

Proficiency testing Food Microbiology

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Abbreviations

Media

ALOA	Agar for <i>Listeria</i> according to Ottaviani & Agosti
APW 2%	Alcaline peptone water, 2 % NaCl
BA	Blood agar
BcsA	<i>Bacillus cereus</i> selective agar
BEA	Bile esculin agar
BGA	Brilliant green agar
BGLB	Brilliant green lactose bile broth
BP	Baird-Parker agar
BPW	Buffered peptone water
BS	Bromthymol blue saccharose agar
CBC	Oxoid Brilliance™ <i>Bacillus cereus</i> agar
CIN	Cefsulodin irgasan novobiocin agar
Compact Dry EC	Compact Dry™ <i>E. coli</i> and coliforms
Compact Dry ETB	Compact Dry™ Enterobacteriaceae
Compact Dry ETC	Compact Dry™ Enterococcus
Compact Dry TC	Compact Dry™ Total Count
COMPASS	COMPASS® Enterococcus agar
CT-SMAC	Cefixime tellurite sorbitol MacConkey agar
DG18	Dikloran glycerol agar
DRBC	Dikloran Rose-Bengal chloramphenicol agar
EC	<i>E. coli</i> broth
EMB	Eosin Methylene Blue agar
ENT	Slanetz & Bartley <i>Enterococcus</i> agar
HEA	Hektoen enteric agar
IA	Iron agar
ISA	Iron sulphite agar
ITC	Irgasan ticarcillin potassium chlorate broth
KEAA	Kanamycin esculin azide agar
LMBA	<i>Listeria monocytogenes</i> blood agar
LSB	Lauryl sulphate broth
LTLSB	Lactose tryptone lauryl sulphate broth
mCCDA	Modified charcoal cephaloperazone deoxycholate agar
mCP	Membrane <i>Clostridium perfringens</i> agar
MKTTn	Muller-Kauffmann tetrathionate/novobiocin broth
MLCB	Manitol Lysine Crystal violet Brilliant green agar
MPCA	Milk plate count agar
MRB	Modified Rappaport broth
MRS	de Man, Rogosa and Sharpe agar
MRS-aB	de Man, Rogosa and Sharpe agar with amphotericin
MRS-S	de Man, Rogosa and Sharpe agar with sorbic acid

MSRV	Modified semi-solid Rappaport-Vassiliadis enrichment media
mTSB	Modified tryptone soya broth
MYP	Mannitol egg yolk polymyxin agar
NAP	Nitrite actidione Polymyxin agar
OCLA	Oxoid Brilliance™ Listeria agar
OGYE	Oxytetracyclin glucose yeast extract agar
OPSP	Oleandomycin, Polymixin, Sulphadiazine, Perfringens agar
PAB	Perfringens agar base
PDA	Potato dextrose agar
PALCAM	Polymyxin acriflavine lithium chloride ceftazidime aesculin mannitol agar
Petrifilm AC	3M™ Petrifilm™ Aerobic Count
Petrifilm CC	3M™ Petrifilm™ Coliform count
Petrifilm Disk	3M™ Petrifilm™ Staph Express Disk
Petrifilm EB	3M™ Petrifilm™ Enterobacteriaceae
Petrifilm EC/CC	3M™ Petrifilm™ <i>E. coli</i> /Coliform count
Petrifilm EL	3M™ Petrifilm™ Environmental Listeria
Petrifilm LAB	3M™ Petrifilm™ Lactic acid bacteria
Petrifilm RAC	3M™ Petrifilm™ Rapid Aerobic Count
Petrifilm REC	3M™ Petrifilm™ Rapid <i>E. coli</i> /Coliform count
Petrifilm RYM	3M™ Petrifilm™ Rapid Yeast and Mold
Petrifilm SEC	3M™ Petrifilm™ Select <i>E. coli</i>
Petrifilm Staph	3M™ Petrifilm™ Staph Express
Petrifilm YM	3M™ Petrifilm™ Yeast and Mold
PEMBA	Polymyxin pyruvate egg yolk mannitol bromothymol blue agar
PSB	Peptone sorbitol bile salts broth
PCA	Plate count agar
RPFA	Baird-Parker agar with rabbit plasma fibrinogen
SFA	Sugar-free agar
RVS	Rappaport-Vassiliadis Soy peptone broth
Saubouraud	Saubouraud chloramphenicol agar
SC	Sulphite cycloserine agar
SCD	Soyabean Casein Digest agar
SFP	Shahidi-Ferguson Perfringens agar
SMAC	Sorbitol MacConkey agar
SP	Salt Polymyxin broth
SSDC	Salmonella/Shigella sodium deoxycholate calcium chloride agar
TBX	Tryptone bile X-glucuronide agar
TCBS	Thiosulphate citrate bile salts sucrose agar
TGE	Tryptone glucose extract agar
TEMPO AC	TEMPO® Aerobic count
TEMPO BC	TEMPO® <i>Bacillus cereus</i>
TEMPO CAM	TEMPO® Campylobacter
TEMPO CC	TEMPO® Coliform count
TEMPO EB	TEMPO® Enterobacteriaceae
TEMPO EC	TEMPO® <i>E. coli</i>

TEMPO RYM	TEMPO® Rapid Yeast/Mould
TEMPO STA	TEMPO® Coagulase-positive staphylococci
TEMPO YM	TEMPO® Yeast/Mould
TGE	Tryptone glucose extract agar
TS	Tryptose sulphite agar
TSA	Tryptic soya agar
TSC	Tryptose sulphite cycloserine agar
TSBY	Tryptone soya broth with yeast extract
XLD	Xylose lysine deoxycholate agar
VIDAS CAM	VIDAS® Campylobacter
VIDAS ECPT	VIDAS® UP E. coli O157 (including H7)
VIDAS LMX	VIDAS® Listeria monocytogenes Xpress
VRB	Violet red bile agar
VRBG	Violet red bile glucose agar
YGC	Yeast extract glucose chloramphenicol agar

Organisations

AFNOR	French National Standardization Association
AOAC	AOAC INTERNATIONAL
ATCC	American Type Culture Collection
CBS	Centraalbureau voor Schimmelcultures (Westerdijk Institute)
CCUG	Culture Collection University of Gothenburg
IDF	International Dairy Foundation
ISO	International Organization for Standardization
NMKL	Nordic-Baltic Committee on Food Analyses
NordVal	NordVal International - NMKL
SLV	Livsmedelsverket/Swedish Food Agency, Sweden
Fohm	Public Health Agency of Sweden

Analyses in this PT round

Quantitative analyses

Aerobic microorganisms, 30 °C

Psychrotrophic microorganisms

Enterobacteriaceae

Escherichia coli

Presumptive *Bacillus cereus*

Coagulase-positive *Staphylococcus*

Lactic acid bacteria

Clostridium perfringens

Anaerobic sulphite-reducing bacteria

Aerobic microorganisms in fish products

H₂S-producing bacteria in fish products

Yeasts

Moulds

Method

Reporting of results and method information

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

It is also mandatory for the participants to report method information for all analyses. This method information is sometimes contradictory or difficult to interpret. For example, when participants state a medium that is not included in the standard method they refer to, or when manual comments by the participant contradict the reported method information. In such cases, the reported method information provided by the participants is generally used in method comparisons “as it is”. Alternatively, method data that are difficult to interpret may be excluded or added to the group “Other”, together with results from methods and media that are only used by 1–2 participants.

Standard deviation and assigned value

Evaluation of the participants’ results and statistical calculations are carried out on the \log_{10} transformed results. Results reported by participants as “> value” are not evaluated. Results reported as “< value” are excluded from the evaluation, or occasionally treated as zero (negative result).

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

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

Outliers

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

Results from different methods

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

Measurement uncertainty for the assigned values

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

$$u_{PT} = 1.25 \times \frac{s_{PT}}{\sqrt{n}}$$

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

$$u_{PT} < 0.3s_{PT}$$

Z-scores

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

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

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

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

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

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

Table legends

- N number of participants that reported results for the analysis
- n number of participants with satisfactory result (false results and outliers excluded)
- m_{PT} assigned value, robust mean value in \log_{10} cfu ml⁻¹
- s_{PT} robust standard deviation
- u_{PT} standard uncertainty of the assigned value

- F number of false positive or false negative results
- $<$ number of low outliers
- $>$ number of high outliers
- results deviating more than 1 s_{PT} from m_{PT} , or unusually many deviating results.

Figure legends

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

Results

General comments

Several participants reported results that – for \log_{10} results – were very large, e.g. 10 or 100. At least some of these are likely due to attempts to report results “less than”, e.g. <10 or <100. Due to technical limitations on the web portal, such results however need to be reported as 0 (zero), which is clearly stated in the instructions. These results have therefore been excluded from the evaluation. In a few cases the participants have commented during the reporting that the intention was to report results “less than”. In these cases, the results have been adjusted accordingly to reflect this.

One participant mixed up samples B and C during the analysis. Since identifying/reporting the correct samples is considered part of the PT, these results are still included in the evaluation.

General outcome

Samples were sent to 152 participants: 35 in Sweden, 104 in Europe, and 13 outside of Europe. Individual results are listed in Appendix 1. Z-scores for individual results are listed in Appendix 2.

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

	Sample A				Sample B				Sample C			
% participants with												
Microorganisms	<i>Bacillus cereus</i> <i>Enterococcus durans</i> <i>Escherichia coli</i> <i>Hafnia alvei</i> <i>Staphylococcus aureus</i>				<i>Aspergillus candidus</i> <i>Candida glabrata</i> <i>Clostridium perfringens</i> <i>Escherichia coli</i>				<i>Bacillus cereus</i> <i>Enterococcus faecalis</i> <i>Rhodotorula minuta</i> <i>Staphylococcus aureus</i>			
Analysis	Target organism	N	F	X	Target organism	N	F	X	Target organism	N	F	X
Aerobic micro-organisms, 30 °C	All	163	0	14	All	162	1	15	All	162	0	13
Psychrotrophic microorganisms	All	20	0	1	All	19	0	0	All	21	0	0
Enterobacteriaceae	<i>E. coli</i> <i>H. alvei</i>	137	1	7	<i>E. coli</i>	136	2	9	-	129	5	0
Escherichia coli	<i>E. coli</i>	115	6	7	<i>E. coli</i>	114	2	10	-	115	6	0
Presumptive <i>Bacillus cereus</i>	<i>B. cereus</i>	100	0	4	-	93	5	0	<i>B. cereus</i>	97	2	4
Coagulase-positive Staphylococcus	<i>S. aureus</i>	105	1	8	-	101	4	0	<i>S. aureus</i>	102	7	13
Lactic acid bacteria	<i>E. durans</i>	61	5	3	-	59	21	0	<i>E. faecalis</i>	59	2	7
<i>Clostridium perfringens</i>	-	47	0	0	<i>C. perfringens</i>	48	2	3	-	46	1	0
Anaerobic sulphite-red. bacteria	-	57	2	0	<i>C. perfringens</i>	58	0	2	-	53	1	0
Aerobic microorganisms in fish products	All	21	0	0	All	21	0	1	All	21	1	2
H2S-producing bacteria in fish products	<i>H. alvei</i>	19	1	1	-	20	1	0	-	20	0	0
Yeasts	-	141	7	0	<i>C. glabrata</i>	143	5	8	<i>R. minuta</i>	142	33	9
Moulds	-	137	4	0	<i>A. candidus</i>	141	15	9	-	133	6	0

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

■ The results are not evaluated.

Aerobic microorganisms, 30 °C

Sample A

All strains in the sample were target organisms and were present in similar concentrations.

In total, 163 results were evaluated. Eight low and six high outliers were identified.

Sample B

E. coli was present in the highest concentration and was thus the main target organism.

In total, 162 results were evaluated. Four low and eleven high outliers were identified, as well as one false negative result.

Sample C

B. cereus, *E. faecalis* and *S. aureus* were present in the highest concentration and were thus the main target organisms.

In total, 162 results were evaluated. Ten low and three high outliers were identified.

General remarks

Most participants followed either ISO 4833-1:2013, NMKL 86:2013, or a method with Petrifilm AC. ISO 4833-1:2013 was last reviewed by ISO in 2019 and remains current. An amendment with a clarification on the scope of the method is available (ISO 4833-1:2013/Amd 1:2022). NMKL 86:2013 was last reviewed by NMKL in 2022 and remains current.

Both NMKL 86:2013 and ISO 4833-1:2013 are based on incubation on PCA or MPCA at 30 °C for 72 h. Users of Petrifilm™ AC can use different incubation times/temperatures, depending on the method validation. There is also a “rapid” version of Petrifilm that gives results in 24 h.

Table 2. Results from analysis of aerobic microorganisms, 30 °C.

Method	Sample A							Sample B							Sample C						
	<i>N</i>	<i>n</i>	<i>m</i> _{PT}	<i>s</i> _{PT}	<i>F</i>	<	>	<i>N</i>	<i>n</i>	<i>m</i> _{PT}	<i>s</i> _{PT}	<i>F</i>	<	>	<i>N</i>	<i>n</i>	<i>m</i> _{PT}	<i>s</i> _{PT}	<i>F</i>	<	>
All results	163	149	5.01	0.13	0	8	6	162	146	4.08	0.16	1	4	11	162	149	5.09	0.12	0	10	3
ISO 4833-1:2013	44	43	5.00	0.10	0	0	1	45	43	4.04	0.10	0	0	2	46	43	5.11	0.09	0	2	1
NMKL 86:2013	42	37	5.02	0.10	0	2	3	39	37	4.03	0.17	0	1	1	37	35	5.08	0.10	0	1	1
Petrifilm™ AC (72 h)	30	26	5.04	0.12	0	3	1	30	24	4.12	0.18	0	3	3	29	25	5.14	0.08	0	3	1
Other	15	14	4.94	0.12	0	1	0	16	14	4.08	0.19	0	0	2	17	16	5.03	0.13	0	1	0
TEMPO® AC	10	10	5.02	0.16	0	0	0	10	9	4.18	0.13	1	0	0	11	10	5.16	0.14	0	1	0
Petrifilm™ AC (48 h)	7	6	5.06	0.09	0	0	1	8	6	3.98	0.09	0	0	2	8	7	5.12	0.11	0	1	0
NMKL 86:2006	6	5	5.03	0.09	0	1	0	7	7	4.01	0.07	0	0	0	7	6	5.17	0.14	0	1	0
ISO 4833-2:2013	5	4	-	-	0	1	0	3	3	-	-	0	0	0	3	3	-	-	0	0	0
Compact Dry™ TC	2	2	-	-	0	0	0	2	2	-	-	0	0	0	2	2	-	-	0	0	0
Petrifilm™ RAC (24 h)	2	2	-	-	0	0	0	2	1	-	-	0	0	1	2	2	-	-	0	0	0

For individual methods: *m*_{PT} = median value and *s*_{PT} = standard deviation for the particular method (outliers and false results excluded).

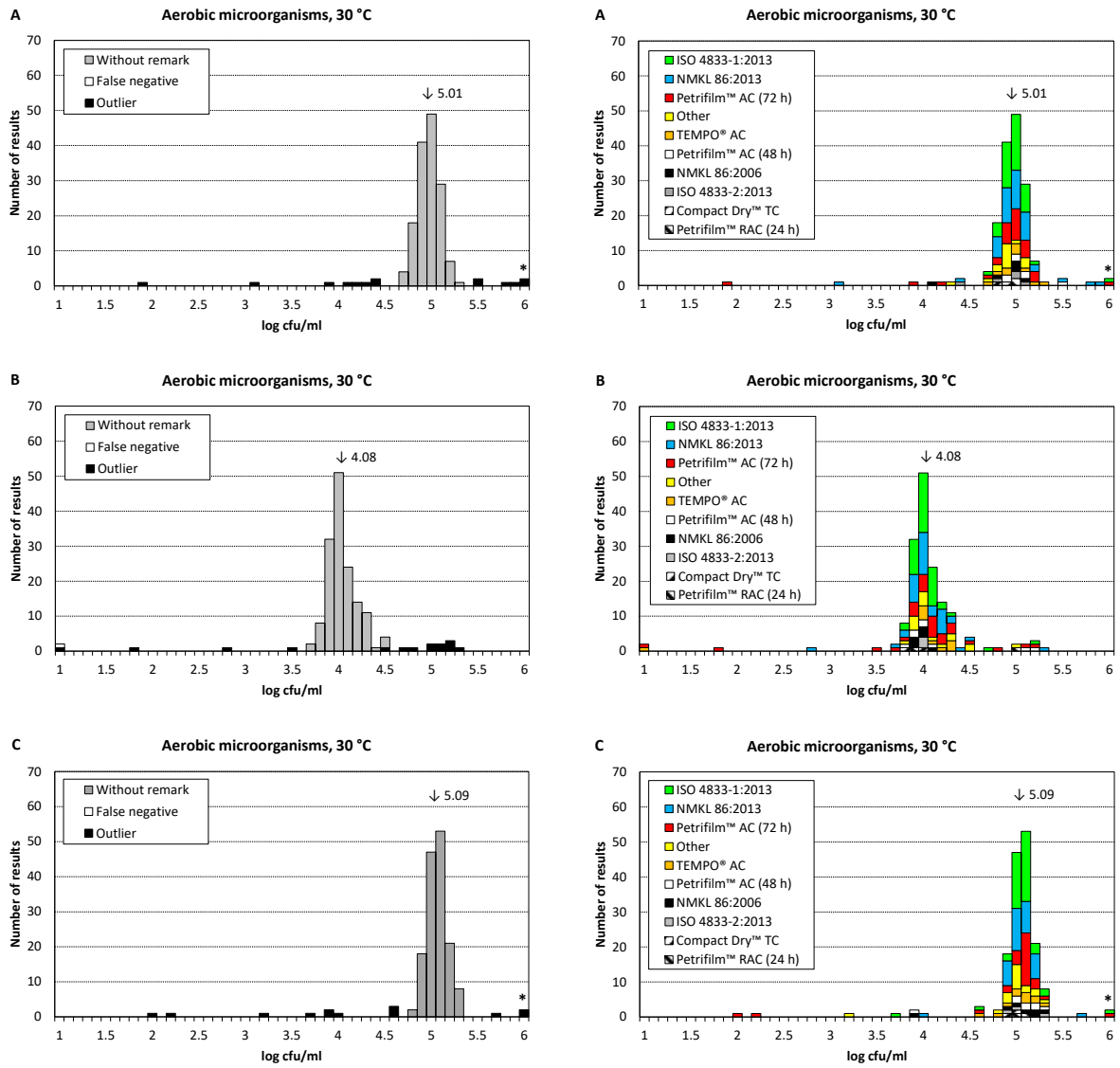


Figure 1. Results from analysis of aerobic microorganisms, 30 °C.

Psychrotrophic microorganisms

Sample A

All strains in the sample were target organisms and were present in similar concentrations.

In total, 20 results were evaluated. One low outlier was identified.

Sample B

At the Swedish Food Agency, none of the microorganisms in the sample formed colonies after incubation on PCA at 6.5 °C for 10 days.

In total, 19 results were evaluated. The results varied considerably, between 0 and 6.1 log₁₀ cfu ml⁻¹. For the most part, the variation appears to be due to method differences. In general, participants that incubated at low temperatures (e.g. 6.5 °C) reported zero (negative) results, whereas participants that incubated at higher temperatures (typically 17–21 °C) reported concentrations centred around 4.0 log₁₀ cfu ml⁻¹. The latter roughly corresponds to the concentration of *E. coli* in the sample.

Note: Due to the low number of positive results, and the high uncertainty of the assigned value, the results are not evaluated, and no z-scores are calculated. the m_{PT} and s_{PT} in Appendix 1 refer to the non-robust median and standard deviation of the 12 positive results, respectively. They should be treated only as informational.

Sample C

At the Swedish Food Agency, *R. minuta* formed distinct colonies at a concentration of 3.26 log₁₀ cfu ml⁻¹ after incubation on PCA at 6.5 °C for 10 days. Other strains in the sample formed pin-point colonies at a concentration of approximately 4.9 log₁₀ cfu ml⁻¹.

In total, 21 results were evaluated. Similar to sample B, the results varied considerably, between 0 and 5.2 log₁₀ cfu ml⁻¹. Again, the variation appears to be at least in part due to method differences, though this was not as clear as for sample B. For example, participants that incubated at 6.5 °C for 10 days reported results over the entire range 0-5.0 log₁₀ cfu ml⁻¹. Likely, the formation and interpretation of pin-point colonies attributed the variation in results between participants.

Note: Due to the low number of positive results, and the high uncertainty of the assigned value, the results are not evaluated, and no z-scores are calculated. the m_{PT} and s_{PT} in Appendix 1 refer to the non-robust median and standard deviation of the 12 positive results, respectively. They should be treated only as informational.

General remarks

The methods used by the participants vary to a great extent in the incubation time and temperature. Users of NMKL 86:2013 can incubate either for 10 days at 6.5 °C, or for 20 h at 17 °C followed by 3 days at 7 °C. For psychrotrophic microorganisms in milk, ISO 6730:2005/IDF 101:2005 stipulates incubation at 6.5 °C. The other method for milk, ISO 8552:2004/IDF 132:2004, instead estimates the number of psychrotrophic microorganisms in a rapid method based on incubation at 21 °C. Both of these have been

replaced by ISO 17410:2019, which stipulates incubation for 10 days at 6.5 °C. This was last reviewed by ISO in 2024 and remains current.

Since the results for samples B and C are not evaluated, participants are encouraged to self-assess their performance for these two samples.

Table 3. Results from analysis of psychrotrophic microorganisms.

Method	Sample A							Sample B*							Sample C*						
	N	n	<i>m</i> _{PT}	<i>s</i> _{PT}	F	<	>	N	n	<i>m</i> _{PT}	<i>s</i> _{PT}	F	<	>	N	n	<i>m</i> _{PT}	<i>s</i> _{PT}	F	<	>
All results	20	19	4.68	0.32	0	1	0	19	19	3.87	2.07	0	-	-	21	21	4.90	2.15	0	-	-
NMKL 86:2013 (17 °C / 7 °C)	5	5	4.64	0.25	0	0	0	0	0	-	-	0	0	0	0	0	-	-	0	0	0
Other	5	5	4.91	0.18	0	0	0	0	0	-	-	0	0	0	0	0	-	-	0	0	0
ISO 8552:2004 (21 °C)	5	4	-	-	0	1	0	0	0	-	-	0	0	0	0	0	-	-	0	0	0
NMKL 86:2013 (6.5 °C)	5	5	4.38	0.20	0	0	0	0	0	-	-	0	0	0	0	0	-	-	0	0	0

* Not evaluated

For individual methods: *m*_{PT} = median value and *s*_{PT} = standard deviation for the particular method (outliers and false results excluded).

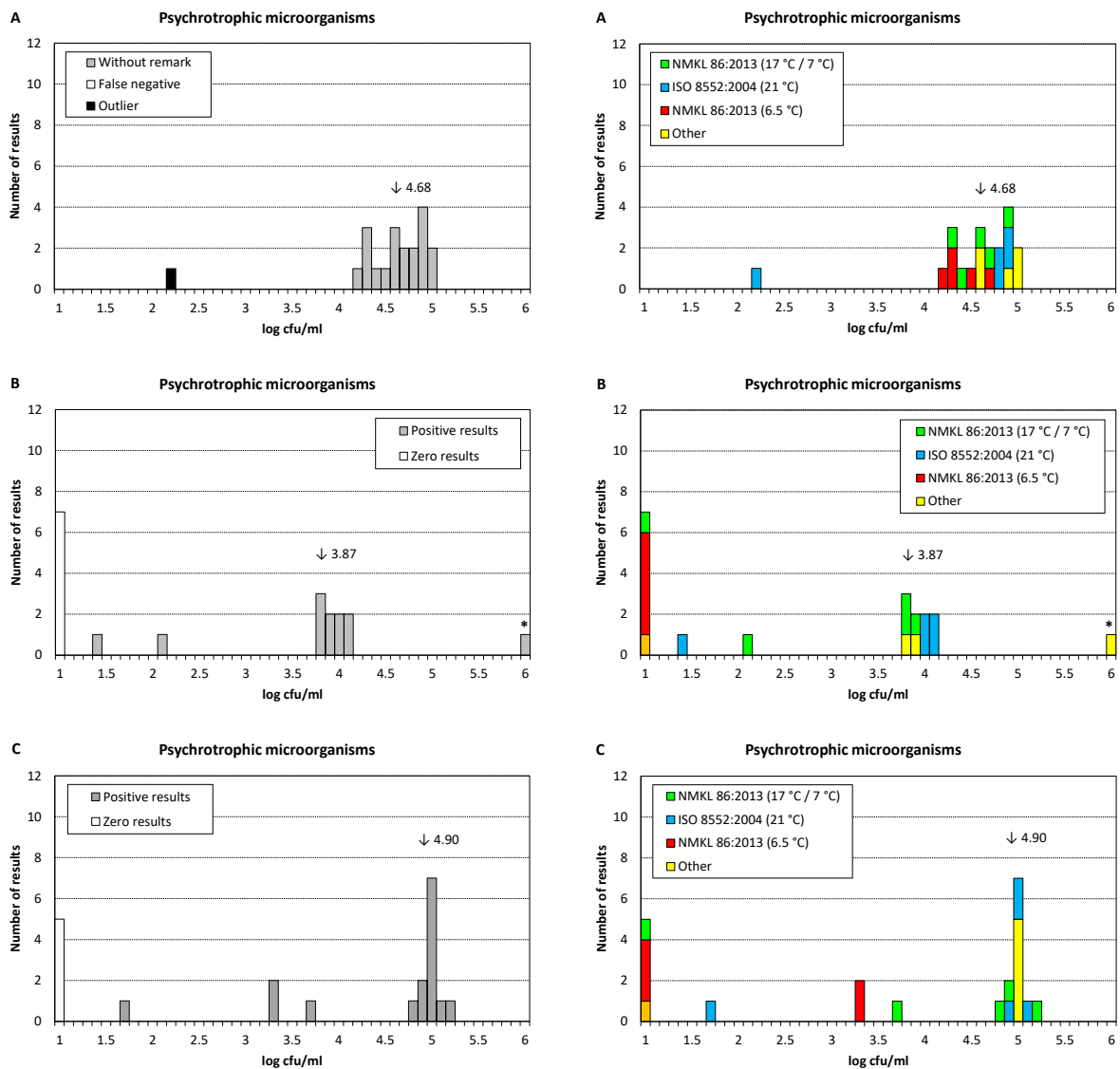


Figure 2. Results from analysis of psychrotrophic microorganisms.

Enterobacteriaceae

Sample A

The strains of *E. coli* and *H. alvei* were target organisms. On VRB, both form typical red colonies that are surrounded by a bile salt precipitation zone. Both strains are oxidase-negative. *H. alvei* was present in a slightly higher concentration than *E. coli*.

In total, 137 results were evaluated. Two low and five high outliers were identified, as well as one false negative result.

Sample B

E. coli was present in the highest concentration and was thus the main target organism. On VRB, it forms typical red colonies that are surrounded by a bile salt precipitation zone. The strain is oxidase-negative.

In total, 136 results were evaluated. Three low and six high outliers were identified, as well as two false negative results.

Sample C

No target organisms were present in the sample. At the Swedish Food Agency, no colonies were observed on VRBG after incubation at 37 °C for 24 h.

In total, 129 results were evaluated. Five false positive results were reported.

General remarks

Enterobacteriaceae are Gram-negative and oxidase-negative bacteria that ferment glucose with the production of acid by-products. On VRBG they therefore form pink/red colonies, with or without a bile salt precipitation zone. The appearance is similar on Petrifilm EB, which also includes a colour indicator for acid by-products and a plastic film for detection of gas production.

The most common methods were NMKL 144:2005, a method with Petrifilm EB and ISO 21528-2:2017. ISO 21528-2:2017 was last reviewed by ISO in 2022 and remains current.

Most methods used by the participants stipulate a 37 °C incubation temperature. With Petrifilm EB, both 30 °C and 37 °C are possible to use. Here, two participants used the lower incubation temperature. One of these reported a low outlier for sample B, but it is difficult to determine if this was due to the incubation temperature or some other factor.

For sample A, the results for TEMPO[®] EB were somewhat lower compared to results from other methods. Differences of this magnitude are not uncommon for TEMPO[®] EB and can be considered normal.

Table 4. Results from analysis of Enterobacteriaceae.

Method	Sample A							Sample B							Sample C						
	N	n	m_{PT}	s_{PT}	F	<	>	N	n	m_{PT}	s_{PT}	F	<	>	N	n	m_{PT}	s_{PT}	F	<	>
All results	137	129	4.51	0.16	1	2	5	136	125	3.97	0.18	2	3	6	129	124	-	-	5	-	-
NMKL 144:2005 (VRBG)	43	39	4.51	0.13	0	0	4	42	38	3.95	0.18	0	0	4	40	39	-	-	1	-	-
Petrifilm™ EB (37 °C)	39	37	4.59	0.15	0	1	1	40	36	3.98	0.16	1	1	2	37	34	-	-	3	-	-
ISO 21528-2:2017 (VRBG)	31	30	4.56	0.14	1	0	0	31	31	3.92	0.12	0	0	0	30	30	-	-	0	-	-
TEMPO® EB	9	8	4.35	0.17	0	1	0	9	8	4.05	0.17	1	0	0	9	9	-	-	0	-	-
Other	7	7	4.31	0.19	0	0	0	7	7	3.78	0.17	0	0	0	6	5	-	-	1	-	-
Compact Dry™ ETB	4	4	-	-	0	0	0	3	3	-	-	0	0	0	3	3	-	-	0	-	-
Petrifilm™ EB (30 °C)	2	2	-	-	0	0	0	2	1	-	-	0	1	0	2	2	-	-	0	-	-
ISO 21528-1:2017 (MPN)	1	1	-	-	0	0	0	1	1	-	-	0	0	0	1	1	-	-	0	-	-
RAPID® Enterobacteriaceae	1	1	-	-	0	0	0	1	0	-	-	0	1	0	1	1	-	-	0	-	-

For individual methods: m_{PT} = median value and s_{PT} = standard deviation for the particular method (outliers and false results excluded).

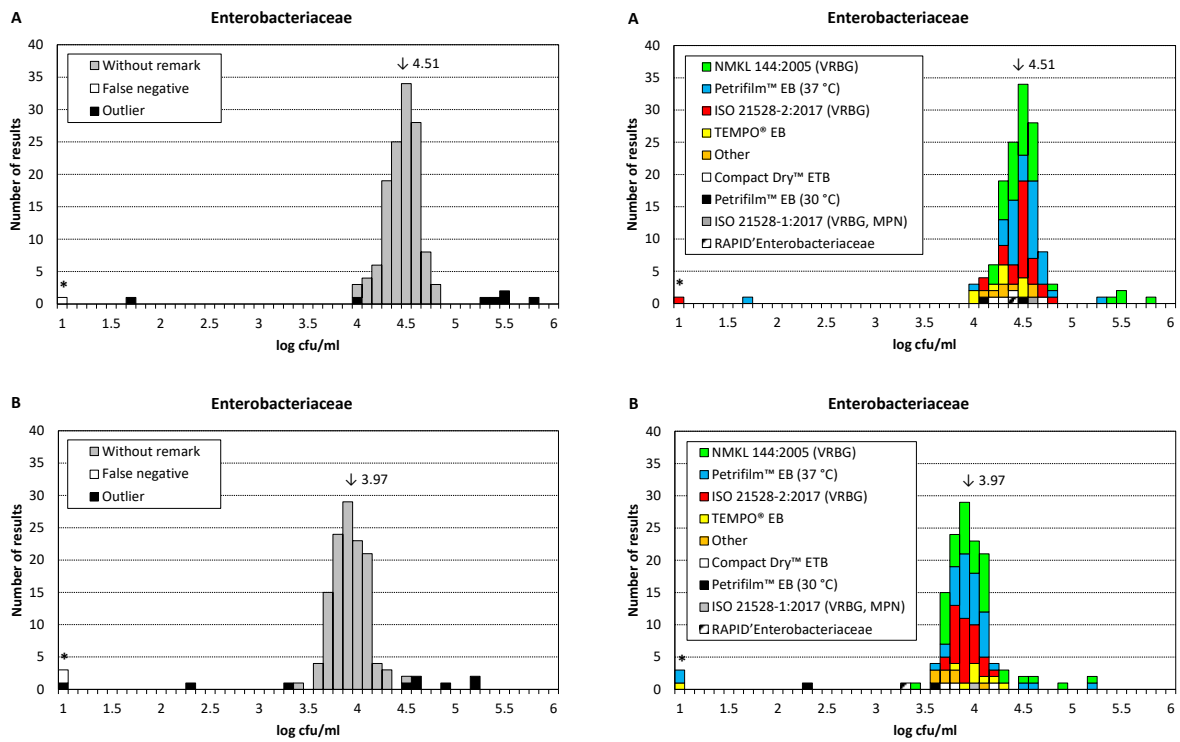


Figure 3. Results from analysis of Enterobacteriaceae.

Escherichia coli

Sample A

The strain of *E. coli* was target organism. On TSA/VRB, it forms typical red colonies surrounded by a bile salt precipitation zone. The strain is positive for indole production and β -glucuronidase activity and produces gas in LTLSB.

In total, 115 results were evaluated. Seven low outliers were identified, as well as six false negative results.

Sample B

The strain of *E. coli* (not identical to that in sample A) was target organism. On TSA/VRB, it forms typical red colonies surrounded by a bile salt precipitation zone. The strain is positive for indole production and β -glucuronidase activity and produces gas in LTLSB.

In total, 114 results were evaluated. Eight low and two high outliers were identified, as well as two false negative results.

Sample C

No target organisms were present in the sample. At the Swedish Food Agency, no colonies were observed on TSA/VRB after incubation at 44 °C for 24 h.

In total, 115 results were evaluated. Six false positive results were reported.

General remarks

The definition of *E. coli* differs between methods, which may sometimes cause problems with non-typical strains. Users of ISO 16649-2:2001 typically count as *E. coli* those bacteria that form blue (i.e. β -glucuronidase positive) colonies on TBX, without further confirmation. Similarly, Petrifilm EC/CC and Petrifilm SEC are also based on media that detect *E. coli* by the activity of β -glucuronidase. The latter media however also have a plastic film that facilitates detection of gas production due to lactose fermentation. In comparison, users of NMKL 125:2005 typically count as *E. coli* those bacteria that form typical dark red colonies surrounded by a red precipitation zone on VRB. Users often, but not always, perform further confirmation test, for example tests for the production of gas and indole. Not performing a confirmation test may partly explain that the mean value for NMKL 125:2005 was somewhat higher compared to other methods.

ISO 16649-2:2001 was last reviewed by ISO in 2019 and remains current. NMKL 125:2005 was recently replaced by NMKL 125:2024, which includes optional enumeration of β -glucuronidase positive *E. coli*. Three participants followed ISO 7251:2005, which is an MPN-based method for the detection *E. coli*. It was last reviewed by ISO in 2019 and remains current. An amendment with performance testing of culture media and reagents was published in 2023.

Table 5. Results from analysis of *Escherichia coli*.

Method	Sample A							Sample B							Sample C						
	N	n	m_{PT}	s_{PT}	F	<	>	N	n	m_{PT}	s_{PT}	F	<	>	N	n	m_{PT}	s_{PT}	F	<	>
All results	115	102	3.98	0.31	6	7	0	114	102	3.95	0.22	2	8	2	115	109	-	-	6	-	-
Petrifilm™ EC/CC	22	19	4.02	0.31	1	2	0	24	21	3.96	0.15	0	2	1	22	22	-	-	0	-	-
Petrifilm™ SEC	20	20	4.07	0.24	0	0	0	20	20	3.95	0.25	0	0	0	19	19	-	-	0	-	-
Other	18	11	3.71	0.39	3	4	0	17	12	3.93	0.24	0	4	1	19	16	-	-	3	-	-
ISO 16649-2:2001 (TBX)	16	15	3.94	0.23	1	0	0	15	15	3.92	0.25	0	0	0	16	14	-	-	2	-	-
NMKL 125:2005 (TSA/VRB)	13	12	4.23	0.22	1	0	0	13	13	4.18	0.22	0	0	0	13	13	-	-	0	-	-
TEMPO® EC	10	10	4.22	0.39	0	0	0	10	9	4.11	0.23	1	0	0	11	11	-	-	0	-	-
NMKL 125:2024(TSA/VRB/TBX)	5	5	4.08	0.09	0	0	0	5	5	3.92	0.05	0	0	0	5	5	-	-	0	-	-
Petrifilm™ REC	4	4	-	-	0	0	0	4	3	-	-	1	0	0	4	3	-	-	1	-	-
ISO 7251:2005 (MPN)	4	3	-	-	0	1	0	4	2	-	-	0	2	0	4	4	-	-	0	-	-
RAPID ¹ E.coli2	3	3	-	-	0	0	0	2	2	-	-	0	0	0	2	2	-	-	0	-	-

For individual methods: m_{PT} = median value and s_{PT} = standard deviation for the particular method (outliers and false results excluded).

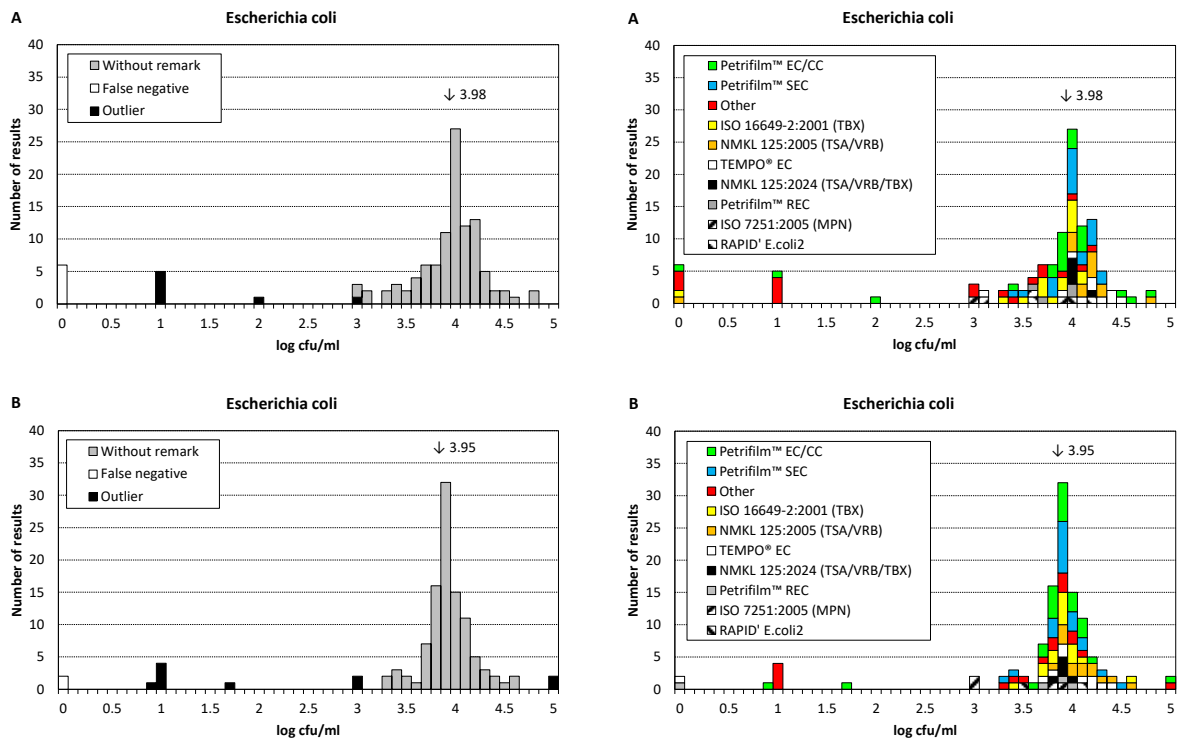


Figure 4. Results from analysis of *Escherichia coli*.

Presumptive *Bacillus cereus*

Sample A

The strain of *B. cereus* was target organism. On BcsA, it forms typical blue colonies surrounded by a blue zone of precipitation. On BA, it forms typical grey colonies surrounded by a zone of haemolysis.

In total, 100 results were evaluated. Three low and one high outlier were identified.

Sample B

No target organism was present in the sample. At the Swedish Food Agency, no colonies were observed on BcsA after incubation at 30 °C for 24 h.

In total, 93 results were evaluated. Five false positive results were reported.

Sample C

The strain of *B. cereus* (not identical to that in sample A) was target organism. On BcsA, it forms irregular colonies surrounded by a blue zone of precipitation. On BA, it forms typical grey colonies surrounded by a zone of haemolysis.

In total, 97 results were evaluated. Three low and one high outlier were identified, as well as two false negative results.

General remarks

B. cereus is a Gram-positive bacterium, which on BA forms large, irregular grey colonies, surrounded by a distinct zone of haemolysis. On the selective medium BcsA, presumptive *B. cereus* instead form bluish colonies that are surrounded by a blue zone of precipitation, due to lecithinase activity on egg yolk present in the medium. On MYP, presumptive *B. cereus* form large pink colonies, usually surrounded by a zone of precipitation, again as a consequence of lecithinase activity.

Most participants followed either NMKL 67:2021 or ISO 7932. NMKL users mainly reported using NMKL 67:2021, but the retracted NMKL 67:2010 is still used by many laboratories. The two methods mainly differ in the order of the selective and non-selective medium. ISO 7932:2004 was last reviewed by ISO in 2021 and remains current. An amendment with optional test was published in 2020.

A few participants used Compact Dry X-BC which contains chromogenic and selective agents that cause *B. cereus* to form blue/green colonies, while other bacteria normally form white colonies. Compact Dry X-BC may give somewhat lower results compared to the reference method ISO 7932:2004, something that is mentioned in both the NordVal 045 and MicroVal 2011-LR41 validations. This was true in this PT as well.

Table 6. Results from analysis of presumptive *Bacillus cereus*.

Method	Sample A							Sample B							Sample C						
	<i>N</i>	<i>n</i>	<i>m</i> _{PT}	<i>s</i> _{PT}	<i>F</i>	<	>	<i>N</i>	<i>n</i>	<i>m</i> _{PT}	<i>s</i> _{PT}	<i>F</i>	<	>	<i>N</i>	<i>n</i>	<i>m</i> _{PT}	<i>s</i> _{PT}	<i>F</i>	<	>
All results	100	96	4.34	0.31	0	3	1	93	88	-	-	5	-	-	97	91	4.41	0.31	2	3	1
NMKL 67:2021 (BcsA → BA)	24	24	4.33	0.27	0	0	0	22	21	-	-	1	-	-	24	24	4.41	0.34	0	0	0
ISO 7932:2004 (MYP)	21	21	4.35	0.35	0	0	0	20	20	-	-	0	-	-	21	19	4.41	0.25	1	1	0
Other	16	13	4.33	0.37	0	2	1	14	10	-	-	4	-	-	16	12	4.43	0.28	1	2	1
NMKL 67:2010 (BA → BcsA)	14	13	4.44	0.25	0	1	0	14	14	-	-	0	-	-	13	13	4.40	0.33	0	0	0
ISO 7932:2004 / Amd 1:2020 (MYP)	9	9	4.34	0.24	0	0	0	9	9	-	-	0	-	-	8	8	4.31	0.31	0	0	0
TEMPO® BC	6	6	4.39	0.24	0	0	0	6	6	-	-	0	-	-	6	6	4.50	0.32	0	0	0
BACARA®	5	5	4.46	0.23	0	0	0	4	4	-	-	0	-	-	5	5	4.62	0.24	0	0	0
Compact Dry™ X-BC	5	5	4.10	0.35	0	0	0	4	4	-	-	0	-	-	4	4	-	-	0	0	0

For individual methods: *m*_{PT} = median value and *s*_{PT} = standard deviation for the particular method (outliers and false results excluded).

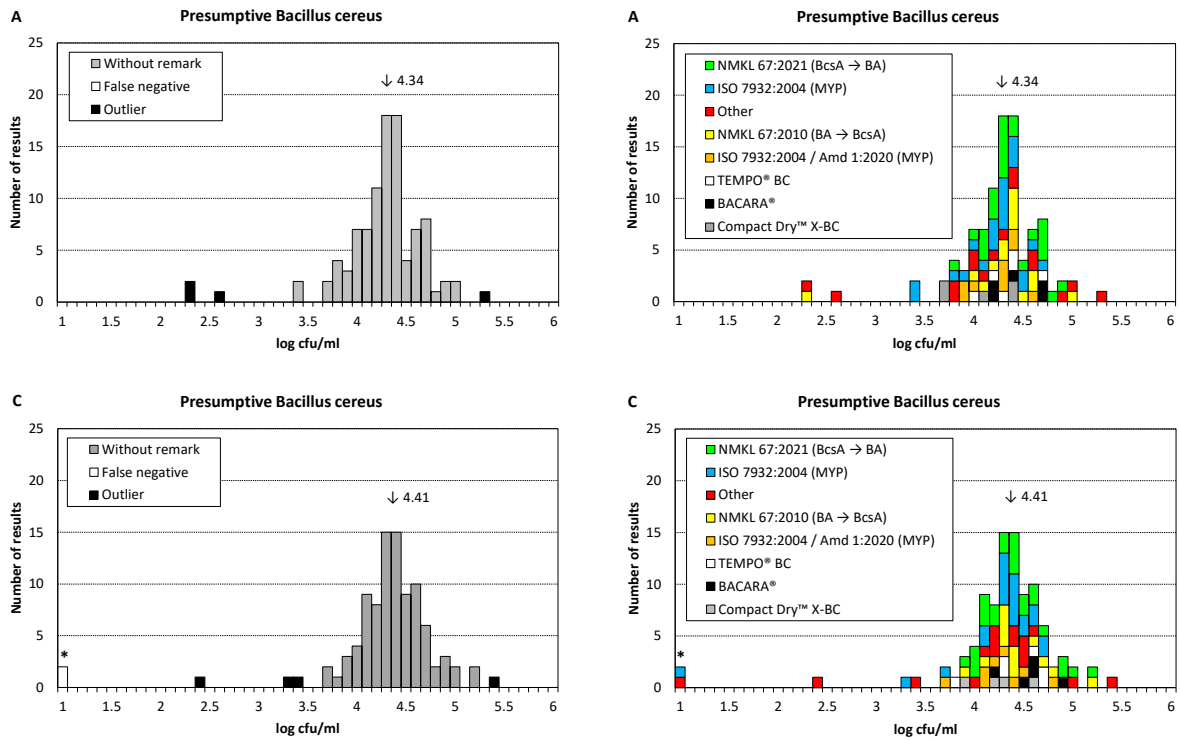


Figure 5. Results from analysis of presumptive *Bacillus cereus*.

Coagulase-positive *Staphylococcus*

Sample A

The strain of *S. aureus* was target organism. On RPFA, it forms typical grey colonies surrounded by a precipitation zone.

In total, 105 results were evaluated. Eight low outliers were identified, as well as one false negative result.

Sample B

No target organism was present in the sample. At the Swedish Food Agency, no colonies were observed on RPFA after incubation at 37 °C for 24 h.

In total, 101 results were evaluated. Four false positive results were reported.

Sample C

The strain of *S. aureus* (not identical to that in sample A) was target organism. On RPFA, it forms typical grey colonies surrounded by a precipitation zone.

In total, 102 results were evaluated. Ten low and three high outliers were identified, as well as seven false negative results.

General remarks

The majority of the participants followed methods based on incubation on BP or RPFA. On BP, *S. aureus* form characteristic convex, shiny colonies that have a grey/black colour due to reduction of tellurite in the medium. The colonies are usually surrounded by a clear zone, due to proteolysis of egg yolk in the medium (lecithinase activity). An opaque halo may also form near the colony, due to precipitation caused by lipase activity. When using BP, a confirmation is typically performed based on coagulase activity, for example a tube coagulase test or the use of RPFA as a secondary medium. With RPFA, the coagulase activity is tested directly in the medium.

In comparison, Petrifilm Staph Express is based on a modified Baird-Parker agar. It contains a chromogenic indicator that causes *S. aureus* to form red/purple colonies. The associated Petrifilm Staph Express Disk facilitates detection of extracellular DNase, which is produced by the majority of coagulase-positive *S. aureus*, but also by the coagulase-positive staphylococci *S. intermedius* and *S. hyicus*. Toluidin blue O in the disks visualises DNase activity as a pink zone around the colonies.

With NMKL 66:2009, incubation is done either with BP and/or RPFA. In comparison, ISO 6888-1:2021 stipulates BP, whereas 6888-2:2021 stipulates the use of RPFA. Amendments with clarifications to ISO 6888-1:2021 and ISO 6888-2:2021 were published in 2023.

Table 7. Results from analysis of coagulase-positive *Staphylococcus*.

Method	Sample A							Sample B							Sample C						
	N	n	m _{PT}	s _{PT}	F	<	>	N	n	m _{PT}	s _{PT}	F	<	>	N	n	m _{PT}	s _{PT}	F	<	>
All results	105	96	4.27	0.12	1	8	0	101	97	-	-	4	-	-	102	82	4.35	0.19	7	10	3
NMKL 66:2009 (BP)	24	23	4.29	0.11	0	1	0	23	23	-	-	0	-	-	26	25	4.39	0.19	1	0	0
Petrifilm™ Staph	20	19	4.26	0.10	0	1	0	18	18	-	-	0	-	-	19	18	4.31	0.18	0	1	0
ISO 6888-1:2021 (BP)	15	13	4.28	0.06	0	2	0	14	14	-	-	0	-	-	13	9	4.30	0.12	2	0	2
Other	13	10	4.25	0.09	0	3	0	15	15	-	-	0	-	-	13	9	4.36	0.10	1	3	0
NMKL 66:2009 (RPFA)	10	9	4.38	0.16	1	0	0	10	9	-	-	1	-	-	9	8	4.50	0.13	0	1	0
ISO 6888-1:2021 Amd 1:2023 (BP)	9	9	4.30	0.13	0	0	0	8	8	-	-	0	-	-	9	3	-	-	1	4	1
ISO 6888-2:2021 (RPFA)	5	5	4.30	0.03	0	0	0	5	3	-	-	2	-	-	5	5	4.40	0.06	0	0	0
Compact Dry™ X-SA	4	3	-	-	0	1	0	3	2	-	-	1	-	-	3	1	-	-	2	0	0
ISO 6888-2:2021 Amd 1:2023 (RPFA)	3	3	-	-	0	0	0	3	3	-	-	0	-	-	3	2	-	-	0	1	0
TEMPO® STA	2	2	-	-	0	0	0	2	2	-	-	0	-	-	2	2	-	-	0	0	0

For individual methods: m_{PT} = median value and s_{PT} = standard deviation for the particular method (outliers and false results excluded).

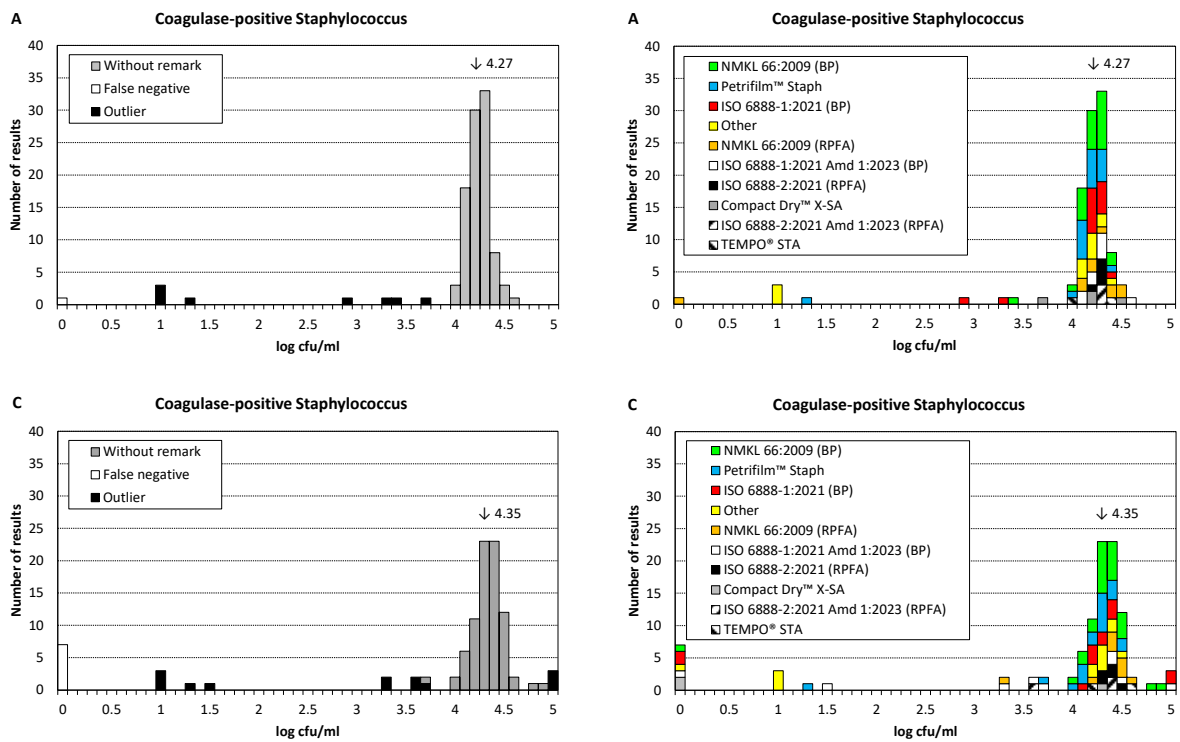


Figure 6. Results from analysis of coagulase-positive *Staphylococcus*.

Lactic acid bacteria

Sample A

The strain of *E. durans* was target organism. On MRS-aB, it forms typical white/grey colonies. The strain is catalase-negative and Gram-positive.

In total, 61 results were evaluated. Two low and one high outlier were identified, as well as five false negative results.

Sample B

No target organism was present in the sample. At the Swedish Food Agency, no colonies were observed on MRS-aB after incubation at 25 °C for 5 days.

In total, 59 results were evaluated. Twenty-one (21) false positive results were reported. False-positive results were reported by most of the different methods used by the participants. The corresponding results were also distributed fairly evenly between 1.5–5 log₁₀ cfu ml⁻¹. It's therefore difficult to say which microorganism was detected by these participants.

Sample C

The strain of *E. faecalis* was target organism. On MRS-aB, it forms typical white/grey colonies. The strain is catalase-negative and Gram-positive.

In total, 59 results were evaluated. Six low and one high outlier were identified, as well as two false negative results.

General remarks

Lactic acid bacteria constitute a heterogeneous group of microorganisms, and therefore have different optimal medium, pH and incubation conditions. Therefore, the choice of media will often have an impact on the results. For example, MRS-aB (pH 6.2) is a less selective medium that allows the growth of a wider range of lactic acid bacteria. This may however also result in the appearance of more false-positive colonies compared to the more acid media MRS and MRS-S (pH 5.7). On Petrifilm LAB, lactic acid bacteria form red colonies. The plates also facilitate distinction between gas producing (heterofermentative) and non-gas producing (homofermentative) lactic acid bacteria. These differences underline the importance of performing a confirmation test in uncertain cases, especially when using a less selective medium. ISO 15214:1998 recommends confirmation of uncertain colonies, and with NMKL 140:2023 confirmation is mandatory. Lactic acid bacteria are Gram positive and normally catalase-negative.

NMKL 140:2007 has been replaced by NMKL 140:2023, which contains changes in the incubation time and the introduction of mandatory confirmation tests. ISO 15214:1998 was reviewed by ISO in 2021 and remains current. ISO 7889/IDF 117:2003, which is a method for characteristic microorganisms in yoghurt at 37 °C, is currently under revision and is scheduled for publication in the coming months.

Table 8. Results from analysis of lactic acid bacteria.

Method	Sample A							Sample B							Sample C						
	N	n	m_{PT}	s_{PT}	F	<	>	N	n	m_{PT}	s_{PT}	F	<	>	N	n	m_{PT}	s_{PT}	F	<	>
All results	61	53	4.48	0.18	5	2	1	59	38	-	-	21	-	-	59	50	4.92	0.16	2	6	1
Petrifilm™ LAB	14	12	4.38	0.17	0	2	0	14	10	-	-	4	-	-	14	11	4.90	0.14	0	3	0
Other	11	10	4.62	0.19	1	0	0	11	5	-	-	6	-	-	11	9	5.00	0.07	1	1	0
ISO 15214:1998	12	11	4.46	0.12	0	0	1	10	7	-	-	3	-	-	11	10	4.95	0.07	0	0	1
NMKL 140:2007 (MRS-aB)	9	8	4.48	0.14	1	0	0	9	5	-	-	4	-	-	9	6	5.04	0.09	1	2	0
NMKL 140:2023 (MRS-aB)	9	6	4.50	0.08	3	0	0	9	6	-	-	3	-	-	9	9	4.92	0.15	0	0	0
TEMPO® LAB	4	4	-	-	0	0	0	4	4	-	-	0	-	-	4	4	-	-	0	0	0
ISO 7889:2003 / IDF 117:2003 (MRS)	2	2	-	-	0	0	0	2	1	-	-	1	-	-	1	1	-	-	0	0	0

For individual methods: m_{PT} = median value and s_{PT} = standard deviation for the particular method (outliers and false results excluded).

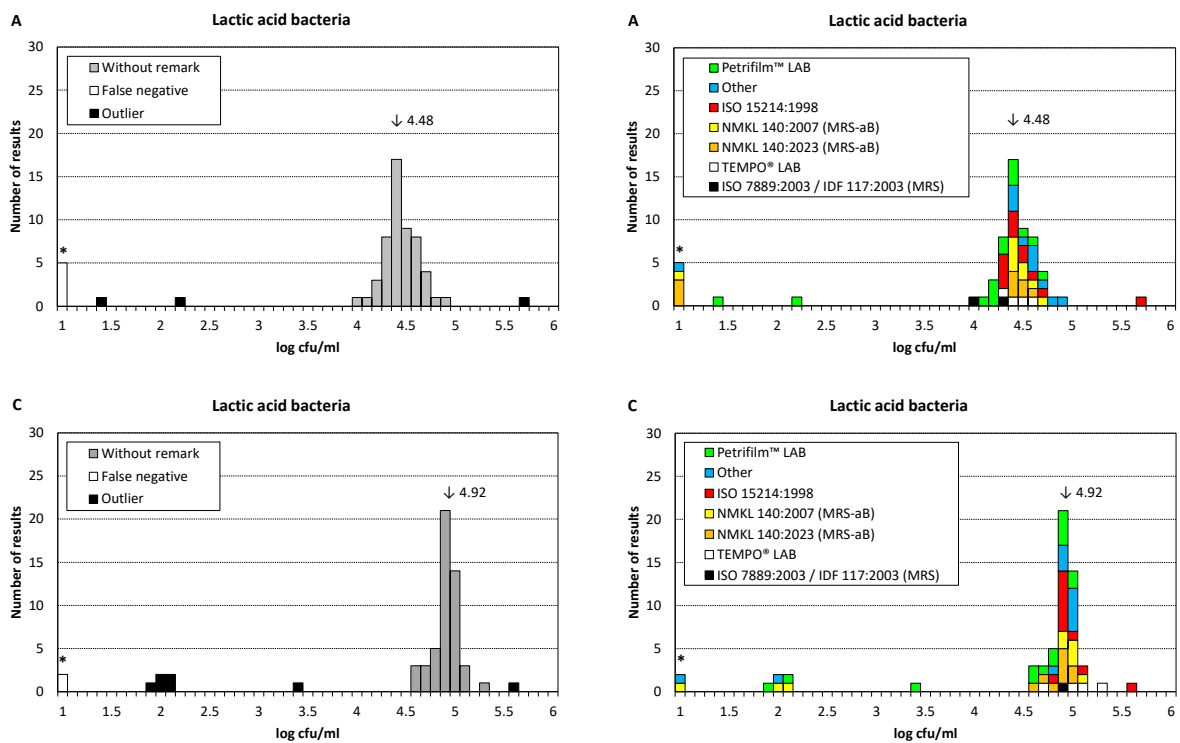


Figure 7. Results from analysis of lactic acid bacteria.

Clostridium perfringens

Sample A

No target organism was present in the sample. At the Swedish Food Agency, no black colonies were observed on TSC after incubation at 37 °C for 24 h.

In total, 47 results were evaluated. All were correct negative.

Sample B

The strain of *C. perfringens* was target organism. It forms black colonies on TSC and displays haemolysis on BA. The strain is non-motile and ferments lactose.

In total, 48 results were evaluated. Three low outliers were identified, as well as two false negative results.

Sample C

No target organism was present in the sample. At the Swedish Food Agency, no black colonies were observed on TSC after incubation at 37 °C for 24 h.

In total, 46 results were evaluated. One false positive result was reported.

General remarks

C. perfringens is a non-motile, Gram-positive, anaerobic spore-forming bacterium. It ferments lactose and sucrose and produces the enzyme acid phosphatase. Common methods for confirmation therefore include a motility test and a test for lactose fermentation. *C. perfringens* can also be confirmed since it forms a double haemolytic zone upon anaerobic incubation on BA.

Most participants followed NMKL 95:2009, with incubation on TSC. Four participants followed the withdrawn ISO 7937:2004, which has been replaced by ISO 15213-2:2023 ("Detection and enumeration of *Clostridium* spp."). Two participants followed NMKL 56:2015 ("Sulphite-reducing Clostridia"), which refers to NMKL 95:2009 for confirmation of *C. perfringens*. No obvious differences could be seen in the results from the different methods.

Table 9. Results from analysis of *Clostridium perfringens*.

Method	Sample A						Sample B						Sample C						
	N	n	m _{PT}	s _{PT}	F	< >	N	n	m _{PT}	s _{PT}	F	< >	N	n	m _{PT}	s _{PT}	F	< >	
All results	47	47	-	-	0	- -	48	43	2.70	0.25	2	3	0	46	45	-	-	1	- -
NMKL 95:2009 (TSC)	29	29	-	-	0	- -	28	25	2.79	0.25	2	1	0	28	27	-	-	1	- -
ISO 15213-2:2023 (TSC)	9	9	-	-	0	- -	10	9	2.63	0.26	0	1	0	8	8	-	-	0	- -
ISO 7937:2004 (TSC)	4	4	-	-	0	- -	5	4	-	-	0	1	0	4	4	-	-	0	- -
Other	3	3	-	-	0	- -	3	3	-	-	0	0	0	3	3	-	-	0	- -
NMKL 56:2015 (ISA)	2	2	-	-	0	- -	2	2	-	-	0	0	0	3	3	-	-	0	- -

For individual methods: m_{PT} = median value and s_{PT} = standard deviation for the particular method (outliers and false results excluded).

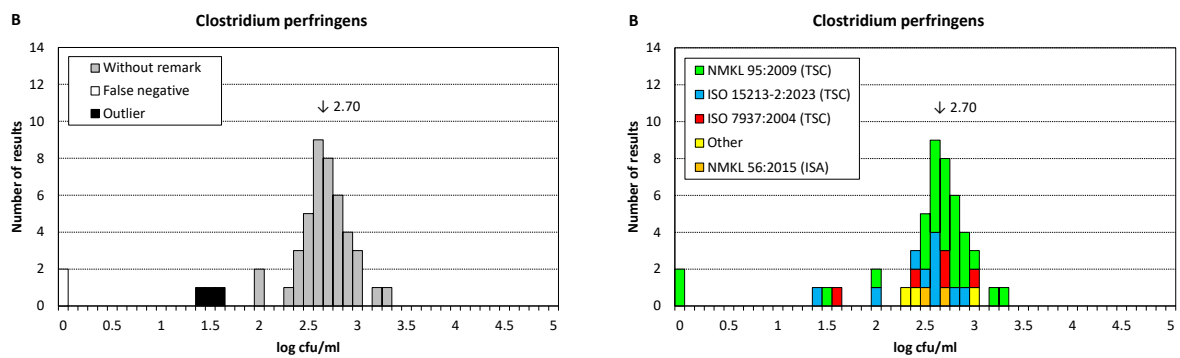


Figure 8. Results from analysis of *Clostridium perfringens*.

Anaerobic sulphite-reducing bacteria

Sample A

No target organism was present in the sample. At the Swedish Food Agency, no black colonies were observed on ISA after incubation on ISA at 37 °C for 48 h.

In total, 57 results were evaluated. Two false positive results were reported.

Sample B

The strain of *C. perfringens* was target organism. It forms black colonies on ISA.

In total, 58 results were evaluated. Two low outliers were identified.

Sample C

No target organism was present in the sample. At the Swedish Food Agency, no black colonies were observed on ISA after incubation on ISA at 37 °C for 48 h.

In total, 53 results were evaluated. One false positive result was reported.

General remarks

The majority of the participants followed NMKL 56:2015, which describes the enumeration of sulphite-reducing Clostridia. This was reviewed by NMKL in 2019 and remains current. Seven participants followed ISO 15213:2003, which has been replaced by ISO 15213-1:2023 ("Enumeration of sulfite-reducing *Clostridium* spp."). Both NMKL 56:2015 and ISO 15213-1:2023 prescribe pour-plate methods with ISA, on which black colonies (possibly surrounded by a black zone) are considered as sulphite-reducing bacteria. The black colour of the colonies comes from iron sulphide, which is formed as a precipitate of Fe³⁺ in the medium, and H₂S that is produced by the reduction of sulphite. Growth of anaerobic bacteria that only produce hydrogen (and not H₂S) may sometimes result in a diffuse and unspecific blackening of the medium.

Two participants reported using ISO 7937:2004, which has been replaced by ISO 15213-2:2023. Five participants specifically stated following ISO 15213-2:2023. Both are methods for the enumeration of *C. perfringens*, based on incubation on TSC. Notably, no participants followed ISO 15213-1:2023. Since the only potential target organism in this PT was *C. perfringens*, the choice of these methods appears to have had no impact on the outcome. It is also possible that the participants have used modified methods.

Table 10. Results from analysis of anaerobic sulphite-reducing bacteria.

Method	Sample A						Sample B						Sample C					
	<i>N</i>	<i>n</i>	<i>m</i> _{PT}	<i>s</i> _{PT}	<i>F</i>	< >	<i>N</i>	<i>n</i>	<i>m</i> _{PT}	<i>s</i> _{PT}	<i>F</i>	< >	<i>N</i>	<i>n</i>	<i>m</i> _{PT}	<i>s</i> _{PT}	<i>F</i>	< >
All results	57	55	-	-	2	- -	58	56	2.67	0.21	0	2 0	53	52	-	-	1	- -
NMKL 56:2015 (ISA)	35	34	-	-	1	- -	34	34	2.69	0.18	0	0 0	32	32	-	-	0	- -
Other	8	7	-	-	1	- -	10	9	2.69	0.24	0	1 0	8	7	-	-	1	- -
ISO 15213:2003 (ISA)	7	7	-	-	0	- -	7	6	2.53	0.36	0	1 0	7	7	-	-	0	- -
ISO 15213-2:2023 (TSC)	5	5	-	-	0	- -	5	5	2.61	0.13	0	0 0	4	4	-	-	0	- -
ISO 7937:2004 (TSC)	2	2	-	-	0	- -	2	2	-	-	0	0 0	2	2	-	-	0	- -

For individual methods: *m*_{PT} = median value and *s*_{PT} = standard deviation for the particular method (outliers and false results excluded).

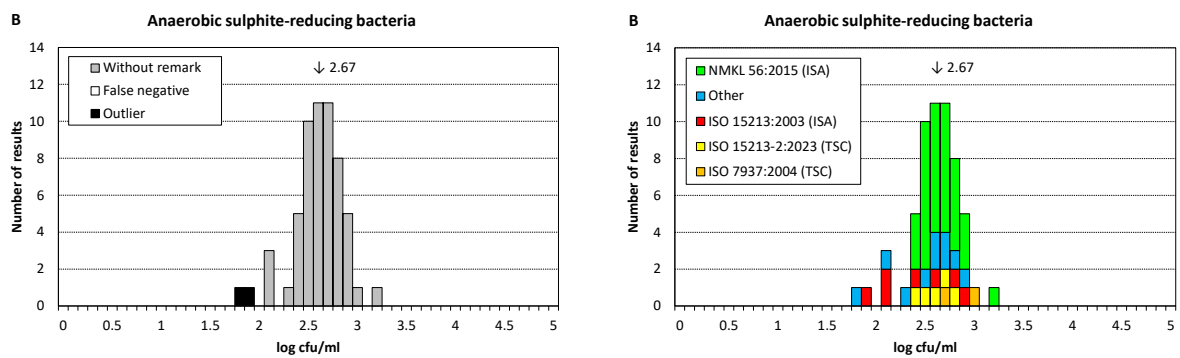


Figure 9. Results from analysis of anaerobic sulphite-reducing bacteria.

Aerobic microorganisms in fish products

Sample A

All strains in the sample were target organisms and were present in similar concentrations.

In total, 21 results were evaluated. No outliers or false negative results were reported.

Sample B

E. coli was present in the highest concentration and was thus the main target organism.

In total, 21 results were evaluated. One high outlier was identified.

Sample C

B. cereus, *E. faecalis* and *S. aureus* were present in the highest concentration and were thus the main target organisms.

In total, 21 results were evaluated. Two low outliers were identified, as well as one false negative result.

General remarks

The vast majority of the participants followed NMKL 184:2006, which is a method for aerobic microorganisms and specific spoilage organisms in fish and fish products. It is based on a pour-plate method with IA. NMKL 184:2006 was reviewed by NMKL in 2022 and remains current.

One participant incubated on Petrifilm AC.

All of the outliers and false negative results were reported by participants that followed NMKL 184:2006.

Table 11. Results from analysis of aerobic microorganisms in fish products.

Method	Sample A							Sample B							Sample C						
	N	n	m _{PT}	s _{PT}	F	<	>	N	n	m _{PT}	s _{PT}	F	<	>	N	n	m _{PT}	s _{PT}	F	<	>
All results	21	21	5.00	0.11	0	0	0	21	20	4.05	0.17	0	0	1	21	18	5.04	0.14	1	2	0
NMKL 184:2006 (IA)	19	19	4.98	0.13	0	0	0	19	18	4.06	0.18	0	0	1	19	16	5.08	0.11	1	2	0
Petrifilm™ AC	1	1	-	-	0	0	0	1	1	-	-	0	0	0	1	1	-	-	0	0	0
Other	1	1	-	-	0	0	0	1	1	-	-	0	0	0	1	1	-	-	0	0	0

For individual methods: m_{PT} = median value and s_{PT} = standard deviation for the particular method (outliers and false results excluded).

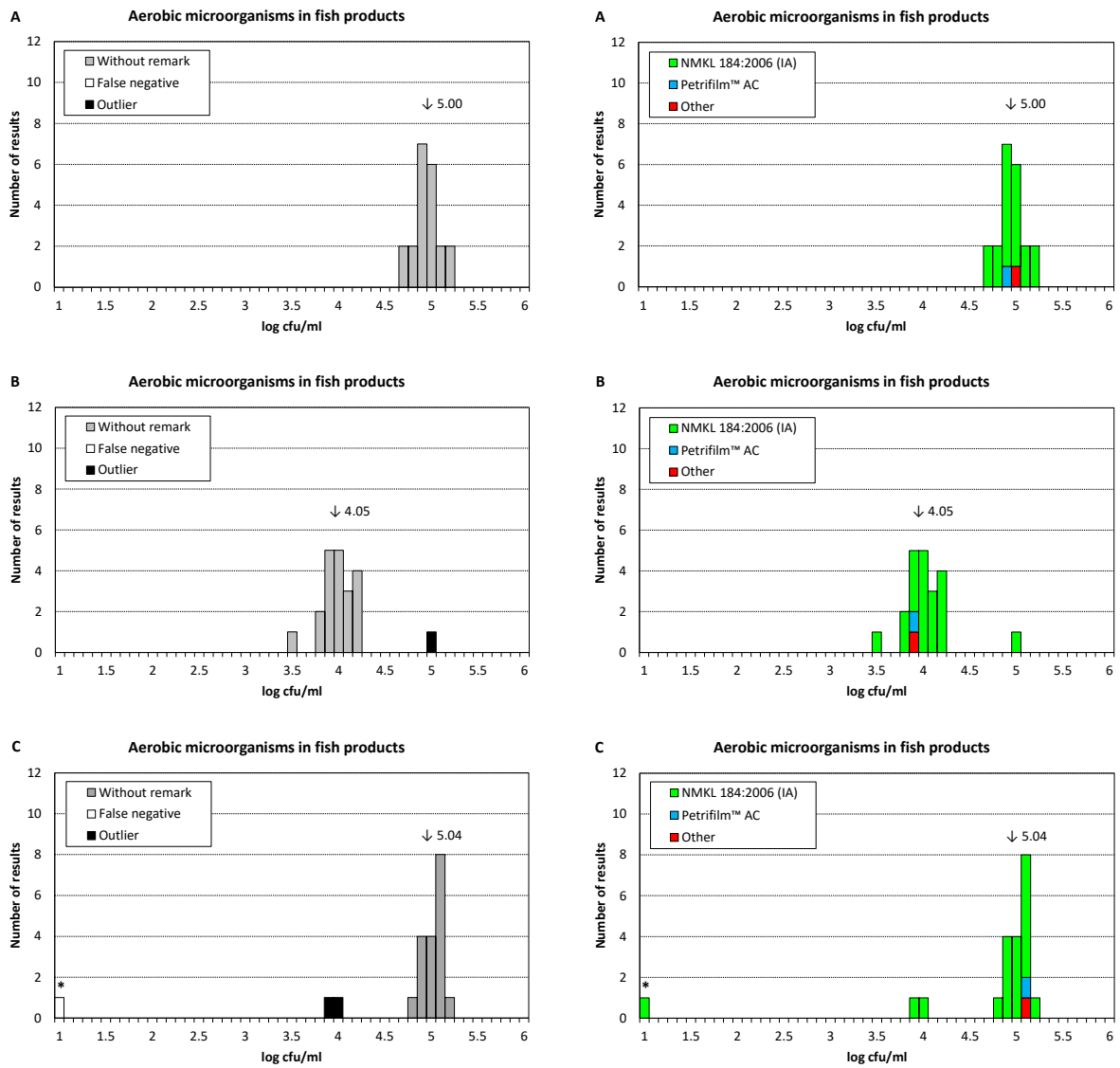


Figure 10. Results from analysis of aerobic microorganisms in fish products.

H₂S-producing bacteria in fish products

Sample A

The strain of *H. alvei* was target organism. It forms black colonies on IA.

In total, 19 results were evaluated. One low outlier was identified, as well as one false negative result.

Sample B

No target organism was present in the sample. At the Swedish Food Agency, no black colonies were observed on IA.

In total, 20 results were evaluated. One false positive result was reported.

Sample C

No target organism was present in the sample. At the Swedish Food Agency, no black colonies were observed on IA.

In total, 20 results were evaluated. No false positive results were reported.

General remarks

The vast majority of the participants followed NMKL 184:2006, which is a method for aerobic microorganisms and specific spoilage organisms in fish and fish products. It is based on a pour-plate method with IA. NMKL 184:2006 was reviewed by NMKL in 2022 and remains current.

With IA, H₂S-producing bacteria form black colonies. It is important to read the plates immediately after the incubation, since the colour of the colonies may fade after a few days' storage in a fridge.

Table 12. Results from analysis of H₂S-producing bacteria in fish products.

Method	Sample A							Sample B							Sample C						
	<i>N</i>	<i>n</i>	<i>m</i> _{PT}	<i>s</i> _{PT}	<i>F</i>	<	>	<i>N</i>	<i>n</i>	<i>m</i> _{PT}	<i>s</i> _{PT}	<i>F</i>	<	>	<i>N</i>	<i>n</i>	<i>m</i> _{PT}	<i>s</i> _{PT}	<i>F</i>	<	>
All results	19	17	4.50	0.10	1	1	0	20	19	-	-	1	-	-	20	20	-	-	0	-	-
NMKL 184:2006 (IA)	19	17	4.50	0.09	1	1	0	20	19	-	-	1	-	-	20	20	-	-	0	-	-

For individual methods: *m*_{PT} = median value and *s*_{PT} = standard deviation for the particular method (outliers and false results excluded).

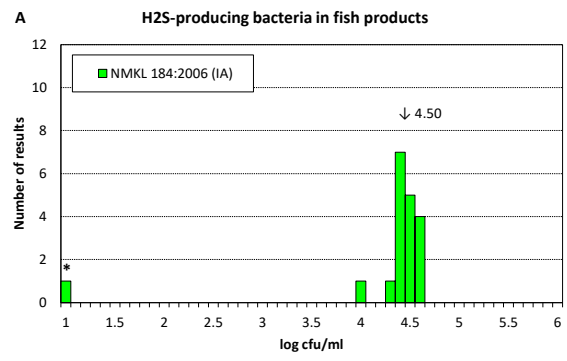
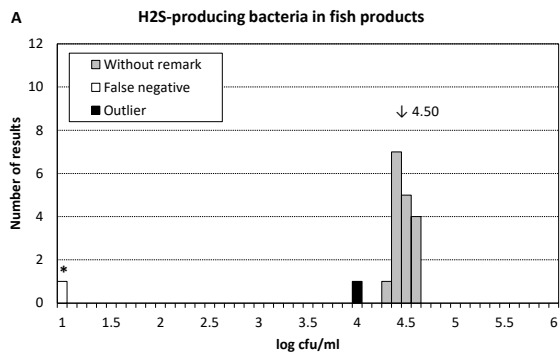


Figure 11. Results from analysis of H₂S-producing bacteria in fish products.

Yeasts and moulds

Sample A

No yeasts or moulds were present in the sample.

In total, 141 results were evaluated for yeasts. Seven false positive results were reported.

In total, 137 results were evaluated for moulds. Four false positive results were reported.

Sample B

The strain of *C. glabrata* was target organism for yeasts. It forms white shiny colonies on DG18.

The strain of *A. candidus* was target organism for moulds. On DG18, it forms white colonies with a distinct mycelium that makes it easy to separate from *C. glabrata*.

In total, 143 results were evaluated for yeasts. Three low and five high outliers were reported, as well as five false negative results.

In total, 141 results were evaluated for moulds. Nine low outliers were reported, as well as fifteen (15) false negative results.

Sample C

The strain of *R. minuta* was target organism for yeasts. On DG18, it forms small pink colonies. On DRBC, it forms orange/pink colonies.

No target organism for moulds was present in the sample.

In total, 142 results were evaluated for yeasts. Eight low and one high outlier were reported, as well as 33 false negative results.

In total, 133 results were evaluated for moulds. Six false positive results were reported.

General remarks

Many different methods and media were used for the analysis of yeast and moulds. With NMKL 98:2005, it is possible to use either DG18, DRBC or OGYE. It was last reviewed by NMKL in 2024 and remains current. With ISO 6611:2004 / IDF 94:2004, which describes the enumeration of yeasts and moulds in milk and milk products, participants mainly used YGC, but OGYE was also reported. ISO 21527-1:2008 and ISO 21527-2:2008 stipulate the use of DRBC and DG18, respectively. ISO 6611:2004/IDF 94:2004 and ISO 21527-1:2008/ISO 21527-2:2008 were last reviewed by ISO in 2020 and 2018, respectively, and remain current.

In general, DRBC is recommended for food with water activity $a_w > 0.95$ (e.g. fresh fruit, vegetables, meat and milk products) while DG18 is recommended for food with $a_w \leq 0.95$ (e.g. dried fruit, dried meat, grains and nuts).

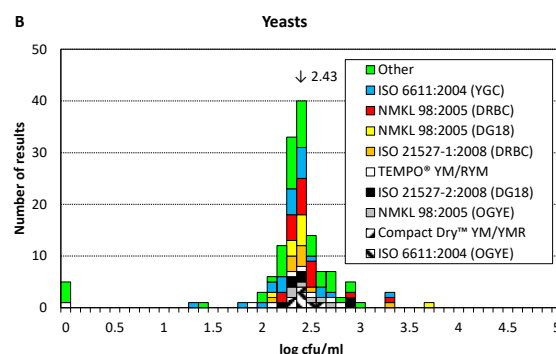
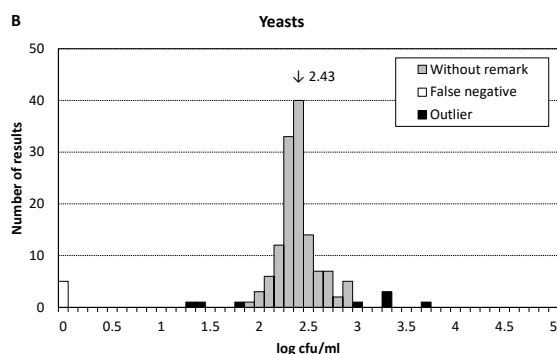
For sample C, many false-negative results were reported for yeasts. Many of these were from participants that incubated on DG18, though DG18 was also used by many participants without problem. Notably, all four results from Compact Dry™ YM/YMR were false negative. The strain of *R. minuta* has not been tested with this medium at the Swedish Food Agency, so it cannot be determined if this is simply by chance, or due to difficulties with identifying *R. minuta* with Compact Dry™ YM/YMR. The AOAC certification for Compact Dry™ YM (100401) does however specify that *R. glutinis* and *R. mucilaginosa* form blue colonies on this medium.

Eight results were reported by participants that used TEMPO® YM or TEMPO® RYM. These MPN-based methods give a combined results for yeast and moulds, which is not the intent in this PT, and may result in misleading evaluations that need to be self-assessed. Though this does not appear to have been a problem in this PT. Rather, all of the deviating results from this method are either low outliers or false negative results.

Table 13. Results from analysis of yeasts.

Method	Sample A						Sample B						Sample C					
	N	n	m _{PT}	s _{PT}	F	< >	N	n	m _{PT}	s _{PT}	F	< >	N	n	m _{PT}	s _{PT}	F	< >
All results	141	134	-	-	7	- -	143	130	2.43	0.18	5	3 5	142	100	3.11	0.18	33	8 1
Other	47	45	-	-	2	- -	48	42	2.43	0.22	4	1 1	48	35	3.18	0.16	9	4 0
ISO 6611:2004 / IDF 94:2004 (YGC)	24	22	-	-	2	- -	24	21	2.39	0.17	0	2 1	23	20	3.16	0.18	1	2 0
NMKL 98:2005 (DRBC)	22	21	-	-	1	- -	21	20	2.41	0.16	0	0 1	22	19	3.08	0.14	2	0 1
NMKL 98:2005 (DG18)	12	12	-	-	0	- -	11	10	2.40	0.09	0	0 1	13	8	3.07	0.14	4	1 0
ISO 21527-1:2008 (DRBC)	8	8	-	-	0	- -	10	9	2.40	0.10	0	0 1	8	7	3.11	0.23	0	1 0
TEMPO® YM/RYM	8	8	-	-	0	- -	8	7	2.40	0.31	1	0 0	8	1	-	-	7	0 0
ISO 21527-2:2008 (DG18)	6	6	-	-	0	- -	7	7	2.41	0.28	0	0 0	6	2	-	-	4	0 0
NMKL 98:2005 (OGYE)	6	4	-	-	2	- -	6	6	2.49	0.15	0	0 0	6	4	-	-	2	0 0
Compact Dry™ YM/YMR	4	4	-	-	0	- -	4	4	-	-	0	0 0	4	0	-	-	4	0 0
ISO 6611:2004 / IDF 94:2004 (OGYE)	4	4	-	-	0	- -	4	4	-	-	0	0 0	4	4	-	-	0	0 0

For individual methods: m_{PT} = median value and s_{PT} = standard deviation for the particular method (outliers and false results excluded).



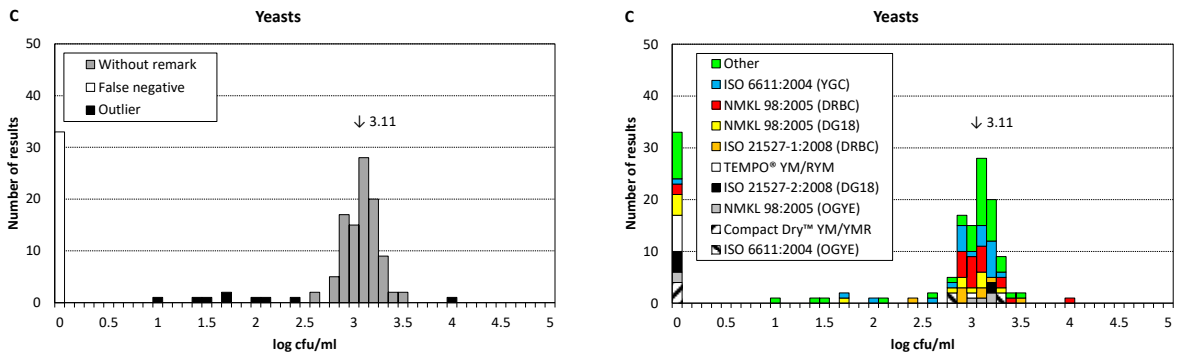


Figure 12. Results from analysis of yeasts.

Table 14. Results from analysis of moulds.

Method	Sample A						Sample B						Sample C						
	N	n	m_{PT}	s_{PT}	F	< >	N	n	m_{PT}	s_{PT}	F	< >	N	n	m_{PT}	s_{PT}	F	< >	
All results	137	133	-	-	4	- -	141	117	2.63	0.20	15	9	0	133	127	-	-	6	- -
Other	45	44	-	-	1	- -	47	39	2.71	0.23	6	2	0	43	41	-	-	2	- -
ISO 6611:2004 / IDF 94:2004 (YGC)	23	21	-	-	2	- -	23	19	2.66	0.14	2	2	0	22	19	-	-	3	- -
NMKL 98:2005 (DRBC)	20	20	-	-	0	- -	20	19	2.56	0.15	1	0	0	21	21	-	-	0	- -
NMKL 98:2005 (DG18)	13	12	-	-	1	- -	12	11	2.61	0.19	1	0	0	14	13	-	-	1	- -
ISO 21527-1:2008 (DRBC)	9	9	-	-	0	- -	9	9	2.67	0.13	0	0	0	6	6	-	-	0	- -
TEMPO® YM/RYM	8	8	-	-	0	- -	8	4	-	-	1	3	0	8	8	-	-	0	- -
ISO 21527-2:2008 (DG18)	5	5	-	-	0	- -	8	6	2.73	0.17	2	0	0	6	6	-	-	0	- -
NMKL 98:2005 (OGYE)	6	6	-	-	0	- -	6	4	-	-	0	2	0	6	6	-	-	0	- -
ISO 6611:2004 / IDF 94:2004 (OGYE)	4	4	-	-	0	- -	4	3	-	-	1	0	0	4	4	-	-	0	- -
Compact Dry™ YM/YMR	4	4	-	-	0	- -	4	3	-	-	1	0	0	3	3	-	-	0	- -

For individual methods: m_{PT} = median value and s_{PT} = standard deviation for the particular method (outliers and false results excluded).

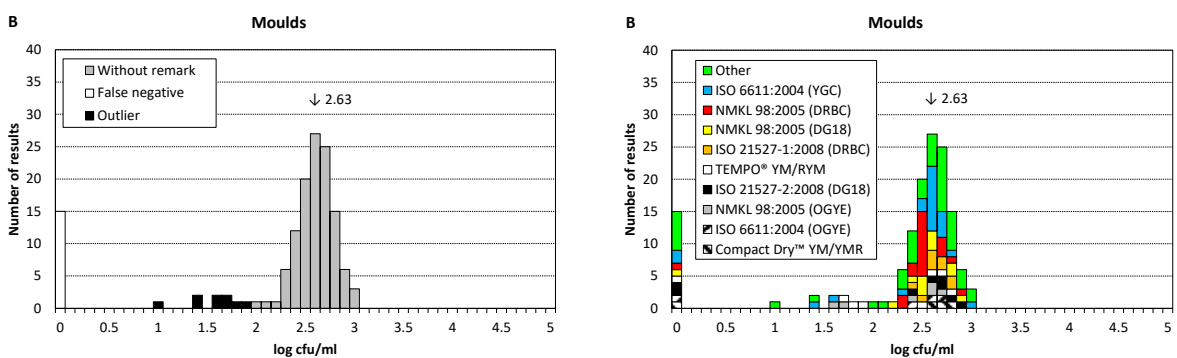


Figure 13. Results from analysis of moulds.

Outcome of the results of individual participants - assessment

Reporting and evaluation of results

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

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

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

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

Box plots

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

The different parts of a box plot are shown in figure 5.

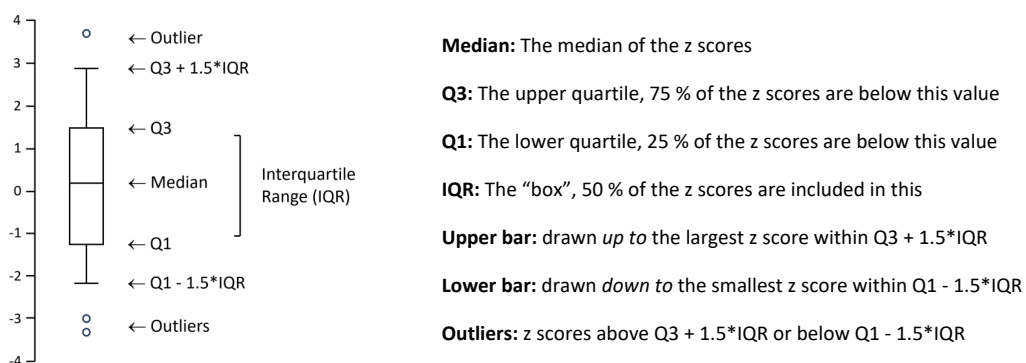
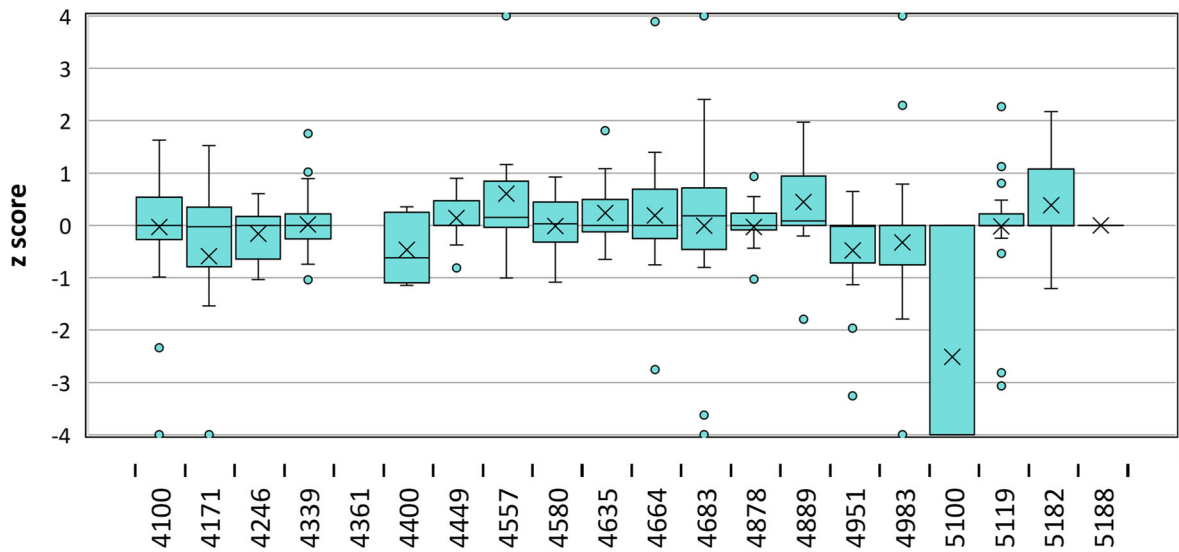
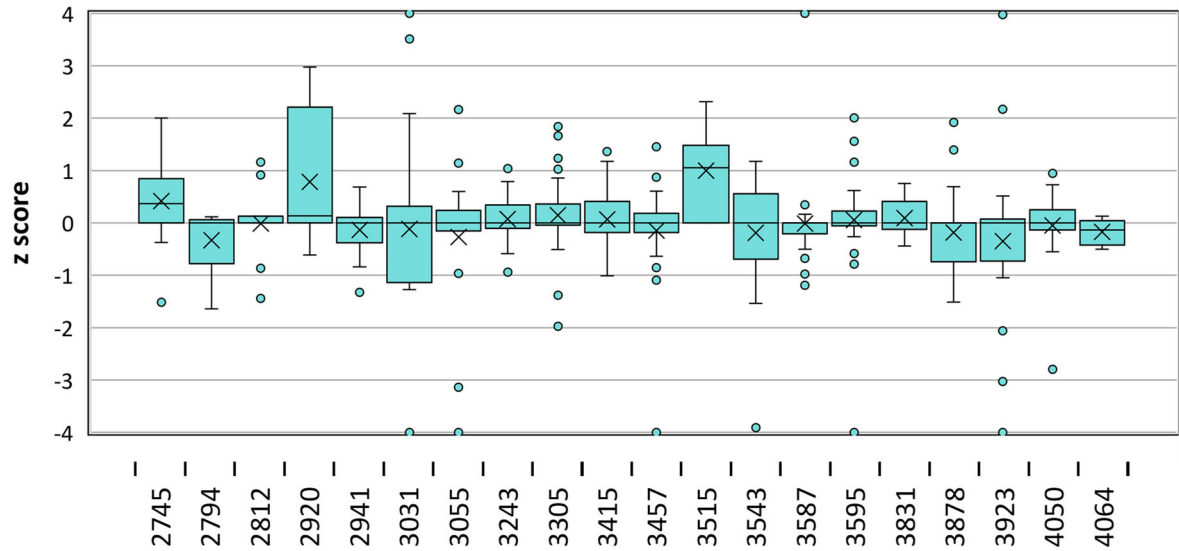
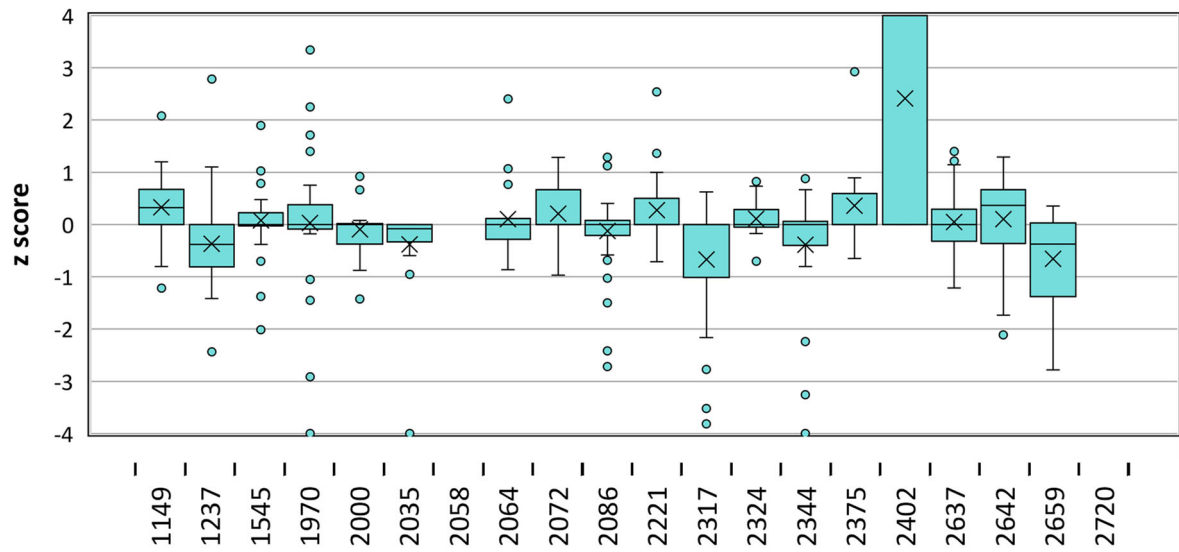
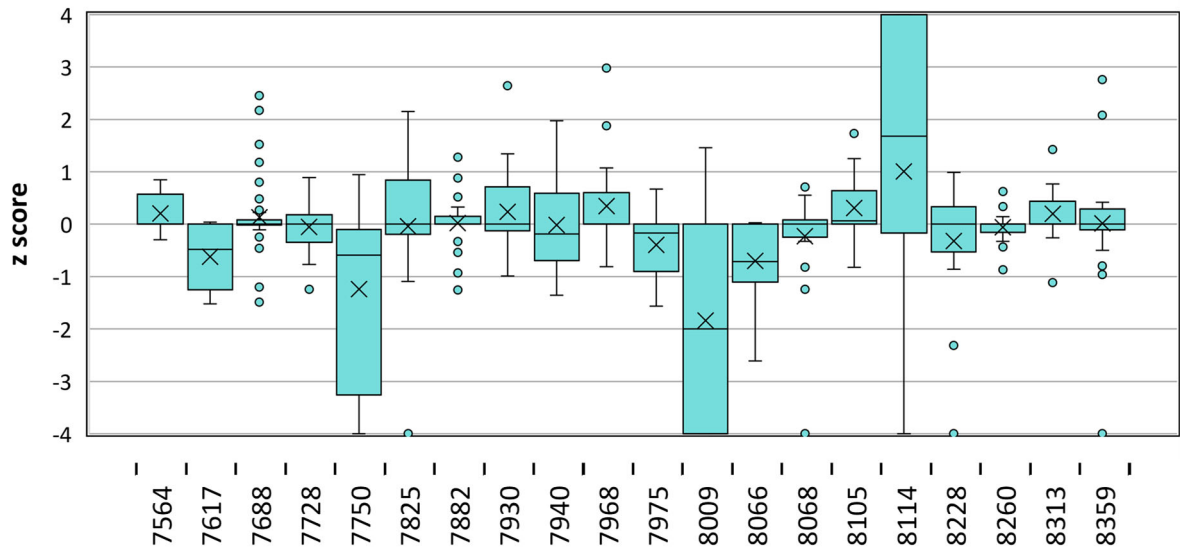
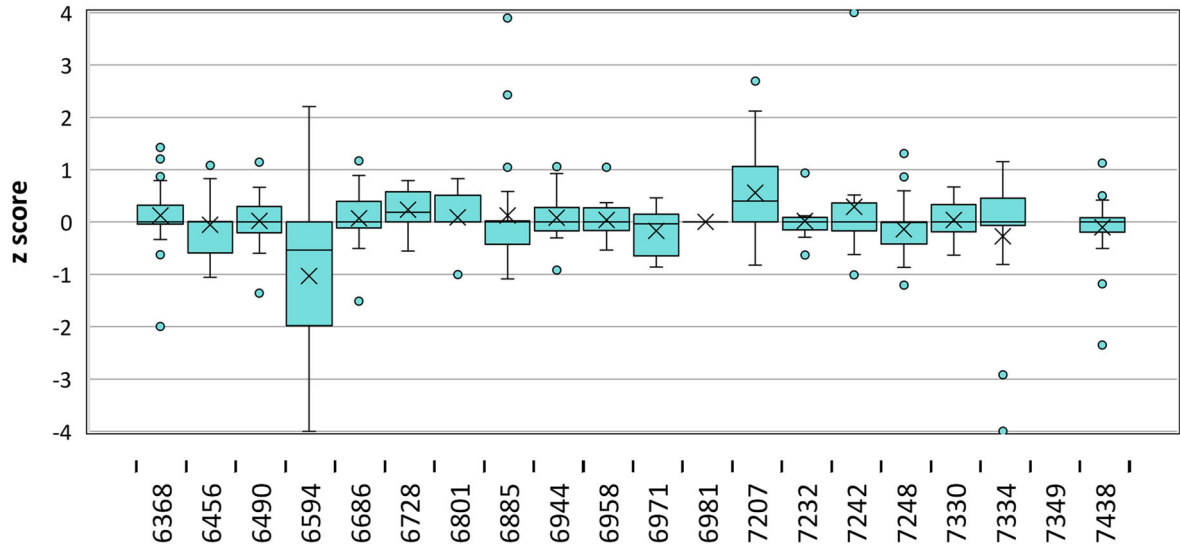
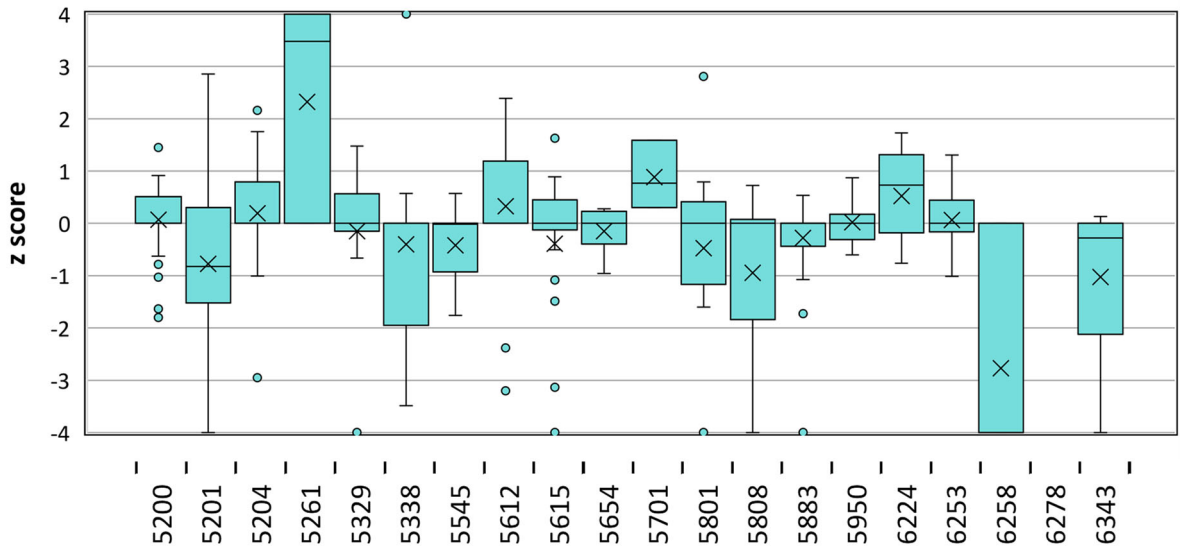


Figure 14. Schematic explanation of a box plot.





Test material and quality control

Test material

Each participant received three samples with freeze-dried microorganisms, designated A–C. The test material was freeze-dried in 0.5 ml portions in glass vials, as described by Peterz and Steneryd [3]. Before analysing the samples, the contents of each vial should be reconstituted in 254 ml of sterile diluent. The microorganism content of the samples and the concentrations determined at the Swedish Food Agency are listed in table 15.

Table 15. Microorganisms and approximate concentrations in the samples.

Sample	Microorganism	Strain			
		SLV no. ¹	Isolated from	Reference ²	log ₁₀ cfu ml ⁻¹
A	<i>Bacillus cereus</i>	SLV-518	Couscous	CCUG 44741	4.3
	<i>Enterococcus durans</i>	SLV-078	Fresh meat	CCUG 44816	4.5
	<i>Escherichia coli</i>	SLV-524	Chicken	CCUG 47554	4.2
	<i>Hafnia alvei</i>	SLV-015	Minced meat	CCUG 45642	4.6
	<i>Staphylococcus aureus</i>	SLV-280	Egg	-	4.4
B	<i>Aspergillus candidus</i>	SLV-541	Wheat flower	-	2.9
	<i>Candida glabrata</i>	SLV-052	-	-	2.5
	<i>Clostridium perfringens</i>	SLV-442	-	CCUG 43593	2.8
	<i>Escherichia coli</i>	SLV-477	Brie cheese	CCUG 43601	4.1
C	<i>Bacillus cereus</i>	SLV-516	Caramel pudding	CCUG 44740	4.3
	<i>Enterococcus faecalis</i>	SLV-051	-	CCUG 45101	5.0
	<i>Rhodotorula minuta</i>	SLV-506	Drinking water	-	3.2
	<i>Staphylococcus aureus</i>	SLV-438	Raw milk	CCUG 44812	4.5

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

² Culture collection. ATCC: American Type Culture Collection, CBS: Centraalbureau voor Schimmelcultures (Westerdijk Institute), CCUG: Culture Collection University of Gothenburg, Sweden; SMI: Public Health Agency of Sweden.

Quality control of the samples

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

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

s_R : the expected laboratory variation, generally assumed to be 0.25 for the Food scheme.

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

Table 16. Concentration mean (m), between-vial variation (s_{bb}) and p values from the quality control of the samples; m is expressed in \log_{10} cfu (colony forming units) per ml of sample.

Analysis and method	A ¹			B ²			C ¹		
	m	s_{bb}	p	m	s_{bb}	p	m	s_{bb}	p
Aerobic microorganisms, 30 °C NMKL method no. 86:2013	5.05	0.01	0.35	4.11	0.00	0.83	5.15	0.04	0.01
Psychrotrophic microorganisms NMKL method no. 86:2013	4.82	0.00	0.79	-	-	-	3.26*	0.05*	0.26*
Enterobacteriaceae NMKL method no. 144:2005	4.59	0.03	0.23	4.03	0.03	0.11	-	-	-
Escherichia coli NMKL method no. 125:2005	4.21	0.02	0.37	4.10	0.06	0.00	-	-	-
Presumptive Bacillus cereus NMKL method no. 67:2021	4.25	0.00	0.53	-	-	-	4.29	0.08	0.26
Coagulase-positive staphylococci NMKL method no. 66:2009	4.39	0.00	0.70	-	-	-	4.47	0.01	0.47
Lactic acid bacteria NMKL method no. 140:2007	4.49	0.03	0.30	-	-	-	4.98	0.02	0.32
Clostridium perfringens NMKL method no. 95:2009	-	-	-	2.81	0.03	0.08	-	-	-
Anaerobic sulphite-reducing bacteria NMKL method no. 56:2015	-	-	-	2.32	0.00	0.74	-	-	-
Aerobic microorganisms in fish products NMKL method no. 184:2006	5.11	0.00	0.70	4.11	0.03	0.05	5.18	0.00	0.54
H2S-producing bacteria in fish products NMKL method no. 184:2006	4.63	0.00	0.64	-	-	-	-	-	-
Yeasts NMKL method no. 98:2005 (DG18)	-	-	-	2.47	0.00	0.93	3.20	0.00	0.54
Moulds NMKL method no. 98:2005 (DG18)	-	-	-	2.88	0.02	0.30	-	-	-

- No target organism or no value

¹ $n = 10$ vials analysed in duplicate

² $n = 5$ vials analysed in duplicate

* Represents only distinct (large) colonies.

References

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

Appendix 1. Results of the participating laboratories

Lab no.	Aerobic microorganisms, 30 °C			Psychrotrophic microorganisms			Enterobacteriaceae			Escherichia coli			Presumptive Bacillus cereus			Coagulase-positive Staphylococcus			Lactic acid bacteria			Clostridium perfringens			Anaerobic sulphite-reducing bacteria			Aerobic microorganisms in fish products			H2S-producing bacteria in fish products			Yeasts			Moulds		
	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C
1149-1	5.06	3.95	4.95	-	-	-	4.613	4.04	0	4.176	4.04	0	4.698	0	4.778	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	2.48	3.26	0	3.04	0		
1149-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
1149-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
1237-1	4.964	3.851	5	-	-	-	4.38	3.806	0	3.799	3.732	0	-	-	-	4.23	0	4.279	4.343	0	4.903	0	3.398	0	4.724	2.58	0	4.716	3.914	4.857	-	-	0	2.431	0	2.845	-		
1237-2	4.857	3.964	5.041	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
1237-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
1545-1	5.03	4.39	5.05	-	-	-	4.51	4.18	0	4.13	4.18	0	4.32	0	4.65	4.03	0	4.09	4.46	0	5.06	0	2.91	0	0	2.91	0	-	-	-	-	-	0	2.3	0	2.5	0		
1545-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	2.36	0	2.63	0		
1545-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
1970-1	5	4.36	5.08	4.34	0	0	4.28	4.57	0	4	4.45	0	4.91	0	4.53	4.26	0	4.32	4.51	0	5.15	0	2.79	0	0	2.48	0	5	3.54	4.08	4.57	0	0	2.57	3.18	0	2.34	0	
1970-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
1970-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
2000-1	5.15	3.94	5.04	-	-	-	4.49	3.71	0	3.71	-	0	4.36	0	4.41	4.28	0	-	2.26	-	-	0	2.61	0	0	-	0	-	-	-	-	0	2.3	3.23	-	2.81	-		
2000-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
2000-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
2035-1	-	-	-	-	-	-	4.36	3.86	0	1	3.88	0	-	-	-	-	-	-	-	-	-	-	0	2.64	0	0	2.62	0	-	-	-	-	0	2.4	2.94	0	2.56	0	
2035-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	2.4	2.94	0	2.56	0	
2035-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
2058-1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
2058-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
2058-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
2064-1	5.11	4.1	5.38	-	-	-	4.44	4.16	0	-	-	0	4.25	0	4.33	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	2.27	2.95	0	2.61	0		
2064-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
2064-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
2072-1	5.11	4.08	5.18	5.04	3.89	5.04	4.72	3.9	0	3.94	3.74	0	4.45	0	4.15	4.36	0	4.4	4.51	0	4.99	0	2.81	0	0	2.81	0	-	-	-	-	0	2.45	3.28	0	2.79	0		
2072-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
2072-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
2086-1	5.171	4.019	5.228	4.684	-	5	4.578	3.883	0	4.023	3.941	0	4.44	0	4.406	4.301	0	4.431	4.464	2.582	5.132	0	2.32	0	0	2.167	0	-	-	-	-	0	2.477	2.926	0	2.67	0		
2086-2	4.984	4.111	5.069	4.683	-	5	4.549	3.862	0	3.918	3.893	0	4.309	0	4.37	4.289	0	4.372	4.363	2.462	4.963	0	2.438	0	0	2.104	0	-	-	-	-	0	2.334	2.932	0	2.56	0		
2086-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
2221-1	5.14	4.03	5.21	-	-	-	4.56	3.95	0	3.76	3.92	0	4.56	0	4.59	4.33	0	4.45	4.56	0	4.97	0	3.04	0	0	2.61	0	-	-	-	-	0	2.9	0	0	0	0		
2221-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
2221-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
2317-1	5.06	4	5.16	-	-	-	4.37	3.95	0	3.31	3.84	0	3.9	0	4.1	4.3	0	3.68	-	-	-	0	2	0	0	1.89	0	-	-	-	-	0	2.28	0	0	2.74	0		
2317-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4.3	0	3.68	-	-	-	-	-	-	-	-	-	-	-	-	-	0	2.19	2.41	0	2.75	0		
2317-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
2324-1	5	4.18	5.09	-	-	-	4.4	4.1	0	-	-	0	4.4	0	4.46	4.25	0	4.36	-	-	-	-	-	-	-	-	-	-	-	-	0	2.41	3.21	0	2.79	0			
2324-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
2324-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
2344-1	4.96	3.95	3.76	-	-	-	4.58	3.84	0	4	3.46	0	4.61	0	-	4.34	0	3.73	4.6	-	-	0	2.67	-	0	2.71	-	-	-	-	0	2.4	-	0	2.62	-			
2344-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
2344-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
2375-1	5.088	3.975	5.129	-	-	-	4.564	3.9	0	-	-	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	2.971	3.272	0	0	0			
2375-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
2375-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
2402-1	6	5.23	6.09	-	-	-	5.34	5.23	0	4.86	5.19	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	3.3	4	0	2.9	0				
2402-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
2402-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
2637-1	4.95	3.94	5.23	-	-	-	4.36	3.76	0	4.36	3.98	0	4.26	0	4.32	4.3	0	4.41	4.41	0	5.09	0	2.97	0	0	2.79	-	-	-	-	0	2.41	2.99	0	2.43	0			
2637-2	4.96	4.18	4.95	-	-	-	4.56	4.04	0	4.4	4.2	0	4.23	0	4.36	-	-	-	4.41	0	5.15	-	-	-	-	0	-	-	-	-	-	-	-	-	-	-			
2637-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
2642-1	4.9	4.04	5.08	4.81	4.04	4.9	4.66	4.15	1	4.08	4.08	1	-	-	-	4.36	1	4.52	-	-	-	-	-	-	-	-	-	-	-	1	2.04	2.98	1	2.76	1				
2642-2	4.91	4.11	5.11	4.85	4.11	5	4.62	4.2																															

Appendix 1. Results of the participating laboratories

Lab no.	Aerobic microorganisms, 30 °C			Psychrotrophic microorganisms			Enterobacteriaceae			Escherichia coli			Presumptive Bacillus cereus			Coagulase-positive Staphylococcus			Lactic acid bacteria			Clostridium perfringens			Anaerobic sulphite-reducing bacteria			Aerobic microorganisms in fish products			H2S-producing bacteria in fish products			Yeasts			Moulds		
	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C
6258-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
6258-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
6278-1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
6278-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
6278-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
6343-1	4.842	-	-	-	-	-	4.423	-	-	4.023	-	-	3.72	-	-	3.778	-	-	4.041	-	-	0	-	-	0	-	-	-	-	-	-	-	0	-	-	0	-		
6343-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
6343-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
6368-1	5.02	4.11	5.13	5.06	3.96	5.01	4.46	4.11	0	4.08	4.04	0	4.32	0	4.36	4.38	0	4.52	4.47	0	4.6	-	-	0	2.54	0	4.98	4.06	5.1	4.5	0	0	0	2.49	3.37	0	2.56	0	
6368-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4.71	0	4.9	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
6368-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
6456-1	4.93	4.12	5.01	-	-	-	-	-	-	-	-	-	4.34	0	4.36	4.2	0	4.2	-	-	-	0	2.48	0	0	2.45	0	-	-	-	-	-	0	2.65	3.26	0	0		
6456-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4.4	0	4.4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-			
6456-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
6490-1	4.96	4.07	5.1	-	-	-	4.6	3.94	0	-	-	-	4.53	0	4.76	4.35	0	4.46	-	-	-	0	2.63	0	-	-	-	-	-	-	-	0	2.32	2.86	0	2.56	0		
6490-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
6490-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
6594-1	4.73	3.87	4.94	-	-	-	-	-	-	3.08	3.56	0.6	4.05	1	4.09	1	0	1	4.44	2	5.04	-	-	0	2.74	0	-	-	-	-	-	0	2.39	0	0	2.52	0		
6594-2	-	-	-	-	-	-	-	-	-	1	1	0	-	-	-	-	-	-	4.87	3.62	4.81	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
6594-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
6686-1	5.08	4.04	5.2	4.91	6.08	5.08	4.48	3.98	0	4.17	3.91	0	-	-	-	4.26	0	0	-	-	-	0	2.68	0	-	-	5.08	4.11	5.2	4.45	0	0	0	2.15	0	0	2.53	0	
6686-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
6686-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
6728-1	5.093	4.13	5.163	-	-	-	4.613	4.068	0	3.985	3.991	0	-	-	-	4.204	0	4.389	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
6728-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4.301	0	4.505	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
6728-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
6801-1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4.15	0	0	-	-	-	-	-	-	-	-	-	-	-	-	-	0	-	3.26	0	2.74	0		
6801-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
6801-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2.49	-	-	-	-		
6885-1	4.89	3.98	4.99	-	-	-	4.36	3.95	0	3.88	3.97	0	4	0	4.3	4.34	0	5.1	-	-	-	0	2.89	0	-	-	-	-	-	0	2.88	0	0	0	0	0			
6885-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
6885-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
6944-1	5.04	4.04	5.22	-	-	-	-	-	-	0	4.13	0	-	-	-	4.26	0	4.3	4.43	0	4.91	-	-	-	-	-	-	-	-	-	0	2.26	3.17	0	2.81	0			
6944-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
6944-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
6958-1	4.99	4.01	5.07	-	-	-	4.56	3.97	0	-	-	-	4.17	0	4.73	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	2.48	3.09	0	2.7	0	0			
6958-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
6958-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
6971-1	4.9	4.07	5.1	-	-	-	4.42	4.05	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
6971-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
6971-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
6981-1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	275	990	0	520	-	-		
6981-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
6981-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
7207-1	5.13	4.52	5.29	-	-	-	4.38	4.04	0	-	-	-	4.71	0	5.06	-	-	4.59	2.95	5.05	-	-	-	-	-	-	-	-	0	2.32	3.06	0	2.79	0	0	0			
7207-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
7207-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
7232-1	4.93	4.08	5.06	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	2.44	3.28	0	2.65	0	0	0			
7232-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
7232-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
7242-1	4.881	3.98	5.074	-	-	-	4.571	4.06	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	3.38	0	0	2.65	-	-	-			
7242-2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
7242-3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0		
7248-1	4.93	3.97	5.02	4.64	3.87	4.91	4.46	3.93	0	4.05	3.91	0	4.2	0	4.04	4.32	0	4.3	0	3.7	4.92	0	2.67	0	0	2.43	0	4.98	3.98	4.93	4.49	0	0	0	2.32	3.03	0	2.54	0
7248-2	5.18	4.03	5.13	4.95	3.91	5.23	4.53	3.9	0	4.08	3.95	0	-	-	-	-																							

Appendix 1. Results of the participating laboratories

Lab no.	Aerobic microorganisms, 30 °C			Psychrotrophic microorganisms			Enterobacteriaceae			Escherichia coli			Presumptive Bacillus cereus			Coagulase-positive Staphylococcus			Lactic acid bacteria			Clostridium perfringens			Anaerobic sulphite-reducing bacteria			Aerobic microorganisms in fish products			H2S-producing bacteria in fish products			Yeasts			Moulds					
	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C			
<i>u_{PT}</i>	0.013	0.016	0.012	0.089	-	-	0.017	0.019	-	0.037	0.026	-	0.039	-	0.039	0.015	-	0.025	0.029	-	0.027	-	0.046	-	-	0.034	-	0.031	0.048	0.038	0.031	-	-	-	0.020	0.022	-	0.022	-			
<i>F+</i>	0	0	0	0	-	-	0	0	5	0	0	6	0	5	0	0	4	0	0	21	0	0	0	1	2	0	1	0	0	0	0	1	0	1	0	0	7	0	0	4	0	6
<i>F-</i>	0	1	0	0	-	-	1	2	0	6	2	0	0	0	2	1	0	7	5	0	2	0	2	0	0	0	0	0	0	1	1	0	0	0	5	33	0	15	0			
<	8	4	10	1	-	-	2	3	0	7	8	0	3	0	3	8	0	10	2	0	6	0	3	0	0	2	0	0	0	2	1	0	0	0	3	8	0	9	0			
>	6	11	3	0	-	-	5	6	0	0	2	0	1	0	1	0	0	3	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	5	1	0	0	0				
<i>Lower</i>	4.62	3.59	4.74	3.72	0	0	4.03	3.43	0	3.05	3.29	0	3.41	0	3.49	3.91	0	3.78	3.96	0	4.44	0	1.94	0	0	2.04	0	4.65	3.52	4.64	4.19	0	0	0	1.88	2.56	0	2.03	0			
<i>Upper</i>	5.40	4.57	5.45	5.63	6.08	5.23	5.00	4.51	0	4.91	4.62	0	5.27	0	5.33	4.63	0	4.93	5.01	0	5.41	0	3.45	0	0	3.30	0	5.34	4.57	5.45	4.82	0	0	0	2.99	3.66	0	3.22	0			

N = number of reported results

n = results without annotation

Min = lowest reported result

Max = highest reported result

Med = median value

m_{PT} = assigned value

s_{PT} = standard deviation

u_{PT} = measurement uncertainty

F+ = false positive

F- = false negative

< = low outlier

> = high outlier

Lower = lowest accepted value

Upper = highest accepted value

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

Appendix 2. Z-scores of all participants

Lab no.	Aerobic microorganisms, 30 °C			Psychrotrophic microorganisms			Enterobacteriaceae			Escherichia coli			Presumptive Bacillus cereus			Coagulase-positive Staphylococcus			Lactic acid bacteria			Clostridium perfringens			Anaerobic sulphite-reducing bacteria			Aerobic microorganisms in fish products			H2S-producing bacteria in fish products			Yeasts			Moulds						
	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C							
5182-1	0.974	1.737	1.857				-0.044	1.450	0			1.032	0	-0.028	0	2.176																0	-0.477	0	0.219	0							
5182-2																															0	-0.477	1.219	0	-1.205	0							
5182-3																																											
5188-1																																											
5188-2																																											
5188-3																																											
5200-1												-1.027	1.449	0			0.164	0	0.502	0.912	0	0.363										0	0.512	0.045	0	-1.638	0						
5200-2												-1.799	0.683				-0.271	0	-0.630	0.706	0	0.629										0	-0.310	0.880	0	-0.783	0						
5200-3																	0.381	0	0.111	0.238	0	0.629														0							
5201-1	-4.000	-0.376	-1.552				-1.262	0.403				-1.519	0.302	-1.474	-0.848	-0.505	2.851																	0.052	-1.194	0.068							
5201-2	-4.000	1.712	-3.488				-0.827	0.901																																			
5201-3																																											
5204-1	0.920	0.791	-0.374	0.327			0.976	2.175	0			1.300	0	0.459	0	0.000	-0.672	0	-0.907	-0.246	0	0.845	0	-0.664	0	0	0.042	0			0	-0.110	-0.812	0	-0.838	0							
5204-2	2.160	1.344	0.384				1.535	0.901	0			0.348	1.753	0			-1.007	0	-0.281													0	1.296	0	-2.951								
5204-3																																											
5261-1	4.000	4.000	4.000				4.000	4.000	0			4.000	0	3.296	0	3.481																		0	4.000	0	0						
5261-2																																											
5261-3																																											
5329-1	0.897	-0.664	0.923				0.192	-0.212	0			-0.111	0	0.233	0	-0.196	1.477	0	1.118	1.077	0.159											0	-4.000	0	-4.000	0							
5329-2																																											
5329-3																																											
5338-1	-1.948	4.000	-3.488				-2.008	0.569	0																											-0.164	-1.358	0	0				
5338-2																																											
5338-3																																											
5545-1	-0.243	-0.683	-1.552				-1.511	-1.758	0					-1.441	0	-0.033	-0.756	0	0.033																0	-0.759	0.553	0	0.571	0			
5545-2																																											
5545-3																																											
5612-1	0.687	2.326	0.047									1.894	2.388	0	0.394	0	0.750						0	2.316	0	0	1.336	0				0	-2.381	0	-3.203	0							
5612-2																																											
5612-3																																											
5615-1	0.532	0.423	0.131				0.541	0.624	0			0.638	0.892	0	-4.000	0	-3.132	0.749	0	0.033	-4.000	0	-4.000	0	-0.505	0	0	-1.491	0			0	-1.083	0.389	0	1.628	0						
5615-2																																											
5615-3																																											
5654-1	-0.398	-0.867	-0.374				-0.019	-0.650	0					-0.958	0	0.228																				0	0.269	0.280	0	0.269	0		
5654-2																																											
5654-3																																											
5701-1	0.765	1.589	0.300																																								
5701-2																																											
5701-3																																											
5801-1	-4.000	-0.253	-4.000				0.603	0.790	0					-0.733	0	-1.598																						2.810	0.225	0	0		
5801-2																																											
5801-3																																											
5808-1	-1.483	0.423	-1.215									-1.680	0.302	0	-4.000	0	-4.000																		0	-2.327	0	0.722	0				
5808-2																																											
5808-3																																											
5883-1	-0.165	-0.560	-0.458				0.478	-0.705	0			0.316	0.030	0	-0.507	0	-1.076	0.080	0	-0.385	-1.730	0	0.536	0	0.210	0	0	0.378	0			0	-0.110	-4.000	0	-0.888	0						
5883-2																																				0	-0.326	-0.321	0	-0.939	0		
5883-3																																											
5950-1				0.171																																							
5950-2																																											
5950-3																																											
6224-1	1.462	0.730	1.731				1.162	0.735	0					-0.765	0	-0.359																											
6224-2																																											
6224-3																																											
6253-1	-0.243	-0.376	0.468											-0.121	0	1.305	-1.007	0	0.659																	0	0.431	1.153	0	-0.133	0		
6253-2																																											
6253-3																																											
6258-1	-4.000	-4.000	-4.000	-4.000								-4.000	-4.000	0																								0	-4.000	-4.000	0	-4.000	0

Appendix 2. Z-scores of all participants

Lab no.	Aerobic microorganisms, 30 °C			Psychrotrophic microorganisms			Enterobacteriaceae			Escherichia coli			Presumptive Bacillus cereus			Coagulase-positive Staphylococcus			Lactic acid bacteria			Clostridium perfringens			Anaerobic sulphite-reducing bacteria			Aerobic microorganisms in fish products			H2S-producing bacteria in fish products			Yeasts			Moulds		
	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C
8228-1	-0.863	0.361	-0.710	0.986			0.105	0.236	0			0.040	0	-2.316																		0	0.539	0.444	0	-4.000	0		
8228-2																																							
8228-3																																							
8260-1	0.145	-0.437	-0.121				-0.205	-0.872	0			-0.314	0	-0.326	-0.171	0	-0.020			0	-0.028	0	0	0.090	0				0	-0.056	0.334	0	0.621	0					
8260-2																																							
8260-3																																							
8313-1	0.765	-1.113	-0.205				0.292	-0.262	0			1.425	0	0.130	0.582	0	0.241					0	1.527	0				0											
8313-2																																							
8313-3																																							
8359-1	2.083	-0.499	-0.794				0.292	0.181	0	0.413	0.166	0	-0.185	0	-0.163	2.757	0											0	-0.380		0	0.420	0						
8359-2	-4.000	-0.069	-0.963							0.413	0.393	0																0	-0.110	0.007	0	0.420	0						
8359-3																																							
8397-1	0.687	4.000	0.805				-1.449	3.726	0	0.735	0.166	0	0.942	0	1.631	0.917	0	-0.072	0.267	0	-0.082							0	0.485	0.389	0	-0.586	0						
8397-2																																							
8397-3																																							
8430-1	-1.948	-3.385	-0.458				-2.071	-4.000	0	-1.616	-2.147	0			-0.338	0	-2.942											0	-0.596	-2.558	0	-1.643							
8430-2																																							
8430-3																																							
8435-1	0.455	0.914	-0.037				0.789	1.012	0	2.827	1.073	0	0.877	0	1.664	0.749	0					-1.011	0	2.042	0.917	-0.014	1.703	0	0	0	1.728		0	0.621	0				
8435-2	1.695	1.344	1.141				0.105	1.732	0	1.443	0.710	0	0.298	0	-0.228	0	-0.333					0						0	2.593	-0.375	0	1.426							
8435-3	1.152	4.000	1.310				0.789	0.181	0							0.582																							
8506-1	0.300	3.125	-0.542				-2.257	-1.481		-2.936	-2.192		0.394		-0.587	-4.000	0	-4.000					0.090					-1.137						-0.737					
8506-2										-4.000	-4.000	0																											
8506-3																																							
8523-1	0.610	-0.007	0.805	0.923			1.100	0.901	0		0.483	0			-0.003	0	0.137											0	-0.380	0.880	0	0.219	0						
8523-2																																							
8523-3																																							
8528-1	-1.251	-0.376	-1.384				-1.387	-0.982	0				-1.763	0	-1.631													0	1.188		0	0.722	0						
8528-2							-1.511	-1.259																															
8528-3																																							
8568-1	-4.000	-0.007	-1.804				-1.325	-0.539	0	-0.875	0.710	0	0.845	0	0.848								0	-0.341	0			0	-0.596		0	-0.687	0						
8568-2																																							
8568-3																																							
8626-1	-1.057	1.067	-1.182				-0.945	-0.018	0	-1.938	-2.600	0																											
8626-2																																							
8626-3																																							
8628-1	-1.173	-0.007	0.552				-1.200	-0.041	0	0.638	-0.786	0			1.753	0	1.755	-0.132	0	0.474	0	0.290	0	0	1.288	0	0.299	-1.426	1.019	1.030	0	0	0	-0.326	-0.048	0.974	0		
8628-2																																							
8628-3																																							
8734-1	-0.243	-0.990	-1.468				0.478	-0.484	0											0.267		0.041						0	1.512	-0.648									
8734-2																																							
8734-3																																							
8742-1	-1.173	-0.499	-0.794							-2.582	-4.000	0			0.582	0	0.555																						
8742-2																																							
8742-3																																							
8756-1	-1.793	1.774	1.141				-1.884	2.120	0	-2.582	1.662	0	0.040	0	1.011	-1.509	0	-0.333																					
8756-2																																							
8756-3																																							
8829-1	1.276	2.842	1.141										0.449	0	0.793													0	0.252	0.203	0								
8829-2													0.401	0	0.940																								
8829-3																																							
8891-1	-0.476	-0.990	-0.037				-2.195	-0.761	0	-0.425	-0.514	0	0.652	0	-0.033	-0.923	0	-0.072					0	1.384			0	-0.596	0.007	0	0.118	0							
8891-2	-0.476	-1.113					-0.951	-0.982																															
8891-3																																							
9002-1	1.307	-0.499	-0.458	-0.927			0.105	-0.761	0	0.702	-0.287	0	-1.087	0	-1.729	-0.087	0	-4.000	-0.817	0	-0.886			0	0.569	0		0	-0.272		0	-0.033	0						
9002-2	0.532	-0.867	-0.458				1.784	-0.262	0	0.895	-0.423	0																											
9002-3																																							
9003-1	-4.000	0.220	0.746				0.074	0.031	0	0.126	0.202	0			-0.681	0	0.320											0	2.923	0.378									

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

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

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

The Swedish Food Agency's PT program offers

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

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

The Swedish Food Agency's reference material

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

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