0	1	0	0
Low limit OK		19	0	140	14	12	100	0	0	22	1*	0	8	23	26	150	1	0	64
High limit OK		300	69	930	58	64	570	54	50	720	49	0	380	84	74	613	24	0	310
mv *(√Mean)*					5.970	5.371	16.795				2.822	0.000	12.382	6.445	7.065	18.116	2.566	0.000	13.793
s *(CV*mv/100)*					0.683	1.062	2.655				1.155	0.000	3.072	0.806	0.779	2.357	0.712	0.000	1.899
$u_{rel,mv}$ (%) *(100*s/ √n_{mv} /mv)*					1.4	2.4	1.9				5.4		2.9	1.6	1.4	1.7	3.6		1.8
x *(√Result)*																			
z *([x-mv]/s)*																			

* The calculated results and acceptance limits are calculated without all the deviating result. However, dependent on method, some of the 15 zero results must be judged

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	
11	0	790	11	0	790	0	8	390	-	-	-	1	30	18	47	35	13	**7962**
7	0	660	7	0	660	0	6	270	0	6	270	1	40	10	59	42	14	**7968**
-	-	-	8	0	740	-	-	-	0	**0**	270	0	41	7	44	43	15	**8068**
-	-	-	8	-	600	-	-	-	<1	-	190	<1	-	15	62	-	15	**8252**
-	-	-	-	-	-	-	-	-	-	-	-	1	42	8	-	-	-	**8260**
6	0	964	6	0	964	-	-	-	0	5	194	1	35	13	52	30	18	**8329**
6	0	730	6	0	730	0	3	220	0	3	220	7	34	13	52	25	12	**8380**
-	-	-	8	0	890	-	-	-	0	3	200	**50**	44	18	49	36	11	**8435**
4	0	640	4	0	640	-	-	-	-	-	-	0	38	24	-	-	-	**8569**
-	-	-	-	-	-	-	-	-	-	-	-	2	42	12	57	35	12	**8626**
-	-	-	7	0	680	-	-	-	0	5	270	0	38	12	50	30	14	**8628**
1	0	870	1	0	870	0	5	340	0	5	200	1	50	23	44	38	8	**8663**
-	-	-	-	-	-	-	-	-	-	-	-	1	34	15	78	40	12	**8742**
10	103	748	10	**103**	748	<1	6	300	<1	6	300	<1	35	14	63	42	16	**8766**
6	76	890	6	**76**	890	-	-	-	-	-	-	0	46	17	57	48	25	**8840**
4	0	873	4	0	873	-	-	-	-	-	-	1	44	17	-	-	-	**8862**
-	-	-	-	-	-	-	-	-	-	-	-	<1	30	9	-	-	-	**8891**
4	0	700	4	0	700	0	3	691	0	3	691	2	47	17	51	42	17	**8898**
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**8998**
-	-	-	**0.7**	0	**2.63**	-	-	-	-	-	-	0	**1.46**	**1.2**	-	-	-	**9002**
-	-	-	-	-	-	-	-	-	-	-	-	0	41	15	61	48	13	**9306**
4	0	745	4	0	745	0	14	318	0	14	318	0	45	21	66	44	23	**9436**
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	**9441**
-	-	-	10	0	683	-	-	-	-	-	-	1	49	17	**0**	47	18	**9524**
6	0	727	6	0	727	0	5	245	0	5	245	0	43	13	21	35	8	**9736**
5	0	871	5	0	871	0	4	329	0	4	329	1	43	19	50	41	22	**9899**
10	0	721	10	0	721	0	3	337	0	3	337	0	46	13	57	43	**42**	**9903**
51	51	51	64	63	64	36	36	36	53	52	53	86	85	85	70	69	70	**n**
0	0	74	0	0	2.63	0	0	66	0	0	2	0	1.46	0	0	0	5	**Min**
13	103	1180	13	103	1000	21	30	691	500	100	691	50	60	160	80	62	42	**Max**
6	0	760	6	0	740	0	4	280	0	4	270	1	39	14	47	38	14	**Median**
			6	**0**	**748**				**0**	**4**	**249**	**1**	**39**	**14**	**46**	**37**	**14**	**Mean**
			22	-	7				-	24	23	90	11	15	15	13	15	**CV (%)**
			0	5	0				2	0	0	0	0	0	0	0	0	**False pos.**
			1	0	0				0	2	0	0	0	3	1	1	0	**False neg.**
			1	0	3				0	0	2	0	4	1	5	1	0	**Outliers <**
			0	0	0				0	2	0	1	0	2	0	0	1	**Outliers >**
0	0	74	1	0	560	0	0	66	0	1	23	0	16	6	16	13	5	**Low limit**
13	103	1180	13	0	1000	21	30	691	0	14	691	14	60	26	80	62	25	**High limit**
			2.452	0.000	27.353				0.000	2.090	15.775	0.943	6.256	3.715	6.812	6.076	3.711	**mv**
			0.530	0.000	1.896				0.000	0.493	3.589	0.852	0.665	0.541	1.015	0.775	0.552	**s**
			2.7		0.9					3.4	3.2	9.8	1.2	1.6	1.9	1.6	1.8	**$u_{rel,mv}$ (%)**
																		x
																		z

as acceptable while others are true false negative results.

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														**2.603**	-1.585	0.660	**3.959**	0.000	0.295
1132												0.000	-0.616	-0.868	1.038	0.420	-0.463	0.000	-0.101
1237					0.747	-0.075	**4.000**				**2.298**	0.000	0.573						
1254					-0.589	-0.640	0.198					0.000	1.608	0.419	**-2.525**	-0.461	0.369	0.000	-0.814
1545					-0.204	0.014	-0.253				-0.323	0.000	1.012	-0.051	-0.850	-0.449	-0.163	0.000	0.368
1594					-0.722	-0.640	-0.023				-0.944	0.000	-0.775	-0.051	0.874	0.584	-0.163	0.000	0.706
1611					-0.330	-0.640	0.198					0.000	0.573	-0.051	1.038	-0.449	0.369	0.000	-0.218
1753																			
1868					1.080	1.045	-0.069				1.428	0.000	0.457	0.689	1.119	-0.728	1.836	0.000	-0.005
1970					-0.722	1.601	1.485				-0.507	0.000	1.701						
2050					-0.330	0.823	-0.103				0.005	0.000	-0.305	-0.051	-0.084	-0.524	0.112	0.000	-0.686
2386					-0.079	1.534	-0.371				1.709	0.000	0.214	**3.374**	0.874	0.628	**3.277**	0.000	1.129
2637														-0.347	1.671	0.408	1.651	0.000	0.313
2670					0.402	0.433	1.016				**3.617**	0.000	**2.315**						
2704					-0.589	-1.533	**2.667**				-0.323	0.000	0.457	1.534	1.671	-0.049	-0.463	0.000	0.033
2745					**2.018**	1.259	-1.870				-0.712	0.000	-0.775						
2915																			
2944														0.131	0.044	**-2.253**	-1.131	0.000	-1.400
3055																			
3057					0.747	-1.533	-1.562					0.000	**-2.339**						
3076																			
3145														1.534	1.671		0.610	0.000	
3159					-0.589	1.329	-0.868				-0.507	0.000	-0.465	-0.510	-0.662	-1.141	0.816	0.000	0.313
3162					0.860	-0.846	0.306				-0.153	0.000	-1.307	-0.247	-0.951	-0.325	-0.463	0.000	**-2.104**
3164					-0.204	-0.640	-0.589				**2.138**		-0.743	-0.149	0.007	-0.240	-0.794	0.000	0.202
3305					-0.589	0.823	0.306				-0.944	0.000	-0.044	-1.917	-0.459	-0.486	-0.794	0.000	-1.260
3533					**-2.884**	-0.640	0.721				0.428	0.000	**2.059**						
3587																			
3730																			
3868					-0.589	-0.256	0.088				-0.712	0.000	0.087	-0.051	-0.459	-0.097	-0.463	0.000	-0.603
4015																			
4288																			
4319					0.402	-0.256	-0.023				0.005	0.000	0.457	0.045	0.276	0.137	-1.171	0.000	0.184
4339					0.284	0.100	0.721				-0.323	0.000	0.457	0.419	1.438	**2.818**	-0.163	0.000	1.979
4343					-0.204	-0.846	0.198				0.154	0.000	-0.111	-0.347	-1.809	-0.845	0.369	0.000	-1.237
4356					1.080	-0.846	1.016				1.330	0.000	0.457	0.864	0.098	-0.845	-0.463	0.000	-0.199
4459					-0.722	-0.952	0.412				-0.712	0.000	-0.319	-0.868	-1.053	-1.538	-1.171	0.000	-0.989
4633														-1.314	-1.809	-0.702	-0.794	0.000	-0.277
4723					0.747	-0.256	-0.651				-0.323	0.000	-1.406	1.121	-0.652	-0.026	-0.163	0.000	-0.337
4889					0.165	1.259	-0.740				-1.577	0.000	-0.044	-1.791	0.450	**2.264**	**-2.199**	0.000	1.063
4980					-0.589	-0.640	-0.023				-1.219	0.000	-0.775	0.582	0.044	1.101	1.836	0.000	1.406
5018					0.165	-1.062	-0.740				-0.712	0.000	0.009	-0.247	-0.176	0.251	1.055	0.000	0.368
5094					0.402	-1.062	1.393				-0.153	0.000	-0.465						
5128											-0.323	0.000	-0.044	-0.347	-1.157	-0.978	-1.171	0.000	-0.603
5188					**-3.262**	-1.290	-0.491				0.154	0.000	-0.044						
5201					0.402	-0.640					-0.712	0.000							
5220					0.284	-1.062	**-2.032**						-1.029						
5352					-1.133	1.329	-0.564				-0.712	0.000	-0.248						
5447					**2.409**	-0.256	1.301					0.000	0.087						
5494																			
5553					1.080	0.513	-0.311				0.005	0.000	1.168						
5858														-0.977	0.791	-1.994	-0.794	0.000	**-3.051**
5950					-0.589	-0.742	0.295				-0.507	0.000	0.573	-0.977	0.098	-0.026	-0.463	0.000	-0.082
6175														-0.051	1.671	-0.216	0.838	0.000	0.202
6180					0.519	-0.742	0.412				0.295	0.000	1.116	0.327	-1.368	-0.097	0.610	0.000	0.368
6233					-0.459	0.513	0.412				-0.944	0.000	0.337	-1.669	-0.555	-0.240	-0.463	0.000	0.202
6253														-1.087	-1.157	-0.216	-0.463	0.000	-0.814
6448											**2.298**	0.000	0.573						
6456					-0.993	-0.742	0.821					0.000	-1.288	0.140	0.276	1.801	-0.463	0.000	**2.009**
6563					1.080	0.100	0.919					0.000	-0.070	-0.449	-0.751	1.213	-0.463	0.000	1.485
6686														**4.000**	-0.195	**-2.490**	0.539	0.000	**-2.704**
7191					**4.000**		**-2.560**				**4.000**	0.000	-0.775						
7248					0.519	0.898	0.821					0.000	-0.648	0.140	0.956	0.660	0.112	0.000	0.202
7282											-1.577	0.000	**-2.539**						
7302					1.080	-0.256	-0.206				0.154	0.000	-0.494	0.327	-1.368	0.660	-1.171	0.000	0.826
7442					-0.079	**2.051**	0.900				0.428	0.000	1.298	**-2.044**	0.187	0.639	-0.794	0.000	0.512
7564					**4.000**	**4.000**	-0.137				0.678	0.000	0.087						
7688					0.860	0.513	-0.868				0.005	0.000	-1.307	0.510	0.622	-0.216	**2.014**	0.000	-0.199
7728					-0.459	-0.444	-1.870				-0.944	0.000	-1.509						
7876					0.284	1.534	0.821				-0.153	0.000	0.337	-0.551	1.594	1.112	-0.163	0.000	-0.218
7930					0.519	-0.742	0.198				-0.323	0.000	0.798	-1.314	-0.176	-0.097	0.369	0.000	-0.814
7962					-0.330	1.259	0.821				0.295	0.000	0.457	0.419	-0.751	-0.449	-0.463	0.000	-0.218
7968					0.634	0.269	0.821				0.295	0.000	0.852	-0.247	-0.084	0.894	-1.171	0.000	1.549
8068					0.747	0.670	0.306					0.000	0.164	-0.051	-0.084	0.021	-0.794	0.000	-0.458
8252														-0.051		-0.715	-0.463		-0.005
8260					-0.589	1.398	-0.829				-0.323	0.000	-0.262						
8329					1.714	-0.742	0.670				0.428	0.000	0.831	-0.761	-0.364	0.420	0.838	0.000	1.485
8380					0.747	-0.256	1.301					0.000	0.573	-1.314	0.956	1.463	-1.171	0.000	1.611
8435					-1.275	-0.640	0.198				0.154	0.000	-0.044						
8569					0.165	-0.742	-0.540				0.295	0.000	-0.841						
8626					0.044	-0.846	-0.253					0.000	0.687						
8628					-1.133	-0.541	-1.000					0.000	-1.447						
8663						-1.410	**-4.000**					0.000	**-3.110**	1.036	1.973	-0.097	0.610	0.000	-0.398
8742					-0.722	0.100	**-2.032**				0.295	0.000	-0.942						

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.

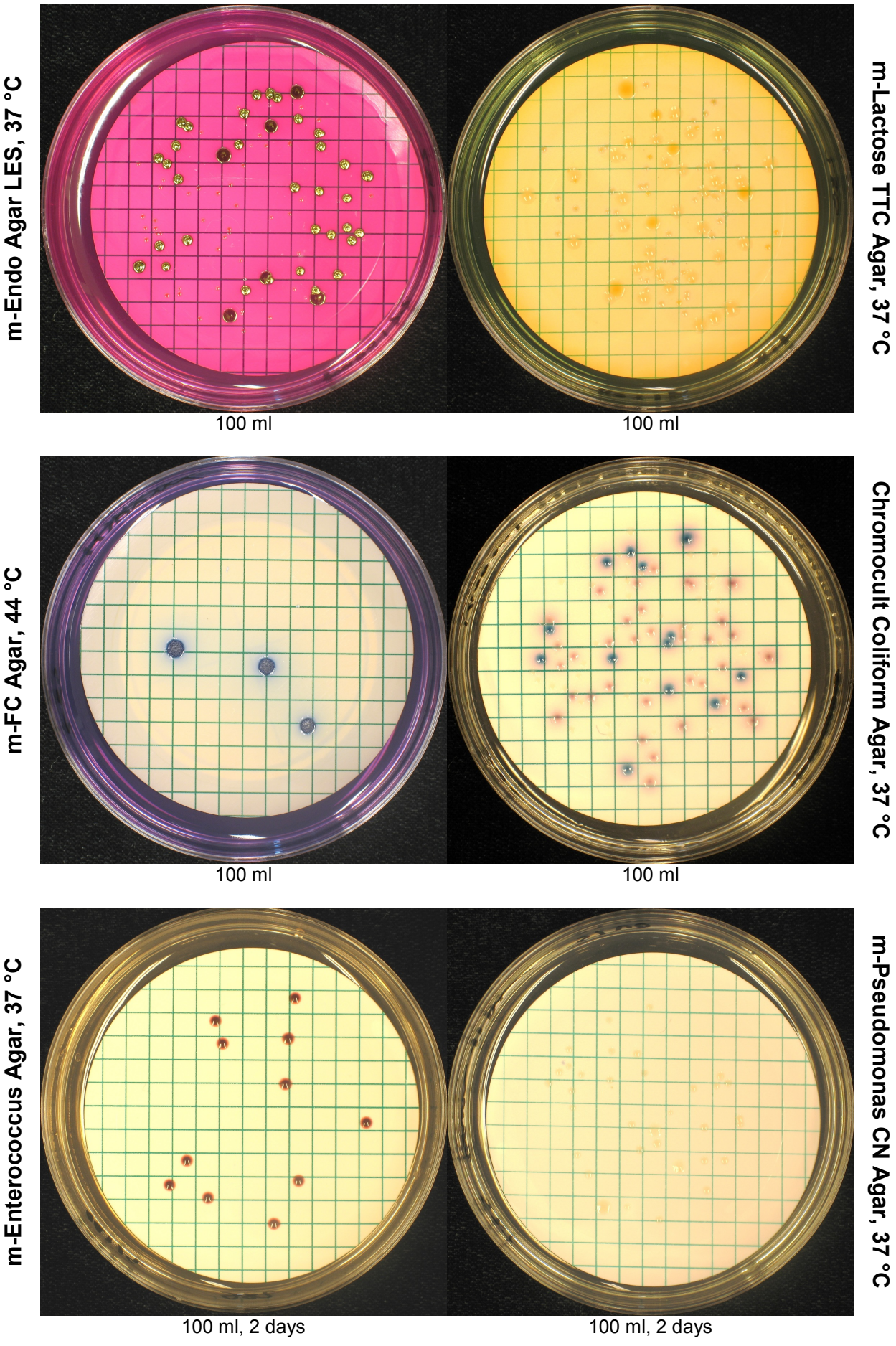
Susp. intestinal enterococci (MF)			Intestinal enterococci (MF)			Susp. *Pseudomonas aeruginosa* (MF)			*Pseudomonas aeruginosa* (MF)			Total plate count 22 °C, 3 days			Total plate count 36±2 °C, 2 days			Lab no.
A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	
												0.067	0.901	**2.560**				**1131**
			-0.005	0.000	0.304							-1.107	-0.138	0.293				**1132**
				0.000	-1.725				0.000	0.730	0.431	0.067	0.679	0.293	0.920	-0.772	1.378	**1237**
			-0.408	0.000	-1.508				0.000	-0.725	0.010	0.067	-0.769	-0.464	0.727	0.522	-0.191	**1254**
			1.034	0.000	0.768				0.000	-0.725	-1.099	0.067	0.102	-0.464	0.595	0.321	0.746	**1545**
			-0.005	0.000	0.491				0.000	-0.182	0.267	0.927	1.435	0.976	-0.030	1.901	-1.288	**1594**
			-0.408	0.000	1.041				0.000	-0.182	0.267	-1.107	0.679	0.527	0.043	0.218	-0.447	**1611**
																		1753
												0.067	1.010	-0.202				**1868**
			-0.005	0.000	**2.252**				0.000	-0.182	0.510	0.067	0.337	1.191	**-2.305**	-0.655	-0.447	**1970**
			-1.359		-0.744				0.000	-1.370	0.431	0.067	1.224	-0.464	-0.327	-0.206	0.746	**2050**
			-0.408	0.000	0.209				0.000	-0.725	0.742	-1.107	-0.017	-1.322	1.170	1.006	0.963	**2386**
												-1.107	1.641	**-2.340**	-1.592	0.422	1.173	**2637**
			-0.854	0.000	-1.294							-1.107	-0.385	**-2.340**				**2670**
			-0.408	0.000	-1.725							0.067	0.221	-1.022	0.856	-0.772	0.523	**2704**
												-1.107	0.337	**4.000**				**2745**
																		2915
			-0.408	0.000	1.130							1.518	-0.385	0.527	0.324	1.006	-0.714	**2944**
												-1.107	-1.035	-0.464				**3055**
			-0.005	0.000	-0.176				0.000		**-2.132**	0.553	0.452	-0.464	-0.327	1.554	0.293	**3057**
									0.000	**4.000**	1.177	0.553	**-2.040**	0.293	-0.883	**-2.069**	-0.994	**3076**
																		3145
			0.710	0.000	0.398				0.000	-0.182	-0.983	0.067	1.118	-0.202	-1.592	0.321	0.523	**3159**
			-0.005	0.000	1.041				0.000	-0.182	0.097	0.067	0.901	1.605	-0.638	0.114	-0.191	**3162**
			-0.408		**-4.000**							**2.787**	**-2.354**		-0.719	-1.260	-1.599	**3164**
			-0.005	0.000	0.768				0.000	-0.182	0.010	0.553	-0.385	-0.202	-0.481	0.114	-0.191	**3305**
			-0.854	0.000	-0.775					**4.000**	**2.429**	**2.606**	**-4.000**	0.050				**3533**
												-1.107	**-4.000**	-0.464	0.043		-0.994	**3587**
												0.553	**-2.195**	0.755				**3730**
			-0.005	0.000	-0.274				0.000	0.297	0.010	0.553	-0.017	-0.737	-0.559	0.218	-0.447	**3868**
																		4015
												-1.107	**2.239**					**4288**
			0.710	0.000	-0.373							-1.107	1.118	0.050	-0.103	0.719	0.523	**4319**
			-0.854	0.000	0.398				0.000	-0.182	1.036	0.067	1.944	0.293	0.528	**2.320**	0.523	**4339**
			2.176	0.000	0.491				0.000	-0.182	-0.445	1.518	-1.171	-0.737	0.856	-0.098	-0.191	**4343**
			-1.959		-0.176				0.000	-0.725	0.964	0.067	0.790	0.050	-0.559	0.218	0.963	**4356**
			1.034	0.000	0.066							0.067	-1.450	-1.322	**-2.305**	0.114	-0.191	**4459**
			0.365	0.000	-1.508				0.000	0.297	0.502	0.067	-0.261	0.755	0.185	-0.772	0.293	**4633**
			1.340	0.000	-0.176							-1.107	0.337	0.293				**4723**
			-0.854	0.000	-1.946				0.000	-0.182	**-3.059**	0.927	-0.901	-0.464	0.595	-1.518	0.293	**4889**
			0.365	0.000	-0.472				0.000	1.128	-0.535	0.927	-0.769	-0.737	**-2.770**	-0.098	0.523	**4980**
			-0.408	0.000	-1.835				0.000	0.730	-0.170	-1.107	-0.261	-0.464	-0.800	-0.655	-0.191	**5018**
												0.553	-1.171	0.755	-0.176	-0.891	-0.994	**5094**
			-1.959	0.000	-0.079				0.000	-1.370	-0.263	**3.286**	**-3.391**	-0.464	**2.100**	-1.926	0.055	**5128**
										-0.182	-0.455							**5188**
												-1.107	0.337					**5201**
									0.000	-0.725	**-4.000**							**5220**
									0.000	0.730	-0.763	0.553	-0.385	-0.737	**-4.000**	-0.540	0.293	**5352**
			1.034	0.000	0.950							-1.107	-0.017	**4.000**	-1.052	0.816	0.963	**5447**
																		5494
																		5553
			-0.005	0.000	-1.084				0.000	-0.725	-1.982	0.927	-1.309	-1.022	**-4.000**	-0.772	-1.288	**5858**
			1.631	0.000	1.710				0.000	-0.725	0.183	0.553	-0.512	-1.022	0.255	-1.012	1.579	**5950**
												0.553	-0.261	0.527	-0.251	-0.655	1.378	**6175**
			0.710	0.000	0.398				0.000	1.128	0.742	0.553	1.743	-0.464	0.324	1.642	0.055	**6180**
			-1.959	0.000	0.491				0.000	0.297	0.431	0.553	-0.017	-0.737	-0.638	0.114	-1.930	**6233**
			-0.005	0.000	1.830							0.067	0.679	-1.022				**6253**
									0.000	**2.176**	-0.871				-0.481	**-2.519**	-0.994	**6448**
												0.067	-0.138	-1.639	**-3.756**	0.321	-0.714	**6456**
			0.365	0.000	0.114				0.000	-1.370	0.589	-1.107	-0.138	-0.464	-0.030	1.284	**-2.285**	**6563**
												1.241	-0.261	1.191	-0.030	-0.427	0.055	**6686**
												1.647	**-4.000**		**-4.000**	**-4.000**	**-2.672**	**7191**
			1.034	0.000	0.584				0.000	**2.176**	-0.555	0.553	1.330	1.191	-1.498	0.321	0.293	**7248**
			-1.959	0.000	**-4.000**				0.000	**-2.210**	**-3.391**				**-4.000**	**-3.187**	-0.714	**7282**
			0.710	0.000	-0.472				0.000	0.297	0.502	0.067	-0.901	0.755	-0.251	-0.540	0.055	**7302**
												-1.107	-0.017	0.976				**7442**
												1.241	-0.901	0.976	-0.103	-0.427	0.523	**7564**
			-0.005	0.000	-0.373				0.000	-0.182	0.267	0.927	-0.261	1.191	1.933	1.284	0.523	**7688**
			-1.359	0.000	-1.294				0.000	-1.370	-1.999	0.067	-1.450	-1.639	0.920	0.218	-1.599	**7728**
			1.034	0.000	0.575				0.000	0.730	0.208	-1.107	0.790	0.527	0.255	0.522	1.173	**7876**
			0.710	0.000	-0.373				0.000	1.128	-0.079	0.067	-0.512	0.293	-0.883	0.218	0.523	**7930**
			1.631	0.000	0.398							0.067	-1.171	0.976	0.043	-0.206	-0.191	**7962**
			0.365	0.000	-0.877				0.000	0.730	0.183	0.067	0.102	-1.022	0.856	0.522	0.055	**7968**
			0.710	0.000	-0.079				0.000		0.183	-1.107	0.221	-1.977	-0.176	0.621	0.293	**8068**
			0.710		-1.508				0.000		-0.555	-1.107		0.293	1.046		0.293	**8252**
												0.067	0.337	-1.639				**8260**
			-0.005	0.000	1.949				0.000	0.297	-0.515	0.067	-0.512	-0.202	0.393	-0.772	0.963	**8329**
			-0.005	0.000	-0.176				0.000	-0.725	-0.263	1.999	-0.639	-0.202	0.393	-1.388	-0.447	**8380**
			0.710	0.000	1.308				0.000	-0.725	-0.455	**4.000**	0.566	0.976	0.185	-0.098	-0.714	**8435**
			-0.854	0.000	-1.084							-1.107	-0.138	**2.190**				**8569**
												0.553	0.337	-0.464	0.727	-0.206	-0.447	**8626**
			0.365	0.000	-0.673				0.000	0.297	0.183	-1.107	-0.138	-0.464	0.255	-0.772	0.055	**8628**
			-2.741	0.000	1.130				0.000	0.297	-0.455	0.067	1.224	1.999	-0.176	0.114	-1.599	**8663**
												0.067	-0.639	0.293	1.989	0.321	-0.447	**8742**

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
8766					-1.873	-0.846	-1.358				-0.153	0.000	0.263	0.510	0.874	0.420	0.610	0.000	0.688
8840					-0.459	1.862	0.088				1.020	0.000	0.263	0.140	-0.459	1.839	-0.794	0.000	0.861
8862					0.747	1.466	1.235				-0.507	0.000	1.348	0.140	0.363	0.831	1.651	0.000	0.929
8891					-0.722	0.100	**-2.376**												
8898					-0.589	**2.475**	0.949				-1.219	0.000	1.157	0.600	-0.364	-0.362	1.055	0.000	-0.277
8998																			
9002					**-4.000**	**-4.000**	**-4.000**				-1.807	0.000	**-3.544**						
9306														0.140	-0.459	-0.625	-0.463	0.000	-0.337
9436					**2.018**	1.189	0.949				-1.577	0.000	0.573	0.600	0.450	-0.002	-0.463	0.000	-0.277
9441																			
9524					-0.856	0.823	-0.491					0.000	1.012	1.288	0.007	-0.486		0.000	0.071
9736					-0.204	-1.795	-0.455				0.154	0.000	0.113	-0.247	-0.951	-1.365	0.610	0.000	-0.708
9899					-0.589	-0.742	0.670				0.556	0.000	0.630	1.371	0.187	0.584	1.055	0.000	0.033
9903					1.296	-0.444	0.629				-0.507	0.000	-0.601						
n		0	0	0	71	71	71	0	0	0	60	73	74	60	59	59	59	59	59
Min					-4.000	-4.000	-4.000				-1.807	0.000	-3.544	-2.044	-2.525	-2.490	-2.199	0.000	-3.051
Max					4.000	4.000	4.000				4.000	0.000	2.315	4.000	1.973	2.818	3.959	0.000	2.009
Median					-0.079	-0.256	0.088				-0.153	0.000	0.087	-0.051	0.007	-0.097	-0.163	0.000	-0.005
Mean					0.056	0.000	-0.056				0.037	0.000	-0.048	0.067	0.000	0.000	0.067	0.000	0.000
SD					1.280	1.195	1.280				1.136	0.000	1.075	1.118	1.000	1.000	1.117	0.000	1.000
z<-3					2	1	2				0	0	2	0	0	0	0	0	1
-3≤z<-2					1	0	4				0	0	2	1	1	2	1	0	2
2<z≤3					3	2	1				3	0	2	1	0	2	1	0	1
z>3					2	1	1				2	0	0	2	0	0	2	0	0

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	
			1.340		-0.002				0.000	0.730	0.431	-1.107	-0.512	0.050	1.108	0.522	0.523	**8766**
			-0.005		1.308							-1.107	0.790	0.755	0.727	1.100	**2.335**	**8840**
			-0.854	0.000	1.157							0.067	0.566	0.755				**8862**
												-1.107	-1.171	-1.322				**8891**
			-0.854	0.000	-0.472				0.000	-0.725	**2.929**	0.553	0.901	0.755	0.324	0.522	0.746	**8898**
																		8998
			-3.049	0.000	**-4.000**							-1.107	**-4.000**	**-4.000**				**9002**
												-1.107	0.221	0.293	0.983	1.100	-0.191	**9306**
			-0.854	0.000	-0.031				0.000	**3.351**	0.573	-1.107	0.679	1.605	1.292	0.719	1.965	**9436**
																		9441
			1.340	0.000	-0.643							0.067	1.118	0.755		1.006	0.963	**9524**
			-0.005	0.000	-0.206				0.000	0.297	-0.034	-1.107	0.452	-0.202	**-2.197**	-0.206	-1.599	**9736**
			-0.408	0.000	1.139				0.000	-0.182	0.658	0.067	0.452	1.191	0.255	0.422	1.774	**9899**
			1.340	0.000	-0.265				0.000	-0.725	0.719	-1.107	0.790	-0.202	0.727	0.621	**4.000**	**9903**

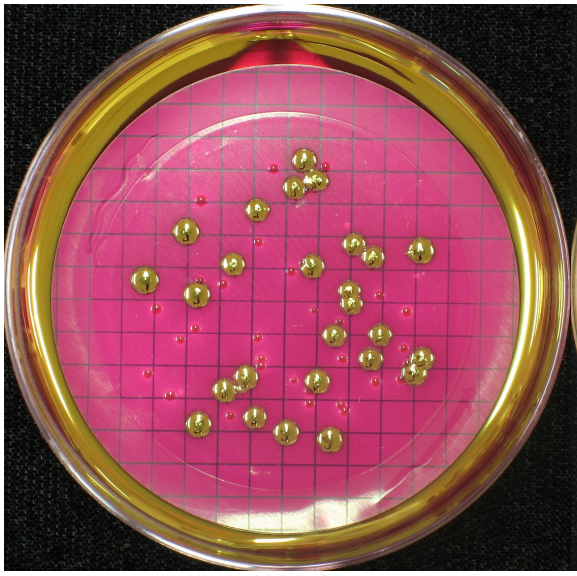
0	0	0	63	58	64	0	0	0	51	50	53	86	85	82	69	68	70	**n**
			-3.049	0.000	-4.000				0.000	-2.210	-4.000	-1.107	-4.000	-4.000	-4.000	-4.000	-2.672	**Min**
			2.176	0.000	2.252				0.000	4.000	2.929	4.000	2.239	4.000	2.100	2.320	4.000	**Max**
			-0.005	0.000	-0.128				0.000	-0.182	0.097	0.067	-0.017	0.050	-0.030	0.114	0.055	**Median**
			-0.048	0.000	-0.187				0.000	0.160	-0.139	0.047	-0.188	0.049	-0.286	-0.059	0.057	**Mean**
			1.064	0.000	1.296				0.000	1.259	1.213	1.084	1.296	1.246	1.411	1.105	1.102	**SD**
																		Summa
			1	0	3				0	0	3	0	5	1	5	2	0	28
			1	0	0				0	1	1	0	3	2	4	2	2	30
			1	0	1				0	2	2	2	1	2	1	1	1	30
			0	0	0				0	3	0	2	0	2	0	0	1	18

Mixture A


m-Endo Agar LES, 37 °C
m-Lactose TTC Agar, 37 °C
100 ml
100 ml
m-FC Agar, 44 °C
Chromocult Coliform Agar, 37 °C
100 ml
100 ml
m-Enterococcus Agar, 37 °C
m-Pseudomonas CN Agar, 37 °C
100 ml, 2 days
100 ml, 2 days

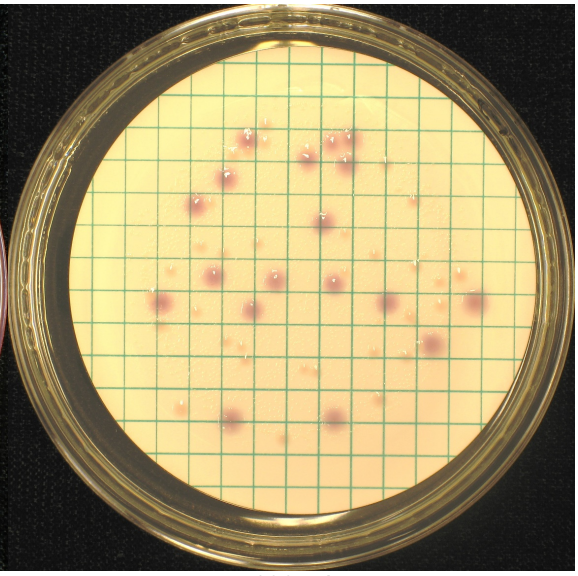
Mixture B

m-Endo Agar LES, 37 °C



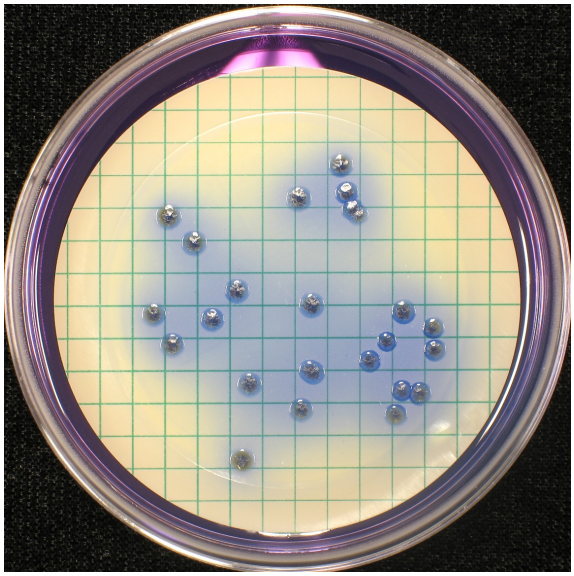
100 ml

Chromocult Coliform Agar, 37 °C



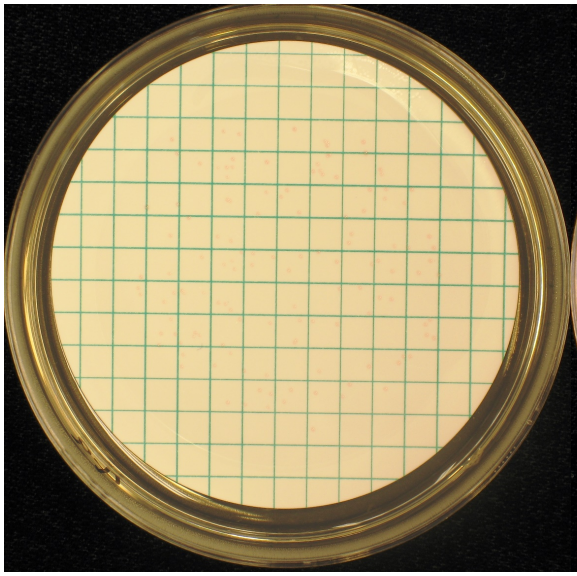
100 ml

m-FC Agar, 44 °C



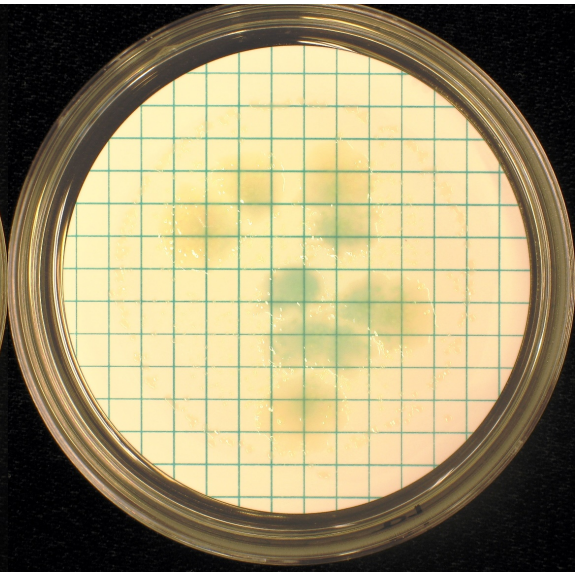
100 ml

m-Enterococcus Agar, 37 °C



100 ml, 2 days

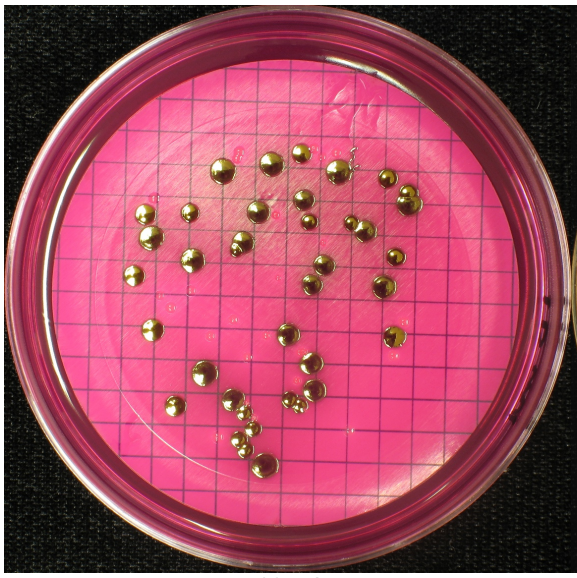
m-Pseudomonas CN Agar, 37 °C



100 ml, 2 days

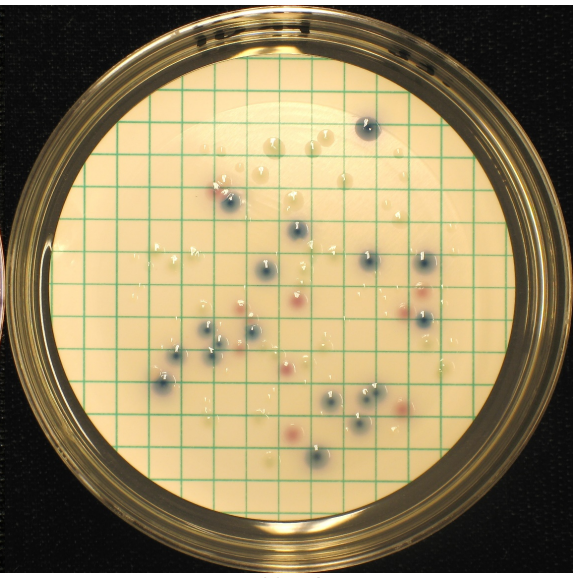
Mixture C

m-Endo Agar LES, 37 °C



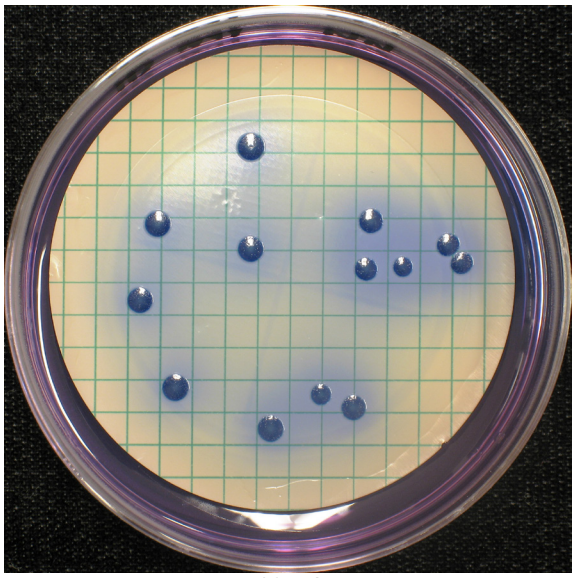
10 ml

Chromocult Coliform Agar, 37 °C



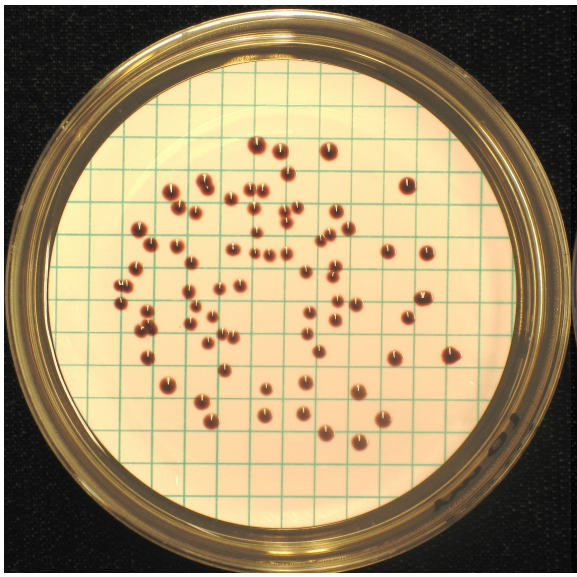
10 ml

m-FC Agar, 44 °C



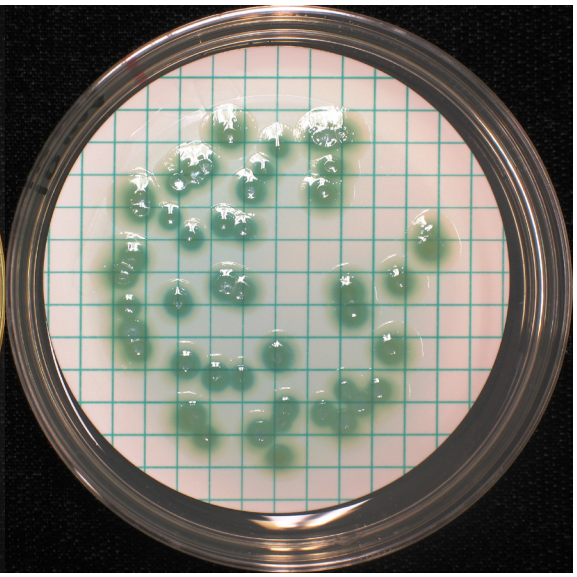
10 ml

m-Enterococcus Agar, 37 °C



10 ml, 2 days

m-Pseudomonas CN Agar, 37 °C



10 ml, 2 days

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

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

Proficiency Testing – Food Microbiology, October 2016

PT reports published 2017

Proficiency Testing – Food Microbiology, January 2017, by Jonas Ilbäck

Proficiency Testing – Drinking Water Microbiology, March 2017, by Tommy Šlapokas

Proficiency Testing – Food Microbiology, April 2017, 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