

## Food Microbiology

April 2014

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*Proficiency Testing*  
**Microbiology – Food**  
April 2014



1457  
ISO/IEC 17043

**Quantitative analyses**

- Aerobic microorganisms, 30 °C
- Psychrotrophs
- Enterobacteriaceae
- *Escherichia coli*
- Presumptive *Bacillus cereus*
- Coagulase positive staphylococci
- Lactic acid bacteria
- *Clostridium perfringens*
- Anaerobic sulphite reducing bacteria
- Aerobic microorganisms in fish products, 20-25 °C
- H<sub>2</sub>S producing bacteria in fish products
- Yeasts
- Moulds

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## Abbreviations

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### Media

BA	Blood Agar
BcS	Bacillus cereus Selective agar
BP	Baird-Parker agar
BP+RPF	Baird-Parker agar with Rabbit Plasma Fibrinogen
Chrom .	Chromogenic medium
DG 18	Dichloran Glycerol agar
DRBC	Dichloran Rose Bengal Chloramphenicol agar
ISA	Iron Sulphite Agar
LTLSB	Lactose-Tryptone-Lauryl Sulphate Broth
MPCA	Milk Plate Count agar
MPN	Most Probable Number
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
MYP	Mannitol egg Yolk Polymyxin agar / Mossel agar
OGYE	Oxytetracycline Glucose Yeast Extract agar
PAB	Perfringens Agar Base
PCA	Plate Count Agar
SFP	Shahidi Ferguson Perfringens agar base
TBX	Tryptone Bile X-glucuronide agar
TSA	Trypticase Soy Agar
TSC	Tryptose Sulphite Cycloserine agar
VRB	Violet Red Bile agar
VRBG	Violet Red Bile Glucose agar
YGC	Yeast extract Glucose Chloramphenicol agar

### Organisations

ISO	International Organization for Standardization
NMKL	Nordic Committee for Food Analyses
SLV/NFA	Livsmedelsverket/National Food Agency, Sweden

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# General information on results evaluation

## Statistical evaluation of the results

Highly deviating values that did not belong to a strictly normal distribution were identified as statistical outliers (Grubbs' test modified by Kelly (1)). In some cases, subjective adjustments were made to set limits, based on knowledge of the mixture's contents. Outliers and false results were not included in the calculations of means and standard deviations. Results reported as ">value" were excluded from the evaluation. Results reported as "<value" were interpreted as being zero (negative result). All reported results are presented in Annex 1.



According to EN ISO/IEC 17043, for which the proficiency testing programme organised by the National Food Agency is accredited since 2012, it is mandatory for the participating laboratories to give method information for all analyses for which they report results. Method information is sometimes difficult to interpret, e.g. many laboratories state a medium that is not mentioned in the standard method. Therefore, in the following section, results have been grouped according to the method or the medium used to perform the analysis.

## Uncertainty of measurement for the assigned values

The uncertainty of measurement for an assigned value is calculated as the standard deviation divided by the square root of the number of correct results ("standard error"). The assigned value of evaluated parameters is the mean value of participants results.




## Tables and figures legend

### Tables

n	number of laboratory that performed the analysis
m	results mean value in $\log_{10}$ cfu/ml (false results and outliers excluded)
s	results standard deviation
F	number of false positive or false negative results
<	number of low outliers
>	number of high outliers
	global results for the analysis
	values discussed in the text

### Figures

Histograms of all analytical results obtained for each mixture are presented. The mean value of the analysis results is indicated in each histogram.

	values within the interval of acceptance (Annex 1)
	outliers
	false negative results
*	values outside of the axis scale

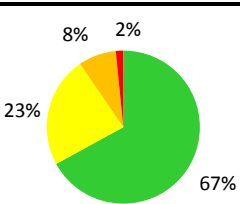
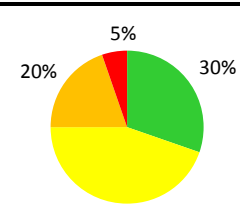
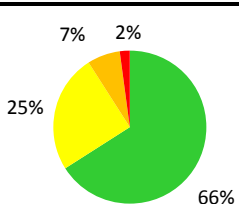
# Results of the PT round April 2014

## General outcome

Samples were sent to 199 laboratories, 46 in Sweden, 137 in other European countries, and 16 outside Europe. Results were reported from 188 laboratories, 81% provided at least one result that received an annotation. In the previous round (April 2013) with similar analyses, the proportion was 57 %.

Individual results for each analysis of the PT round are listed in annex 1 and are also available on the website after logging in: [www.slv.se/absint/index.aspx](http://www.slv.se/absint/index.aspx).

**Table 1: Microorganisms in each mixture and % of deviating results (F%: false positive or false negative, Out: outliers).**

	Mixture A			Mixture B			Mixture C		
% participants with									
Organisms	<i>Pseudomonas aeruginosa</i> <i>Staphylococcus aureus</i> <i>Lactobacillus plantarum</i> <i>Clostridium perfringens</i> <i>Candida glabrata</i> <i>Cladosporium cladosporioides</i>			<i>Enterobacter cloacae</i> <i>Bacillus cereus</i> <i>Staphylococcus hyicus</i> <i>Carnobacterium piscicola</i> <i>Clostridium bifermentas</i> <i>Shewanella putrefaciens</i> <i>Zygosaccharomyces rouxii</i> <i>Penicillium roqueforti</i>			<i>Escherichia coli</i> <i>Bacillus thuringiensis</i> <i>Staphylococcus saprophyticus</i> <i>Shewanella putrefaciens</i>		
Analysis	Target	F%	Out	Target	F%	Out	Target	F%	Out
Aerob. microorg, 30 °C	<i>P. aeruginosa</i> <i>S. aureus</i> <i>L. plantarum</i>	1	3	<i>S. hyicus</i> <i>C. piscicola</i>	0	1	<i>S. saprophyticus</i>	0	1
Psychrotroph	<i>C. cladosporioides</i>	-	-	<i>S. hyicus</i> <i>C. piscicola</i>	0	15	-	15	0
Enterobacteriaceae	-	7	-	<i>E. cloacae</i>	1	6	<i>E. coli</i>	1	5
<i>E. coli</i>	-	1	-	-	8	-	<i>E. coli</i>	18	3
Presump. <i>B. cereus</i>	-	4	-	<i>B. cereus</i>	2	9	<i>B. thuringiensis</i>	2	3
Coag. pos. Staph.	<i>S. aureus</i>	4	9	<i>S. hyicus</i>	-	-	( <i>S. saprophyticus</i> )	1	0
Lactic acid bacteria	<i>L. plantarum</i>	1	1	<i>C. piscicola</i>	53	1	( <i>S. saprophyticus</i> )	24	0
<i>C. perfringens</i>	<i>C. perfringens</i>	3	5	( <i>C. bifermentas</i> )	24	-	-	1	-
Anaerob. sulph. red	<i>C. perfringens</i>	4	3	<i>C. bifermentas</i>	3	6	-	3	-
Aerob. microorg. in fish prod., 20-25 °C	<i>P. aeruginosa</i> <i>S. aureus</i> <i>L. plantarum</i>	0	0	<i>S. hyicus</i> <i>C. piscicola</i>	3	6	<i>S. saprophyticus</i>	0	0
H <sub>2</sub> S producing bact. in fish products	-	7	-	<i>S. putrefaciens</i>	17	3	<i>S. putrefaciens</i>	34	0
Yeasts	<i>C. glabrata</i>	1	6	<i>Z. rouxii</i>	45	0	-	1	-
Moulds	<i>C. cladosporioides</i>	9	4	<i>P. roqueforti</i>	5	2	-	2	-

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

## Aerobic microorganisms, 30 °C

### Mixture A

The colonies counted were mainly from the strains of *Pseudomonas aeruginosa* and *Lactobacillus plantarum* present at the highest concentration in mixture A.

### Mixture B

The colonies counted were mainly from the strains of *Carnobacterium piscicola*, *Staphylococcus hyicus*, *Bacillus cereus* and *Enterobacter cloacae* present at the highest concentration in mixture B.

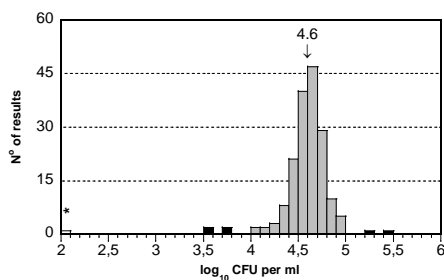
### Mixture C

The colonies counted were mainly from the strain of *Staphylococcus saprophyticus* present at the highest concentration in mixture C. Independently of the medium used, the results were more spread than for the other mixtures.

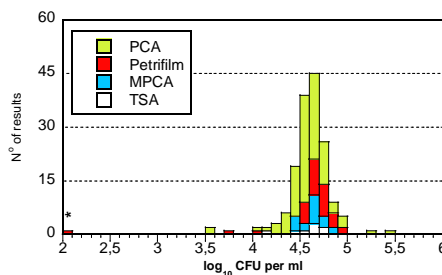
### Results of aerobic microorganisms analysis

Medium	Mixture A						Mixture B						Mixture C					
	n	m	s	F	<	>	n	m	s	F	<	>	n	m	s	F	<	>
Total	174	4.60	0.16	1	4	2	174	4.66	0.18	0	2	0	173	4.55	0.28	0	2	0
PCA	101	4.57	0.16	0	2	2	102	4.65	0.17	0	0	0	100	4.55	0.27	0	0	0
Petrifilm™	34	4.68	0.15	1	1	0	34	4.70	0.19	0	0	0	34	4.56	0.25	0	0	0
MPCA	19	4.62	0.12	0	0	0	19	4.64	0.23	0	1	0	19	4.55	0.30	0	1	0
TSA	8	4.57	0.20	0	0	0	8	4.61	0.11	0	0	0	8	4.48	0.31	0	0	0

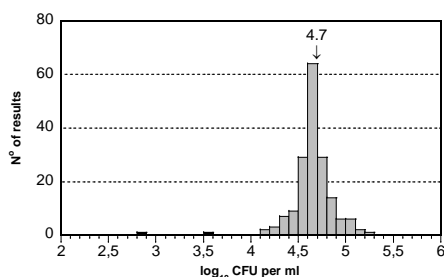
A



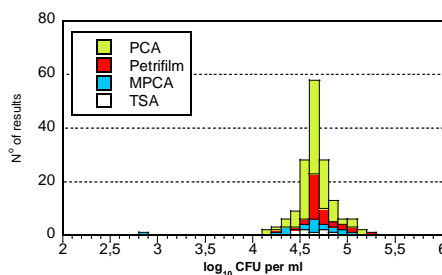
A



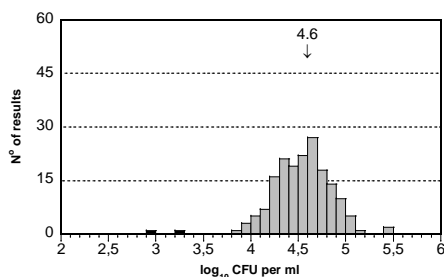
B



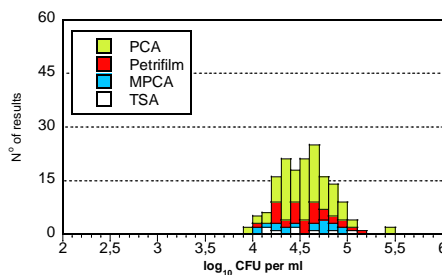
B



C



C



There is no differences in results depending on the medium chosen to perform the analysis.



## Psychrotrophic microorganisms

### Mixture A

At NFA, the mould *Cladosporium cladosporioides* formed colonies in PCA after 10 days of incubation at 6.5 °C. The colonies were however very small and a magnifying glass was used for the enumeration. 11 of the 13 laboratories that performed the analysis reported a negative result.

Due to the difficulty of the analysis, the results are not evaluated and therefore no z-scores are calculated. Moreover, these results are not taken into account in the tables under the box plots.

### Mixture B

Colonies from the same microorganisms than for the analysis of aerobic microorganisms at 30°C were counted.

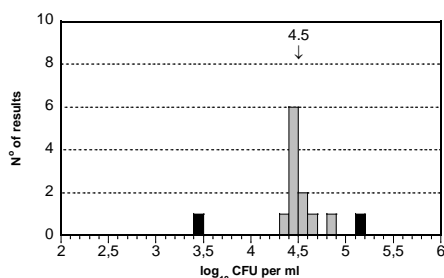
### Mixture C

At NFA, none of the strains present in mixture C formed colonies on PCA after 10 days of incubation at 6.5°C.

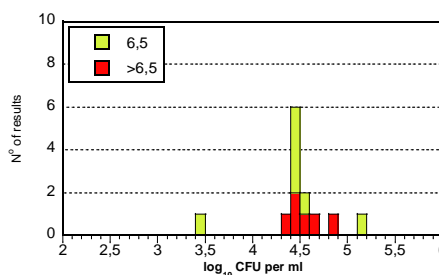
### Results of psychrotrophic microorganisms analysis

T°C	Mixture A					Mixture B					Mixture C							
	n	m	s	F	<	>	n	m	s	F	<	>	n	m	s	F	<	>
Total	13	3.40	1.53	11	0	0	13	4.50	0.13	0	1	1	13	-	-	2	-	-
6,5	7	2.32	-	6	0	0	7	4.47	0.04	0	1	1	7	-	-	0	-	-
>6,5	6	4.48	-	5	0	0	6	4.52	0.18	0	0	0	6	-	-	2	-	-

B



B



Only 13 laboratories performed this analysis, and although most of them used PCA as medium, the time and temperature of incubation varied : 6.5°C / 10 days, 17°C / 20h + 7°C / 3 days, 20°C / 20h + 7°C / 3 days, 15°C / 7 days or 21°C / 24h. This variation reflects the different definition that laboratories have of psychrotrophic microorganisms and makes the statistical evaluation of the results quite difficult.

It should be noticed that the NMKL methods 86:2006 and 74:2000 have been replaced by the NMKL method 86:2013 which prescribes the following incubation: 6.5°C / 10 days or 17°C / 24h + 7°C / 3 days.

## Enterobacteriaceae and *Escherichia coli*

### Mixture A

There was no target organism for these analyses in mixture A. At NFA, the strain of *Pseudomonas aeruginosa* formed small atypical beige colonies on VRBG. This could explain the 10 false positive results reported for the analysis of Enterobacteriaceae, especially as seven of these laboratories did not perform any confirmation.

## Mixture B

The strain of *Enterobacter cloacae* present in mixture B was only target organism for the analysis of Enterobacteriaceae. Even though there was no target organism for the analysis of *E. coli*, 10 false positive results were reported. At NFA *E. cloacae* formed colonies on TSA/VRB after 24h of incubation at 37°C, but not at 44°C. Moreover, unlike *E. coli*, *E. cloacae* does not produce indole from tryptophane.

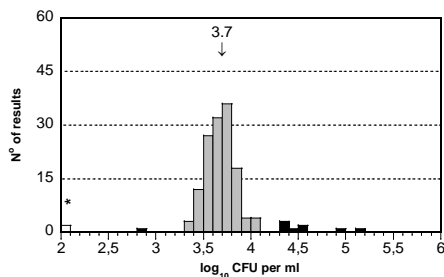
## Mixture C

Although a strain of *E. coli* was target organism for both analyses, 23 laboratories reported an absence of *E. coli* in mixture C. Among them, 15 used Petrifilm™ E.coli/Coliform Count plate which indicates that the strain was difficult to identify using this method (see below).

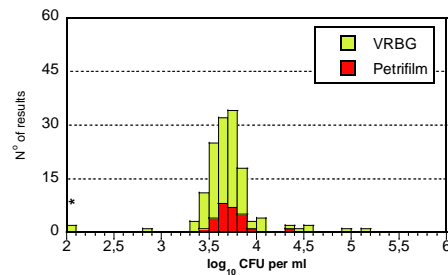
### Results of Enterobacteriaceae analysis

Medium	Mixture A					Mixture B					Mixture C				
	n	m	s	F	< >	n	m	s	F	< >	n	m	s	F	< >
Total	146	-	-	10	- -	147	3.67	0.15	2	1 8	146	3.09	0.12	1	3 4
VRBG	112	-	-	8	- -	113	3.67	0.15	2	1 6	112	3.08	0.12	1	2 4
Petrifilm™ Entero	27	-	-	2	- -	27	3.70	0.11	0	0 1	27	3.14	0.09	0	1 0

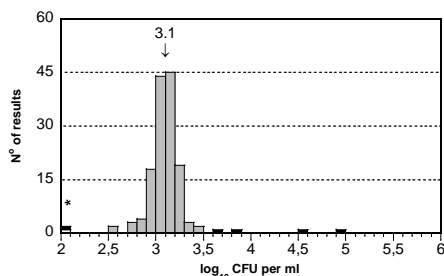
B



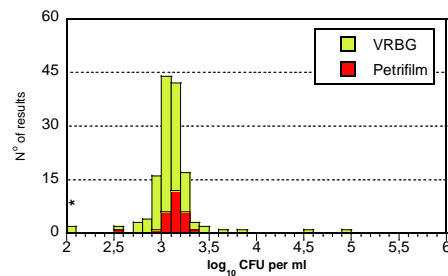
B



C



C

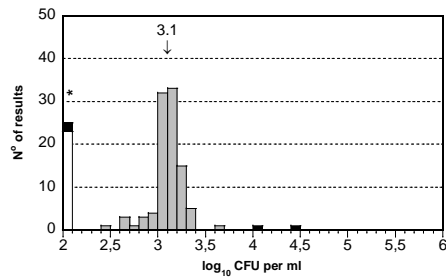


Most of the laboratories used VRBG plates or Petrifilm™ Enterobacteriaceae as medium and similar average values were reported.

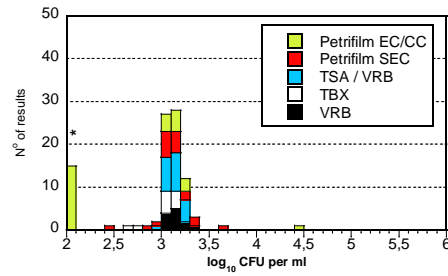
### Results of E.coli analysis

Medium	Mixture A					Mixture B					Mixture C				
	n	m	s	F	< >	n	m	s	F	< >	n	m	s	F	< >
Total	126	-	-	1	- -	126	-	-	10	- -	125	3.10	0.16	23	2 2
Petrifilm™ EC/CC	28	-	-	1	- -	28	-	-	6	- -	28	3.14	0.08	15	0 1
Petrifilm™ SEC	19	-	-	0	- -	19	-	-	0	- -	20	3.11	0.24	1	0 0
TSA/VRB	24	-	-	0	- -	24	-	-	0	- -	23	3.11	0.08	0	0 0
TBX	14	-	-	0	- -	14	-	-	0	- -	14	3.02	0.16	2	1 0
VRB	14	-	-	0	- -	14	-	-	0	- -	14	3.16	0.09	1	1 0
MPN-baserad	8	-	-	0	- -	8	-	-	0	- -	7	3.09	0.28	2	0 0

C



C



At NFA, the *E. coli* strain present in mixture C formed typical colonies on TSA/VRB and produced gas and indole in LTLNB after incubation at 44°C. Laboratories that used methods based on these characteristics did not have problem with the analysis.

Other methods using for example Petrifilm™ or TBX are based on the detection of  $\beta$ -glucuronidase, but previous trial performed at NFA showed that this *E. coli* strain has a weak  $\beta$ -glucuronidase activity. However false negative results appeared essentially linked to the use of Petrifilm™ EC/CC which were incubated at 35 or 37°C, while most laboratories using Petrifilm™ SEC or TBX performed an incubation at 42 or 44°C. This suggests that the  $\beta$ -glucuronidase activity of the *E. coli* strain is higher at 42-44°C and could explain the difference of results depending on the method chosen.

## Presumptive *Bacillus cereus*

### Mixture A

Mixture A did not contain any strain belonging to the *B. cereus* group.

### Mixture B

A strain of *Bacillus cereus* was target organism for the analysis.

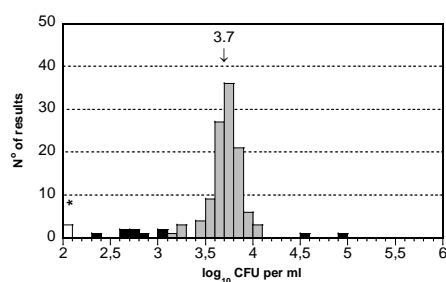
### Mixture C

A strain of *Bacillus thuringiensis* which belongs to the *B. cereus* group was target organism for the analysis.

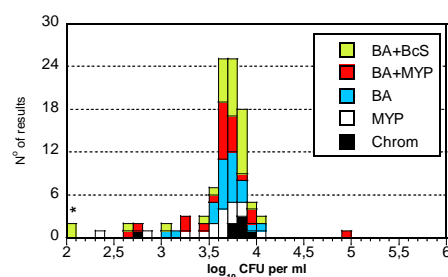
### Results of presumptive *B. cereus* analysis

Medium	Mixture A						Mixture B						Mixture C					
	n	m	s	F	<	>	n	m	s	F	<	>	n	m	s	F	<	>
Total	123	-	-	5	-	-	124	3.71	0.15	3	9	2	124	3.16	0.25	3	3	1
BA+BcS	32	-	-	3	-	-	32	3.76	0.13	2	3	0	31	3.21	0.20	0	0	0
BA+MYP	22	-	-	1	-	-	23	3.66	0.18	0	2	1	23	3.09	0.28	0	1	1
BA	23	-	-	0	-	-	24	3.70	0.16	0	1	0	24	3.09	0.26	1	0	0
MYP	17	-	-	0	-	-	16	3.67	0.18	0	1	0	17	3.09	0.36	0	0	0
Chrom	7	-	-	0	-	-	7	3.84	0.08	0	1	0	7	3.34	0.09	0	1	0

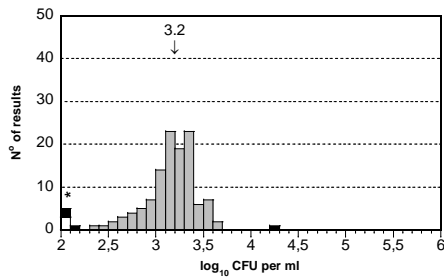
B



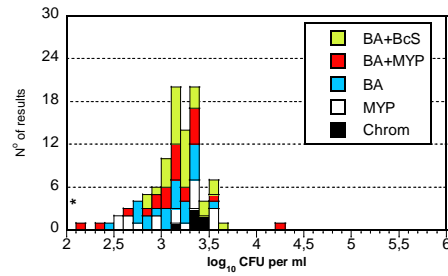
B



C



C



The results are more spread for mixture C than for mixture B with a tail of lower values that cannot be linked to a specific medium or method. For both mixtures, results connected to the use of chromogenic medium tend to be higher and less spread. The indicator dye revealing  $\beta$ -glucosidase activity might facilitate the enumeration of colonies and therefore leads to higher and more reproducible counts.

## Coagulase-positive *Staphylococci*

### Mixture A

A strain of *Staphylococcus aureus* was target organism for this analysis.

### Mixture B

Mixture B contained a strain of *Staphylococcus hyicus*. The analysis was performed by 115 laboratories; 97 reported the absence of target organism.

The identification of coagulase positive staphylococci is traditionally based on the detection of extracellular coagulase (tube coagulase test) or bound coagulase, also called clumping factor (slide coagulase test, haemagglutination test). Other identification tests allow the detection of protein A and/or polysaccharides also present on the bacterial cell surface (latex agglutination test) or the detection of DNase production.

At NFA colonies of *S. hyicus* grown on Baird-Parker agar with RPF did not present any precipitation zone. The strain was also negative for the coagulase test in tube. Therefore negative results based on confirmation tests for coagulase activity should be considered as correct.

Laboratories that counted colonies of coagulase positive staphylococci did not perform any confirmation or used confirmation tests detecting the presence of DNase activity, protein A or capsular polysaccharides. Therefore these results should also be considered as correct.

Considering the strain's characteristics and the variability in interpretation depending on the confirmation method used, the results are not evaluated and therefore no z-scores are calculated. Moreover, these results are not taken into account in the tables under the box plots.

### Mixture C

There was no target organism for this analysis in mixture C.

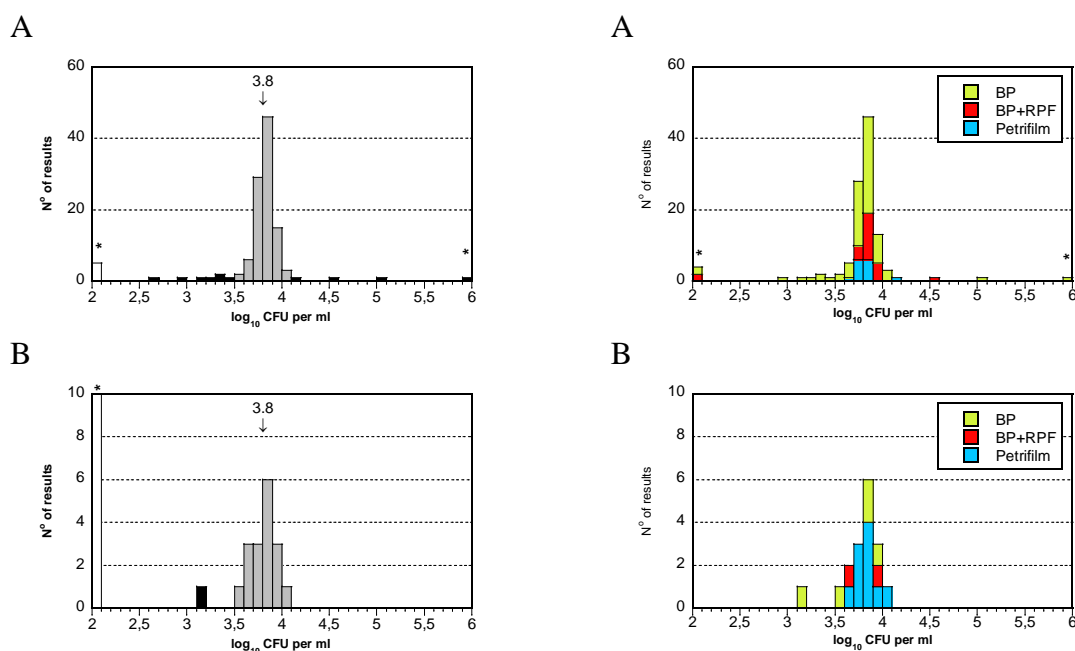
### Results of coagulase-positive *Staphylococci* analysis

Medium	Mixture A					Mixture B*					Mixture C				
	n	m	s	F	< >	n	m	s	F	< >	n	m	s	F	< >
Total	117	3.82	0.10	5	7 4	115	3.80	0.13	97	1 0	115	-	-	1	- -
BP	73	3.82	0.11	2	6 2	70	3.78	0.19	65	1 0	70	-	-	1	- -
BP+RPF	25	3.84	0.07	2	0 1	25	3.79	-	23	0 0	25	-	-	0	- -
Petrifilm™	14	3.78	0.06	0	0 1	14	3.82	0.11	4	0 0	14	-	-	0	- -

\* = Results not evaluated. Negative and positive results are correct depending on the confirmation test used.

### Results for mixture B depending on the confirmation method

Test	n	m	s	F	<	>
Coagulase	53	-	-	53	-	-
Latex agglutination	22	3.87	0.03	18	1	0
DNase	8	3.79	0.11	1	0	0



Without considering the negative results reported for mixture B, no results difference could be seen depending on the medium used.

## Lactic acid bacteria

### Mixture A

A strain of *Lactobacillus plantarum* was target organism for this analysis.

### Mixture B

Although a strain of *Carnobacterium piscicola* was target organism, 53% of the laboratories that performed the analysis reported a false negative result. Carnobacteria are more sensitive to low pH than other lactic acid bacteria. This characteristic could explain that all laboratories that used MRS-S or Rogosa agar reported the absence of target organism for the analysis: these two media have a pH of 5.7 and 5.4, respectively while MRS and MRS-aB have a pH of 6.2.

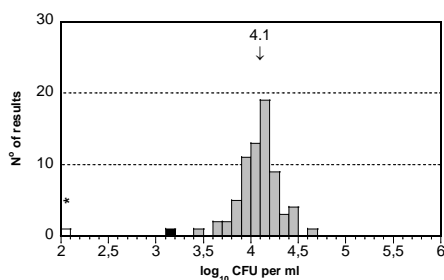
### Mixture C

Mixture C did not contain any target organism for this analysis but at NFA, the strain of *Staphylococcus saprophyticus* formed small colonies on MRS-aB after 5 days of incubation in anaerobiosis at 25°C and previous trial showed that it also formed colonies on MRS. This could explain the report of 17 false positive results. However unlike lactic acid bacteria, *S. saprophyticus* is catalase positive. Catalase test is recommended in case of doubt in the methods NMKL 140:2007 and ISO 15214:1998.

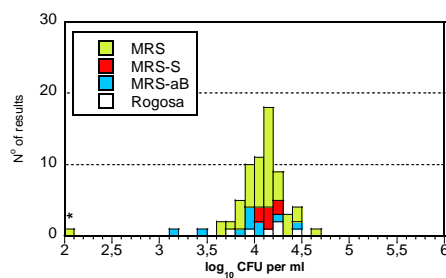
## Results of lactic acid bacteria analysis

Medium	Mixture A						Mixture B						Mixture C					
	n	m	s	F	<	>	n	m	s	F	<	>	n	m	s	F	<	>
Total	72	4.08	0.20	1	1	0	70	4.26	0.46	37	1	0	71	-	-	17	-	-
MRS	45	4.08	0.20	1	0	0	43	4.31	0.42	22	1	0	43	-	-	11	-	-
MRS-aB	10	3.98	0.26	0	1	0	10	4.14	0.56	0	0	0	10	-	-	2	-	-
MRS-S	7	4.15	0.09	0	0	0	7	-	-	7	0	0	7	-	-	1	-	-
Rogosa	6	4.14	0.24	0	0	0	6	-	-	6	0	0	6	-	-	0	-	-

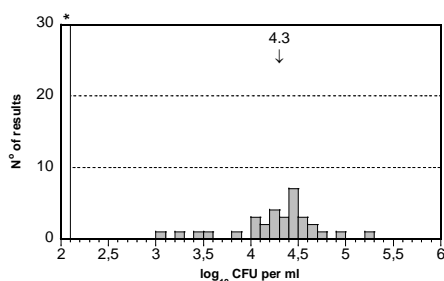
A



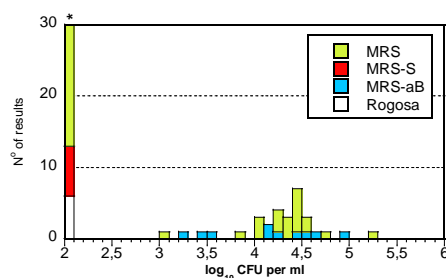
A



B



B



The enumeration of *L. plantarum* in mixture A did not cause any difficulties and all media led to similar results. For mixture B, results are very spread independently of the medium used, MRS or MRS-aB. This can be due to the bacteria's sensitivity to lower pH if pH media were not adjusted.

## *C. perfringens* and anaerobic sulphite-reducing bacteria

### Mixture A

Mixture A contained a strain of *C. perfringens* that was target organism for both analyses.

### Mixture B

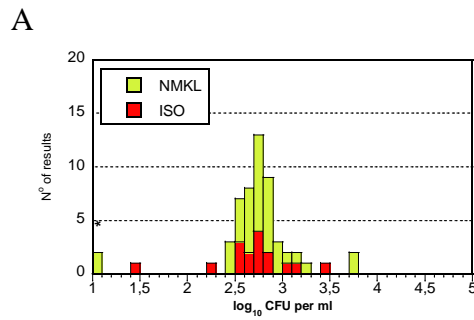
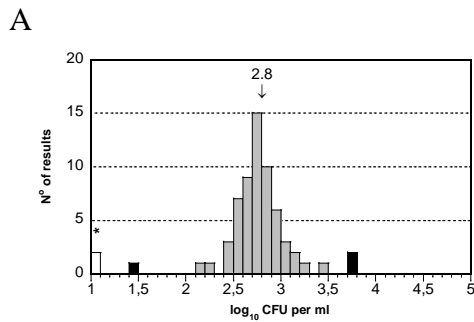
Mixture B contained a strain of *Clostridium bifermentas* that was only target organism for the analysis of anaerobic sulphite-reducing bacteria. *C. bifermentas* forms colonies on TSC plates that can be differentiated from *C. perfringens* in the confirmation steps of the analysis. Unlike *C. perfringens*, *C. bifermentas* is motile.

### Mixture C

Mixture C did not contain any target organisms for these analyses.

## Results of *C. perfringens* analysis

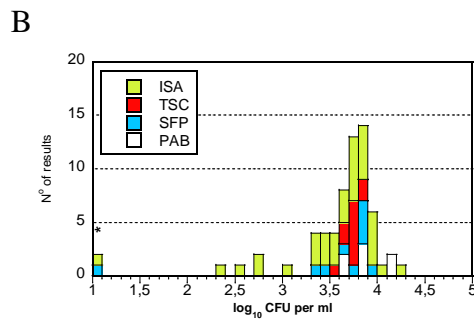
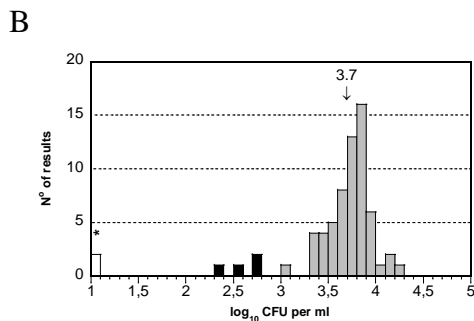
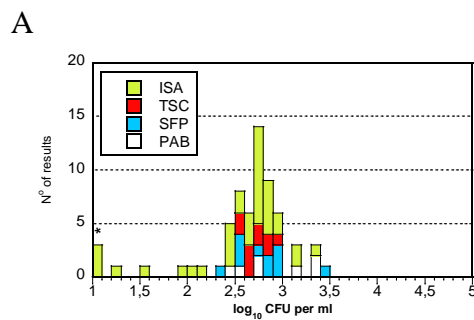
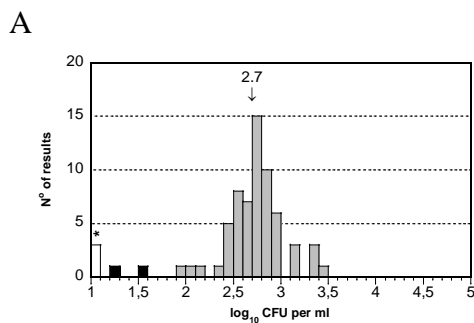
Method	Mixture A						Mixture B						Mixture C					
	n	m	s	F	<	>	n	m	s	F	<	>	n	m	s	F	<	>
Total	64	2.75	0.22	2	1	2	62	-	-	15	-	-	64	-	-	1	-	-
NMKL 95:2009	39	2.75	0.19	2	0	2	37	-	-	6	-	-	38	-	-	0	-	-
EN ISO 7937:2004	16	2.76	0.28	0	1	0	16	-	-	3	-	-	16	-	-	0	-	-



Almost all laboratories used TSC medium and the method NMKL 95:2009 or EN ISO 7937:2004 which led to similar results.

### Results of anaerobic sulphite-reducing bacteria analysis

Medium	Mixture A						Mixture B						Mixture C					
	n	m	s	F	<	>	n	m	s	F	<	>	n	m	s	F	<	>
Total	67	2.73	0.28	3	2	0	67	3.72	0.22	2	4	0	68	-	-	2	-	-
ISA	36	2.68	0.29	3	2	0	36	3.69	0.26	1	4	0	36	-	-	2	-	-
TSC	10	2.72	0.13	0	0	0	11	3.71	0.08	0	0	0	11	-	-	0	-	-
SFP	11	2.78	0.30	0	0	0	10	3.72	0.20	1	0	0	11	-	-	0	-	-
PAB	7	2.89	0.37	0	0	0	7	3.84	0.21	0	0	0	7	-	-	0	-	-



Almost all laboratories used the method NMKL 56:2008 or ISO 15213:2003. Even though both methods prescribe the use of ISA as medium, many laboratories performed the analysis with another medium like TSC or SFP which are selective. Therefore the detection of anaerobic sulfite bacteria other than clostridia could be missed with these media.

## Aerobic microorganisms and H<sub>2</sub>S producing bacteria in fish products

### Mixture A

Colonies counted for the analysis of aerobic microorganisms were mainly from the strains of *P. aeruginosa* and *L. plantarum*. Mixture A did not contain any H<sub>2</sub>S producing bacteria.

## Mixture B

*C. piscicola*, *S. hyicus*, *B. cereus* and *E. cloacae* formed the colonies counted for the analysis of aerobic microorganisms. A strain of *Shewanella putrefaciens* was target organism for the analysis of H<sub>2</sub>S producing bacteria.

## Mixture C

Colonies of *S. saprophyticus* were counted for the analysis of aerobic microorganisms.

Even though mixtures C and B contained the same strain of *Shewanella putrefaciens* at a similar concentration, here one third of the laboratories reported a false negative result for the analysis of H<sub>2</sub>S producing bacteria. This can be due to the background flora of the mixture that affected the growth of *S putrefaciens*: at NFA, colonies were very small on Iron agar and were counted using a magnifying glass.

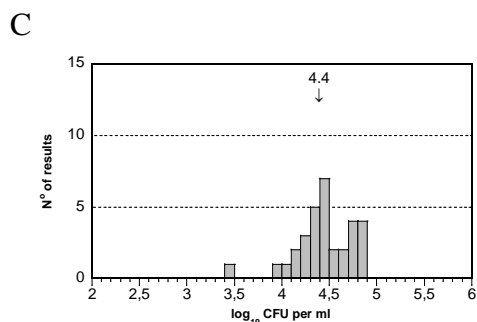
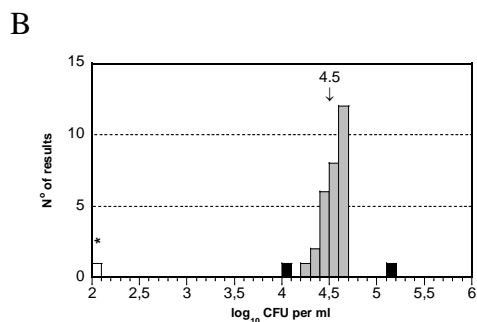
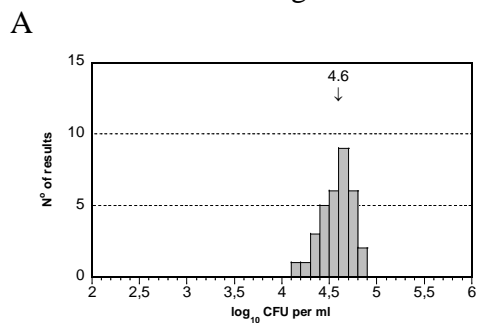
### Results of aerobic microorganisms in fish products analysis

Method	Mixture A					Mixture B					Mixture C							
	n	m	s	F	<	>	n	m	s	F	<	>	n	m	s	F	<	>
Total	33	4.57	0.17	0	0	0	32	4.54	0.10	1	1	1	32	4.44	0.30	0	0	0

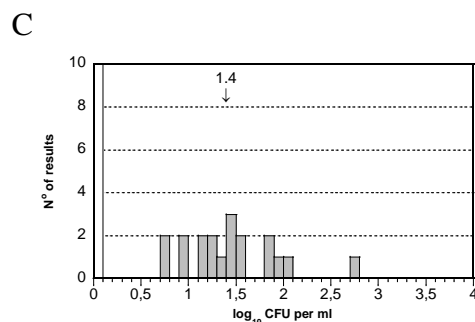
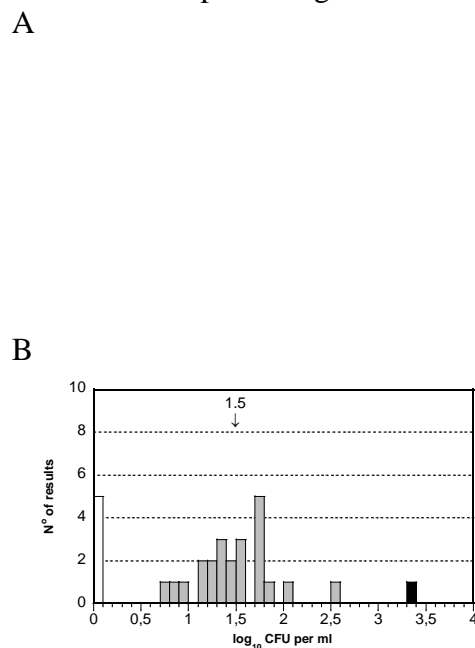
### Results of H<sub>2</sub>S producing bacteria in fish products analysis

Method	Mixture A					Mixture B					Mixture C							
	n	m	s	F	<	>	n	m	s	F	<	>	n	m	s	F	<	>
Total	30	-	-	0	-	-	29	1.46	0.41	5	0	1	29	1.42	0.50	10	0	0

#### Aerobic microorganisms 20-25°C



#### H<sub>2</sub>S producing bacteria



The 30 laboratories that performed both analyses all used Iron agar as medium and 26 the method NMKL 184:2006, therefore no distribution of results according to medium or method is presented here.



## Yeasts and moulds

### Mixture A

A strain of *Candida glabrata* and *Cladosporium cladosporioides* were target organism for the analysis of yeasts and moulds, respectively. Thirteen laboratories reported the absence of moulds in mixture A, but no correlation with the method and/or medium used could be seen.

### Mixture B

A strain of *Zygosaccharomyces rouxii* was target organism for the analysis of yeasts. The results are widely spread without forming a main peak. At NFA, we observed that this yeast strain formed less and smaller colonies on DRBC than DG18, which is in line with the results of the proficiency testing. The mixture contained also a strain of *Penicillium roquefortii*, target organism for the analysis of moulds; the colonies of which could make the reading of yeasts colonies difficult. This could partly explain the fact that 45% of the laboratories that performed the yeasts analysis reported a false negative result.

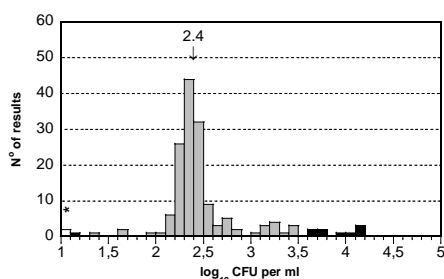
### Mixture C

Mixture C did not contain any target organisms for these analyses.

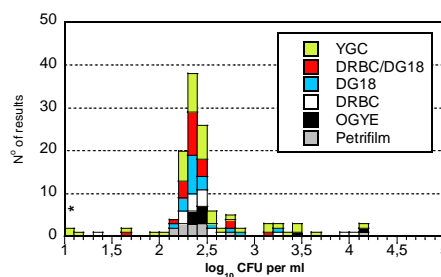
### Results of yeasts analysis

Medium	Mixture A						Mixture B						Mixture C					
	n	m	s	F	<	>	n	m	s	F	<	>	n	m	s	F	<	>
Total	156	2.43	0.31	2	1	9	152	1.51	0.50	69	0	0	151	-	-	2	0	0
YGC	44	2.50	0.39	2	1	2	41	0.71	0.5	20	0	0	41	-	-	2	-	-
DRBC/DG18	23	2.37	0.27	0	0	0	23	1.88	0.52	11	0	0	22	-	-	0	-	-
DG18	20	2.43	0.25	0	0	0	20	1.80	0.32	3	0	0	20	-	-	0	-	-
DRBC	18	2.38	0.35	0	0	2	18	0.91	0.21	13	0	0	18	-	-	0	-	-
Petrifilm™ YM	13	2.34	0.16	0	0	1	13	1.65	0.45	7	0	0	13	-	-	0	-	-
OGYE	9	2.52	0.36	-	-	1	9	1.35	0.5	1	0	0	9	-	-	0	-	-

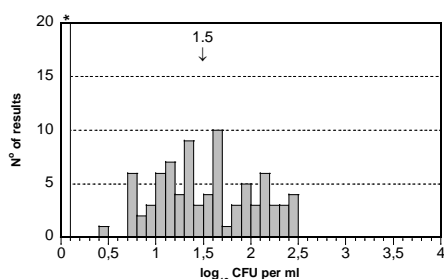
A



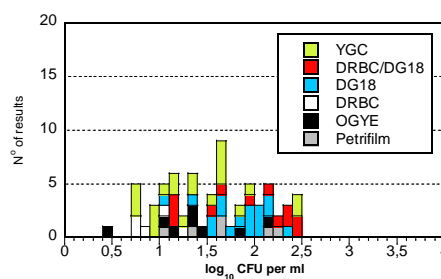
A



B



B

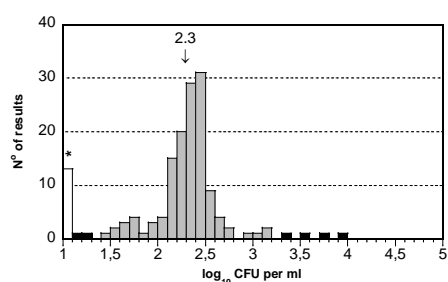


The results of mixture A analysis form a major peak with a tail of higher values but they cannot be linked to any medium or method. For mixture B, results obtained with the use of YGC or DRBC only were lower while those obtained with DG18 were higher than average. DG18 contains glycerol and is recommended for the analysis of products with a water activity lower than 0.95. This medium might be more adapted for the growth of *Z. rouxii* that is known to have a high tolerance to osmotic stress.

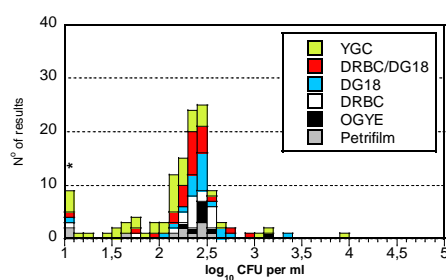
## Results of moulds analysis

Medium	Mixture A						Mixture B						Mixture C					
	n	m	s	F	<	>	n	m	s	F	<	>	n	m	s	F	<	>
Total	151	2.30	0.28	13	2	4	152	2.01	0.38	8	0	3	149	-	-	3	-	-
YGC	43	2.16	0.37	4	2	1	44	1.95	0.38	3	0	1	41	-	-	0	-	-
DRBC/DG18	25	2.33	0.23	1	0	0	25	2.11	0.35	0	0	0	24	-	-	0	-	-
DG18	20	2.41	0.18	1	0	1	20	2.01	0.43	0	0	0	20	-	-	1	-	-
DRBC	17	2.34	0.19	1	0	0	17	2.13	0.24	1	0	1	17	-	-	1	-	-
Petrifilm™ YM	11	2.28	0.28	2	0	0	11	1.82	0.40	1	0	0	11	-	-	0	-	-
OGYE	8	2.51	0.25	0	0	0	8	2.13	0.48	0	0	0	8	-	-	0	-	-

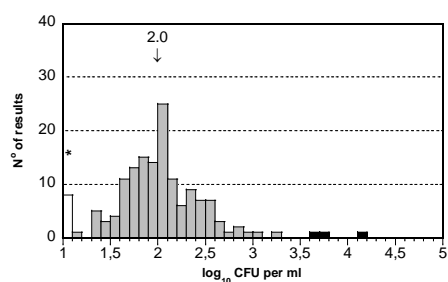
A



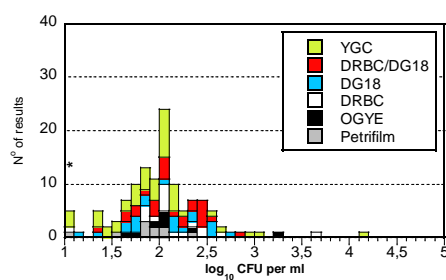
A



B



B



For mixture A, results of the moulds analysis form a major peak around 2.4 and a minor peak of lower values centered round 1.7 linked mainly to the use of YGC. The values obtained for mixture B are more spread, forming a wide peak, but no correlation between results and medium can be seen.

## Outcome of the results of individual laboratory - assessment

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In order to allow comparison of the results from different analyses and mixtures, all the results of the analyses were transformed into standard values (z-scores). For quantitative analyses, a z-score is either positive or negative, depending on whether the individual result is higher or lower than the mean value calculated from all laboratory results for each analysis. For qualitative analyses, a z-score of zero is attributed for a correct answer. The z-scores obtained, which are listed in Annex 2, can be used as a tool by laboratories when following up on the results.

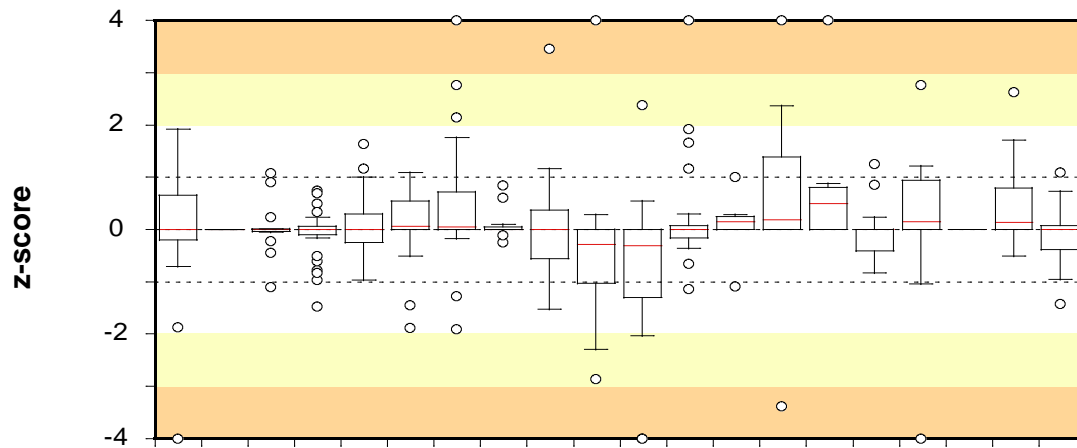
All the results from each laboratory – outliers included and false results excluded – were compiled into a box plot based on their z-scores. The smaller and more centred round zero the box of a laboratory is, the closer its results are to the general mean values calculated for all laboratory results.

The laboratories were not grouped or ranked based on their results. However, for each laboratory, the numbers of false results and outliers are presented below the box plots. These results are also highlighted in Annex 1, where all the reported results are listed, and the minimum and maximum accepted values for each analysis are stated.

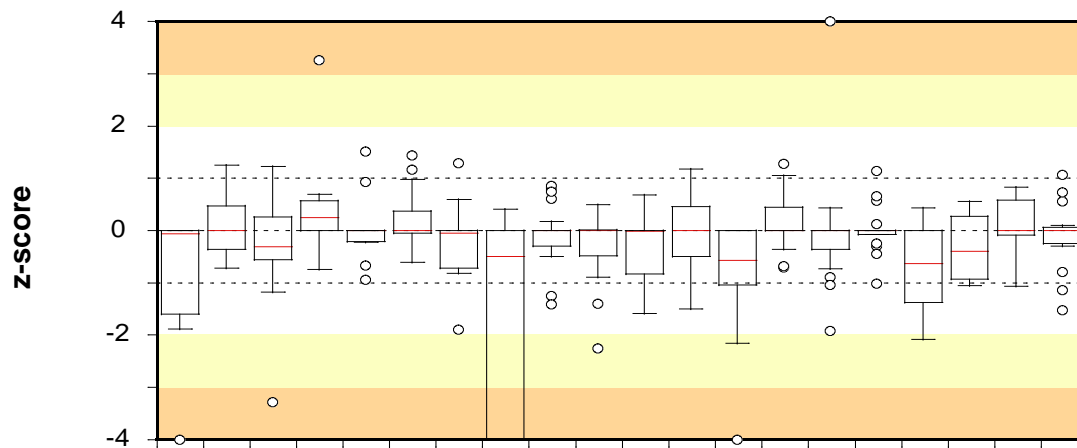
Information on the results processing and recommendations for follow-up work are given in the Scheme Protocol (2). Samples for follow-up can be ordered, free of charge via our website: [www.slv.se/pt\\_extra](http://www.slv.se/pt_extra)

### Box plots and numbers of deviating results for each laboratory

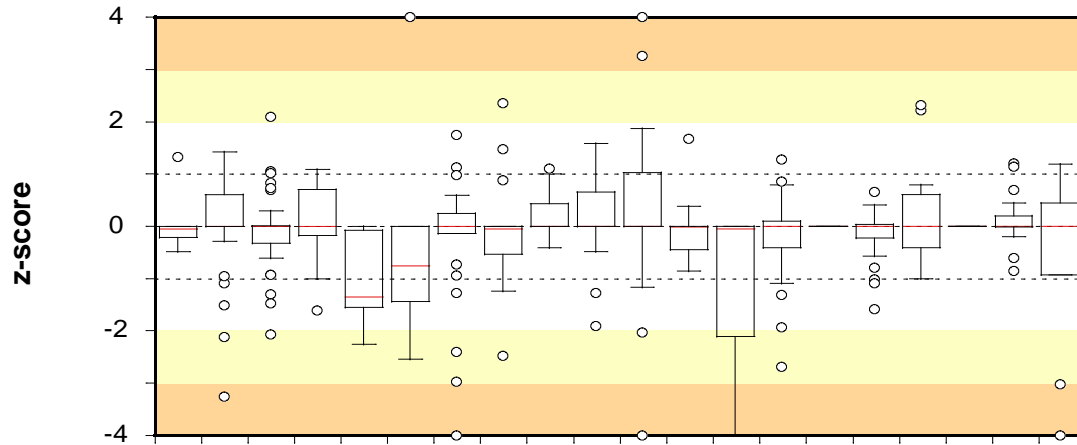
- *The plots are based on the laboratory results from all analyses transformed into z-scores calculated according to the formula:  $z = (x-m)/s$ , where  $x$  is the result of the individual laboratory,  $m$  is the mean of the results of all participating laboratories, and  $s$  is the standard deviation.*
- *Correct results for quantitative analyses without target organism and for qualitative analyses generate a z-value of 0.*
- *The laboratory median value is illustrated by a horizontal red line in the box.*
- *The box includes 50 % of a laboratory'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.*
- *Very deviating results are represented by circles and are calculated as follow: the lowest result in the box  $- 1.5 \times$  (the highest result in the box  $-$  the lowest result in the box) or the highest result in the box  $+ 1.5 \times$  (the highest result in the box  $-$  the lowest result in the box). z-scores higher than +4 and less than  $-4$  are positioned at +4 and  $-4$ , respectively, in the plot.*
- *The background is divided by lines and shaded fields to indicate ranges in order to simplify location of laboratory results.*



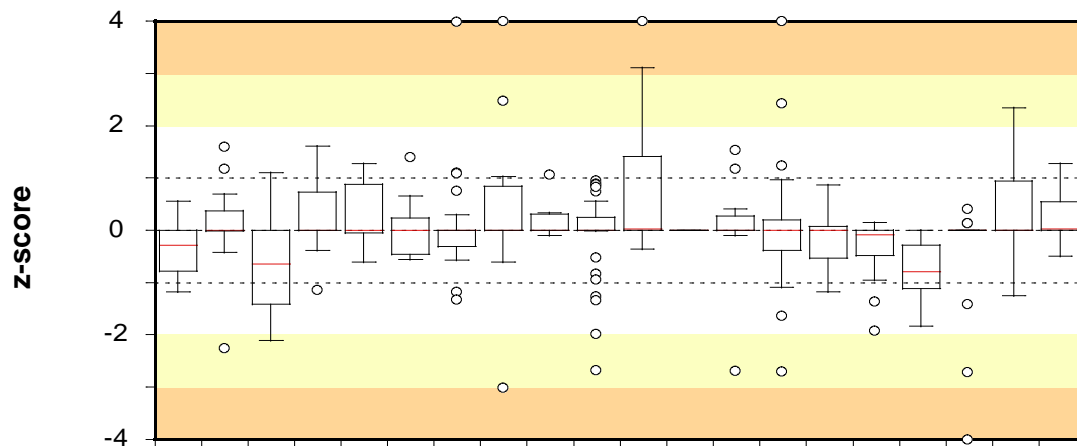
Lab no	1000	1081	1149	1254	1290	1594	1970	2035	2058	2072	2324	2344	2386	2402	2459	2637	2704	2720	2745	2764
No. of results	37	-	17	31	22	24	33	11	18	23	20	26	8	12	13	26	19	-	17	20
False positive	-	-	-	-	-	1	-	-	2	2	2	1	-	1	1	-	-	-	-	-
False negative	-	-	3	1	1	1	1	1	1	1	1	-	-	2	-	3	1	-	-	1
Low outliers	1	-	-	-	-	-	-	-	-	-	4	-	-	-	-	-	1	-	-	-
High outliers	-	-	-	-	-	-	1	-	-	1	-	1	-	1	2	-	-	-	-	-



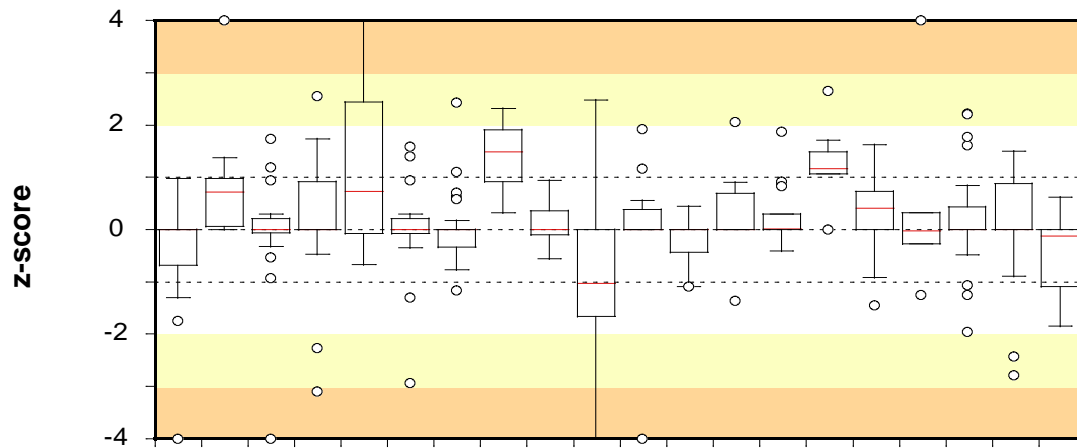
Lab no	2842	2920	2941	3055	3126	3159	3225	3243	3305	3347	3457	3543	3587	3588	3595	3626	3831	3925	4047	4050
No. of results	9	12	14	14	12	24	14	6	27	13	22	17	22	27	24	17	14	4	20	17
False positive	-	-	-	1	-	1	-	-	-	1	-	-	-	1	-	-	1	-	-	-
False negative	3	-	-	-	2	1	1	-	1	1	1	-	1	1	-	-	-	2	-	1
Low outliers	1	-	-	-	-	-	-	2	-	-	-	-	1	-	-	-	-	-	-	-
High outliers	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-



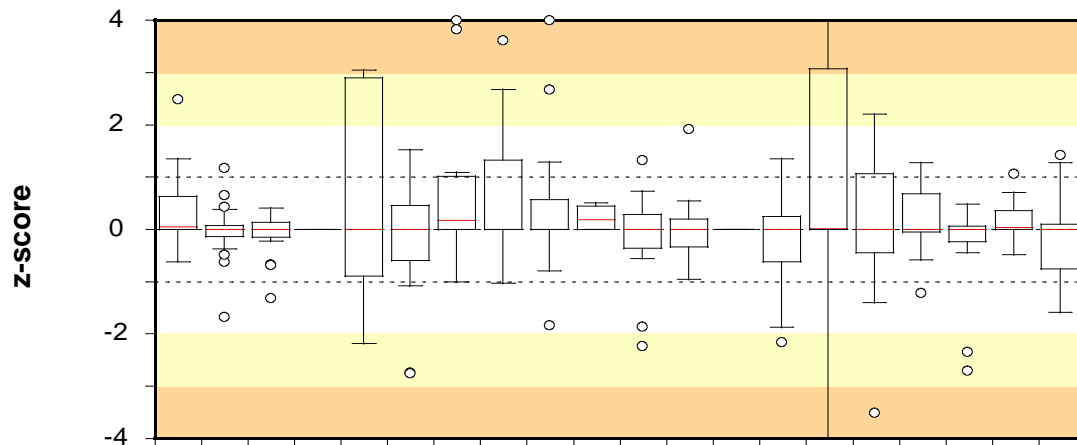
Lab no	4064	4100	4153	4171	4246	4278	4288	4305	4339	4352	4400	4538	4557	4562	4586	4635	4664	4713	4817	4840	
No. of results	6	29	32	20	11	14	25	18	34	22	13	14	7	26	-	22	14	-	20	14	
False positive	-	-	-	-	2	-	1	-	-	1	-	1	-	-	-	-	-	-	-	-	2
False negative	-	3	-	1	1	1	-	1	1	4	2	2	1	-	-	1	3	-	-	-	1
Low outliers	-	-	-	-	-	-	1	-	-	-	1	-	1	-	-	-	-	-	-	-	2
High outliers	-	-	-	-	-	1	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-



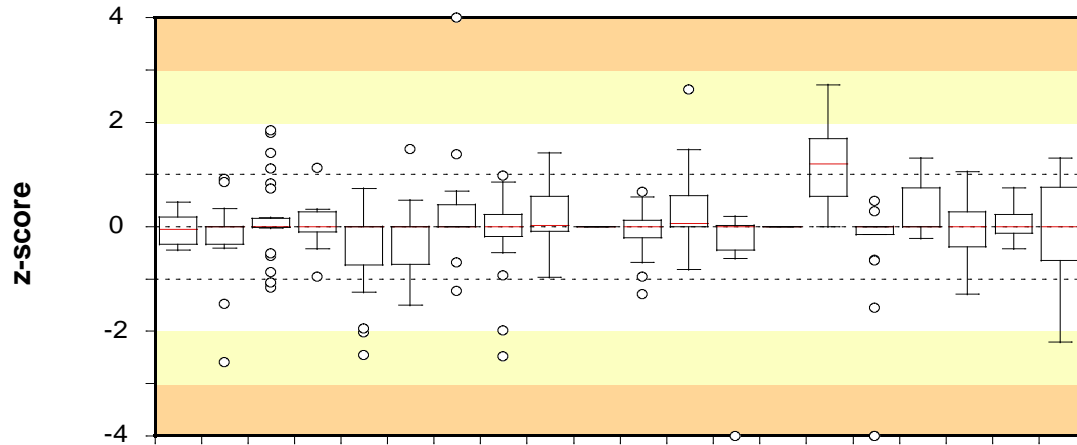
Lab no	4873	4889	4951	4955	4980	4998	5018	5100	5119	5120	5162	5188	5197	5200	5201	5204	5220	5250	5304	5329	
No. of results	12	28	14	29	16	9	27	12	7	33	14	-	15	21	14	27	8	13	17	18	
False positive	-	-	1	-	-	-	-	-	-	1	-	-	1	-	-	-	-	-	-	-	-
False negative	-	1	-	-	1	-	1	3	2	1	1	-	4	1	-	1	1	2	-	-	2
Low outliers	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-
High outliers	-	-	-	-	-	-	1	1	-	-	1	-	-	1	-	-	-	-	-	-	-



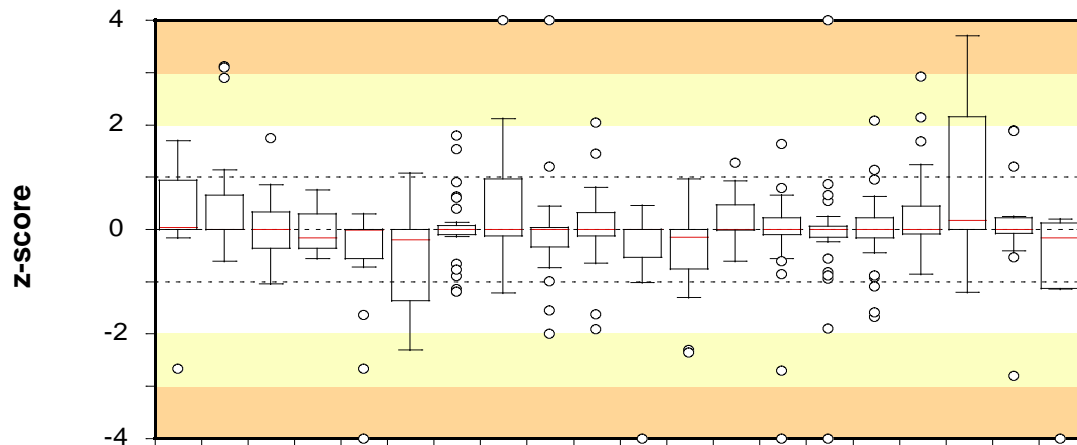
Lab no	5333	5338	5352	5380	5545	5553	5615	5701	5774	5801	5808	5883	5993	6109	6175	6224	6232	6253	6343	6352
No. of results	22	9	22	14	8	16	29	3	6	13	12	23	7	17	9	9	6	23	21	18
False positive	-	-	-	-	-	-	3	-	-	1	-	-	-	-	-	-	-	-	1	2
False negative	1	-	1	-	-	-	5	-	-	1	3	-	2	1	-	-	-	-	1	3
Low outliers	1	-	1	-	-	-	-	-	-	2	2	-	-	-	-	-	-	-	-	-
High outliers	-	1	-	-	1	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-



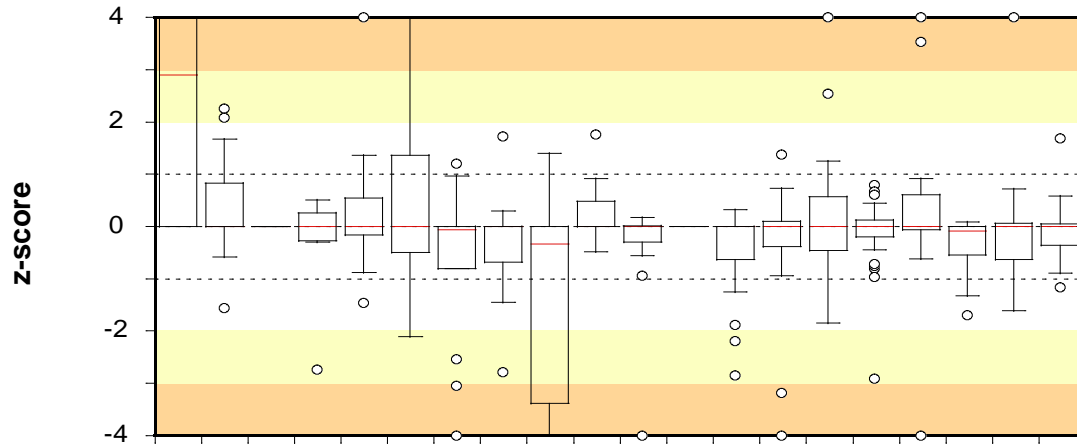
Lab no	6368	6456	6490	6594	6628	6647	6658	6686	6707	6728	6730	6762	6852	6944	6958	6971	7024	7096	7182	7207
No. of results	23	25	20	-	8	12	14	21	29	4	17	9	-	21	13	14	15	15	16	17
False positive	-	-	-	-	-	-	1	1	-	-	2	-	-	2	1	-	-	-	2	-
False negative	3	-	-	-	1	-	-	1	2	1	1	-	-	-	1	1	-	2	-	1
Low outliers	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-
High outliers	-	-	-	-	-	-	2	1	1	-	-	-	-	-	3	-	-	-	-	-



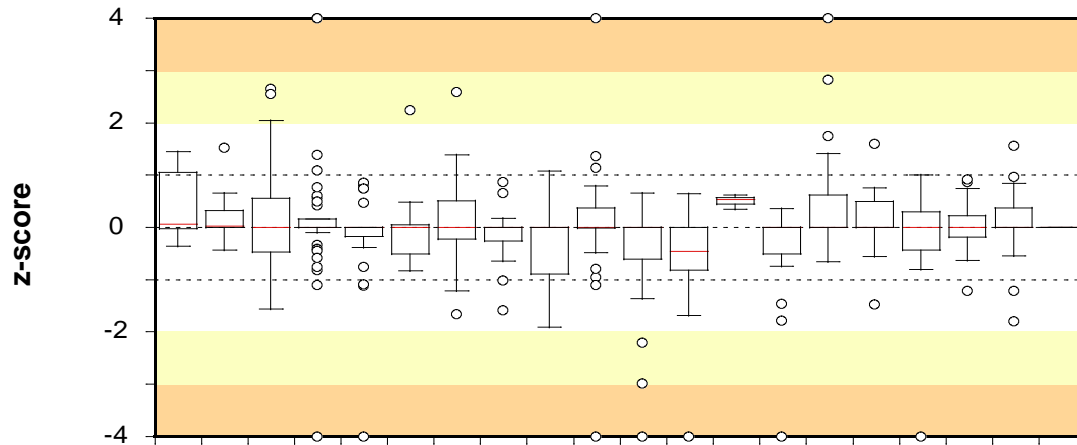
Lab no	7232	7242	7248	7253	7282	7330	7334	7438	7449	7543	7564	7596	7617	7627	7655	7688	7728	7750	7825	7828
No. of results	8	17	28	14	19	22	14	25	12	-	32	21	7	-	6	22	22	16	18	11
False positive	-	1	-	-	-	-	-	-	-	-	1	1	1	-	-	-	-	-	-	1
False negative	1	-	1	-	-	1	2	1	-	-	-	1	-	-	2	1	1	2	2	-
Low outliers	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	2	-	-	-	-
High outliers	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-



Lab no	7876	7906	7930	7940	7962	8066	8068	8105	8180	8255	8260	8313	8333	8352	8380	8397	8428	8430	8435	8523
No. of results	16	16	14	3	20	15	27	11	24	27	25	20	20	25	29	27	26	16	21	8
False positive	3	1	-	-	-	-	-	2	-	-	-	-	-	-	-	1	2	-	2	1
False negative	4	3	1	-	-	2	2	1	2	2	1	3	1	1	-	1	1	4	-	-
Low outliers	-	-	-	-	1	-	-	-	-	-	1	-	-	1	1	-	-	-	-	1
High outliers	-	-	-	-	-	-	-	1	1	-	-	-	-	-	1	-	-	1	-	-



Lab no	8528	8529	8568	8626	8628	8657	8734	8742	8756	8766	8891	8909	8918	8955	8961	9002	9003	9034	9051	9217
No. of results	14	28	-	11	33	12	13	21	18	22	18	-	23	27	15	25	15	12	16	15
False positive	-	-	-	1	-	-	1	1	-	-	-	-	-	-	-	-	1	-	-	-
False negative	1	1	-	-	2	-	1	1	2	1	2	-	3	-	-	1	1	2	1	3
Low outliers	-	-	-	-	-	-	1	-	4	-	1	-	-	1	-	-	1	-	-	-
High outliers	7	-	-	-	1	1	-	-	-	-	-	-	-	-	1	-	1	-	1	-



Lab no	9408	9429	9436	9441	9451	9453	9512	9555	9559	9569	9662	9747	9783	9853	9886	9890	9903	9923	9950
No. of results	12	29	28	37	23	18	11	22	22	35	27	13	3	16	29	22	25	17	13
False positive	-	1	1	-	-	-	-	1	2	-	1	-	-	-	2	-	-	1	-
False negative	-	1	2	-	-	2	1	-	2	-	1	2	-	1	-	1	-	2	2
Low outliers	-	-	-	1	1	-	-	-	-	1	1	1	-	1	-	-	2	-	-
High outliers	-	-	-	2	-	-	-	-	-	1	-	-	-	-	1	-	-	-	-



## Test material and quality control

### Test material

Each laboratory received three freeze-dried microbial mixtures designated A-C. The manufactured test material was freeze-dried in portions of 0.5 ml in vials, as described by Peterz and Steneryd (3). Before analysing the samples, the contents of each vial had to be dissolved in 254 ml of diluent. The organisms present in the mixtures are listed in Table 2.

**Table 2.** *Microorganisms present in mixture A-C supplied to participants*

Mixture <sup>1</sup>	Microorganism	Strain no.
A	<i>Pseudomonas aeruginosa</i>	SLV- 429
	<i>Staphylococcus aureus</i>	SLV- 280
	<i>Lactobacillus plantarum</i>	SLV- 475
	<i>Clostridium perfringens</i>	SLV- 442
	<i>Candida glabrata</i>	SLV- 052
	<i>Cladosporium cladosporioides</i>	SLV- 488
B	<i>Enterobacter cloacae</i>	SLV- 011
	<i>Bacillus cereus</i>	SLV- 516
	<i>Shewanella putrefaciens</i>	SLV- 520
	<i>Staphylococcus hyicus</i>	SLV- 546
	<i>Carnobacterium piscicola</i>	SLV- 519
	<i>Clostridium bifermentas</i>	SLV- 009
	<i>Zygosaccharomyces ruoxii</i>	SLV- 434
	<i>Penicillium roquefortii</i>	SLV- 510
C	<i>Staphylococcus saprophyticus</i>	SLV- 013
	<i>Escherichia coli</i>	SLV- 295
	<i>Bacillus thuringiensis</i>	SLV- 564
	<i>Shewanella putrefaciens</i>	SLV- 520

<sup>1</sup>The links between the mixtures and the randomised sample numbers are shown in annex 1

### Quality control of the mixtures

It is essential to have aliquots of homogeneous mixture and equal volume in all vials in order to allow comparison of all freeze-dried samples from one mixture. Quality control was performed in conjunction with manufacturing of the mixtures according to Scheme Protocol (2). The results are presented in Table 3. Homogeneity requires that the standard deviation and the difference between the highest and lowest value of results from 10 samples analysed do not exceed 0.15 log<sub>10</sub> units and 0.5 log<sub>10</sub> units, respectively.

**Table 3.** Concentration mean (*m*) and standard deviation (*s*) from analyses of 10 randomly selected vials per mixture, expressed in log<sub>10</sub> cfu (colony forming units) per ml of sample.

Analysis and method	A		B		C	
	m	s	m	s	m	s
Aerobic microorganisms, 30 °C NMKL method no. 86	4.76	0.06	4.69	0.07	4.52	0.10
Psychotrophic microorganisms NMKL method no. 83	2,40	0,13	4.52	0.07	-	-
Enterobacteriaceae NMKL method no. 144	-	-	3.74	0.08	3.20	0.05
<i>Escherichia coli</i> NMKL method no. 125	-	-	-	-	3.22	0.06
Presumptive <i>Bacillus cereus</i> NMKL method no. 67	-	-	3.73	0.05	3.26	0.09
Coagulase-positive staphylococci NMKL method no. 66	3.91	0.03	4.00*	0.03*	-	-
Lactic acid bacteria NMKL method no. 140	4.14	0.05	4.39	0.08	-	-
<i>Clostridium perfringens</i> NMKL method no. 95	2.57	0.08			-	-
Anaerobic sulphite-reducing bacteria NMKL method no. 56	2.80	0.05	3.76	0.06	-	-
Aerobic microorganisms in fish products NMKL method no. 184. JA	4.77	0.06	4.72	0.07	4.52	0.08
H <sub>2</sub> S-producing bacteria in fish products NMKL method no 184. JA	-	-	1.57	0.11	2.23	0.08
Yeasts NMKL method no. 98. DG18	2.35	0.10	2.57	0.09	-	-
Moulds NMKL method no. 98. DG18	2.58	0.06	2.40	0.14	-	-

- No target organism

\* Count of colonies without precipitation halo on BP+RPF

## References

1. Kelly. K. 1990. Outlier detection in collaborative studies. *J. Assoc. Off. Anal. Chem.* 73:58-64.
2. Anonymous. 2012. Protocol. Microbiology. Drinking Water & Food. The National Food Agency.
3. Peterz. M. Steneryd. A.C. 1993. Freeze-dried mixed cultures as reference samples in quantitative and qualitative microbiological examinations of food. *J. Appl. Bacteriol.* 74:143-148.





Lab n°	Vial	Aerobic microorganisms 30°C			Psychotrophic microorganisms			Enterobacteriaceae			Escherichia coli			Presumptive Bacillus cereus			Coagulase-positive staphylococci			Lactic acid bacteria			Clostridium perfringens			Anaerobic sulphite-reducing bacteria			Aerobic m.o. in fish products, 20-25°C			H <sub>2</sub> S producing bacteria			Yeasts			Moulds			Lab n°			
		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							
6628	2 1 3	4.41	4.27	4.37	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3.37	0	0	3.14	3.07	0	6628			
6647	3 1 2	4.71	4.64	4.64	-	-	-	-	-	-	<0.48	<0.48	2.66	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2.61	0.98	<1	1.54	2.6	<1	6647		
6658	3 2 1	4.72	4.84	4.61	-	-	-	3.6	4.31	3	-	-	-	<1	3.56	3.2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3.62	1.6	<1	2.6	2.08	<1	6658			
6686	3 1 2	-	-	-	-	-	-	<1	3.52	3.11	<1	<1	3.08	-	-	-	3.89	<1	<1	-	-	-	2.77	3.82	<1	-	-	-	4.57	4.68	4.74	<1	2	<1	3.26	2.3	<1	3.3	2.7	<1	6686			
6707	2 3 1	4.3	4.62	4.48	-	-	-	0	3.69	3.23	0	0	4.48	0	3.72	3.3	3.94	0	0	-	-	-	2.78	-	0	2.51	3.59	0	4.48	4.62	4.48	0	1.7	2.04	3.26	0	0	0	1.9	0	6707			
6728	3 2 1	-	4.75	4.65	-	-	-	-	-	-	<1	<1	<1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	6728			
6730	3 2 1	4.69	4.71	4.39	-	-	-	-	-	-	<1	4	3	<1	3.43	3	3.78	<1	<1	4	4.60	3	-	-	-	-	-	-	-	-	-	-	-	-	-	2	0	0.00	2.20	3	0	6730		
6762	2 1 3	4.63	4.60	4.28	-	-	-	<1	4	3.32	<1	<1	3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	6762		
6852	2 3 1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	6852		
6944	2 3 1	-	-	-	-	-	-	-	-	-	<1	4	3.32	<1	3.72	3.32	3.76	<1	<1	4.18	4.38	4.9	-	-	-	-	-	4.2	4.43	4.46	<1	1.3	1.11	2.23	1.9	<1	2.41	1.3	<1	6944				
6958	1 2 3	4.6	4.78	5.4	-	-	-	<1	5.18	3.6	<1	<1	3	<1	4.52	1.85	<1	<1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2.04	<1	3.8	2.3	2.11	<1	6958			
6971	3 1 2	4.95	4.92	5.16	-	-	-	0	3.83	3.06	-	-	-	0	3.18	3.07	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2.2	1.3	0	0	1.48	0	6971		
7024	1 2 3	4.6	4.84	4.81	-	-	-	<1	3.86	3.14	<1	<1	2.9	<1	3.7	3.4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2.44	1.23	<1	2.23	1.55	<1	7024		
7096	1 3 2	4.67	4.68	4.47	-	-	-	<1	3.69	2.77	<1	<1	3.18	-	-	-	3.81	<1	<1	-	-	-	-	-	-	-	4.17	4.52	4.31	<1	<1	<1	-	-	-	-	-	-	-	-	-	-	7096	
7182	2 3 1	4.77	4.67	4.47	-	-	-	<1	3.71	3.13	<1	3.6	3.07	-	-	-	-	-	-	4.22	4.55	4.4	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2.28	1.63	<1	2.41	2.02	<1	7182	
7207	1 2 3	4.34	4.54	4.9	-	-	-	<1	3.56	2.93	-	-	-	<1	3.71	3.18	-	-	-	4.32	<1	<1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2.15	1	<1	2.41	2.56	<1	7207	
7232	2 1 3	4.58	4.6	4.65	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2.29	<1	<1	2.43	1.89	<1	7232		
7242	2 3 1	4.53	4.62	4.61	-	-	-	-	0	3.62	3.2	-	-	0	3.77	3.37	-	-	-	-	-	-	2.74	2.3	0	-	-	-	-	-	-	-	-	-	-	-	2.38	0.78	0	1.59	1.86	0	7242	
7248	2 3 1	4.42	4.56	4.54	-	-	-	-	0	3.5	3.26	0	0	3.13	0	3.84	3.34	3.77	0	0	3.91	4.27	0	0	0	2.77	4.11	0	-	-	-	-	-	-	-	-	2.1	2.46	0	2.32	2.44	0	7248	
7253	1 2 3	4.58	4.71	4.28	-	-	-	<1	3.61	3.08	-	-	-	-	-	-	3.85	<1	<1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2.42	1.67	<1	2.61	2.05	<1	7253	
7282	2 3 1	4.27	4.69	4.68	-	-	-	<1	3.31	2.86	<1	<1	2.9	<2	3.63	3.34	3.76	<2	<2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2.17	1.6	<1	-	1.77	<1	7282	
7330	3 2 1	4.48	4.75	4.96	-	-	-	<1	3.55	2.92	<1	<1	2.86	<2	3.65	3.23	3.8	<2	<2	4.12	<2	<2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2.38	1.12	<1	2.23	1.74	<1	7330	
7334	3 1 2	5.46	4.44	4.56	-	-	-	-	-	-	<1	<1	>1	-	-	-	3.95	<1	<1	-	-	-	-	-	-	2.92	3.81	<1	-	-	-	-	-	-	-	-	2.22	0	<1	<1	2.03	<1	7334	
7438	2 1 3	4.56	4.57	4.65	-	-	-	<1	3.79	3.07	<1	<1	3.03	<1	3.75	3.37	3.63	<1	<1	-	-	-	-	-	2.2	<1	<1	2.47	3.89	<1	-	-	-	-	-	-	2.37	<1	<1	2.44	2.39	<1	7438	
7449	2 3 1	4.72	4.73	4.78	-	-	-	<1	3.53	3.26	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2.38	1.15	0	2.4	2.04	0	7449	
7543	1 2 3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7543	
7564	1 3 2	4.51	4.69	4.36	<0	4.48	<0	<1	3.69	3.15	<1	<1	3	<1	3.61	3.11	-	-	-	4.04	4.57	<2	2.82	3.64	<0	2.79	3.51	<0	4.67	-	4.36	<0	0	0.78	2.36	1.59	<0	2.36	1.96	<0	7564			
7596	3 1 2	4.67	4.67	4.32	-	-	-	0	3.76	3.13	0	0	0	4.2	3.83	3.23	3.85	0	0	-	-	-	-	-	3.14	3.91	0	4.7	4.54	4.36	0	1.43	2.72	-	-	-	-	-	-	-	-	-	7596	
7617	1 2 3	4.55	4.55	4.6	-	-	-	<1	3.8	3.11	<1	<1	3.11	-	-	-	2.97	3.5	<1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7617	
7627	2 1 3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7627
7655	1 2 3	4.85	>6.8	4.78	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	4.86	<6	4.62	<1	2.56	<1	7655	
7688	3 2 1	-	-	-	-	-	-	-	-	-	<1	<1	3	<1	3.76	3.28	3.81	<1	<1	3.15	3.56	<1	2.61	<1	<1	2.72	2.52	<1	-	-	-	-	-	-	-	2.42	<1	<1	2.27	1.96	<1	7688		
7728	3 2 1	4.81	4.82	4.89	-	-	-	0	0	3.29	0	0	3.29	0	3.86	3.1	3.81	0	0	-	-	-	2.81	0	0	2.71	3.88	0	-	-	-	-	-	-	-	-	2.6	0	0	2.26	2.04	0	7728	
7750	2 3 1	4.65	4.7	4.19	-	-	-	<1	3.73	3.02	-	-	-	<1	3.73	3.42	-	-	-	4.23	<3	<3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2.2	0	0	2.25	1.73	0	7750	
7825	2 1 3	4.61	4.78	4.51	-	-	-	<1	3.76	3.08	<1	<1	3.14	-	-	-	3.89	<1	<1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2.35	<1	<1	2.46	1.97	<1	7825	
7828	2 3 1	4.81	4.75	4.36	-	-	-	4.08	3.4	3.21	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2.24	2.1	<1	1.69	2.11	<1	7828		
7876	3 1 2	4.76	4.96	4.5	-	-	-	3.41	<1	3.11	<1	<1	3.21	3.7	<1	3.38	<2	3.87	<2	-	-	-	<1	2.74	<1	-	-	-	-	-	-	-	-	-	-	1.6	2.3	<1	2.32	2.4	<1	7876		
7906	2 1 3	4.6	4.6	4.5	-	-	-	<1	3.7	3.1	<1	<1	<1	3.6	<1	3	<1	<1	<1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3.4	2.1	0	3.1	3.2	0	7906		
7930	2 1 3	4.53	4.81	-	-	-	-	<1	3.79	-	<1	<1	-	<1	3.98	-	3.85	<1	-	-	-	2.52	<1	-	-	-	-	-	-	-	-	-	-	-	-	2.32	<1	-	2.29	1.71	-	7930		
7940	3 2 1	4.72	4.63	4.39	-	-	-	<1	3.79	-	<1	<1	-	<1	3.98	-	3.85	<1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	7940
7962	3 2 1	4.57	4.63	4.41	-	-	-	<1	3.58	3.09	<1	<1	3.15	<1	3	2.48	3.84	<1	<1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2.33	0.7	0	2.1	2.06			









Lab n°	vial	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 m.o. in fish products, 20-25°C			H2S producing bacteria			Yeasts			Moulds			Lab n°	
		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					
6343	2 1 3	0.823	1.358	1.278							0	0		0	-2.780	-2.429	1.074	0					0.073	0	-0.896	0.107	0						1.259	0.884	0	-0.722	1.504	0	6343			
6352	3 2 1	-1.341	-1.676	-0.921				0	-1.840		0	0	-0.013	0	-0.745	-1.402		0					-0.953	0				0.752	1.100	1.349	0			-0.222	0	-1.084	0.616	0	6352			
6368	2 1 3	0.514	0.122	1.133				0	2.490	-0.156	0	0	0.049				0.020	0	-0.612	0.472	0												-0.415	0	0.148	1.086	0	6368				
6456	3 1 2	0.081	-1.676	-0.272				0	-0.623	-0.096	0	0	-0.137		0	-0.483	0.654	1.180	0				0.386	0	0.253	-0.076	0					-0.222	-0.364	0	0.438	0.250	0	6456				
6490	2 1 3	0.081	-0.664	-1.317				0	-0.014	0.240				0	-0.680	-0.216	0.125	0							0.145	-0.076	0						-0.222	0.329	0	0.256	0.407	0	6490			
6594	3 1 2																																						6594			
6628	2 1 3	-1.156	-2.181	-0.633																														3.030	0	3.046	2.759	0	6628			
6647	3 1 2	0.699	-0.103	0.341							0	0	-2.739																				0.583	-1.077	0	-2.751	1.530	0	6647			
6658	3 2 1	0.761	1.021	0.232					4.000	-0.769				0	-1.008	0.179																		3.835	0.151	0	1.090	0.172	0	6658		
6686	3 1 2										0	-1.029	0.156				0.758	0					0.073	0			-0.005	1.398	0.985	0	1.327		2.676	1.537	0	3.626	1.792	0	6686			
6707	2 3 1	-1.836	-0.215	-0.236					0	0.122	1.165			0	0.042	0.575	1.285	0					0.118	0	-0.788	-0.580	0	-0.530	0.802	0.125	0	0.586	1.255	2.676	0		-0.299	0	6707			
6728	3 2 1		0.515	0.377							0	0																												6728		
6730	3 2 1	0.576	0.291	-0.561							0	0	0.483		0	-1.861	-2.232	-0.402	0	-0.106	0.735																-0.351	0	-0.360	1.321	0	6730
6762	2 1 3	0.205	-0.327	-0.957					0	-0.352	1.921			0	0	0.545																									6762	
6852	2 3 1																																								6852	
6944	2 3 1										0	1.351		0	0.042	0.654	-0.613	0	0.501	0.253							-2.161	-1.086	0.059	0	-0.403	-0.624			-0.640	0.745	0	0.401	-1.866	0	6944	
6958	1 2 3	0.019	0.684	3.080					4.000	4.000				0	4.000	-4.000																									6958	
6971	3 1 2	2.184	1.470	2.215					0	1.069	-0.264																														6971	
7024	1 2 3	0.019	1.021	0.953					0	0.122	0.408						0.272	0																							7024	
7096	1 3 2	0.452	0.122	-0.272					0	0.122	-2.702			0	0	0.483												-2.336	-0.192	-0.437	0											7096
7182	2 3 1	1.071	0.066	-0.272					0	0.257	0.324			0	-0.199				0.704	0.625																					7182	
7207	1 2 3	-1.589	-0.664	1.278					0	-0.758	-1.357								1.210																						7207	
7232	2 1 3	-0.105	-0.327	0.377																																					7232	
7242	2 3 1	-0.408	-0.198	0.214					0	-0.332	0.913			0	0.351	0.859							-0.043	0			-0.158	-1.477	0						-2.588	-0.403	0			7242		
7248	2 3 1	-1.094	-0.552	-0.020					0	-1.164	1.417			0	0.830	0.733	-0.507	0	-0.865	0.012	0			0	0	0.145	1.802	0												7248		
7253	1 2 3	-0.105	0.291	-0.957					0	-0.420	-0.096						0.336	0																							7253	
7282	2 3 1	-2.022	0.178	0.485					0	-2.449	-1.946			0	-1.252	0	-0.549	0.733	-0.613	0																					7282	
7330	3 2 1	-0.723	0.515	1.494					0	-0.826	-1.441			0	-1.500	0	-0.417	0.298	-0.191	0	0.197	0																			7330	
7334	3 1 2	4.000	-1.226	0.052													1.391	0								0.683	0.428	0													7334	
7438	2 1 3	-0.228	-0.496	0.377					0	0.799	-0.180			0	0	-0.446	0	0.239	0.851	-1.983	0		-2.471	0	0	-0.932	0.794	0													7438	
7449	2 3 1	0.761	0.403	0.845					0	-0.961	1.417																															7449
7543	1 2 3																																									7543
7564	1 3 2	-0.537	0.178	-0.669	-0.120	0			0	0.122	0.492			0	0	-0.632	0	-0.680	-0.176					0.296	0	0.217	-0.946	0	0.577		-0.272	0		-1.291	-0.222	0.131	0	0.220	-0.142	0	7564	
7596	3 1 2	0.452	0.066	-0.813					0	0.596	0.324						0.764	0.298	0.336	0						1.473	0.886	0	0.752	0.007	-0.272	0	-0.082	2.629								7596
7617	1 2 3	-0.290	-0.608	0.196						0	0.049						-4.000	0																								7617
7627	2 1 3																																									7627
7655	1 2 3	1.565		0.845																								1.685		0.588	0	2.712										7655
7688	3 2 1																																									7688
7728	3 2 1	1.318	0.909	1.242					0	0	-0.632			0	0.305	0.496	-0.086	0	-4.000	-1.543	0		-0.641	0	0	-0.035	-4.000	0													7728	
7750	2 3 1	0.328	0.234	-1.281					0	0.393	-0.601			0	0.108	1.049									0.252	0	0	-0.070	0.749	0												7750
7825	2 1 3	0.100	0.695	-0.139					0	0.616	-0.122			0	0	0.242		0.748	0	-0.425	0																					7825
7828	2 3 1	1.318	0.515	-0.669						-1.840	0.997																															7828
7876	3 1 2	1.009	1.695	-0.164						0.156				0	0	0.669		0.891																								7876
7906	2 1 3	0.019	-0.327	-0.164					0	0.190	0.072			0	0																											7906
7930	2 1 3	-0.414	0.852						0	0.799				0	1.749		0.336							-1.043	0																	7930
7940	3 2 1	0.761	-0.159	-0.561																																						7940
7962	3 2 1	-0.166	-0.159	-0.488					0	-0.623	-0.012			0	0	0.297		-4.000	-2.666	0.231	0																					7962
8066	3 2 1								0	-0.352	1.081			0	0													-1.579	-0.887	-1.529	0	-1.194	-0.200									8066
8068	3 1 2	0.143	0.403	-0.020					0	1.543	-1.189			0	-0.137		0	0.633	-0.88																							



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

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

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

### **The National Food Agency's PT program offers**

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

For more information visit our website: [www.slv.se/absint](http://www.slv.se/absint)



### **The National Food Agency's reference material**

As a complement to the proficiency testing, National Food Agency produces also reference material (RM) for internal quality control: a total of 8 RM for food and drinking water microbiological analyses, including pathogens, are available.

Information available on our website: [www.slv.se/RM-micro](http://www.slv.se/RM-micro)