

Proficiency testing Food Microbiology

April 2023

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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
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
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 SEC	3M™ Petrifilm™ Select <i>E. coli</i>
Petrifilm Staph	3M™ Petrifilm™ Staph Express
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
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
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 staphylococci

Lactic acid bacteria

Clostridium perfringens

Anaerobic sulphite-reducing bacteria

Aerobic microorganisms in fish products

H₂S-reducing 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 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 5 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 Annex 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 , or unusually many deviating results.

Figure legends

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

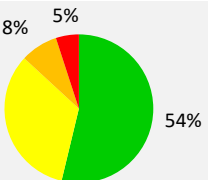
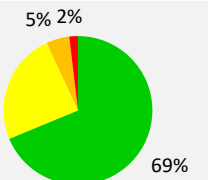
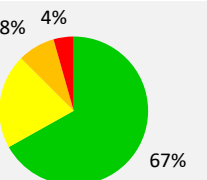
Results

General outcome

Samples were sent to 168 participants; 38 in Sweden, 114 in Europe, and 16 outside of Europe. Of the 160 participants that reported results, 102 (64 %) provided at least one result that received an annotation. In the previous PT round with similar analyses (April 2022) the proportion was 62 %.

Individual results are listed in Annex 1 and on the website: <https://www2.slv.se/absint>. Z-scores for individual results are listed in Annex 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>Clostridium bifermentans</i> <i>Carnobacterium maltaromaticum</i> <i>Hafnia alvei</i> <i>Penicillium verrucosum</i>				<i>Clostridium perfringens</i> <i>Hanseniaspora uvarum</i> <i>Staphylococcus aureus</i> <i>Serratia marcescens</i> <i>Shewanella putrefaciens</i>				<i>Cladosporium cladosporioides</i> <i>Escherichia coli</i> <i>Staphylococcus aureus</i> <i>Saccharomyces cerevisiae</i>			
Analysis	Target organism	N	F	X	Target organism	N	F	X	Target organism	N	F	X
Aerobic microorganisms, 30 °C	All	148	0	7	All	148	0	7	All	148	0	6
Psychrotrophic microorganisms	All	21	0	1	All	21	0	0	Method depend.	21	-	-
Enterobacteriaceae	<i>H. alvei</i>	127	0	3	<i>S. marcescens</i>	126	4	3	<i>E. coli</i>	127	1	7
<i>Escherichia coli</i>	-	105	2	0	-	105	0	0	<i>E. coli</i>	104	2	6
Presumptive <i>Bacillus cereus</i>	<i>B. cereus</i>	102	11	4	(<i>S. aureus</i>)	101	4	0	(<i>S. aureus</i>)	102	4	0
Coagulase-positive staphylococci	-	92	1	0	<i>S. aureus</i>	91	4	3	<i>S. aureus</i>	92	1	7
Lactic acid bacteria	<i>C. maltaromaticum</i>	46	25	2	(<i>S. aureus</i>)	46	21	0	(<i>S. aureus</i>)	47	15	0
<i>Clostridium perfringens</i>	(<i>C. bifermentans</i>)	51	13	0	<i>C. perfringens</i>	50	1	1	-	51	0	0
Anaerob. sulphite red. bacteria	<i>C. bifermentans</i>	60	3	3	<i>C. perfringens</i>	59	1	6	-	62	1	0
Aerobic microorg. in fish products	All	22	0	1	All	22	-	-	All	22	0	2
H2S-prod. bacteria in fish products	<i>H. alvei</i>	19	0	0	<i>S. putrefaciens</i>	19	-	-	-	19	0	0
Yeasts	-	130	12	0	<i>H. uvarum</i>	131	0	6	<i>S. cerevisiae</i>	131	9	8
Moulds	<i>P. verrucosum</i>	130	11	10	-	127	3	0	<i>C. cladosporioides</i>	129	9	7

- 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

H. alvei and *C. maltaromaticum* were the main target organisms.

In total, 148 participants reported results. Four low and three high outliers were reported.

Sample B

S. putrefaciens and *S. aureus* were the main target organisms.

In total, 148 participants reported results. Three low and four high outliers were reported.

Sample C

E. coli and *S. aureus* were the main target organisms.

In total, 148 participants reported results. Four low and two high outliers were reported.

General remarks

Most participants followed either NMKL 86:2013, ISO 4833-1:2013 or used 3M Petrifilm AC. The withdrawn NMKL 86:2006 and ISO 4833:2003 were used by eleven and six participants, respectively.

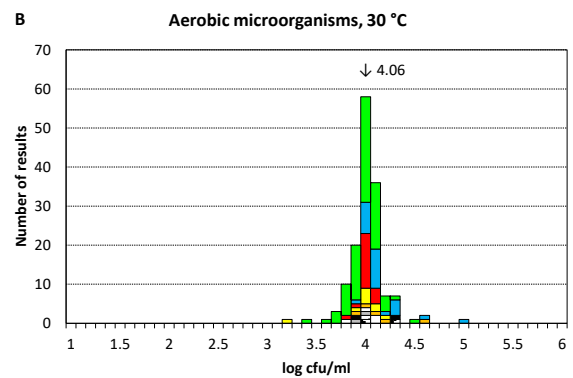
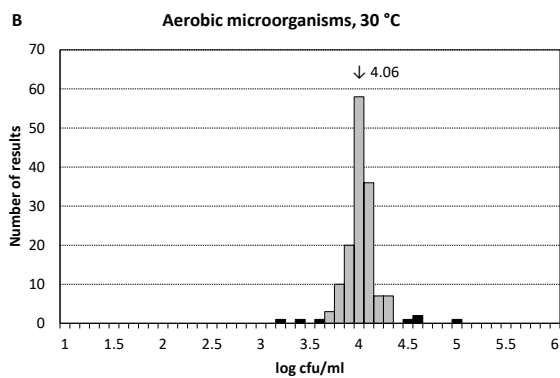
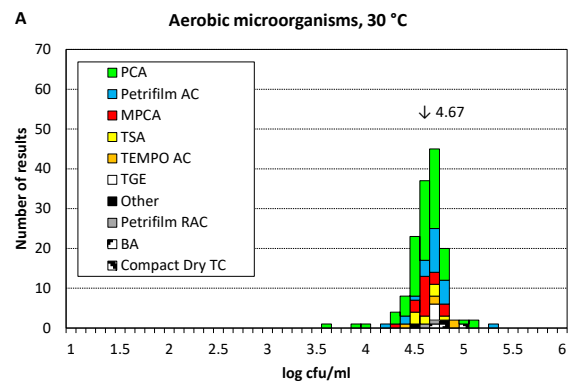
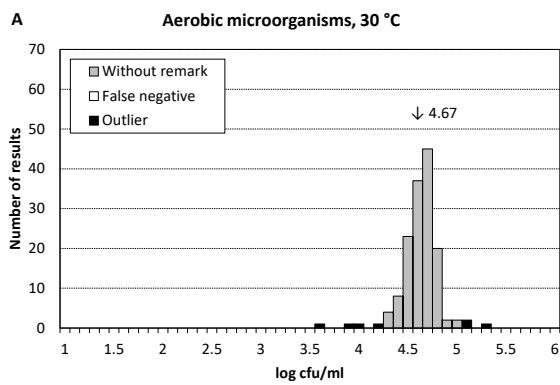
Both NMKL 86:2013 and ISO 4833-1:2013 are based on incubation on PCA or MPCA at 30 °C for 72 h. Users of Petrifilm AC can use different times/temperatures, depending on the method validation. For example, AOAC[®] prescribes incubation at 35 °C for 48 h while AFNOR prescribes 30 °C for either 48 h or 72 h, depending on which product that is analysed. 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.

The majority of the participants incubated on PCA, but Petrifilm AC was also common. Incubation on MPCA was mainly done by laboratories within the dairy industry. Incubation on TSA was mainly done by users of a company-specific method. A few participants used TEMPO AC, which is based on MPN (Most Probable Number). With this method, the sample is incubated in a card that contains different-sized wells. A substrate in the medium emits fluorescence when hydrolysed by the microorganisms. The number of microorganisms is determined statistically by the number and size of the fluorescing wells.

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

Medium	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	148	141	4.67	0.13	0	4	3	148	141	4.06	0.12	0	3	4	148	142	4.32	0.10	0	4	2
PCA	77	72	4.66	0.13	0	3	2	77	74	4.04	0.13	0	2	1	77	72	4.28	0.09	0	4	1
Petrifilm AC	26	24	4.72	0.12	0	1	1	26	24	4.12	0.12	0	0	2	26	25	4.39	0.10	0	0	1
MPCA	20	20	4.66	0.11	0	0	0	20	20	4.08	0.08	0	0	0	20	20	4.32	0.10	0	0	0
TSA	9	9	4.68	0.11	0	0	0	9	8	4.04	0.08	0	1	0	9	9	4.34	0.06	0	0	0
TEMPO AC	5	5	4.79	0.17	0	0	0	5	4	-	-	0	0	1	5	5	4.39	0.10	0	0	0
TGE	4	4	-	-	0	0	0	4	4	-	-	0	0	0	4	4	-	-	0	0	0
Other	2	2	-	-	0	0	0	2	2	-	-	0	0	0	2	2	-	-	0	0	0
Petrifilm RAC	2	2	-	-	0	0	0	2	2	-	-	0	0	0	2	2	-	-	0	0	0
BA	2	2	-	-	0	0	0	2	2	-	-	0	0	0	2	2	-	-	0	0	0
Compact Dry TC	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).



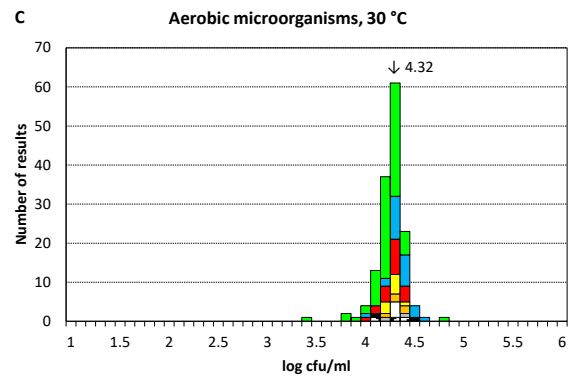
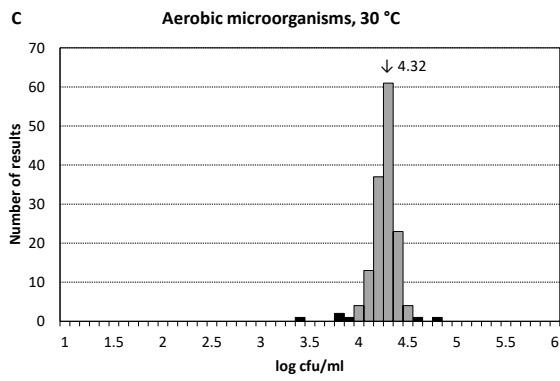


Figure 1. Results from analysis of aerobic microorganisms, 30 °C.

Psychrotrophic microorganisms

Sample A

H. alvei and *C. maltaromaticum* were the main target organisms.

In total, 21 participants reported results. One low outlier was reported.

Sample B

S. putrefaciens and *S. aureus* were the main target organisms. In the quality control at the Swedish Food Agency (ten days incubation on PCA at 6.5 °C), two types of colonies were observed; larger white colonies and very small transparent colonies.

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

Sample C

In the Swedish Food Agency's quality control, no colonies were observed on PCA after ten days incubation at 6.5 °C. Similar results were found for the participants; 9 of the 11 participants that incubated at low temperatures (6–7 °C) reported zero results. In contrast, the remaining 10 participants (of which most incubated at 15–22 °C) reported results in the range of 3.48–4.32 log₁₀ cfu ml⁻¹, corresponding to *E. coli* and *S. aureus* in the sample.

Despite the stark differences in results, participants are not encouraged to repeat the analysis. Rather, since the differences in results align very well with the choice of method, they are likely to reflect the “true” results of the respective methods.

The results for sample C are not evaluated, and no z-scores are calculated for the analysis.

Note: The assigned value (m_{PT}) and standard deviation (s_{PT}) provided in Annex 1 are calculated only from the positive results, and can thus be used by participants that want to evaluate their own performance. They should however be used carefully, and only as a guidance, since the measurement uncertainty of the assigned value is not negligible ($u_{PT} = 0.118$).

General remarks

In summary, the results are difficult to evaluate. This is mainly due to the differences between the methods, but also due to the fact that several participants used modified methods. Users of NMKL 86:2013 typically incubated for 10 days at 6.5 °C, but 20 h at 17 °C followed by 3 days at 7 °C was also used. 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 6.5 °C as the primary incubation temperature.

Several methods were referenced by only one participant each. These included NMKL 74:2000, ISO 4833-1:2013, ISO 6730:2005/IDF 101:2005 and NMKL 184:2006. NMKL 74:2000 has been replaced

by NMKL 86:2013. NMKL 184 is mainly adapted for analysis of aerobic count and specific spoilage organisms in fish and fish products.

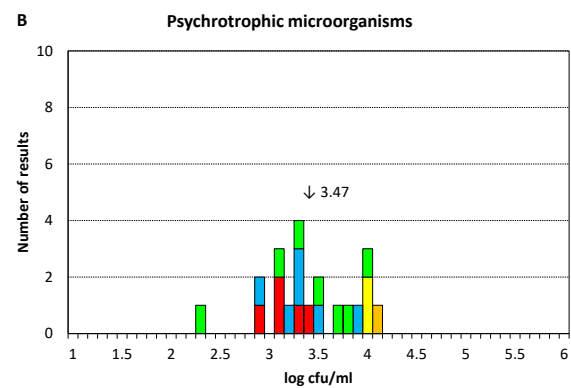
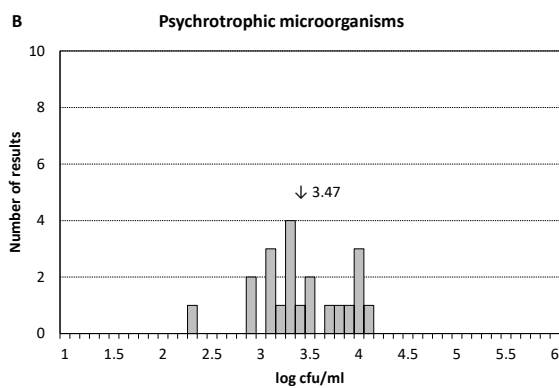
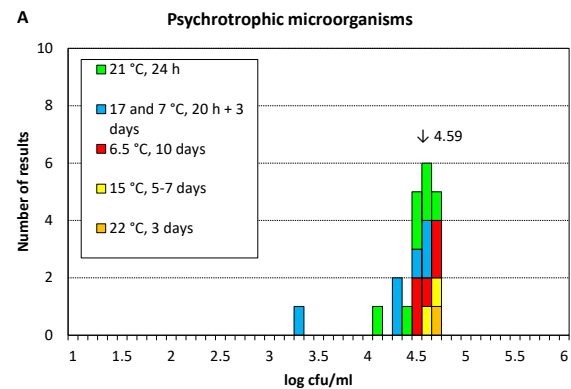
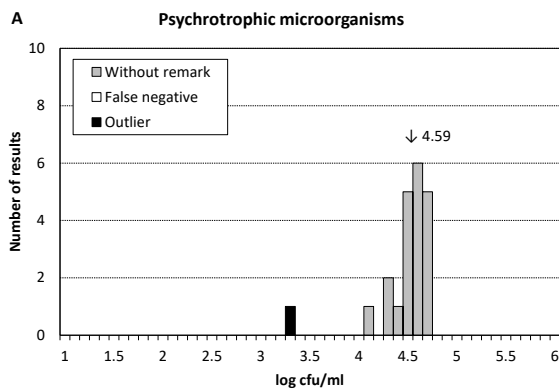
Fourteen of the 21 participants incubated on PCA, three on MPCA, two on Petrifilm AC and two on Long & Hammer agar.

Table 3. Results from analysis of psychrotrophic microorganisms.

Incubation	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	21	20	4.59	0.16	0	1	0	21	21	3.47	0.47	0	0	0	21	21	3.94*	0.33*	-	-	-
21 °C, 24 h	7	7	4.57	0.20	0	0	0	7	7	3.51	0.58	0	0	0	7	-	-	-	-	-	-
17 and 7 °C, 20 h + 3 days	6	5	4.53	0.14	0	1	0	6	6	3.31	0.34	0	0	0	6	-	-	-	-	-	-
6.5 °C, 10 days	5	5	4.66	0.08	0	0	0	5	5	3.16	0.21	0	0	0	5	-	-	-	-	-	-
15 °C, 5-7 days	2	2	-	-	0	0	0	2	2	-	-	0	0	0	2	-	-	-	-	-	-
22 °C, 3 days	1	1	-	-	0	0	0	1	1	-	-	0	0	0	1	-	-	-	-	-	-

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

*The sample is not evaluated. The values are shown only as an information to the participants. The measurement uncertainty of the assigned value is not negligible.



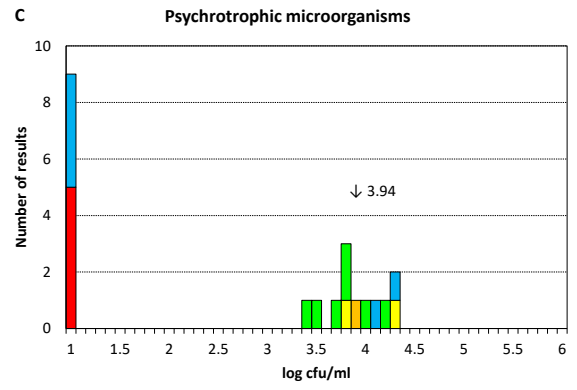
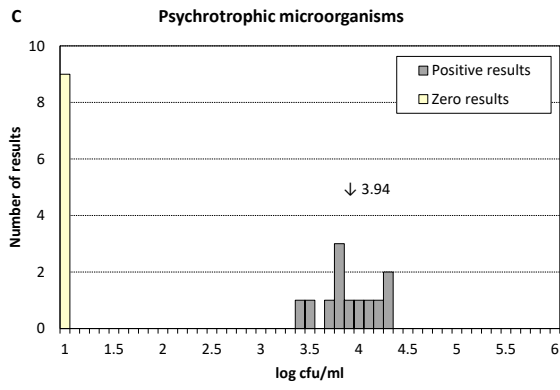


Figure 2. Results from analysis of psychrotrophic microorganisms

Enterobacteriaceae

Sample A

H. alvei was target organism. On VRBG, it forms typical red colonies that are surrounded by a bile salt precipitation zone. The strain is oxidase negative.

In total, 127 participants reported results. Two low and one high outliers were reported.

Sample B

S. marcescens was target organism. On VRBG, it forms small pink/red colonies that are surrounded by a less prominent bile salt precipitation zone. The strain is oxidase negative.

In total, 126 participants reported results. Two low and one high outliers were reported, as well as four false-negative results.

Sample C

E. coli was target organism. On VRBG, it forms dark red colonies that are surrounded by a distinct bile salt precipitation zone. The strain is oxidase negative.

In total, 127 participants reported results. Two low and five high outliers were reported, as well as one false negative result.

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.

Most participants followed either NMKL 144:2005 (42 %), a method with Petrifilm EB (24 %), or an ISO method (24 %). Among the latter, the majority followed ISO 21528-2:2017, which is based on colony-count. In comparison, ISO 21528-1:2017 is based on MPN. The latter method is recommended when the expected level of Enterobacteriaceae is lower than 100 cfu g⁻¹. Both ISO standards were last reviewed by ISO in 2022 and remain current. Ten participants still followed either of the previous – and now withdrawn – ISO 21528-2:2004 and ISO 21528-1:2004.

For sample B, the median value for participants that incubated on TSA/VRB, or that used TEMPO EB, differed by more than one *s*_{PT} from the assigned value. However only five and six participants used these media, respectively, so it might not reflect a true difference in the results between these methods.

Confirmation was performed by 61 % of the participants, and most often consisted of an oxidase test.

Table 4. Results from analysis of Enterobacteriaceae.

Medium	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	127	124	4.14	0.15	0	2	1	126	119	2.63	0.17	4	2	1	127	119	3.80	0.14	1	2	5
VRBG	80	77	4.12	0.13	0	2	1	80	75	2.60	0.17	2	2	1	80	74	3.80	0.15	1	2	3
Petrifilm EB	32	32	4.21	0.15	0	0	0	32	31	2.67	0.12	1	0	0	32	31	3.84	0.10	0	0	1
TSA/VRBG	6	6	4.13	0.16	0	0	0	5	5	2.38	0.25	0	0	0	6	6	3.71	0.11	0	0	0
TEMPO EB	6	6	4.03	0.17	0	0	0	6	6	2.84	0.15	0	0	0	6	6	3.81	0.17	0	0	0
Compact Dry ETB	2	2	-	-	0	0	0	2	1	-	-	1	0	0	2	2	-	-	0	0	0
Other	1	1	-	-	0	0	0	1	1	-	-	0	0	0	1	0	-	-	0	0	1

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

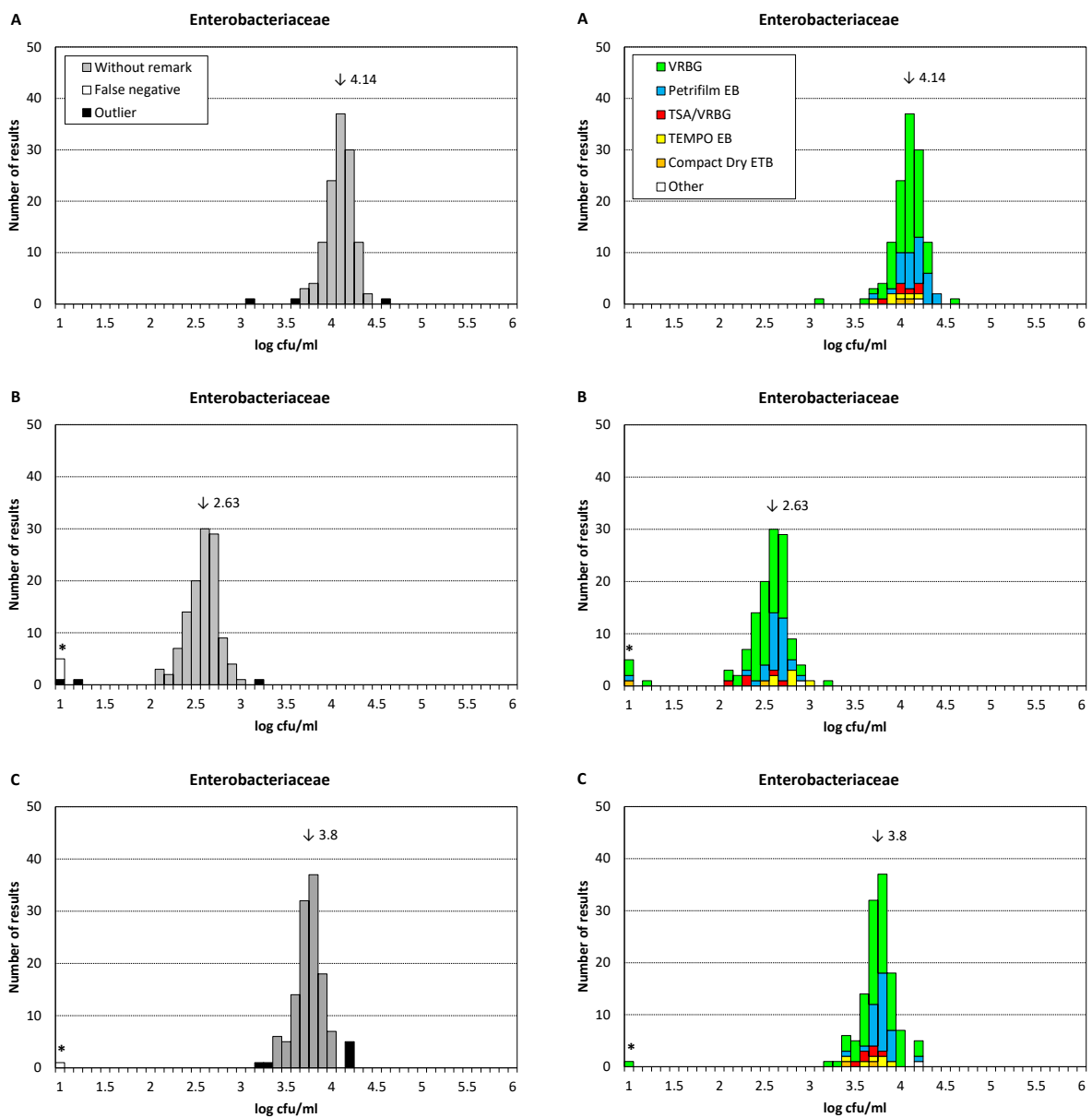


Figure 3. Results from analysis of Enterobacteriaceae

Escherichia coli

Sample A

No target organism was present in the sample.

In total, 105 participants reported results. Two false positive results were reported.

Sample B

No target organism was present in the sample.

In total, 105 participants reported results. No false positive results were reported.

Sample C

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

In total, 104 participants reported results. Four low and two high outliers were reported, as well as two false negative results.

General remarks

In total, 32 % of the participants used a method based on 3M™ Petrifilm™. NMKL 125:2005 and ISO 16649-2:2001 were in comparison used by 23 % and 22 % of the participants, respectively. A few of the participants that followed NMKL 125:2005 and ISO 16649-2:2001 used media other than those stipulated by the respective standards, for example Petrifilm EC/CC or Brilliance EC/CC. 16649-2:2001 was last reviewed by ISO in 2019, and remains current.

ISO 7251:2005 and NMKL 96:2009 were used by four and one participants, respectively. ISO 7251 is an MPN-based method for the detection *E. coli*. NMKL 96 is also based on MPN, and is adapted for analysis of coliform bacteria, thermotolerant coliform bacteria and *E. coli* in fish and seafood. ISO 7251:2005 was last reviewed by ISO in 2019, and remains current.

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* 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. Other media, e.g. Brilliance™ EC/CC, facilitate detection and distinction between coliform bacteria and *E. coli*, based their differences in β -glucuronidase and β -galactosidase activity.

Despite these differences, altogether, the results from the different methods and media were similar. This is true also when considering differences in the incubation temperature, where participants typically incubated either at 41.5–44 °C (53 %) or at 35–37 °C (44 %).

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

Medium	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	105	103	-	-	2	-	-	105	105	-	-	0	-	-	104	96	3.78	0.20	2	4	2
Petrifilm EC/CC ¹	23	23	-	-	0	-	-	23	23	-	-	0	-	-	24	24	3.84	0.15	0	0	0
TBX	24	23	-	-	1	-	-	24	24	-	-	0	-	-	24	22	3.62	0.20	0	2	0
TSA/VRB ²	18	18	-	-	0	-	-	18	18	-	-	0	-	-	18	18	3.86	0.15	0	0	0
Petrifilm SEC	15	15	-	-	0	-	-	15	15	-	-	0	-	-	15	13	3.83	0.12	1	0	1
Other	12	12	-	-	0	-	-	12	12	-	-	0	-	-	10	8	3.84	0.23	0	1	1
TEMPO EC	6	6	-	-	0	-	-	6	6	-	-	0	-	-	6	6	3.95	0.15	0	0	0
Rapid'E.coli 2	3	3	-	-	0	-	-	3	3	-	-	0	-	-	3	3	-	-	0	0	0
VRB	2	1	-	-	1	-	-	2	2	-	-	0	-	-	2	1	-	-	1	0	0
Brilliance EC/CC	2	2	-	-	0	-	-	2	2	-	-	0	-	-	2	1	-	-	0	1	0

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

¹ TSA/VRB includes one participant that incubated on TSA/VRBG

² Petrifilm EC/CC includes one participant that used Petrifilm REC

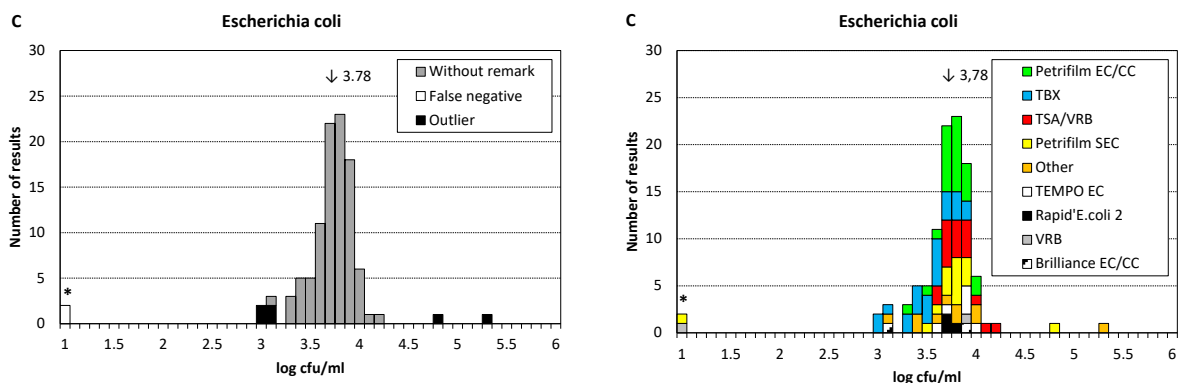


Figure 4. Results from analysis of *Escherichia coli*

Presumptive *Bacillus cereus*

Sample A

B. cereus was target organism. On BA, it forms typical grey colonies with a narrow zone of haemolysis. On BcsA, it forms typical blue colonies surrounded by a blue zone of precipitation. With some chromogenic media, the blue colour may be less prominent.

In total, 102 participants reported results. Two low and two high outliers were reported, as well as eleven false negative results. The false results were almost exclusively reported by users of NMKL67:2010 and ISO 7932:2004.

Sample B

No target organism was present in the sample. *S. aureus* may form atypical colonies on BA and BcsA.

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

Sample C

No target organism was present in the sample. *S. aureus* may form atypical colonies on BA and BcsA.

In total, 102 participants reported results. Four false positive results were reported.

General remarks

Most participants followed either NMKL 67:2010 (35 %) or ISO 7932:2004 (31 %). The new NMKL 67:2021 – which replaces NMKL 67:2010 – was in contrast only followed only by twelve participants (12 %). Notably, users of the new NMKL 67:2021 reported no false results or outliers, whereas false results and outliers were reported by users of the old NMKL 67:2010 for all three samples. The new version of NMKL 67 stipulates a different primary incubation medium. ISO 7932:2004 was last reviewed by ISO in 2021, and remains current.

The most common selective media were MYP and BcsA. On BcsA, presumptive *B. cereus* 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 that are normally surrounded by a zone of precipitation, again as a consequence of lecithinase activity. MYP and BcsA were often used together with a non-selective medium, typically BA. On BA, *B. cereus* forms large, irregular grey colonies, surrounded by a distinct zone of haemolysis.

Other fairly common selective media were Brilliance™ *B. cereus*, PEMBA and Compact Dry X-BC. Brilliance™ *B. cereus* contains the substrate X-Gluc, which is cleaved by *B. cereus* β -glucuronidase. Colonies of *B. cereus* are therefore white with a blue/green centre on this medium. Similarly, the chromogenic and selective agents in Compact Dry X-BC cause *B. cereus* to form blue/green colonies, whereas 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. PEMBA is almost identical to BcsA in its

composition, and was similarly often used together with BA. In contrast, Brilliance™ B. cereus and Compact Dry X-BC were most often used as standalone media.

Table 6. Results from analysis of presumptive *Bacillus cereus*. Only the main (selective) media are shown.

Medium	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	102	87	3.31	0.19	11	2	2	101	97	-	-	4	-	-	102	98	-	-	4	-	-
MYP	33	30	3.29	0.24	2	0	1	33	32	-	-	1	-	-	33	32	-	-	1	-	-
BcsA	25	20	3.26	0.21	4	1	0	24	22	-	-	2	-	-	25	22	-	-	3	-	-
BA	13	11	3.37	0.23	1	1	0	13	12	-	-	1	-	-	13	13	-	-	0	-	-
Brilliance™ B. cereus	7	7	3.34	0.09	0	0	0	7	7	-	-	0	-	-	7	7	-	-	0	-	-
PEMBA	6	4	-	-	2	0	0	6	6	-	-	0	-	-	6	6	-	-	0	-	-
Compact Dry X-BC	5	5	3.30	0.12	0	0	0	5	5	-	-	0	-	-	5	5	-	-	0	-	-
Other	5	3	-	-	1	0	1	5	5	-	-	0	-	-	5	5	-	-	0	-	-
TEMPO BC	3	3	-	-	0	0	0	3	3	-	-	0	-	-	3	3	-	-	0	-	-
BACARA™	3	3	-	-	0	0	0	3	3	-	-	0	-	-	3	3	-	-	0	-	-
COMPASS® B. cereus	2	1	-	-	1	0	0	2	2	-	-	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).

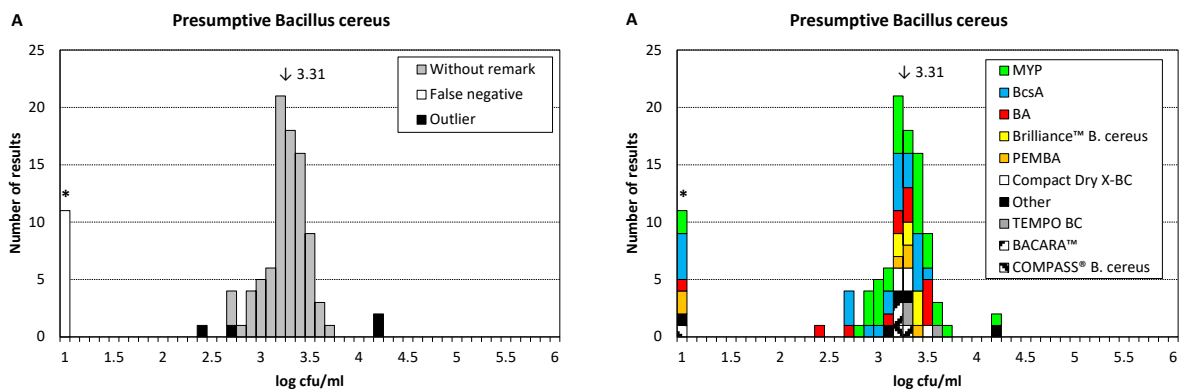


Figure 5. Results from analysis of presumptive *Bacillus cereus*.

Coagulase-positive staphylococci

Sample A

No target organism was present in the sample.

In total, 92 participants reported results. One false positive result was reported

Sample B

S. aureus was target organism. This particular strain often grows slow on RPFA, and notably not all colonies may display a typical appearance and/or a distinct precipitation zone after 24 h incubation at 37 °C. Incubation for 48 h is therefore usually necessary to allow all bacteria in the sample to form typical colonies.

In total, 91 participants reported results. Three low outliers were reported, as well as four false negative results. All of the low outliers and false negative results were reported by participants that incubated for 48 h. Thus, the slow-growing characteristics of the particular *S. aureus* does not appear to have caused any problem for the participants.

Sample C

S. aureus (different strain than in sample B) was target organism. On RPFA, it forms typical grey colonies surrounded by a precipitation zone.

In total, 92 participants reported results. Five low and two high outliers were reported, as well as one false negative result.

General remarks

Most participants incubated on BP. On this medium, *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. Participants that used BP typically performed a confirmation based on coagulase activity, for example a tube coagulase test or the use of RPFA as a secondary medium.

The second most common media were RPFA and Petrifilm Staph. With RPFA, the coagulase activity is tested directly in the medium. Petrifilm Staph is based on a modified Baird-Parker agar. It also contains a chromogenic indicator that causes *S. aureus* to form red/purple colonies. Participants that used Petrifilm Staph typically performed a confirmation with Petrifilm Staph Express Disk. This is based on 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.

Most participants (40 %) followed NMKL 66:2009, where 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. Most participants that followed an ISO method, referenced the withdrawn versions ISO 6888-1:1999

and ISO 6888-2:1999. One participant followed the MPN-based ISO 6888-3:2003, which is adapted for use when low numbers of stressed coagulase-positive staphylococci are expected. This was last reviewed by ISO in 2022 and remains current.

Table 7. Results from analysis of coagulase-positive staphylococci.

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	92	91	-	-	1	-	-	91	84	3.95	0.09	4	3	0	92	84	4.10	0.09	1	5	2
BP	46	45	-	-	1	-	-	44	40	3.97	0.09	3	1	0	45	41	4.11	0.09	1	1	2
RPFA	21	21	-	-	0	-	-	22	20	4.00	0.08	1	1	0	22	20	4.11	0.10	0	2	0
Petrifilm Staph	14	14	-	-	0	-	-	14	13	3.86	0.09	0	1	0	14	13	4.07	0.06	0	1	0
Compact Dry X-SA	4	4	-	-	0	-	-	4	4	-	-	0	0	0	4	4	-	-	0	0	0
TEMPO STA	2	2	-	-	0	-	-	2	2	-	-	0	0	0	2	1	-	-	0	1	0
Brilliance Staph 24	2	2	-	-	0	-	-	2	2	-	-	0	0	0	2	2	-	-	0	0	0
Other	2	2	-	-	0	-	-	2	2	-	-	0	0	0	2	2	-	-	0	0	0
EASY Staph®	1	1	-	-	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).

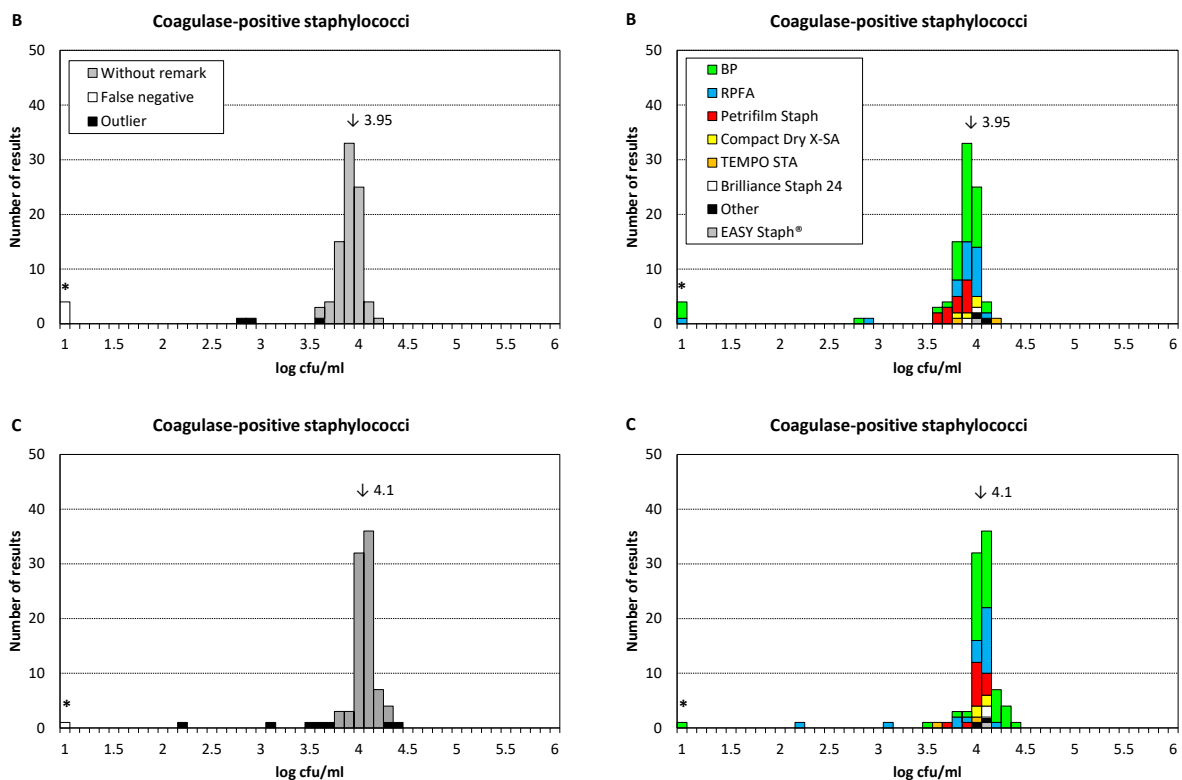


Figure 6. Results from analysis of coagulase-positive staphylococci.

Lactic acid bacteria

Sample A

C. maltaromaticum was target organism. On MRS-aB, it forms typical shiny, white colonies. The strain is catalase-negative and Gram-positive.

In total, 46 participants reported results. Two low outliers were reported, as well as 25 false negative results.

Compared to other lactic acid bacteria, the strain of *C. maltaromaticum* has a higher sensitivity to low pH, as for example in the media MRS, MRS-S and Rogosa agar. Users of these media often reported false negative results.

Sample B

No target organism was present in the sample. *S. aureus* may cause false positive results.

In total, 46 participants reported results. Of these, 21 reported a false positive result.

False positive results are likely due to detection of *S. aureus*. Strains of *S. aureus* have in previous PT rounds formed small colonies on MRS and MRS-aB. In the initial quality control at the Swedish Food Agency, small transparent colonies were observed on MRS-aB at a concentration of 3.9 log₁₀ cfu ml⁻¹. In the subsequent confirmation these were catalase positive, and they were therefore not considered as lactic acid bacteria.

Sample C

No target organism was present in the sample. *S. aureus* may cause false positive results.

In total, 47 participants reported results. Of these, 15 reported a false positive result. Similar to sample B, false positive results are likely due to detection of *S. aureus*.

General remarks

Most of the participants followed NMKL 140, either NMKL 140:2007 (39 %), or the withdrawn NMKL 140:1991 (6 %). In comparison, ISO 15214:1998 was used by 23 % of the participants. It was reviewed by ISO in 2021, and remains current. One participants followed ISO 7889/IDF 117:2003, which is a method for characteristic microorganisms in yoghurt at 37 °C.

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 more wide 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). Such differences between media and incubation conditions underline the importance of performing a confirmation test in uncertain cases, especially when using a less selective medium.

Both the ISO and the NMKL methods recommend confirmation of uncertain colonies. Lactic acid bacteria are Gram positive and normally catalase-negative. Confirmation of some kind was here performed by roughly half (55 %) of the participants. It often consisted of a catalase test or microscopy. For sample A, 8 false positive results were reported by the 23 participants that performed a catalase test, and 17 false positive results were reported by those that did not.

Table 8. Results from analysis of lactic acid bacteria.

Medium	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	46	19	3.81	0.68	25	2	0	46	25	-	-	21	-	-	47	32	-	-	15	-	-
MRS	25	8	4.03	0.68	17	0	0	25	12	-	-	13	-	-	26	15	-	-	11	-	-
MRS-aB	7	7	4.21	0.42	0	0	0	7	4	-	-	3	-	-	7	5	-	-	2	-	-
Rogosa	5	0	-	-	5	0	0	5	5	-	-	0	-	-	5	5	-	-	0	-	-
Petrifilm LAB	4	2	-	-	0	2	0	4	0	-	-	4	-	-	4	2	-	-	2	-	-
MRS-S	2	1	-	-	1	0	0	2	2	-	-	0	-	-	2	2	-	-	0	-	-
TEMPO LAB	2	1	-	-	1	0	0	2	2	-	-	0	-	-	2	2	-	-	0	-	-
Other	1	0	-	-	1	0	0	1	0	-	-	1	-	-	1	1	-	-	0	-	-

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

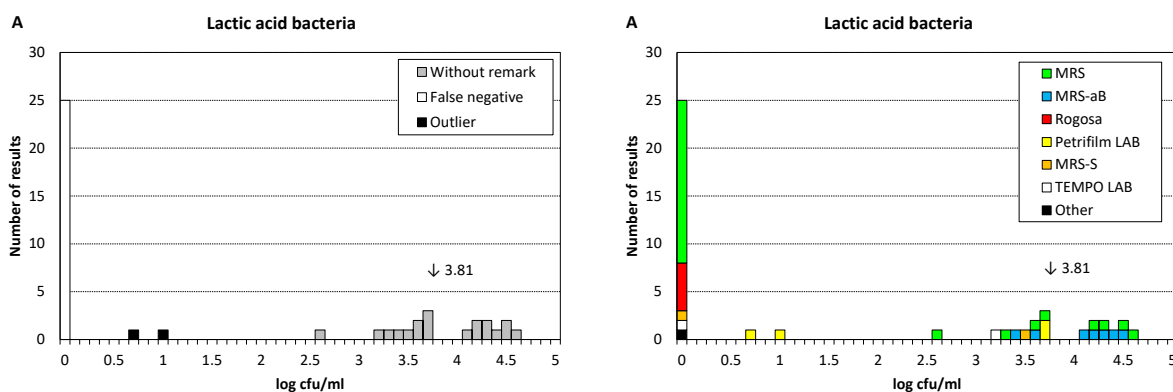


Figure 7. Results from analysis of lactic acid bacteria.

Clostridium perfringens

Sample A

No target organism was present in the sample. It did however contain *C. bifermentans*, which is false positive for the analysis. It forms black colonies on TSC, but can be distinguished from *C. perfringens* after confirmation, for example since *C. bifermentans* is motile.

In total, 51 participants reported results. Of these, 13 reported a false positive result.

The reported concentrations of the false positive results corresponded to that of *C. bifermentans* in the sample (2.3 log₁₀ cfu ml⁻¹).

Sample B

C. perfringens was target organism. It forms black colonies on TSC. The strain is non-motile and ferments lactose. It grows on BA under anaerobic conditions, but not under aerobic conditions.

In total, 50 participants reported results. One low outlier was reported, as well as one false negative result.

Sample C

No target organism was present in the sample.

In total, 51 participants reported results. No false positive results were reported.

General remarks

Most participants followed either NMKL 95:2009 (59 %) or ISO 7937:2004 (33 %). One participant followed the withdrawn NMKL 95:1997 and one participant analysed according to NMKL 56:2015 (Sulphite-reducing Clostridia). ISO 7937:2004 was reviewed by ISO in 2015 and remains current. It is however scheduled to be replaced by ISO 15213-2 ("Enumeration of *Clostridium perfringens* by colony-count technique"), which is currently under development. No obvious differences could be seen in the results from the different methods.

In line with ISO 7937:2004 and NMKL 95:2009, the majority (92 %) of the participants reported the use of TSC. On TSC, *C. perfringens* form black colonies after anaerobic incubation at 37 °C. The media ISA and SC were used by one each. Comparisons with TSC are difficult to make – due to the low number of users of these media – but TSC has by some been recommended for the analysis of *C. perfringens* in food samples [2, 3].

Two common methods for confirmation of *C. perfringens* are motility test and test for lactose fermentation; *C. perfringens* is non-motile and forms acid and gas as a consequence of lactose fermentation. *C. perfringens* can also be confirmed since it forms a double haemolytic zone upon anaerobic incubation on BA. In total, 90 % of the participants stated they performed some kind of confirmation. Common confirmation methods were motility test, test for lactose fermentation, test for haemolysis on BA, and test for absence of growth in aerobic conditions.

C. perfringens normally grows both at 37 °C and at 44 °C. Here, the majority of the participants (94 %) incubated at 37 °C, while only a few (6 %) incubated at 44 °C. It is therefore difficult to say if the choice of incubation temperature had an impact on the outcome, but it does not appear to be the case.

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

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	51	38	-	-	13	-	-	50	48	2.66	0.29	1	1	0	51	51	-	-	0	-	-
NMKL 95:2006	30	20	-	-	10	-	-	30	30	2.70	0.30	0	0	0	30	30	-	-	0	-	-
ISO 7937:2004	17	16	-	-	1	-	-	16	15	2.66	0.24	0	1	0	17	17	-	-	0	-	-
Other	2	1	-	-	1	-	-	2	2	-	-	0	0	0	2	2	-	-	0	-	-
NMKL 95:1997	1	1	-	-	0	-	-	1	1	-	-	0	0	0	1	1	-	-	0	-	-
NMKL 56:2015	1	0	-	-	1	-	-	1	0	-	-	1	0	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).

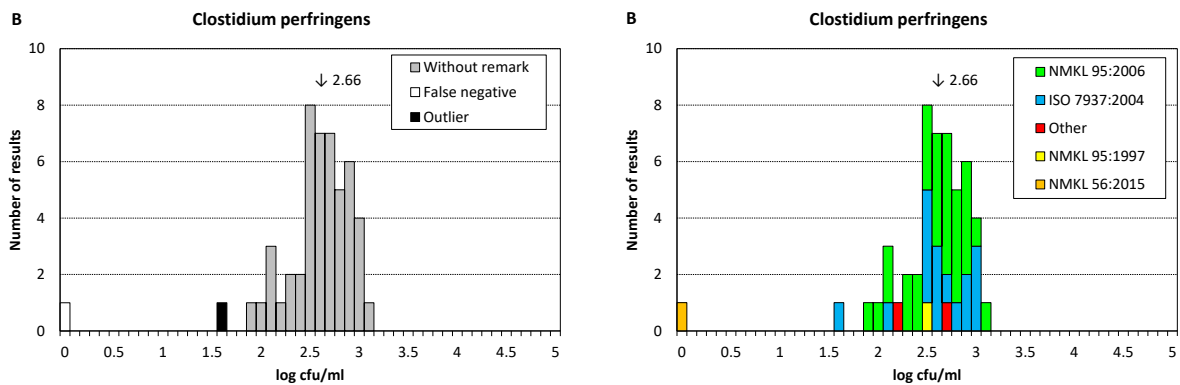


Figure 8. Results from analysis of *Clostridium perfringens*.

Anaerobic sulphite-reducing bacteria

Sample A

C. bifermentans was target organism. It forms typical black colonies on ISA.

In total, 60 participants reported results. Two low and one high outliers were reported, as well as three false negative results.

Sample B

C. perfringens was target organism. It forms black colonies on ISA. The black colour may be more distinct after 48 h incubation, compared to after 24 h incubation.

In total, 59 participants reported results. Four low and two high outliers were reported, as well as one false negative result.

Sample C

No target organism was present in the sample.

In total, 62 participants reported results. Of these, one reported a false positive result.

General remarks

The majority of the participants (63 %) followed a version of NMKL 56. However most followed the withdrawn NMKL 56:2008 (42 %) or even NMKL 56:1994 (3 %), and few (18 %) followed the current NMKL 56:2015. ISO 15213:2003 was used by 16 % of the participants. This was last reviewed by ISO in 2015, and remains current. It is however scheduled to be replaced by ISO 15213-1 ("Enumeration of sulphite-reducing *Clostridium* spp. by colony-count technique"), which is currently under development. Four participants followed ISO 7937:2004 ("Horizontal method for the enumeration of *Clostridium perfringens*"), which will be replaced by the future ISO 15213-2 ("Enumeration of *Clostridium perfringens* by colony-count technique").

Both NMKL 56:2015 and ISO 15213:2003 prescribe pour-plate methods with ISA, which was consequently the medium most frequently used by the participants (42 %). With ISA, 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 Fe^{3+} in the medium, and H_2S that is produced by the reduction of sulphite. Growth of anaerobic bacteria that only produce hydrogen (and not H_2S) may sometimes result in a diffuse and unspecific blackening of the medium.

Other media that were used were TSC (24 %), SFP (19 %), PAB (6 %) and TS (3 %). These media are often used when identifying *C. perfringens*, and it should therefore be mentioned that for that purpose, colonies should be confirmed using the methods in for example NMKL 95.

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	60	54	2.34	0.26	3	2	1	59	52	2.74	0.24	1	4	2	62	61	-	-	1	-	-
NMKL 56:2008	25	21	2.40	0.28	2	1	1	26	22	2.70	0.27	1	2	1	26	25	-	-	1	-	-
NMKL 56:2015	11	10	2.34	0.33	0	1	0	11	10	2.86	0.17	0	1	0	11	11	-	-	0	-	-
ISO 15213:2003	10	10	2.35	0.15	0	0	0	8	8	2.73	0.16	0	0	0	9	9	-	-	0	-	-
EB-SM-3013	6	6	2.26	0.17	0	0	0	6	6	2.77	0.10	0	0	0	6	6	-	-	0	-	-
ISO 7937:2004	4	3	-	-	1	0	0	4	4	-	-	0	0	0	4	4	-	-	0	-	-
Other	3	3	-	-	0	0	0	3	1	-	-	0	1	1	4	4	-	-	0	-	-
NMKL 56:1994	1	1	-	-	0	0	0	1	1	-	-	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).

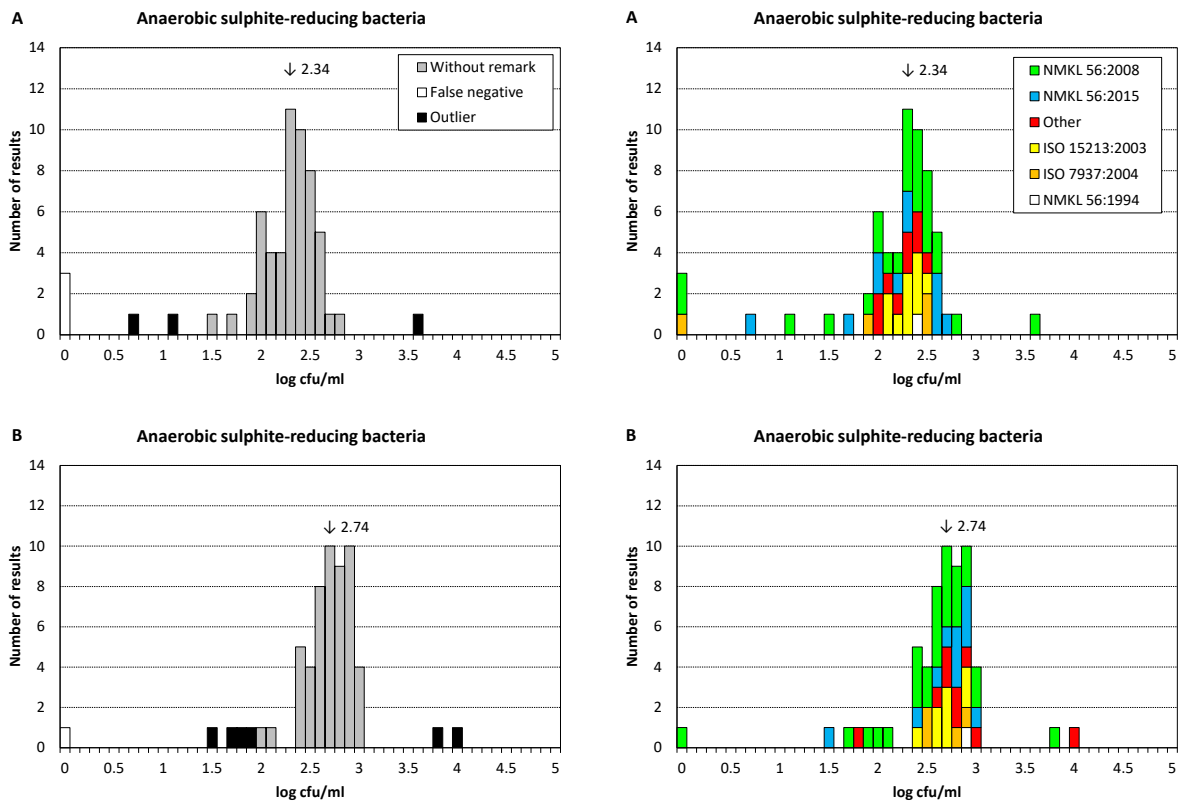


Figure 9. Results from analysis of anaerobic sulphite-reducing bacteria.

Aerobic microorganisms in fish products

Sample A

H. alvei and *C. maltaromaticum* were the main target organisms.

In total, 22 participants reported results. One high outlier was reported.

Sample B

S. putrefaciens and *S. aureus* were the main target organisms.

During the initial quality control at the Swedish Food Agency the parameter did not fulfil the requirements for homogeneity, and a larger than usual distribution of the results can thus be expected. No values have therefore been considered as outliers.

In total, 22 participants reported results. All participants reported positive results. The majority of these were close to the assigned value ($4.04 \log_{10} \text{cfu ml}^{-1}$) and only one of the results could be seen as a potential low outlier.

The results for sample B are not evaluated, and no z-scores are calculated for the analysis.

Sample C

E. coli and *S. aureus* were the main target organisms.

In total, 22 participants reported results. Two low outliers were reported.

General remarks

Nineteen of the 22 participants followed the method for aerobic microorganisms and specific spoilage organisms in fish and fish products, NMKL 184:2006. This prescribes a pour-plate method with IA, which was consequently the medium most frequently used by the participants (86 %). Two and one participants followed ISO 4833-1:2013 and NMKL 86:2006, respectively, and thus incubated on PCA.

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	22	21	4.59	0.19	0	0	1	22	22	4.04*	0.24*	-	-	-	22	20	4.18	0.23	0	2	0
NMKL 184:2006	19	18	4.63	0.15	0	0	1	0	0	-	-	-	-	-	19	17	4.26	0.13	0	2	0
ISO 4833-1:2013	2	2	-	-	0	0	0	0	0	-	-	-	-	-	2	2	-	-	0	0	0
NMKL 86:2006	1	1	-	-	0	0	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).

* The sample is not evaluated. The values are shown only as an information to the participants.

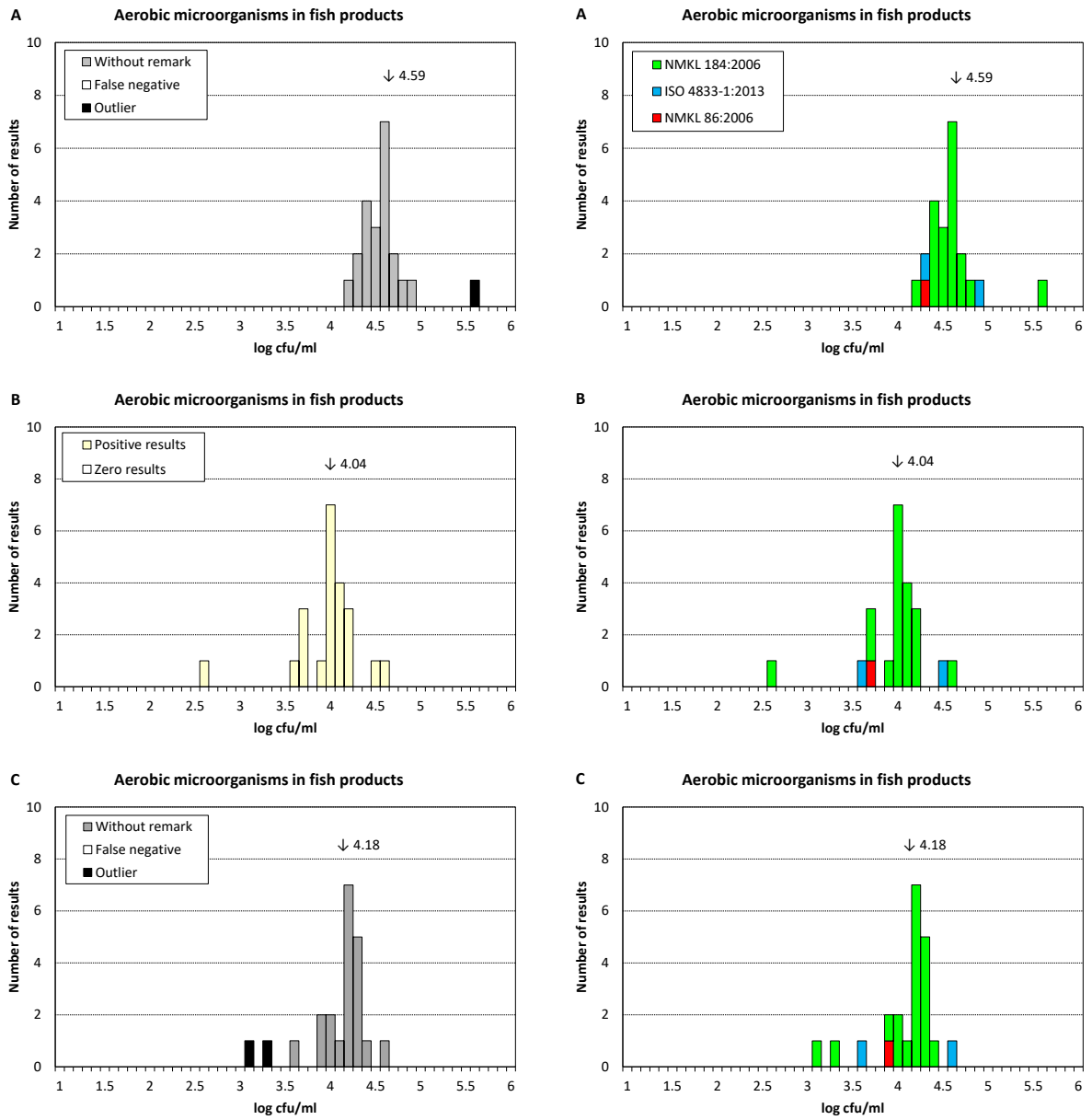


Figure 10. Results from analysis of aerobic microorganisms in fish products.

H₂S-reducing bacteria in fish products

Sample A

H. alvei was target organism. It forms typical black colonies on IA.

In total, 19 participants reported results. All reported results were correct.

Sample B

S. putrefaciens was target organism.

During the initial quality control at the Swedish Food Agency the parameter did not fulfil the requirements for homogeneity, and a larger than usual distribution of the results can thus be expected. No values have therefore been considered as outliers.

In total, 19 participants reported results. All of these were close to the assigned value (3.35 log₁₀ cfu ml⁻¹), and no potential outliers could be identified.

The results for sample B are not evaluated, and no z-scores are calculated for the analysis.

Sample C

No target organism was present in the sample.

In total, 19 participants reported results. All reported results were correct.

General remarks

All of the 19 participants followed the method for aerobic microorganisms and specific spoilage organisms in fish and fish products, NMKL 184:2006, and all of the participants incubated on IA. With IA, H₂S-producing bacteria form black colonies.

Table 12. Results from analysis of H₂S-reducing bacteria 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	19	19	4.23	0.13	0	0	0	19	19	3.35*	0.34*	-	-	-	19	19	-	-	0	-	-
NMKL 184:2006	19	19	4.26	0.12	0	0	0	0	0	-	-	-	-	-	19	19	-	-	0	-	-

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

* The sample is not evaluated. The values are shown only as an information to the participants.

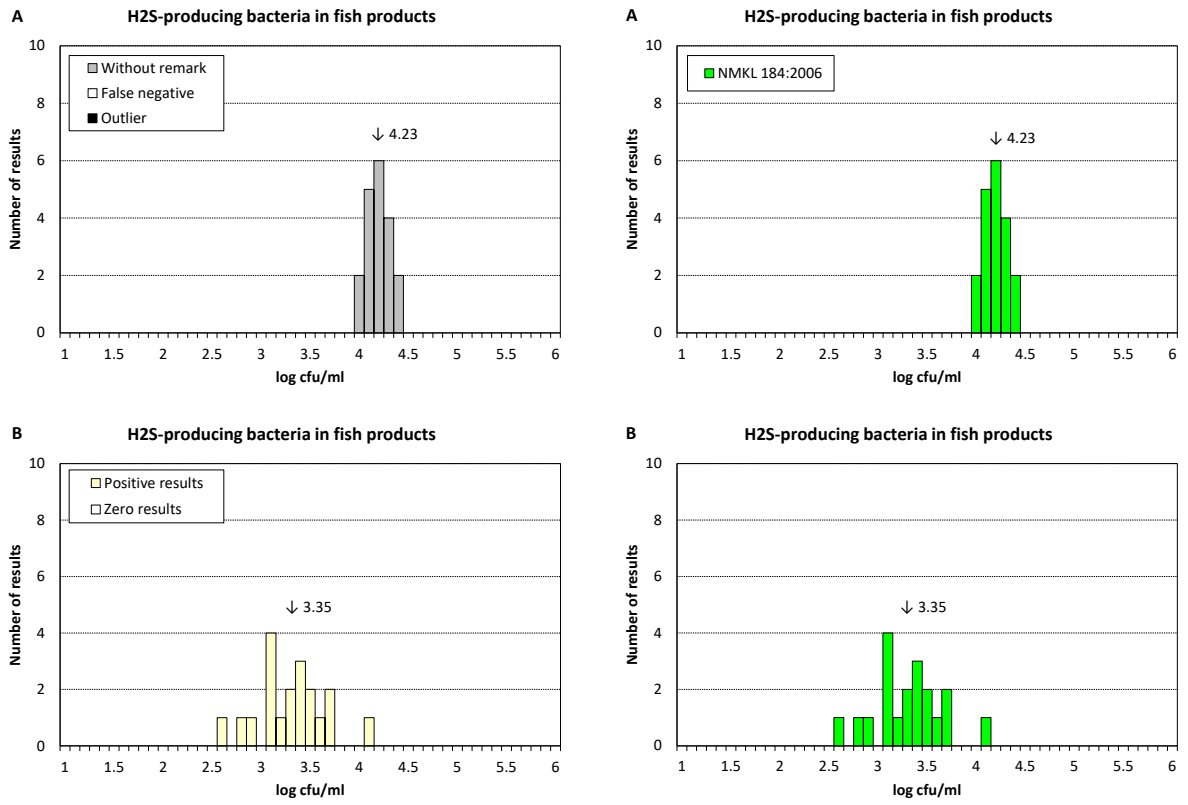


Figure 11. Results from analysis of H₂S-reducing bacteria in fish products.

Yeasts and moulds

Sample A

No target organism was present for yeasts. *P. verrucosum* was target organism for moulds; it forms typical colonies on both DG18 and DRBC.

In total, 130 participants reported results for yeasts. Of these, 12 reported a false positive result.

In total, 130 participants reported results for moulds. Eight low and two high outliers were reported, as well as 11 false negative results.

Four participants reported false positive results for yeasts, and simultaneously false negative results for moulds.

Sample B

H. uvarum was target organism for yeasts. It forms typical pink colonies on DRBC. No target organism was present for moulds.

In total, 131 participants reported results for yeasts. Five low and one high outliers were reported.

In total, 127 participants reported results for moulds. Three false positive results were reported.

Sample C

S. cerevisiae was target organism for yeasts. *C. cladosporioides* was target organism for yeasts.

In total, 131 participants reported results for yeasts. Three low and five high outliers were reported, as well as nine false negative results.

In total, 129 participants reported results for moulds. Three low and four high outliers were reported, as well as nine false negative results.

Five participants reported false negative results for both yeasts and moulds.

General remarks

In essence, the same participants analysed both yeasts and moulds, and they generally reported identical methods for both parameters. In order, the most common methods were NMKL 98:2005, ISO 6611:2004/IDF 94:2004, 3M™ Petrifilm™ and ISO 21527-1:2008 / ISO 21527-2:2008. In addition, two participants followed ISO 7954:1987 ("General guidance for enumeration of yeasts and moulds"), which has been replaced by ISO 21527-1:2008 and ISO 21527-2:2008. Both ISO 21527-1:2008 and ISO 21527-2:2008 were last reviewed by ISO in 2018 and remain current.

With NMKL 98:2005, participants mainly used either DRBC and/or DG18. With ISO 6611:2004 / IDF 94:2004, which describes the enumeration of yeasts and moulds in milk and milk products, participants instead mainly used YGC. ISO 21527-1:2008 and ISO 21527-2:2008 stipulate the use of DRBC and

DG18, respectively. 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). Outliers and false results were for the most part evenly distributed between the main methods and media that were used.

Note: Two participants used TEMPO YM, which gives a combined value for yeasts and moulds. These results were excluded from calculations of the assigned value and standard deviations. Due to the low number of participants that use this methods, results from TEMPO YM need to be evaluated by the individual participants themselves.

Table 13. Results from analysis of yeasts.

Medium	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	130	118	-	-	12	-	-	131	125	3.31	0.20	0	5	1	131	114	2.02	0.18	9	3	5
YGC	37	36	-	-	1	-	-	38	36	3.28	0.20	0	2	0	37	34	2.01	0.14	1	0	2
DG18 + DRBC	23	22	-	-	1	-	-	22	22	3.36	0.15	0	0	0	23	22	2.02	0.17	0	1	0
DG18	16	16	-	-	0	-	-	16	16	3.38	0.25	0	0	0	16	13	2.07	0.24	1	2	0
Other ¹	15	12	-	-	3	-	-	15	13	3.30	0.19	0	2	0	15	10	2.11	0.12	4	0	1
Petrifilm YM	14	11	-	-	3	-	-	14	13	3.31	0.19	0	0	1	14	11	2.00	0.17	2	0	1
DRBC	10	10	-	-	0	-	-	11	10	3.22	0.21	0	1	0	11	9	2.08	0.24	1	0	1
Petrifilm RYM	10	6	-	-	4	-	-	10	10	3.30	0.16	0	0	0	10	10	2.02	0.21	0	0	0
OGYE	5	5	-	-	0	-	-	5	5	3.42	0.22	0	0	0	5	5	1.98	0.08	0	0	0

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

¹ Other media includes e.g. Compact Dry YM, TEMPO YM, MEA, Sabouraud and PDA.

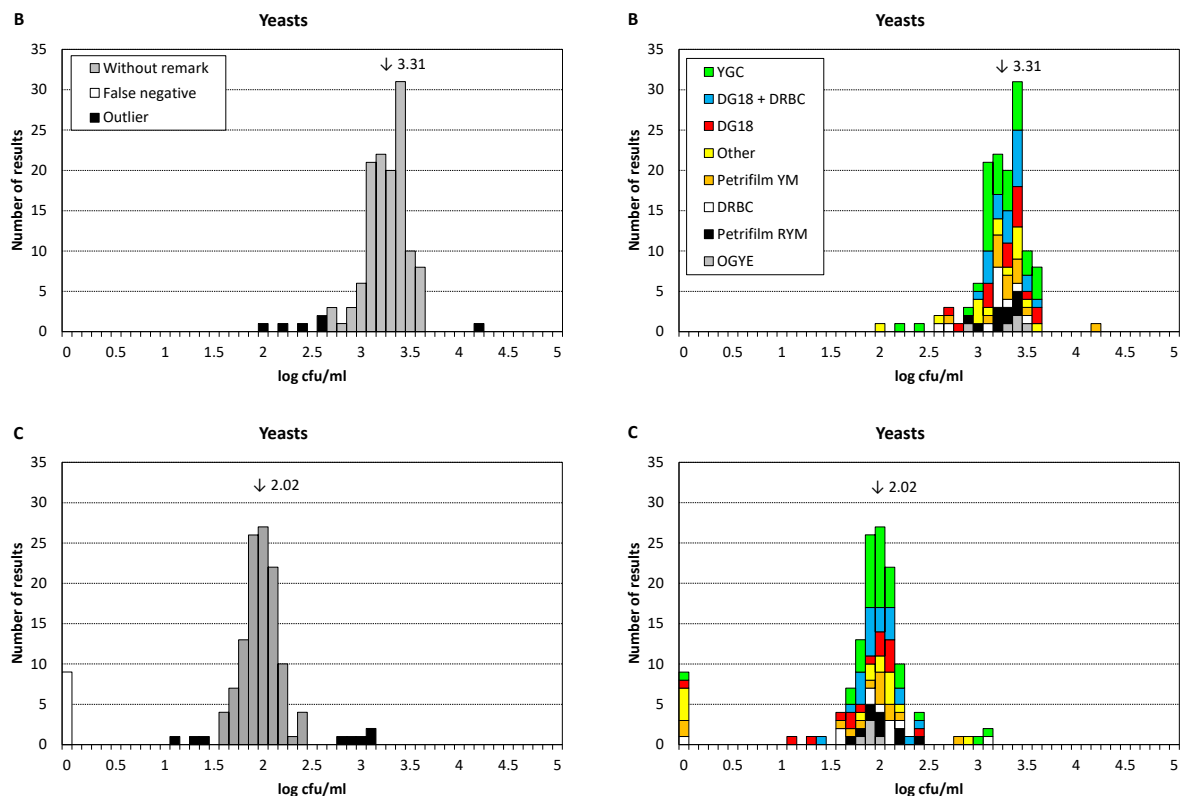


Figure 12. Results from analysis of yeasts.

Table 14. Results from analysis of moulds.

Medium	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	130	109	2.67	0.15	11	8	2	127	124	-	-	3	-	-	129	113	1.64	0.19	9	3	4
YGC	39	36	2.71	0.12	1	1	1	38	38	-	-	0	-	-	38	34	1.60	0.22	1	2	1
DG18 + DRBC	22	21	2.70	0.15	0	0	1	21	20	-	-	1	-	-	22	21	1.68	0.17	0	0	1
DG18	17	14	2.71	0.09	1	2	0	17	17	-	-	0	-	-	17	17	1.70	0.15	0	0	0
Petrifilm YM	15	10	2.69	0.18	2	3	0	15	15	-	-	0	-	-	15	13	1.71	0.19	1	0	1
Other ¹	13	8	2.73	0.16	3	2	0	13	12	-	-	1	-	-	13	7	1.65	0.19	4	1	1
DRBC	11	11	2.67	0.16	0	0	0	10	10	-	-	0	-	-	11	10	1.63	0.11	1	0	0
Petrifilm RYM	8	4	-	-	4	0	0	8	7	-	-	1	-	-	8	6	1.72	0.16	2	0	0
OGYE	5	5	2.74	0.21	0	0	0	5	5	-	-	0	-	-	5	5	1.67	0.26	0	0	0

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

¹ Other media includes e.g. Compact Dry YM, TEMPO YM, MEA, Saubouraud and PDA.

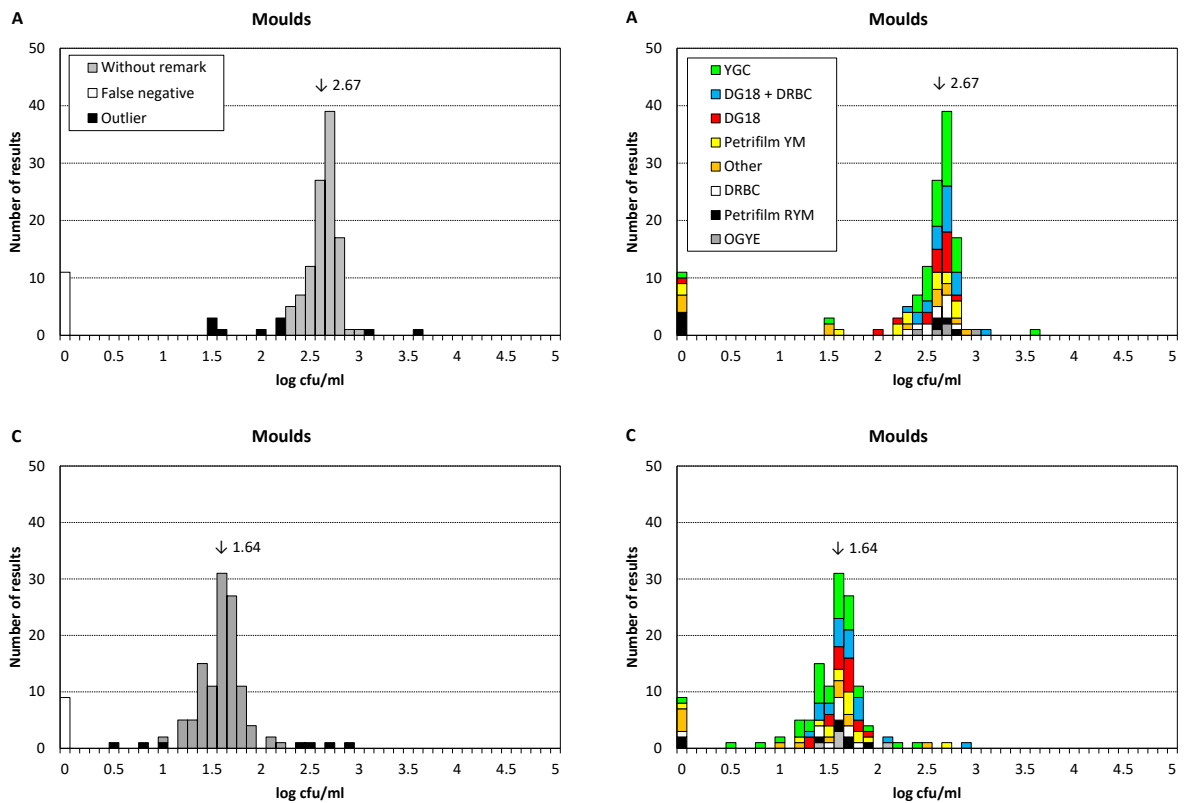


Figure 13. Results from analysis of moulds.

Outcome of the results of individual participants - assessment

Reporting and evaluation of results

The results of all participants are listed in Annex 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 [4].

Samples for follow-up analyses can be ordered at: www.livsmedelsverket.se/en/PT-extra

Box plots and numbers of deviating results for each participant

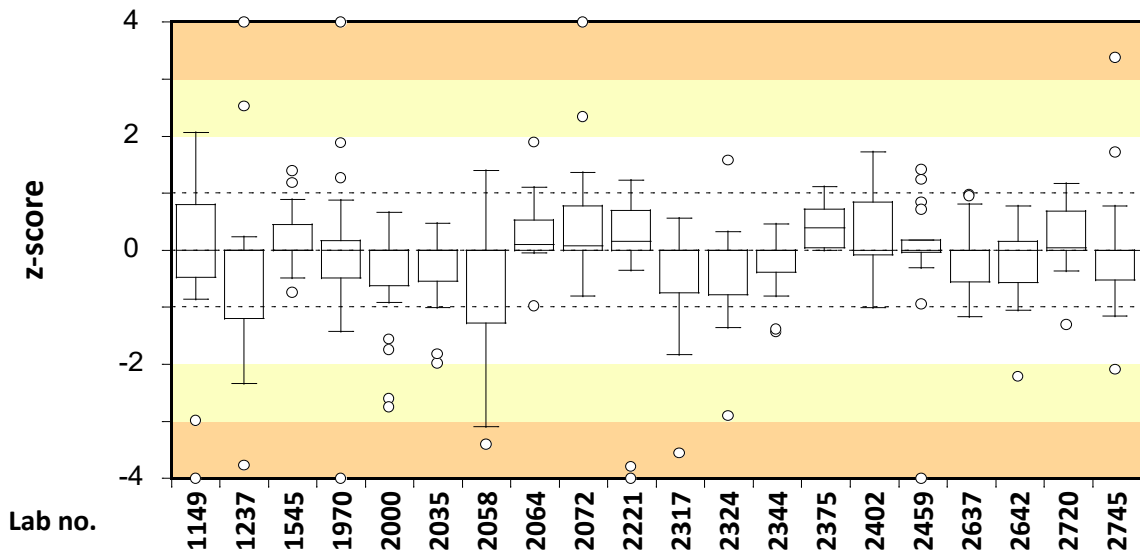
Box plots are based on the z -scores listed in Annex 2, and give a comprehensive view of the performance of each participant. The range of z -scores is indicated by the size of the box and, for most participants, by lines and/or circles above and beneath the box. A small range of values, centred around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

Outliers are included in the figures after being calculated to z -scores in the same way as for other results. Correct results for qualitative analyses and correct negative results for quantitative analyses without target organism are given a z -score of 0. False results do not generate any z -scores, and are not included in “No. of results”.

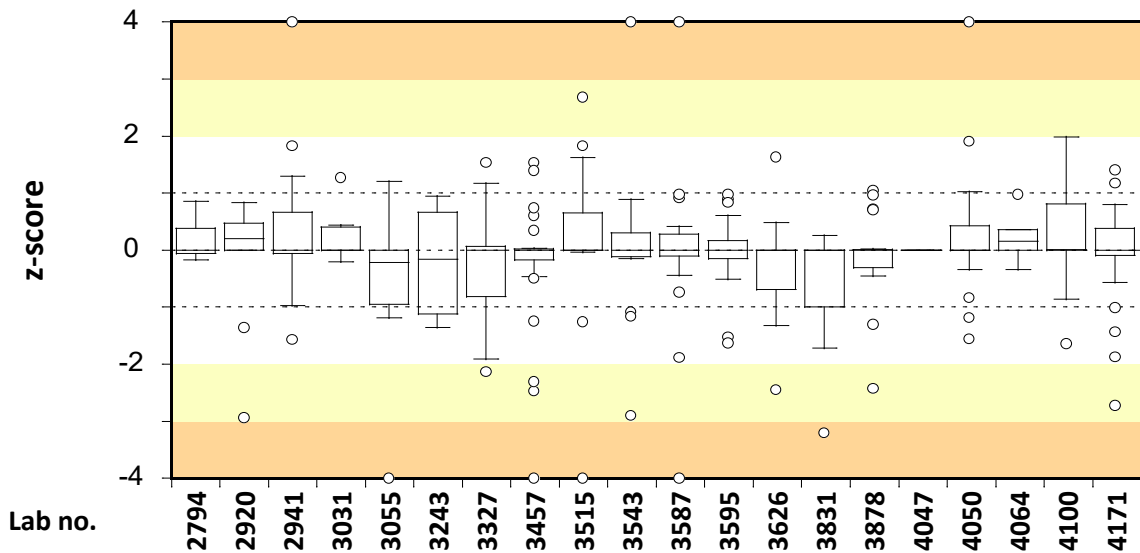
The participant’s median value is illustrated by a horizontal line in the box. Each box includes 50 % of a participant’s results (25 % of the results above the median and 25 % of the results below the median). The remaining 50 % are illustrated by lines and circles outside the box. A circle is for technical reasons shown in the plot when a value deviates to certain degree* from the other values. This does not by itself indicate that the value is an outlier.

Z -scores $>+4$ and <-4 are positioned at $+4$ and -4 , respectively, in the plot. The background is divided by lines and shaded fields to simplify identifying the range in which the results are located.

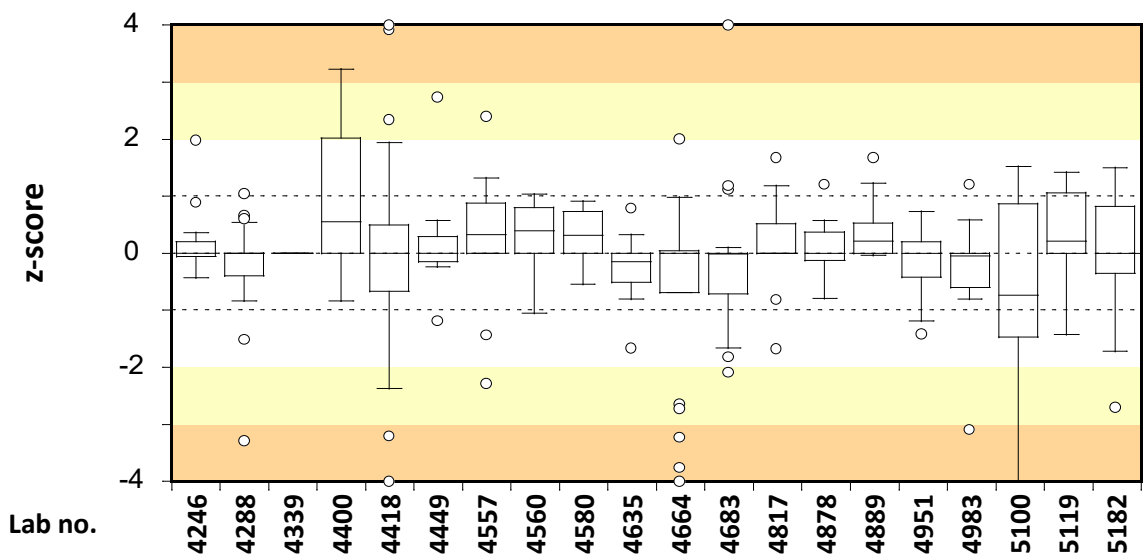
* $< [\text{lowest value in the box} - 1.5 \times (\text{highest value in the box} - \text{lowest value in the box})]$
or
 $> [\text{highest value in the box} + 1.5 \times (\text{highest value in the box} - \text{lowest value in the box})].$



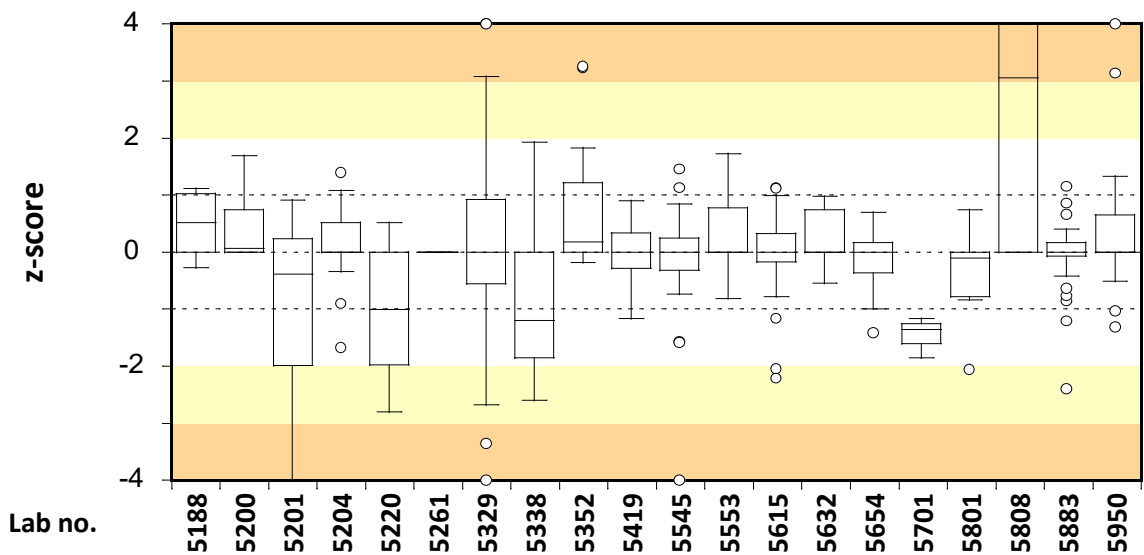
Lab no.	1149	1237	1545	1970	2000	2035	2058	2064	2072	2221	2317	2324	2344	2375	2402	2459	2637	2642	2720	2745
No. of results	15	23	30	36	27	18	15	15	31	30	25	22	23	12	9	21	30	20	15	27
False positive	0	1	2	0	0	0	0	0	0	2	0	0	1	0	0	0	2	0	0	1
False negative	0	3	3	0	0	0	0	0	1	1	0	0	0	0	0	1	1	1	0	2
Low outliers	1	1	0	1	0	0	2	0	0	2	1	0	0	0	0	1	0	0	0	0
High outliers	0	1	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1



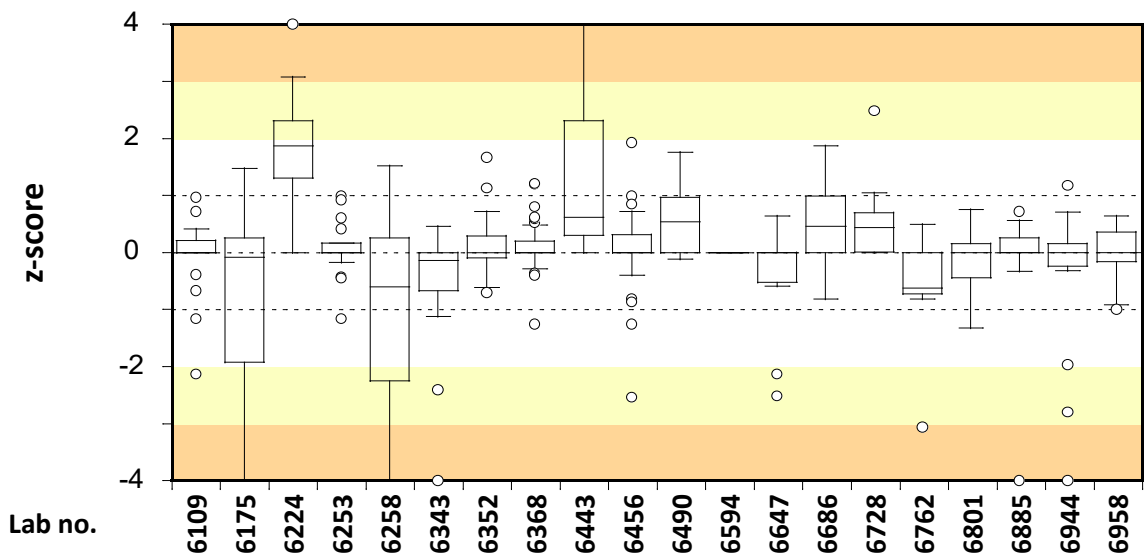
Lab no.	2794	2920	2941	3031	3055	3243	3327	3457	3515	3543	3587	3595	3626	3831	3878	4047	4050	4064	4100	4171
No. of results	9	12	26	10	15	6	21	28	15	15	24	27	18	15	21	0	18	6	33	25
False positive	0	0	3	0	1	0	0	3	0	0	0	0	0	1	0	0	0	0	3	0
False negative	2	0	3	0	0	0	0	0	0	0	0	0	0	1	2	0	1	0	1	1
Low outliers	0	0	0	0	1	0	0	1	1	0	1	0	0	1	0	0	0	0	0	0
High outliers	0	0	1	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0	0



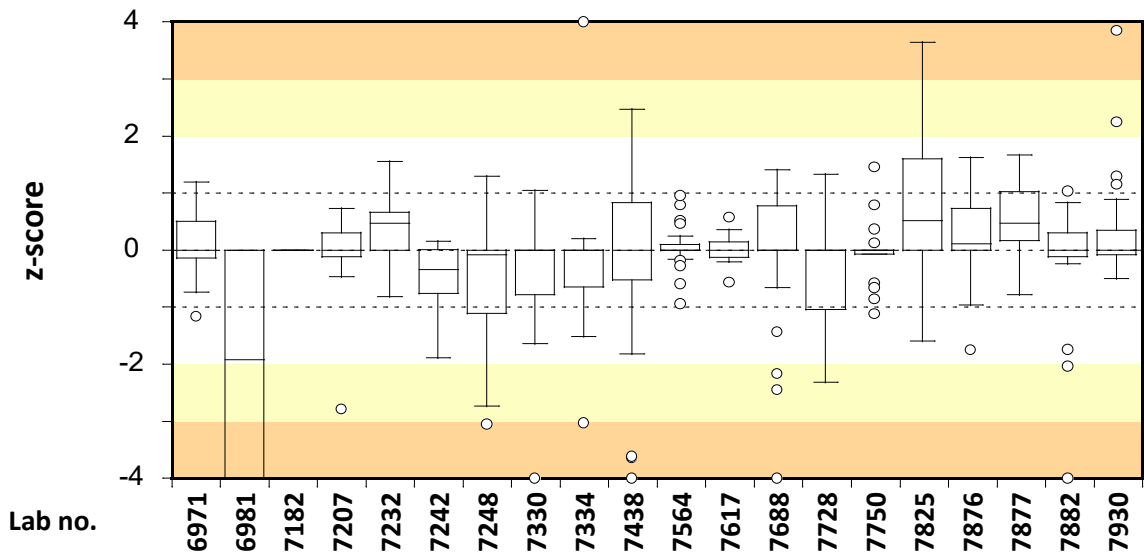
Lab no.	4246	4288	4339	4400	4418	4449	4557	4560	4580	4635	4664	4683	4817	4878	4889	4951	4983	5100	5119	5182
No. of results	12	27	0	18	31	15	12	6	15	19	21	30	21	15	22	15	15	7	9	18
False positive	0	1	0	0	4	0	0	0	1	0	0	2	0	0	0	0	1	0	0	0
False negative	1	0	0	2	2	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0
Low outliers	0	1	0	0	2	0	0	0	0	0	3	0	0	0	0	0	1	1	0	0
High outliers	0	0	0	1	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0



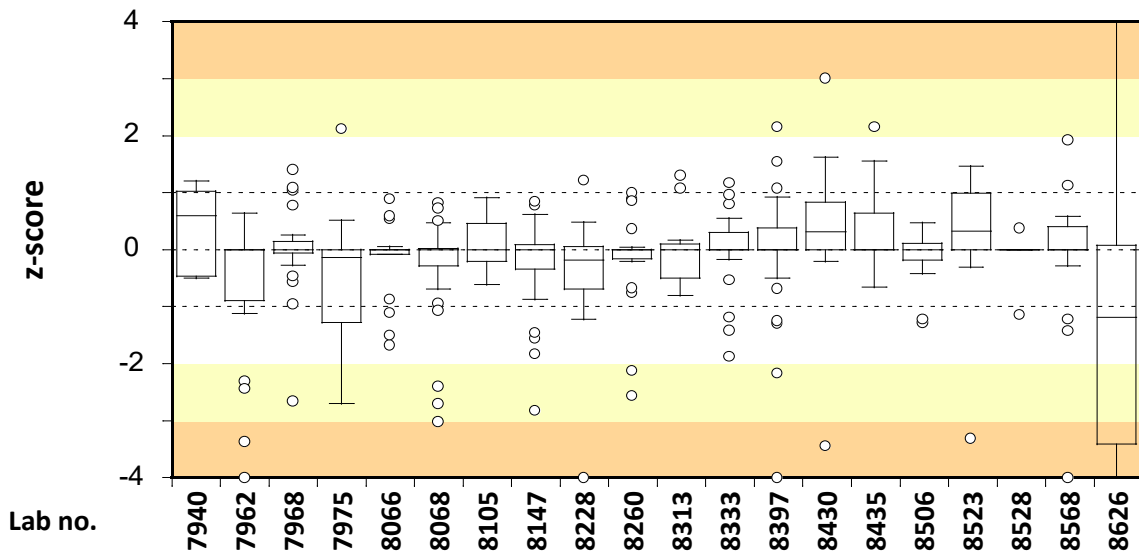
Lab no.	5188	5200	5201	5204	5220	5261	5329	5338	5352	5419	5545	5553	5615	5632	5654	5701	5801	5808	5883	5950
No. of results	6	9	12	32	20	0	24	12	24	17	18	18	30	15	15	3	15	12	30	30
False positive	0	0	0	1	0	0	5	0	0	0	0	0	2	0	1	0	0	0	2	1
False negative	0	0	0	0	0	0	5	0	1	0	1	0	1	0	1	0	1	2	0	0
Low outliers	0	0	2	0	0	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0
High outliers	0	0	0	0	0	0	3	0	2	0	0	0	0	0	0	0	0	5	0	2



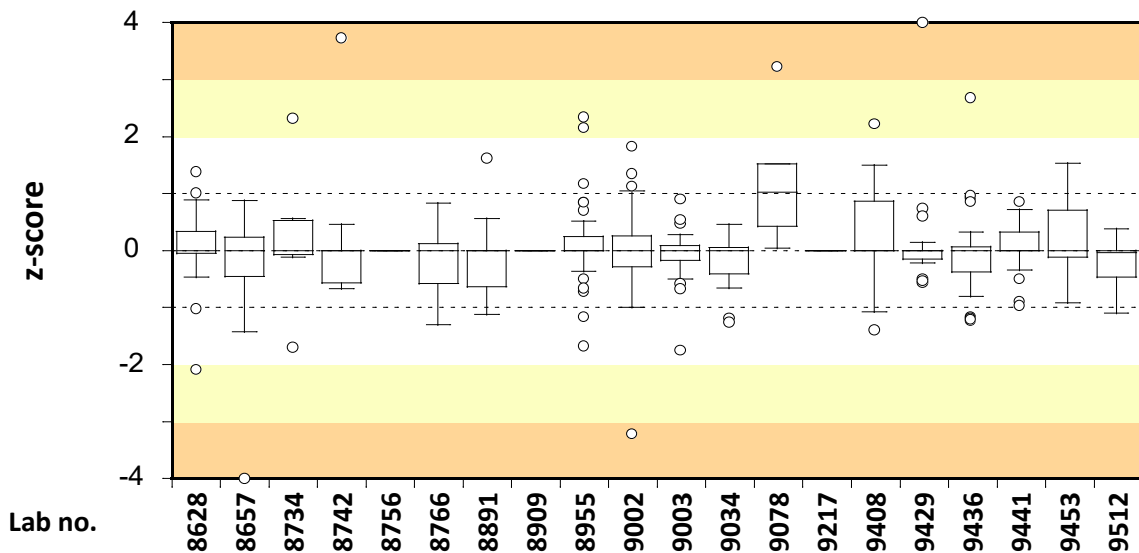
No. of results	21	12	9	18	11	30	24	33	3	21	21	0	11	27	12	9	9	24	18	15
False positive	0	0	0	0	0	2	1	0	0	0	0	0	0	2	0	0	2	0	1	0
False negative	1	0	0	0	0	2	0	0	0	0	0	0	0	1	0	0	0	0	1	0
Low outliers	0	2	0	0	1	1	0	0	0	0	0	0	0	0	0	1	0	1	1	0
High outliers	0	0	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0



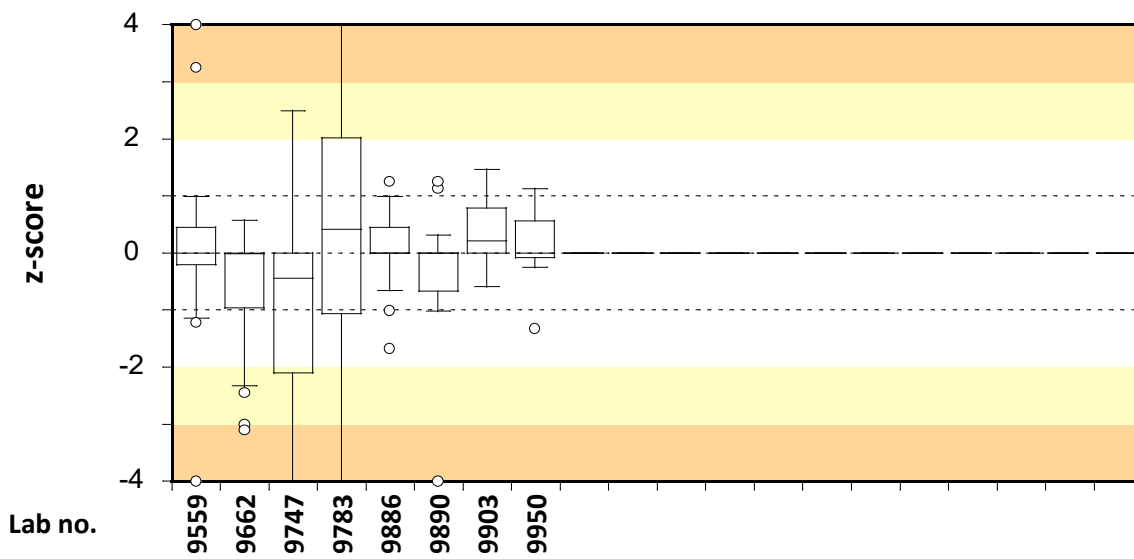
No. of results	9	6	0	18	9	12	36	21	20	24	21	12	32	27	18	18	24	14	30	28
False positive	0	0	0	0	0	0	1	0	0	2	0	0	1	1	0	2	0	1	3	0
False negative	0	0	0	3	0	0	0	1	1	0	0	0	0	0	1	2	0	0	1	1
Low outliers	0	3	0	0	0	0	0	1	0	3	0	0	1	0	0	0	0	0	1	0
High outliers	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	1



Lab no.	7940	7962	7968	7975	8066	8068	8105	8147	8228	8260	8313	8333	8397	8430	8435	8506	8523	8528	8568	8626
No. of results	6	21	32	15	19	27	18	30	14	24	18	24	31	18	15	18	20	9	24	11
False positive	0	0	0	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
False negative	0	0	0	0	0	0	1	0	0	1	0	1	1	0	1	0	0	3	1	0
Low outliers	0	2	0	0	0	0	0	0	1	0	0	0	1	1	0	0	1	0	1	3
High outliers	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1



Lab no.	8628	8657	8734	8742	8756	8766	8891	8909	8955	9002	9003	9034	9078	9217	9408	9429	9436	9441	9453	9512
No. of results	34	12	15	9	0	24	19	0	34	29	18	11	6	0	31	21	32	28	18	18
False positive	1	0	2	0	0	0	0	0	0	0	0	0	0	0	1	0	2	1	0	1
False negative	1	0	3	0	0	0	0	0	1	1	0	0	0	0	0	0	1	0	0	3
Low outliers	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
High outliers	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0



No. of results	21	34	15	12	29	24	24	15	0	0	0	0	0	0	0	0	0	0
False positive	1	1	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
False negative	1	1	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Low outliers	1	1	3	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0
High outliers	2	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0

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 [5]. 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 the table below.

Table 15. Microorganisms and approximate concentrations in the samples.

Sample	Microorganism	Strain			
		SLV no. ¹	Origin	Reference ²	log ₁₀ cfu ml ⁻¹
A	<i>Bacillus cereus</i>	SLV-517	Cream sauce	CCUG 44739	3.5
	<i>Clostridium bifermentans</i>	SLV-009	Fish	CCUG 43592	2.3
	<i>Carnobacterium maltaromaticum</i>	SLV-519	Smoked salmon	CCUG 46539	4.2
	<i>Hafnia alvei</i>	SLV-015	Minced meat	CCUG 45642	4.3
	<i>Penicillium verrucosum</i>	SLV-544	Soil	CBS 112488	2.9
B	<i>Clostridium perfringens</i>	SLV-442	-	CCUG 43593	2.9
	<i>Hanseniaspora uvarum</i>	SLV-555	-	-	3.5
	<i>Staphylococcus aureus</i>	SLV-539	Mastitis	-	4.1
	<i>Serratia marcescens</i>	SLV-040	Pond water	-	2.7
	<i>Shewanella putrefaciens</i>	SLV-520	-	CCUG 46538	3.8
C	<i>Cladosporium cladosporioides</i>	SLV-488	Meat	CBS 812.96	2.0
	<i>Escherichia coli</i>	SLV-524	Chicken	CCUG 47554	3.9
	<i>Staphylococcus aureus</i>	SLV-350	-	CCUG 45099	4.2
	<i>Saccharomyces cerevisiae</i>	SLV-375	Baker's yeast	-	2.4

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; Fohm: Public Health Agency of Sweden.

Quality control of the samples

In order to allow comparison of the freeze-dried samples, it is essential to have aliquots of homogeneous test material and equal volume in all vials. Quality control is performed on 10 randomly chosen vials in conjunction with manufacturing of the samples or on 5 vials if an “old” sample mixture was used and the last quality control was performed more than 6 months ago. Homogeneity of a test material is approved if, for each analysis, the values obtained for the test for “Index of dispersion” between vials (I_2) and the test for reproducibility (T) do not simultaneously exceed 2.0 and 2.6, respectively. (For definitions of I_2 , and T , see references [6] and [7] respectively.)

Table 16. Concentration mean (m), I_2 and T 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 ¹			C ²		
	m	I_2	T	m	I_2	T	m	I_2	T
Aerobic microorganisms, 30 °C NMKL method no. 86:2013	4.77	1.29	1.34	4.64	0.91	1.48	4.37	1.33	1.60
Psychrotrophic microorganisms NMKL method no. 86:2013	4.70	0.36	1.19	4.38	0.98	1.52	-	-	-
Enterobacteriaceae NMKL method no. 144:2005	4.18	0.81	1.23	2.69	1.28	1.37	3.85	1.54	1.49
<i>Escherichia coli</i> NMKL method no. 125:2005	-	-	-	-	-	-	3.98	1.98	1.50
Presumptive <i>Bacillus cereus</i> NMKL method no. 67:2021	3.52	0.32	1.21	-	-	-	-	-	-
Coagulase-positive staphylococci NMKL method no. 66:2009	-	-	-	4.07	0.82	1.26	4.18	0.87	1.23
Lactic acid bacteria NMKL method no. 140:2007	4.22	3.40	2.13	-	-	-	-	-	-
<i>Clostridium perfringens</i> NMKL method no. 95:2009	-	-	-	2.84	0.97	1.27	-	-	-
Anaerobic sulphite-reducing bacteria NMKL method no. 56:2015	2.30	0.67	1.44	2.96	2.81	1.40	-	-	-
Aerobic microorganisms in fish products NMKL method no. 184:2006	4.67	0.55	1.23	4.24	5.53	1.42	4.01	1.88	2.31
H ₂ S-producing bacteria in fish products NMKL method no. 184:2006	4.31	1.88	1.85	3.78	4.33	1.73	-	-	-
Yeasts NMKL method no. 98:2005 (DRBC)	-	-	-	3.47	2.10	1.62	2.37	2.01	1.78
Moulds NMKL method no. 98:2005 (DRBC)	2.93	4.53	1.88	-	-	-	1.96	1.56	2.65

- No target organism or no value

¹ n = 5 vials analysed in duplicate

² n = 10 vials analysed in duplicate

References

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Annex 1. Results of the participating laboratories

Lab no.	Aerobic microorganisms, 30 °C			Psychrotrophic microorganisms			Enterobacteriaceae			<i>Escherichia coli</i>			Presumptive <i>Bacillus cereus</i>			Coagulase-positive staphylococci			Lactic acid bacteria			<i>Clostridium perfringens</i>			Anaerobic sulphite-reducing bacteria			Aerobic microorganisms in fish products			H ₂ S-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	
7750	4.53	3.99	4.31	-	-	-	-	-	-	-	-	3.46	0	0	-	-	-	0	0	0	-	-	-	2.17	2.72	0	-	-	-	-	-	-	0	3.33	2.09	2.54	0	1.91		
7825	4.83	4.39	4.42	-	-	-	4.37	3.26	4.09	<1	<1	<1	-	-	-	-	-	-	<1	3.36	1.3	-	-	-	-	-	-	-	-	-	-	-	<1	3.6	1.73	2.59	<1	1.53		
7876	4.55	4.15	4.34	-	-	-	4.1	2.32	3.95	<1	<1	3.94	3.41	<1	<1	<1	3.99	4.16	-	-	-	<1	2.73	<1	-	-	-	-	-	-	-	<1	3.46	2.32	2.72	<1	1.83			
7877	4.89	4.08	4.42	4.79	3.72	4.29	4.34	2.79	3.84	-	-	3.34	<1	<1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2.65	3.4	1.88	-	-				
7882	4.45	4.16	4.36	-	-	-	4.12	2.74	3.86	0	0	3.84	3.3	0	0	0	4.02	4.09	3.7	3.19	2.88	2.61	0	0	2.61	1.57	0	-	-	-	-	0	3.26	1.65	2.65	0	1.66			
7930	4.61	4	4.28	-	-	-	4.18	2.85	3.75	0	0	4.22	0	0	0	0	4.03	4.43	-	-	-	0	2.71	0	-	-	-	4.81	4.1	4.26	4.28	3.75	0	0	3.41	1.95	2.6	0	1.61	
7940	4.83	4	4.42	-	-	-	4.07	2.76	3.86	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
7962	4.72	4.09	4.36	-	-	-	4.23	2.43	3.79	0	0	3.9	2.46	0	0	0	3.89	4.02	-	-	-	-	-	-	-	-	-	-	-	-	-	0	2.64	1.6	2.3	0	1.62			
7968	4.81	4.04	4.26	-	-	-	4.16	2.46	3.78	0	0	3.83	2.79	0	0	0	3.92	4.11	4.55	0	0	0	2.68	0	2.22	3.08	0	-	-	-	4.22	3.32	0	0	3.46	2.06	2.68	0	1.67	
7975	4.52	4.06	4.53	-	-	-	3.77	2.39	3.78	-	-	-	-	-	-	<1	3.69	3.93	-	-	-	-	-	-	-	-	-	-	-	-	-	-	<1	3.22	1.96	2.75	<1	1.71		
8066	-	-	-	-	-	-	-	-	-	0	0	3.79	3.41	0	0	0	4.03	4.09	4.21	0	0	3.58	2.7	2.18	0	-	-	4.43	4.06	3.92	4.04	3.49	0	-	-	-	-	-	-	-
8068	4.78	4.03	4.3	-	-	-	4	2.62	3.81	<1	<1	3.79	2.78	0	0	<1	3.66	3.89	-	-	-	0	2.87	0	2.26	2.86	0	-	-	-	-	-	0	3.17	2.11	2.51	0	1.66		
8105	4.76	4.17	4.4	-	-	-	-	-	-	0	0	3.7	3.24	0	0	0	3.97	4.08	-	-	-	-	-	-	-	-	-	-	-	-	-	2.55	3.48	1.91	0	0	1.6			
8147	4.63	3.72	4.16	-	-	-	4.15	2.58	3.71	<1	<1	3.65	2.95	<1	<1	<2	4.02	4.13	3.6	<2	<1	<1	2.82	<1	2.56	2.82	<1	-	-	-	-	<1	3.43	2.04	2.45	<1	1.48			
8228	4.62	4.03	4.35	4.57	4.04	4.05	3.96	2.71	3.7	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	<0	3.12	1.9	2.68	<0	0.8			
8260	4.67	4.04	4.24	-	-	-	4.04	2.69	3.78	-	-	-	0	0	0	4.03	4.08	-	-	-	0	2.05	0	2.6	2.11	0	-	-	-	-	-	0	3.3	2.18	2.65	0	1.65			
8313	4.61	4.08	4.24	-	-	-	4.02	2.59	3.69	-	-	-	3.56	0	0	-	-	-	-	-	-	-	-	2.38	3	0	-	-	-	-	-	-	0	3.3	1.92	2.67	0	1.66		
8333	4.73	4.04	4.35	-	-	-	4.06	2.38	3.63	<0	<0	3.41	3.33	<0	<0	-	-	-	<1	<1	<1	-	-	-	2.34	2.87	<0	-	-	-	-	<0	3.36	2.17	2.85	<0	1.82			
8397	4.71	4.19	4.41	-	-	-	3.95	2.41	4.02	0	0	3.78	0	0	0	4.15	4.11	3.34	0	0	-	-	-	-	-	2.44	2.93	0	4.65	3.74	3.15	4.17	3.15	0	0	3.48	1.95	2.34	0	1.72
8430	4.86	4.16	4.48	-	-	-	4.29	2.76	3.91	<1	<1	3.94	-	-	-	<1	3.62	4.11	-	-	-	-	-	-	-	-	-	-	-	-	-	<1	3.36	2.09	2.64	<1	2.2			
8435	-	-	-	-	-	-	4.23	3	3.79	<1	<1	3.65	3.61	<1.7	<1.7	<2	<2	4.09	-	-	-	-	-	-	2.66	2.86	0	-	-	-	-	-	-	-	-	-	-	-	-	
8506	4.51	4.01	4.35	-	-	-	-	-	-	0	0	3.54	3.27	0	0	-	-	-	-	-	-	-	-	-	2.37	2.71	0	-	-	-	-	-	0	3.4	2.11	2.61	0	1.67		
8523	4.74	4.16	4.38	4.6	3.32	3.83	4.35	2.8	3.95	<1	<1	3.13	-	-	-	<1	3.96	4.11	-	-	-	-	-	-	-	-	-	-	-	-	<1	3.55	2.2	2.88	<1	1.74				
8528	-	-	-	-	-	-	-	-	-	-	-	3.38	<1	<1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	<1	3.08	<1	<1	<1	<1			
8568	4.73	3.25	4.37	-	-	-	4.14	2.96	3.85	0	0	3.5	3.25	0	0	-	-	-	0	0	0	-	-	-	2.44	2.67	0	-	-	-	-	0	3.53	1.8	2.75	0	1.75			
8626	4.08	3.72	3.85	-	-	-	4.2	1.04	3.82	0	0	5.38	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4.36	3.72	3.9	-	-	-	-	-	-	-	-	-	-	
8628	4.65	4.05	4.27	-	-	-	3.99	2.63	3.81	0	0	3.85	3.26	0	0	0	4.03	4.13	0	3.16	0	0	2.95	0	2.7	2.84	0	4.2	4.28	4.25	4.2	3.57	0	0	3.4	2.16	2.64	0	1.66	
8657	4.63	4.04	4.32	-	-	-	3.93	1.23	3.82	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0	3.48	1.92	2.74	0	1.7			
8734	4.7	4.34	4.37	-	-	-	4.12	2.62	3.88	-	-	-	-	-	-	-	-	-	0	2.81	2.06	-	-	-	-	-	-	-	-	-	0	2.97	2.01	0	0	0	0	0		
8742	4.66	4.51	4.26	-	-	-	-	-	-	<1	<1	3.66	-	-	-	<1	3.99	4.04	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
8756	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
8766	4.59	4.16	4.3	-	-	-	4	2.4	3.7	0	0	3.62	3.38	0	0	0	3.91	4.15	-	-	-	0	2.73	0	-	-	-	-	-	-	-	0	3.43	1.93	2.77	0	1.45			
8891	4.59	4.06	4.48	-	-	-	4	2.52	3.88	0	0	3.83	3.32	0	0	0	3.84	4	-	-	-	-	-	-	-	-	-	-	-	-	0	3.15	-	2.59	0	-				
8909	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
8955	4.65	4	4.28	-	-	-	4.26	2.66	3.9	<1	<1	3.88	3.08	<1	<1	<1	3.97	4.3	<1	<1	<1	<1	2.18	<1	2.56	2.56	<1	4.65	4.08	4.45	4.15	3.15	<1	<1	3.32	1.99	3	<1	1.65	
9002	4.91	3.94	4.26	4.59	3.11	0	4.08	2.86	3.95	0	0	3.98	3.3	0	0	0	3.93	4.15	0	0	0	-	-	-	2.36	1.95	0	-	-	-	-	0	3.53	1.85	2.74	0	1.46			
9003	4.6	4	4.3	-	-	-	4.15	2.63	3.84	<1	<1	3.78	-	-	-	<1	3.78	4.04	-	-	-	-	-	-	-	-	-	-	-	-	-	<1	3.32	2.11	2.81	<1	1.74			
9034	4.59	4.04	4.32	4.66	2.91	<1	4.15	2.6	3.62	<1	<1	3.83	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
9078	4.68	4.18	4.47	-	-	-	4.29	2.7	4.26	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
9217	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
9408	4.6	3.93	4.38	-	-	-	4.34	2.79	3.93	<1	<1	3.95	3.2	<1	<1	<1	3.95	4.03	-	-	-	2.42	2.26	<1	2.42	2.95	<1	4.67	3.77	4.01	4.43	2.83	<1	<1	3.42	2.43	2.81	<1	1.78	
9429	4.61	4.15	4.26	-	-	-	-	-	-	-	-	3.28	<1	<1	<1	<1	3.96	4.15	-	-	-	<1	2.66	<1	2.3	2.7	<1	-	-	-	-	<1	3.2	2	3.62	<1	1.6			
9436	5.02	4.07	4.35	4.39	2.92	<1	4.1	2.56	3.63	<1	<1	3.67	3.26	<1	<1	<1	3.87	4.05	4.45	3.96	3.49	<1	2.56	<1	<1	2.44	<1	-	-	-	<1	3.32	2.19	2.82	<1	1.8				
9441	4.56	4	4.34	-	-	-	-	-	-	<1	<1	3.89	-	-	-	<1	3.94	4.11	4.3	3.85	<1	0	2.79	0	2.4	2.79	0	4.53	4.04	4.32	4.11	3.38	<1	0	3.26	1.18	2.76	0	1.72	
9453	4.71	3.95	4.28	-	-	-	4.18	2.48	3.91	-	-	-	3.6	<1	<1	<1	3.99																							

Annex 1. Results of the participating laboratories

Lab no.	Aerobic microorganisms, 30 °C			Psychrotrophic microorganisms			Enterobacteriaceae			<i>Escherichia coli</i>			Presumptive <i>Bacillus cereus</i>			Coagulase-positive staphylococci			Lactic acid bacteria			<i>Clostridium perfringens</i>			Anaerobic sulphite-reducing bacteria			Aerobic microorganisms in fish products			H ₂ S-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			
Min	3.65	3.25	3.45	3.34	2.32	0	3.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4.20	2.65	3.15	4.01	2.61	0	0	2.06	0	0	0	0				
Max	5.34	5.03	4.81	4.79	4.11	4.32	4.61	3.26	4.26	3.93	0	5.38	4.24	3.38	3.62	4.21	4.20	4.43	4.64	3.96	3.58	2.95	3.14	0	3.68	4.00	2.79	5.60	4.69	4.60	4.43	4.14	0	2.95	4.21	3.17	3.62	3.29	2.91			
Med	4.69	4.06	4.32	4.61	3.34	3.53	4.13	2.63	3.80	0	0	3.80	3.30	0	0	0	3.96	4.11	3.79	0	0	0	2.69	0	2.39	2.78	0	4.60	4.08	4.26	4.26	3.38	0	0	3.32	2.02	2.70	0	1.66			
m _{PT}	4.675	4.060	4.317	4.586	3.467	3.943	4.137	2.625	3.799	-	-	3.780	3.306	-	-	-	3.946	4.097	3.805	-	-	-	2.659	-	2.341	2.735	-	4.594	4.044	4.178	4.235	3.349	-	-	3.307	2.023	2.672	-	1.641			
s _{PT}	0.129	0.121	0.101	0.160	0.470	0.326	0.145	0.174	0.143	-	-	0.197	0.195	-	-	-	0.095	0.087	0.681	-	-	-	0.287	-	0.259	0.244	-	0.188	0.242	0.233	0.130	0.339	-	-	0.198	0.183	0.153	-	0.186			
u _{PT}	0.013	0.012	0.010	0.044	0.128	-	0.016	0.020	0.016	-	-	0.024	0.026	-	-	-	0.013	0.011	0.186	-	-	-	0.051	-	0.043	0.040	-	0.050	-	0.062	0.037	-	-	-	0.022	0.021	0.017	-	0.021			
F+	0	0	0	0	0	-	0	0	0	2	0	0	0	4	4	1	0	0	0	21	15	13	0	0	0	0	0	1	0	0	0	-	0	0	-	0	12	0	0	0	3	0
F-	0	0	0	0	0	-	0	4	1	0	0	2	11	0	0	0	4	1	25	0	0	0	1	0	3	1	0	0	-	0	0	-	0	0	0	0	9	11	0	9		
<	4	3	4	1	0	-	2	2	2	0	0	4	2	0	0	0	3	5	2	0	0	0	1	0	2	4	0	0	-	2	0	-	0	0	5	3	8	0	3			
>	3	4	2	0	0	-	1	1	5	0	0	2	2	0	0	0	0	2	0	0	0	0	0	0	1	2	0	1	-	0	0	-	0	0	1	5	2	0	4			
Lower	4.29	3.70	4.01	4.11	2.06	0	3.70	2.10	3.37	0	0	3.19	2.72	0	0	0	3.66	3.84	1.76	0	0	0	1.80	0	1.56	2.00	0	4.03	3.32	3.48	3.84	2.33	0	0	2.71	1.47	2.21	0	1.08			
Upper	5.06	4.42	4.62	5.07	4.88	4.32	4.57	3.15	4.23	0	0	4.37	3.89	0	0	0	4.23	4.36	5.85	0	0	0	3.52	0	3.12	3.47	0	5.16	4.77	4.88	4.63	4.37	0	0	3.90	2.57	3.13	0	2.20			

N = number of reported results Min = lowest reported result Med = median value s_{PT} = standard deviation F+ = false positive < = low outlier Lower = lowest accepted value
n = results without annotation Max = highest reported result m_{PT} = assigned value u_{PT} = measurement uncertainty F- = false negative > = high outlier 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 not evaluated
- u_{PT} > 0,3 s_{PT} and/or > 20 % outliers and/or fewer than 12 evaluated results

Annex 2. Z-scores of all participants

Lab no.	Aerobic microorganisms, 30 °C			Psychrotrophic microorganisms			Enterobacteriaceae			Escherichia coli			Presumptive Bacillus cereus			Coagulase-positive staphylococci			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	-4.000	-2.985	-0.861				0.293	0.889	1.405	0	0	-0.405																				0	-0.537	2.057	0.708	0	1.128		
1237	2.525	-0.498	-1.655				0.087		-2.236	0	0	-2.339				0	-1.016	-0.662		0	0.229	-1.375	0	4.000		-3.771					0	-0.789							
1545	0.896	0.331	0.232				1.393	0.544	0.005	0	0	0.002	0.278	0	0	0	0.568	1.186		0	0.456	0	-0.157	0.470	0					0	-0.486		-0.733	0					
1970	-1.277	-0.581	-1.357	-4.000	-0.355		-1.425	-1.124	-1.186	0	0	0.511	0.638	0	0	0	-0.382	1.879	-0.023	0	0	0.874	0	4.000	0.101	0	-0.711	0.225	-0.651	0	0	1.277	0.313	-0.012	0	0.643			
2000	-2.596	-1.741	-2.747				-1.562	-0.606	-0.626	0	0	-0.914	-0.646	0	0	0	-0.171	0.146	0.667	0	0	0.002	0							0	-0.386	-0.178	0.053	0	-0.166				
2035							-1.975	-0.779	-1.816				-0.544	0	0							-0.312	0	-1.007	-0.432	0				0	0.169	0.476	-0.340	0	0.320				
2058	-1.277	-3.399	-1.655				0	0	-1.270												0	-0.556	0							0	0.471	-0.123	-3.091	0	1.398				
2064	0.197	0.248	0.430				-0.050	0.717	1.895				1.100	0	0															0	0.622	0.095	-0.012	0	-0.974				
2072	0.353	1.160	0.629	0.774	1.368		0.431	0.141	0.775	0	0	0.511	1.100	0	0	0		2.341	0	0	0	-0.416	0	0.770	-0.801	0				0	-0.386	4.000	1.101	0	0.859				
2221	1.051	0.828	0.232				0.156	0.256	0.565	0	0	-0.354	0.638	0	0	0	1.096	-4.000		0	0.909	0	0.499	-3.793	0				0	1.227	0.749	1.167	0	0.481					
2317	0.120	-0.747	-0.165				-0.394	-0.491	0.565	0	0	0.358	-1.828	0	0	0	-1.227	0.146		0	-3.556	0	-0.891						0	-0.386	-0.287	-1.715	0	-1.513					
2324	-0.889	-0.912	-1.357				-1.150	-2.907	0.075	0	0	0.053	-0.030	0	0	0	-0.382	-0.200											0	1.580	-0.777	0.250	0	0.320					
2344	-1.432	-0.166	-0.364				-0.806	-0.491	-0.415	0	0	-1.372	-0.389	0	0	0	0.463	0.146			0	0	0.113	0					0		-0.287	0.315	0	0.050					
2375	0.741	-0.001	0.132				1.118	0.774	0.425																					0	0.370	0.095	0.708	0	0.643				
2402	0.353	-0.083	1.721				-0.531	-1.009	0.845	0	0	1.020																											
2459	-0.268	0.165	1.423				0.843	1.234	0.145	0	0	-0.303		0	0	0	-0.065	0.724											0	-0.940	-4.000	0.184	0	0.158					
2637	0.197	-0.664	0.033				0.637	-0.319	-1.116	0	0	-0.303		0	0	0	-1.121	-0.200	0.814		0	0.979	0	-1.162	0.962	0			0	-1.142	-0.886	-0.995	0	-0.435					
2642	0.197	0.165	-0.165	-0.667	-0.696		0.774	0.165	-0.145	0	0	0.664				0	0.568	0.146												0	-0.789	-1.050	-0.471	0	-2.214				
2720	1.129	0.663	-0.364				0.362	0.256	0.705				-0.235	0	0														0	1.177	0.040	0.839	0	-1.298					
2745	3.379	-0.995	-0.463				0.293	0.774	-0.836	0	0	-0.150	-2.084	0	0	0	1.730	0.377		0	0	-0.242	0							-0.587	-1.159		0	-0.705					
2794	-0.113	-0.166	0.033				-0.113	-0.166	0.033																					0	0.723	0.858		0					
2920	0.197	0.414	-1.357				0.431	0.832	0.215	0	0	0.511												0.693	-2.932	0													
2941	0.197	0.828	-0.463				-0.119	-0.491	-0.976	0	0	0.002	1.152	0	0	0		0.493											0	1.832	4.000	1.298	0	-1.567					
3031							0	0	0.104							0	-0.065	-0.200					0.406		0.440	1.270	0												
3055	-0.035	-0.829	-1.158				0.981	-0.951	0.915				1.203	0															0		-4.000	-0.396	-1.191	0	-0.866				
3243	-1.122	0.663	-1.357				-0.119	0.947	-0.205																														
3327	-0.811	-1.907	-0.563				-1.425	-0.549	-0.626	0	0	-2.135				0	0.568	1.533											0	0.068	-0.941	1.167	0	0.751					
3457	-0.113	-0.498	-0.463				1.530	0.026	-0.065	0	0	-0.100				0	-0.171	0.608	-4.000	0		-2.474	0	0.033	0.741	0.348	0			-0.134	1.403	-2.305	0	-1.244					
3515	1.827	0.497	1.622				0.293	-0.031	-1.256	0	0	0.816	0.124	0	0	0	2.680	-4.000																					
3543	0.896	4.000	0.728				-1.081	-0.031	0.565				-1.160	0	0	0	0.040	-0.085																					
3587	-0.113	0.082	0.331				0.912	0.371	0.985	0	0	4.000	-0.441	0	0	0	-4.000	-0.085																					
3595	0.197	0.082	-0.165				-0.119	0.889	0.145	0	0	-0.303	-1.519	0	0	0	0.251	0.608											0	-0.033	0.422	-0.733	0	-1.891					
3626	0.197	-1.327	-1.158				-0.256	-2.447	-0.696	0	0	1.631	-1.057	0	0	0	-0.488	0.031			0	0.979	0	-1.625	0.839	0			0	-0.486	-0.505	0.184	0	-0.273					
3831	0.120	-0.001	-0.960				0	0	-3.204																					0	-0.990	0.258	-1.715	0	-1.136				
3878	0.717	-1.302	1.046				0.974	-0.175	-0.226	0	0	0.715	-0.456	0	0	0	-2.430	-0.397												0	-0.456	0.024		0					
4047																																							
4050	0.353	1.906	-1.556				0.018	0.429	-0.345				4.000	0	0																								
4064	-0.346	-0.001	0.232				0.981	0.084	0.355																														
4100	1.129	1.989	1.225	0.210	-0.313		0.981	0.947	0.005	0	0	-0.863	-0.235	0	0							-1.637	0	0.229	0.839	0	0.725	0.655	0.809	0	0	0.874	-0.123	0.315	0	0.589			
4171	0.042	1.409	-0.563				-0.188	1.177	-2.726	0	0	-1.881	0.535	0	0	0														0	0.521	-1.432	0.250	0	0.805				
4246	0.042	1.989	-0.165				-0.119	0.889	0.005	0	0	0.358				0		-0.431																					
4288	-1.510	-0.415	-0.364				-0.394	0.544	-3.286	0	0	0.664	1.049	0	0	0	-0.276	0.608											0	-0.033	-0.559	0.446	0	0.320					
4339																																							
4400	1.361	2.321	2.416				0.637	1.867	3.225	0	0	1.478	2.179	0	0															0	-0.839	0.476							
4418	3.922	0.497	-4.000	0.335	0.155		-0.188	-0.664	-1.606	0	0	0.104				0	1.941	2.341													-3.208	4.000	-1.846		-2.376				
4449	-0.113	0.165	0.232				-0.188	-1.181	0.355				-0.235	0	0														0	0.572	-0.232	0.446	0	2.745					
4557	0.197	2.404	1.324				0.981	0.774	0.775	0	0	0.460				0	-1.438	-2.280																					
4560																																							
4580	0.353	0.911	0.728				0.774	0.832	0.425	0	0	-0.201																											
4635	-1.665	-0.664	-0.165				-0.463	-0.204	-0.555				0.792	0	0	0	-0.804	-0.200												0	0.320	-0.668	-0.143	0	0.050				

Annex 2. Z-scores of all participants

Lab no.	Aerobic microorganisms, 30 °C			Psychrotrophic microorganisms			Enterobacteriaceae			Escherichia coli			Presumptive Bacillus cereus			Coagulase-positive staphylococci			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
7750	-1.122	-0.581	-0.066									0.792	0	0						0	0			-0.659	-0.063	0					0	0.118	0.367	-0.864	0	1.452			
7825	1.206	2.735	1.026				1.599	3.650	2.035	0	0																			0	1.479	-1.595	-0.536	0	-0.597				
7876	-0.966	0.746	0.232				-0.256	-1.757	1.055	0	0	0.816	0.535	0	0	0	0.463	0.724											0	0.773	1.621	0.315	0	1.020					
7877	1.672	0.165	1.026	1.276	0.538		1.393	0.947	0.285			0.176	0	0															0	0.471	-0.777								
7882	-1.742	0.828	0.430				-0.119	0.659	0.425	0	0	0.308	-0.030	0	0	0	0.779	-0.085	-0.155					1.040	-4.000	0			0	-0.235	-2.031	-0.143	0	0.104					
7930	-0.501	-0.498	-0.364				0.293	1.292	-0.345	0	0	2.241	0	0	0	0.885	3.843							1.150		0.354	0.348		0	0.521	-0.396	-0.471	0	-0.166					
7940	1.206	-0.498	1.026				-0.463	0.774	0.425																														
7962	0.353	0.248	0.430				0.637	-1.124	-0.065	0	0	0.613	-4.000	0	0	0	-0.593	-0.893											0	-3.359	-2.304	-2.436	0	-0.112					
7968	1.051	-0.166	-0.563				0.156	-0.951	-0.135	0	0	0.257	-2.650	0	0	0	-0.276	0.146	1.093	0	0	0	0	0.072	0		-0.466	1.413	0		0	0.773	0.204	0.053	0	0.158			
7975	-1.199	-0.001	2.119				-2.525	-1.354	-0.135						0	-2.705	-1.933													0	-0.436	-0.341	0.512	0	0.373				
8066										0	0	0.053	0.535	0	0	0	0.885	-0.085	0.594	0			-0.871				-0.871		-1.107	-1.496									
8068	0.818	-0.249	-0.165				-0.944	-0.031	0.075	0	0	0.053	-2.701	0	0	0	-3.022	-2.395											0	-0.688	0.476	-1.060	0	0.104					
8105	0.663	0.911	0.828				0	0	-0.405	-0.338	0	0	0	0	0	0.251	-0.200												0	0.874	-0.614		0	-0.220					
8147	-0.346	-2.819	-1.556				0.087	-0.261	-0.626	0	0	-0.659	-1.828	0	0	0	0.779	0.377	-0.301	0	0	0	0.560	0	0.847	0.347	0		0	0.622	0.095	-1.453	0	-0.866					
8228	-0.423	-0.249	0.331	-0.103	1.219		-1.219	0.486	-0.696																				0	-0.940	-0.668	0.053	0	-4.000					
8260	-0.035	-0.166	-0.761				-0.669	0.371	-0.135					0	0	0	0.885	-0.200					0	-2.126	0	1.002	-2.563	0		0	-0.033	0.858	-0.143	0	0.050				
8313	-0.501	0.165	-0.761				-0.806	-0.204	-0.766			1.306	0	0															0	-0.033	-0.559	-0.012	0	0.104					
8333	0.430	-0.166	0.331				-0.531	-1.412	-1.186	0	0	-1.881	0.124	0	0				0	0								0	0.269	0.803	1.167	0	0.966						
8397	0.275	1.077	0.927				-1.287	-1.239	1.545	0	0	0.002	0	0	0	2.152	0.146	-0.683	0	0						0.299		-4.000	-0.497		0	0.874	-0.396	-2.174	0	0.427			
8430	1.439	0.828	1.622				1.049	0.774	0.775	0	0	0.816			0	-3.444	0.146												0	0.269	0.367	-0.209	0	3.015					
8435							0.637	2.154	-0.065	0	0	-0.659	1.562	0	0	0		-0.085																					
8506	-1.277	-0.415	0.331				0	0	-1.219	-0.184	0	0																	0	0.471	0.476	-0.405	0	0.158					
8523	0.508	0.828	0.629	0.085	-0.313		1.462	1.004	1.055	0	0	-3.305			0	0.146	0.146												0	1.227	0.967	1.363	0	0.535					
8528												0.381	0	0															0	-1.142			0						
8568	0.430	-4.000	0.530				0.018	1.924	0.355	0	0	-1.423	-0.287	0	0														0	1.126	-1.214	0.512	0	0.589					
8626	-4.000	-2.819	-4.000				0.431	-4.000	0.145	0	0	4.000																	0										
8628	-0.191	-0.083	-0.463				-1.013	0.026	0.075	0	0	0.358	-0.235	0	0	0	0.885	0.377		0			0	1.014	0	1.388	0.429	0	-2.094	0.311	-0.267		0	0.104					
8657	-0.346	-0.166	0.033				-1.425	-4.000	0.145																				0	0.874	-0.559	0.446	0	0.320					
8734	0.197	2.321	0.530				-0.119	-0.031	0.565																				0	-1.696	-0.069		0						
8742	-0.113	3.730	-0.563							0	0	-0.608			0	0.463	-0.662																						
8756																																							
8766	-0.656	0.828	-0.165				-0.944	-1.296	-0.696	0	0	-0.812	0.381	0	0	0	-0.382	0.608					0	0.246	0				0	0.622	-0.505	0.643	0	-1.028					
8891	-0.656	-0.001	1.622				-0.944	-0.606	0.565	0	0	0.257	0.073	0	0	0	-1.121	-1.125											0	-0.789		-0.536	0						
8909																																							
8955	-0.191	-0.498	-0.364				0.843	0.199	0.705	0	0	0.511	-1.160	0	0	0	0.251	2.341		0	0						0.299		1.171	-0.651		0	0.068	-0.178	2.149	0	0.050		
9002	1.827	-0.995	-0.563	0.022	-0.759		-0.394	1.349	1.055	0	0	1.020	-0.030	0	0	0	-0.171	0.608		0	0								0	1.126	-0.941	0.446	0	-0.974					
9003	-0.578	-0.498	-0.165				0.087	0.026	0.285	0	0	0.002			0														0	0.068	0.476	0.905	0	0.535					
9034	-0.656	-0.166	0.033	0.461	-1.185		0.087	-0.146	-1.256	0	0	0.257																											
9078	0.042	0.994	1.523				1.049	0.429	3.225																														
9217																																							
9408	-0.578	-1.078	0.629				1.393	0.947	0.915	0	0	0.867	-0.544	0	0	0	0.040	-0.778									0.406		-0.720	1.501		0	0.572	2.221	0.905	0	0.751		
9429	-0.501	0.746	-0.563				-0.256	-0.376	-1.186	0	0	-0.558	-0.235	0	0	0	0.146	0.608												0	-0.537	-0.123	4.000	0	-0.220				
9436	2.680	0.082	0.331	-1.232	-1.164		-0.256	-0.376	-1.186	0	0	-0.558	-0.235	0	0	0	-0.804	-0.547	0.946										0	0.068	0.912	0.970	0	0.859					
9441	-0.889	-0.498	0.232				0	0	0.562																														
9453	0.275	-0.912	-0.364				0.293	-0.836	0.775			1.511	0	0	0	0.463	1.533												0	-0.235	0.858	0.577	0	0.427					
9512	-0.191	-0.001	-0.463				-1.013	-0.146	-0.065			0.381	0	0															0	0.925	-0.450	0.708	0	-0.112					
9559	0.508	0.994	0.232				3.249	0.947	-0.415	0	0	0.358	0.381	0	0	0	-1.227	-1.125											0	-1.091	-0.941		0						
9662	-0.191	-1.824	-0.463				-1.837		-2.446	0	0	-3.000	-3.112	0	0	0	0.568	0.146	-0.287	0	0							0	-0.033	-0.668	-1.322	0	-0.166						
9747	-0.889	-0.498	-4.000				-4.000	1.062	1.405			-0.441	0	0															0	-2.805	2.493	-3.091	0	-1.405					
9783	-2.130	0.414	3.409																											0	0.622		-4.000	0	4.000				
9886	-0.113	0.165	0.033	-0.479	0.092		-0.188	-1.009	-1.676	0	0	-0.659	0.587	0	0																								

Annex 2. Z-scores of all participants

Lab no.	Aerobic microorganisms, 30 °C			Psychrotrophic microorganisms			Enterobacteriaceae			Escherichia coli			Presumptive Bacillus cereus			Coagulase-positive staphylococci			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
	The parameter is not evaluated																																						
	The result is not evaluated																																						

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: <https://www2.slv.se/absint>

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