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**AFNOR VALIDATION certification of the CFB broth
(Reference 42642/42643) / CampyFood Agar (CFA)
(Reference 43471) method for the detection of
Campylobacter spp.**

*Comparative and interlaboratory studies according to the
EN ISO 16140 standard*

SUMMARY REPORT

Certificate number :	BIO 12/30 – 05/10
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CFB broth / CampyFood Agar CFA - summary 2010 v01

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1 Introduction

1.1 Validation references

The CFB broth / CampyFood Agar (CFA) method was validated in May 2010 according to the reference method EN ISO 16140:2003, with respect to the reference method EN ISO 10272-1:2006, for poultry products, other meat products and for environmental samples.

1.2 Protocol and principle of the alternative method

1.2.1 Protocol

The diagram summarising the method is shown in Appendix A.

The method consists of :

- an enrichment in CampyFood broth (CFB), in Combibag with a microaerobic atmosphere generator, incubated for **48h ± 4h at 41.5°C +/- 1°C** ,
- followed by inoculation with a 10 µl sterile loop a specific CampyFood Agar (or CFA), incubated for **44h ± 4h at 41.5°C ± 1°C** in a microaerobic atmosphere.

The incubation of CFB (bioMérieux reference 42642/42643) in microaerophilic atmosphere is achieved in Combibag (bioMérieux, reference 30551) provided with GENbox microaer atmosphere generator (bioMérieux, reference 96125, 1 generator by bag) closed by a clip seal provided in the kit.

Note 1: CFB have to be pre-heated at room temperature before use.

Note 2: The time between opening the GENbox bag and closing the Combibag must not exceed 30 seconds.

Characteristic colonies on CFA have to be confirmed by :

- Conventional tests described in the standardized methods : purification on Columbia blood agar, then examination of morphology and motility, microaerobic growth at 25°C, aerobic growth at 41,5 °C, detect ion of oxidase activity,
- Realization of VIDAS CAM test from 1 to 5 characteristic isolate or not colonies, after resuspension of the colony in 2 ml tryptone saltdfqsd,df,
- Simplified conventional tests : inoculation of a Columbia blood agar followed by incubation, for 48 to 72 hours at 41.5°C in a microaerobic atmosphere, and streaking on a Columbia blood agar followed by incubation for 48 to 72 hours at 41.5°C in an aerobic atmosphere (inoculation of a maximum of 5 streaks of colonies maximum per plate). The microscopic examination of morphology and motility, and detection of oxidase activity are performed only on strict microaerobic colonies.

Note : Before 48 hours of incubation, colonies are not big enough for confirmations. All confirmations were done from 48 hours isolated colonies.

1.2.2 Principle of the alternative method

The CampyFood Agar contains specific activators facilitating the growth of *Campylobacter*, a selective mixture allowing the inhibition of most of the contaminants and a colored indicator that facilitates the reading. The characteristic colonies seem red orange-coloured in red Bordeaux, with sometimes a metallic reflection.

Note: the metallic reflection remains a criterion of orientation, the other microorganisms can also present this characteristic.

Sometimes, the colonies of *Campylobacter* can present a tint going from pink-red to dark brown, or spread out and to present a dark red-orange-coloured center, a suburb of granular aspect and irregular edges.

1.3 Application scope

- Fresh and frozen raw meats of poultry and preparations with poultry,
- Other raw fresh and frozen meats (eg. pork, beef) and preparations with these products,
- Samples of production environment.

1.4 Reference method

The validation study was carried out by EN ISO Standard 10272-1 :2006: « Microbiology of food and animal feeding stuffs. Horizontal method for detection and enumeration of *Campylobacter* spp. Part 1: Detection method" #

The incubation of Bolton broth is carried out in anaerobic jar with the microaerobic atmosphere generator, GENbox microaer. The diagram of the method is shown in Appendix A.

1.5 Background of certification

Initial validation.

2 Comparative study of methods

2.1 Relative accuracy, relative specificity and relative sensitivity

The aim of the study, according to the reference document EN ISO 16140, is to compare the performances of the two methods :

- the reference method EN ISO 10272-1 :2006 and,
- the CFB – CFA method,

on naturally contaminated or spiked samples and uncontaminated samples.

2.1.1 Number and nature of the samples

According to the EN ISO 16140 standard, a minimum of 60 products per category must be analysed, with around 50% of positive products (at least 30 results) and 50% of negative products.

Each category was divided into various types and the overall results are displayed in the following tables :

Category	Types	Positive*	Negative	Total
Products with poultry	Raw, frozen	15	14	29
	Preparations with poultry, raw or cooked	4	10	14
	Rinsed carcass	8	0	8
	Skin of poultry neck	9	4	13
	Total		36	28
Other meat products	Raw meat	20	27	47
	Raw flavored meats	7	12	19
	Ready-made meal	6	10	16
	Total	33	49	82
Environment	Various waters	8	11	19
	Surface samples	13	12	25
	Residues and scraps	9	9	18
	Total	30	32	62
TOTAL		99	109	208

*these are positive results by either one or two methods

2.1.2 Artificial contamination of the samples and percentage

Artificial contamination was achieved by using stressed bacterial suspensions, the stress treatment and efficiency of which have been determined according to EN ISO 16140 and AFNOR validation rules.

Fifty five samples were positive for *Campylobacter* spp after artificial contamination out of a total of 99 positive.

Overall, 55.5% of the positive results were due to artificial contamination.

2.1.3 Results of assays

The analyses were performed in single using the two methods. Individual results are shown in Appendix B.

- **Case 1 : confirmation with the VIDAS CAM test**
- **Case 2 : confirmation with conventional tests of the EN ISO 10272-1 method or with the simplified conventional tests.**

The overall results are shown in the summary table below :

Case1 : CFA + VIDAS CAM Confirmation			
And			
Case2 : CFB – CFA confirmed by conventional simplified or not tests			
	Positive reference method (R+)	Negative reference method (R-)	Total
Positive alternative method (A+)	83	14	97
Negative alternative method (A-)	2*	109*	111
Total	85	123	208

Legend :
 A+ = positive confirmed
 A- = immediate negatives **and** negatives after confirmation when presumed positive
 *Including 2 non-confirmed results (G11 et G12)

Identical results were found using both confirmation methods.

The results for each of the sample categories are presented below :

<u>Products with poultry (64)</u>	Positive reference method (R+)	Negative reference method (R-)
Positive alternative method (A+)	Positive agreement (A+/R+) PA = 31	Positive deviation (R-/A+) PD = 5
Negative alternative method (A-)	Negative deviation (A-/R+) ND = 0	Negative agreement (A-/R-) NA = 28

<u>Other meat products (82)</u>	Positive reference method (R+)	Negative reference method (R-)
Positive alternative method (A+)	Positive agreement (A+/R+) PA = 28	Positive deviation (R-/A+) PD = 4
Negative alternative method (A-)	Negative deviation (A-/R+) ND = 1	Negative agreement (A-/R-) NA = 49

<u>Environment (62)</u>	Positive reference method (R+)	Negative reference method (R-)
Positive alternative method (A+)	Positive agreement (A+/R+) PA = 24	Positive deviation (R-/A+) PD = 5
Negative alternative method (A-)	Negative deviation (A-/R+) ND = 1	Negative agreement (A-/R-) NA = 32

2.1.4 Calculation of relative accuracy (AC), relative specificity (SP) and relative sensitivity (SE)

All previous results were used to calculate the relative accuracy, relative sensitivity and relative specificity for each category, according to the EN ISO 16140 standard.

The results obtained with CFA + VIDAS CAM (case 1) confirmations or CFA + conventional methods (case 2) are summarised in the table below :

Category	PA	NA	ND	PD	Sum N	Relative accuracy AC (%) [100x(PA+NA)]/N	N+ PA + ND	Relative sensitivity SE (%) [100xPA]/N+	N- NA + PD	Relative specificity SP (%) [100xNA]/N-
Poultry products	31	28	0	5	64	92.2	31	100	33	84.8
Other meat product	28	49	1	4	82	93.9	29	96.6	53	92.5
Environmental samples	24	32	1	5	62	90.3	25	96.0	37	86.5
TOTAL	83	109	2	14	208	92.3	85	97.6	123	88.6

The percentage values of the alternative method calculated for the following three criteria according to the EN ISO 16140 standard were :

	Case 1 or Case 2
Relative accuracy : AC	92.3%
Relative specificity : SP	88.6%
Relative sensitivity : SE	97.6%

The AFNOR technical committee asks the sensitivity of both methods to be calculated with consideration of all the confirmed positives (this includes the additional positives of the alternative method) :

	Alternative method: (PA + PD) / (PA + PD + ND)	Reference method: (PA + ND) / (PA + PD + ND)
Case 1 or Case 2	98.0	85.9

2.1.5 Analysis of discrepant results

2.1.5.1 Statistic test

According to Annex F of the EN ISO 16140 standard, the minimum number of discordances for which a statistical test must be conducted in order to compare the two methods is 6.

As the number of discordances is between 6 and 22, the aim is then to determine the M value, according to the EN ISO 16140 (Appendix F) and to compare it to the m-value, defined as the smallest values between PD and ND. Both methods are considered as equivalent if $m > M$.

In this study, 16 results were discordant between both methods whatever the confirmation option. A statistic test (binomial law) was performed.

	Additional positive results confirmed with the alternative method	False negative results obtained with the alternative method
Case 1 : CFA + VIDAS CAM confirmation	14	2
Case 2 : CFA + conventional simplified or not tests confirmation	14	2

	Number of discordances	M	m	Conclusion
Case 1 : CFA + VIDAS CAM confirmation	16	3	2	No equivalence
Case 2 : CFA + conventional simplified or not tests confirmation	16	3	2	No equivalence

The performances of the alternative method and of the reference method are considered as no equivalent ($p < 0.05$), whatever the confirmation option. However this result is explained by a significant number of additional positive results obtained by the alternative method (PD = 14).

2.1.5.2 Conclusion

The alternative method detected 97 confirmed positive versus 85 by the reference method.

The CFB associated with the Combibag system allowed a better enrichment of *Campylobacter* spp. compared to the Bolton broth of the reference method and the CFA allowed a better recovery of *Campylobacter* spp than the selective media of the reference method.

Finally, both methods were not considered statistically equivalent.

However, the alternative method performed better than the reference method with 14 additional positives and 2 false negatives.

2.1.6 Comments on confirmations

The characteristic colonies were confirmed :

- Without a purification step, 1 to 5 characteristic colonies, isolated or not, were tested by the VIDAS CAM test to confirm the presence of *Campylobacter* spp.

And

- From isolated colonies, by the tests described in the ISO method, in the cases where the colonies were not isolated, purification steps were undertaken.

It was noted that a minimum of 48 h incubation of Columbia blood agar plates were required prior confirmation, in order to produce sufficient size colonies.

2.2 Relative detection level

The objective was to determine the level of contamination that can be detected in the sample in 50% occasions by the alternative and reference methods.

Three different « food matrix/strain » associations were studied in parallel with the reference method and the CFB/CFA alternative method.

The artificial contaminations were carried out according to EN ISO 16140 and the AFNOR rules.

The levels of detection, calculated according to the Spearman – Kärber⁽¹⁾ method (LOD₅₀), obtained for each combination “matrix-strain” are the following:

Matrix	Strain	Relative detection level(CFU/ 25 g or 25 ml) with confidence interval ⁽²⁾ LOD ₅₀	
		Reference method	Alternative method
Poultry meat	<i>Campylobacter jejuni</i>	0.9 [0.3 – 2.4]	0.7 [0.3 – 1.8]
Pork	<i>Campylobacter jejuni</i>	0.9 [0.4 – 1.8]	0.9 [0.4 – 1.8]
Process water	<i>Campylobacter coli</i>	0.3 [0.2 – 0.4]	0.3 [0.2 – 0.4]

⁽¹⁾Hitchins A. *Proposed Use of a 50% Limit of Detection Value in Defining Uncertainty Limits in the Validation of Presence-Absence Microbial Detection Methods*, Draft 10th December, 2003.

⁽²⁾ LOD₅₀: estimation of level of contamination enabling positive detection by alternative method in 50 % of cases

The level of detection obtained for the CFB / CFA method was between 0.2 and 1.8 CFU/ 25 g, compared with 0.2 to 2.4 CFU/ 25 g for the reference method.

2.3 Inclusivity / exclusivity

The inclusivity and the exclusivity of the alternative method were determined using 50 positive strains and 30 negative strains, respectively.

2.3.1 Protocols

Protocol for inclusivity

Each *Campylobacter* strain was prepared and incubated in CFB for 48 hours at 41.5°C in microaerobic atmosphere. Then, a new CFB was inoculated with around 10 to 100 *Campylobacter* per 225 ml and incubated for 48 hours at 41.5°C in a microaerobic atmosphere. Ten microliters were then used to inoculate CFA which was incubated for 44 h +/- 4h at 41.5°C in microaerobic atmosphere.

Protocol for exclusivity

The pure negative strains were inoculated at a level of around 10⁵ CFU/ ml in a nutrient broth which was incubated in aerobic atmosphere for 24 h at 37°C. Ten microliters were then used to inoculate CFA which was incubated for 44 h +/- 4h at 41.5°C in microaerobic atmosphere.

Note : *C. fetus* is part of the *Campylobacter* genus, but does not grow at 41.5°C.

The protocol for *Campylobacter fetus* strains was the same as the one used to study inclusivity, but all incubation temperatures were 25°C instead of 41.5°C.

2.3.2 Results and conclusion

The results are presented in Appendix C.

All the 50 strains of *Campylobacter* tested (*C. coli*, *C. jejuni*, *C. upsaliensis*, *C. lari*), produced characteristic colonies on CFA : red orange-coloured in Bordeaux, with sometimes a metallic sheen.

The 2 strains of *C. fetus* were characteristic when incubated at 25°C, but there was no growth when incubation was at 41,5°C.

The 30 non *Campylobacter* spp strains did not grow or did not give characteristic colonies, except in 4 cases.

Colonies of 3 strains were coloured in red Bordeaux, with irregular edges. :

- One strain of *Enterobacter cloacae* (EN16),
- One strain of *Escherichia coli* (accuracy assay),
- One strain of *Acinetobacter baumannii* (reference 40).

And the 4th strain, isolated during the accuracy study, gave purplish red colonies without metallic sheen on CFA, and was identified as *Aeromonas hydrophila*.

3 Interlaboratory study

The aim of the interlaboratory study was to determine the variability of the results obtained in different laboratories using identical samples and to compare these results with those obtained during the methods comparison study.

3.1 Study organization

- Number of participating laboratories: 17 laboratories received samples. The laboratories list is presented in Appendix D.
- Matrix: poultry minced meat
- Strain: *Campylobacter jejuni* (origin "turkey").
- Number of samples per laboratory: 24 samples per method were prepared to represent 3 levels of contamination, with 8 samples per level for each method.

3.2 Control of experimental parameters

3.2.1 Contamination rate before artificial inoculation

The uncontaminated meat was analyzed according to the reference EN ISO 10272-1:2006 method, to verify absence of *Campylobacter* spp. None of the 25 g samples contained *Campylobacter* spp.

The MPN enumeration of *Campylobacter* was carried out by preparing 3 dilutions, 3 tubes per dilution in CFB, streaking on mCCDA and CFA. The result of the enumeration was < 3 CFU / 25g.

The total viable count at 30°C in the matrix was estimated at $1.5 \cdot 10^6$ CFU/g.

3.2.2 Stability of inoculated samples and inoculation level

3.3.2.1 Stability of samples

Preliminary assays demonstrated stability of *Campylobacter* spp in the poultry meat, under the conditions used in the study.

3.3.2.2 Contamination rate after artificial inoculation

The following table shows the contamination rates obtained and estimated precisions:

Level	Samples	Targeted theoretical rate (CFU/25g)	Real rate (CFU/25g)	Estimated lower contamination limit per 25 g sample	Estimated upper contamination limit per 25 g sample
Level 0 (L0)	5-6-9-10-13-14-19-20 27-28-35-36-41-42-43-44	0	0	/	/
Low level (L1)	3-4-11-12-17-18-23-24 29-30-31-32-39-40-45-46	3	4.4	1.2	11.2
High level (L2)	1-2-7-8-15-16-21-22 25-26-33-34-37-38-47-48	30	26.0	17.0	38.2

3.2.3 Problems of temperature recorded during transport, temperature on reception and reception times

a) *Analysis of temperature monitoring curves during transport*

The curves obtained further to the temperature recording by thermobutton show that temperatures were stable during transport and inferior to 8°C until the reception of samples in the most of the laboratories, excepted for 4 laboratories (I, J, L and P) (cf table below).

b) *Temperatures at reception and reception times*

The temperatures obtained are recorded in the following table :

Laboratory	Temperatures at receipt (°C)		Comments
	Measured by the laboratory	Thermobutton record	
A	5.5	4.5	
B	4.6	4.0	
C	6.5	0.0	Reception at D1 (11am), but samples analyses at D2
D	7.6	5.0	
E	5.8	5.5	
F	5.0	1.2	Reception at D1 (11am), but samples analyses at D2
G	1.0	3.6	
H	5.0	7.3	
I	14.4	14.3	Reception at D2
J	13.0	13.1	Reception at D2
K	8.5	7.8	
L	9.0	8.7	
M	8.0	7.5	
N	7.8	6.6	
O	7.8	8.0	
P	10.0	9.1	Reception at D1 (at midday), and samples analyses at D2
Q	8.2	5.1	

3.2.4 Conclusion

Of the 17 laboratories, 6 were excluded because of temperature out of range during the shipment (Laboratories I, J and L), shipment received at D2 (laboratories I and J) or samples received at D1 but analysed at D2 (laboratories C, F and P).

3.3 Results

3.3.1 Enumeration of aerobic mesophilic flora

A sample of the uninoculated poultry meat was sent to all laboratories for enumeration of the aerobic mesophilic microorganisms.

The results of enumerations varied between $2.9 \cdot 10^7$ and $1.1 \cdot 10^9$ UFC / g.

3.3.2 Results obtained by cooperating laboratories

The detailed results are presented in Appendix D and the following Tables give a summary for all the laboratories.

Positive results obtained with the reference method

Laboratory	Levels of contamination					
	L0		L1		L2	
	Positive results	Total samples	Positive results	Total samples	Positive results	Total samples
A	0	8	0	8	0	8
B	0	8	6	8	8	8
C	0	8	0	8	0	8
D	2	8	3	8	5	8
E	6	8	6	8	4	8
F	/	/	/	/	/	/
G	4	8	1	8	5	8
H	0	8	1	8	7	8
I	/	/	/	/	/	/
J	0	8	0	8	0	8
K	0	8	0	8	0	8
L	5	8	5	8	6	8
M	3	8	4	8	6	8
N	0	8	0	8	0	8
O	0	8	1	8	1	8
P	0	8	0	8	0	8
Q	0	8	1	8	5	8
Total selected laboratories	15 (a)	88	23 (b)	88	41 (c)	88

Positive results obtained with the alternative method

Laboratory	Levels of contamination					
	L0		L1		L2	
	Positive results	Total samples	Positive results	Total samples	Positive results	Total samples
A	2	8	8	8	8	8
B	0	8	8	8	8	8
C	2	8	8	8	8	8
D	0	8	8	8	8	8
E	0	8	8	8	8	8
F	/	/	/	/	/	/
G	2	8	8	8	8	8
H	0	8	8	8	8	8
I	/	/	/	/	/	/
J	4	8	8	8	8	8
K	0	8	8	8	8	8
L	0	8	5	8	6	8
M	1	8	7	8	8	8
N	1	8	8	8	8	8
O	1	8	7	8	8	8
P	1	8	8	8	8	8
Q	0	8	8	8	8	8
Total selected laboratories	7 (a)	88	86 (b)	88	88 (c)	88

(a) : False positive

(b) : True positive at level 1

(c) : True positive at level 2

3.3.3 Conclusion with comments (discordances with expected results, exclusions... for instance)

The results of 11 laboratories were finally integrated in the statistical analysis.

Results of the CFB – CFA method

- Five of the 11 laboratories (A, G, M, N and O) found 1 or 2 positives among the 8 replicates of the uncontaminated samples.
- Two of the 11 laboratories (M and O) showed a negative result for 1 sample contaminated at the low level : the strain of *Campylobacter* was not recovered after streaking on CFA.
- All of the eleven laboratories were able to detect *Campylobacter* in all the samples contaminated at the highest level.

Results of the standard method

- Three of the 11 laboratories (A, K, N) did not find *Campylobacter* spp whatever the contamination level due to the presence of an important interfering flora.
- Four laboratories (B, H, O and Q) showed negative results as expected for the uncontaminated samples. However, they showed varying extend positives results for the spiked samples, comprised between 1 to 6 and 1 to 8 for the low and the high contamination levels respectively.
- Four of the 11 laboratories (D, E, G, and M) showed varying extend positive results for the uncontaminated samples as well as for the spiked samples..

For the ISO method, the Campyloset agar was used in addition to the mCCD agar. Most of the plates showed the following characteristics :

- Characteristic macroscopic colonies on mCCDA which turned out negative after confirmation.
- And, no characteristic colonies, strongly hemolytic or not on Campyloset.

Further investigations of trials plates from the participating laboratories were done by the expert laboratory.

Strains of *Escherichia coli* were identified and studied for their resistance to antibiotics.

These strains presented a β -phenotype lactamines - β -lactamase explaining their growth.

The high bacterial background flora , consisted of multi-resistant *Escherichia coli* and lactic flora, normally inhibited in the Bolton broth and on selective agars of *Campylobacter* spp. was able to grow and inhibit and/or mask the presence of *Campylobacter* spp.

Note: the CampyFood Broth and CampyFood Agar appeared to be more selective towards the background flora.

Finally, the results of the reference method and the alternative method were not considered as equivalent.

The results of the reference method were not in accordance with the expected results, for all 11 laboratories in this study.

The alternative method showed 174 positive results out of a total of 176 expected positive results.

3.4 Calculations

The results of 11 laboratories were considered.

Note : the positive results of the alternative method were all confirmed.

3.4.1 Specificity (% SP) and Sensitivity (% SE)

The percentages of specificity (SP) and sensitivity (SE) were calculated according to the EN ISO 16140.

At level L0, the specificity (%SP) is calculated as follows :

$$SP = \{1 - (FP/N_-)\} \times 100$$

where FP, number of false positives
N-, total number of tests L0

At levels L1 and L2, the sensitivity (%SE) is as follows :

$$SE = (TP/N_+) \times 100$$

where TP, number of true positives
N+, total number of tests L1 or L2

The results are given in the following Table :

	Reference method	Alternative method
L0	SP% = 83.0	SP% = 92.1
L1	SE% = 26.1	SE% = 97.8
L2	SE% = 46.6	SE% = 100.0
L1+L2	SE% = 36.4	SE% = 98.9

3.4.2 Relative accuracy (AC)

The relative accuracy is calculated using the following formula:

$$AC = \{(PA + NA) / N\} \times 100$$

where PA, number of positive agreements
NA, number of negative agreements

The results for all the samples are presented below.

	Positive reference method (R+)	Negative reference method (R-)	Total
Positive alternative method (A+)	Positive agreement (A+/R+) PA = 67	Positive Deviation (R-/A+) PD = 114	(N+) = 181
Negative alternative method (A-)	Negative deviation (A-/R+) ND = 12*	Negative agreement (A-/R-) NA = 71*	(N-) = 83
Total	(N+) = 79	(N-) = 185	N = 264

* None of the presumptive positive samples were negative after confirmation

The values of relative accuracy of the alternative method compared with the reference method were calculated for each of the levels and are reported in the table below.

	AC %
Level L0	81.8
Level L1	28.4
Level L2	46.6
Level L1 + L2	37.5
All levels	52.3

3.4.3 Analysis of discordances

As defined in Annex F of the EN ISO 16140 standard, the minimum number of discordances beyond which a statistical test must be carried out to compare the two methods is 6. In this study the number of discrepant results was 126.

When the number of discordances is above 22, the test of McNemar with the χ^2 distribution for 1 degree of freedom is used. Determination of $d = |PD - ND|$ to calculate χ^2 is carried out according to the formula:

$$\chi^2 = d^2 / (PD + ND)$$

Number of discordances	d minimal	χ^2	Conclusion
126	$ 114 - 12 $ = 102	$(102 \times 102) / 126$ = 83	No Equivalence

Both methods were not considered as **equivalent** because $\chi^2 > 3,84$ (Annex F).

Note: *Analysis of discordances*

• **false negatives results** : positive by reference method and negative by alternative method

Among 8 concerned results, 6 correspond to not contaminated samples (level L0), 2 in a sample contaminated at the low level (3 UFC / 25g).

• « **false positives** » results : positive by CFB broth - CFA and unconfirmed

No results.

3.5 Interpretation

3.5.1 Relative accuracy (AC), specificity (SP) and sensitivity (SE)

The values obtained in the two parts of the validation study are given in the following Table:

	Interlaboratory study	Comparative study
Relative accuracy (AC)	52.3 %	92.3 %
Sensitivity (SE)	98.9 %	97.6 %
Specificity (SP)	92.1 %	88.6 %

The values obtained through the interlaboratory study and the preliminary study were not equivalent.

The AFNOR Technical Board requests the calculation of the sensitivity of both methods taking account of all confirmed positives (true positive results):

Alternative method	Reference method
$(PA + PD) / (PA + PD + ND) = 93.8 \%$	$(PA + ND) / (PA + PD + ND) = 40.9 \%$

3.5.2 Accordance (DA)

The accordance is the percentage chance of finding the same result from two identical test portions analyzed in the same laboratory under repeatability conditions: a single operator using the same instrument and the same reagents within the shortest feasible time interval.

The first step to calculate the accordance is to calculate the probability that two identical samples give the same result for each of the participating laboratories, and then to determine the average of the probabilities of all laboratories.

The different Tables used to determine the accordance are given in Appendix E and the accordance of each method at each level is given in the following Table:

Level	Reference method	Alternative method
L0	DA % = 84 %	DA % = 87 %
L1	DA % = 76 %	DA % = 96 %
L2	DA % = 75 %	DA % = 100 %

3.5.3 Concordance

The concordance is the percentage chance of finding the same result for two identical samples analyzed in two different laboratories.

The objective is to calculate the percentage of all pairs giving the same results on all possible pairs of results.

Results of the calculations are shown in Tables in Appendix F and the concordance of each method at each level is given in the following Table:

Level	Reference method	Alternative method
L0	Concordance % = 70.5 %	Concordance % = 85.2 %
L1	Concordance % = 59.9 %	Concordance % = 95.5 %
L2	Concordance % = 47.7 %	Concordance % = 100.0 %

3.5.4 Odds Ratio (COR)

The concordance odds ratio is calculated using the following formula:

$$COR = \frac{\text{accordance} \times (100 - \text{concordance})}{\text{concordance} \times (100 - \text{accordance})}$$

The concordance odds ratio of each method and at each level is given in the following Table:

Level	Reference method	Alternative method
L0	COR = 1.20	COR = 1.02
L1	COR = 2.17	COR = 1.13
L2	COR = 3.33	COR = 1.00

A value of 1.00 for the Odds ratio means that accordance and concordance are equal.

When the Odds ratio increases, the interlaboratory variation becomes more predominant.

4 Praticability

Praticability is studied as a function of the 13 criteria defined by the technical board in comparing the reference method EN ISO 10271-1 (2006) with the CFB / CFA method.

1. Packaging mode of the components of the method (cf package insert) 2. Reagent volumes (cf package insert and vial packaging)	CFB (reference 42 643) : Broths are packaged in 10 × 225 ml minibags CFB (reference 42 642) : Broths are packaged in 10 × 90 ml minibags CFA (reference 43 471) : Plates are packaged in 2x10 plates of 90 mm diameter.
3. Storage conditions of the components (cf package insert) – Expiry of products not opened (cf package insert)	The CFB minibags must be stored at 2-8°C in their box until the expiry date, protected from light. The plates must be kept between +2°C and +8°C. The expiry date is shown on each vial.
4. Modalities of use after first use (cf package insert)	The CFB minibags must be stored at 2-8°C in their box until the expiry date, protected from light. The plates must be kept between +2°C and +8°C in their box up to expiry date.
5. Equipments or necessary specific premises (cf package insert)	Normal configuration and common material of a laboratory of microbiology. Necessary equipment: 1) Combibag + microaerobic atmosphere generator 2) Or jar and GENbox microaer, GENbag microaer, GENbox Jar, microaerobic atmosphere generators, 3) Mixer typifies to stomacher 4) Air incubator at 41.5°C+/-1.0°C 5) Air incubator at 25.0°C+/-1.0°C
6. Reagents ready for use or to be reconstituted (cf package insert)	/
7. Duration of training of the operator not familiar with the method	For an operator trained in standard techniques of microbiology, training in the technique requires less than 1 day.

8. Real time handling – Flexibility of the technique relative to the number of samples to be analysed

Steps	Average time for a sample (min)		Average time for 20 samples (min)	
	EN ISO 10272-1 Standard	CFB- CFA method	EN ISO 10272-1 Standard	CFB- CFA method
Preparation, weighing, dilution in CFB and stomaching	/	7		60
Preparation, weighing, dilution in BOLTON broth and stomaching	7	/	60	
Streaking on CFA	/	1	/	8
Streaking on mCCDA and 2nd agar	1		10	/
Agar readings and typical colonies selection	2	1	15	12
Average total time (per sample)	10 min	9 min	5 min	4 min

These times correspond to negative samples for which no confirmation is necessary.
In the case of positive samples, it is necessary to add the time necessary for the confirmations.

The interest of the alternative method is the possibility of screening the negative samples and of reducing the number of confirmations (only one selective chromogenic medium).

Furthermore, time of manipulations is reduced in comparison with the reference method for each negative (5 confirmations of suspect colonies by agar - mCCDA and 2nd agar of different principle).

The average time for the confirmation of 5 colonies by a reference method can be evaluated at around 31 minutes, excluding media preparation.

For the alternative method, the confirmations according to the same protocol require less time : generally, the confirmation of a single characteristic colony leads to a positive result.

9. Time to result

Step	Time required (Day)	Time required (Day)
	CFB broth –CFA method	EN ISO 10272-1 :2006 standard
Realization of pre-enrichment	D0	D0
Streaking on selective media in a microaerobic atmosphere	/	D2
Streaking on CFA	D2	/
Reading the plates	D3 to D4	D4
Obtaining negative results (if no characteristic colony)	D4	D4
Confirmation by reference method tests : GRAM, motility, oxidase, microaerobic growth at 25°C, aerobic growth at 41, 5°C, including purification	D6 to D7	D6 to D8
Simplified confirmation tests : conventional method	D6 to D7	/
Confirmation tests : VIDAS CAM test from colony isolate or no	D4	/
Obtaining negative results (after negative confirmations if necessary)	D4 to D7	D6 to D8
Obtaining positive results		
- Confirmation by reference method tests, including purification	D6 to D7	D6 to D8
- Confirmation by VIDAS CAM test from colony isolate or no	D4 (to D6 purification)	/

10. Type de qualification of the operator	Staff trained in microbiology. Level identical to that for the reference method
11. Steps common to the reference method	Confirmations (option 1)
12. Traceability of the analysis results	/
13. Maintenance by the laboratory	/

5 General conclusion

The validation study of the CampyFood agar method was conducted according to the reference document EN ISO 16 140 (2003).

During the **comparative study** the following parameters were determined :

- Relative accuracy, relative sensitivity and relative specificity,
- Relative detection level,
- Inclusivity and exclusivity.

The performance of the CFB broth/CampyFood Agar CFA method was compared with the EN ISO 10272-1 2006 reference method by the analysis of 208 samples distributed in three categories of products.

The relative accuracy was 92.3 %, the relative sensitivity 97.6 % and the relative specificity 88.6 %, according to the calculations required by the EN ISO 16140 standard.

Overall both methods were not considered statistically equivalent. The alternative method was better than the reference method with 14 additional positives and 2 false negatives. The enrichment in CampyFood broth performed in the individual Combibag system to promote microaerobic atmosphere was better than the enrichment of the reference method. CFA allowed a better recovery of *Campylobacter* spp than the selective media of the reference method

According to the calculations recommended by the AFNOR, and whatever the confirmation option, the sensitivity of the CFB - CFA method was 98.0 % and that of the reference method was 85.9 %.

The relative detection level for the CFB / CFA method and the reference method was evaluated by artificial contamination of 3 products, representative of the three categories tested.

It was between 0.2 and 1.8 CFU/ 25 g for alternative method and between 0.2 and 2.4 CFU/ 25 g for the reference method.

The inclusivity of the method was excellent since all the 50 strains of thermotolerant *Campylobacter* spp were detected.

The study of the exclusivity of the 32 strains not belonging to *Campylobacter* genus did not give any characteristic colonies and generally no growth, except in 4 cases, where suspect colonies were observed (*Enterobacter cloacae*, *Escherichia coli*, *Acinetobacter baumannii* and one strain of *Aeromonas hydrophila*). No growth of the 2 strains of *Campylobacter fetus* was observed on CFA incubated at 41.5°C+/-1.0°C.

The **interlaboratory study** did not show comparable values of relative accuracy, specificity and sensitivity for the alternative and the reference methods. For the reference method, the results were also different from those obtained during the preliminary study.

The sensitivity of the alternative method by taking into account the set of confirmed positive (this includes additional positive of the alternative method) was of the same order as that obtained during the preliminary study (93.8 % / 98.9%), while that of the standard method was reduced more than a factor 2 (40.9 % / 97.6 %).

The variability of the alternative method (accordance, concordance, odds ratio) was not comparable to that of the reference method.

The interlaboratory variability of the alternative method was much lower than that of the reference method.

In conclusion, this study demonstrated that the alternative method was much better than the reference method for the recovery of thermotolerant *Campylobacter*, in samples containing high background flora.

Based on the results of this study carried out according the EN ISO 16140 method, the CampyFood agar method was certified **AFNOR validation** (certificate n° BIO 12/30 – 05/10), for the detection of *Campylobacter* spp. in poultry products, other meat products and environmental samples, **for a period of 4 years**.

Lille, December 10th 2010

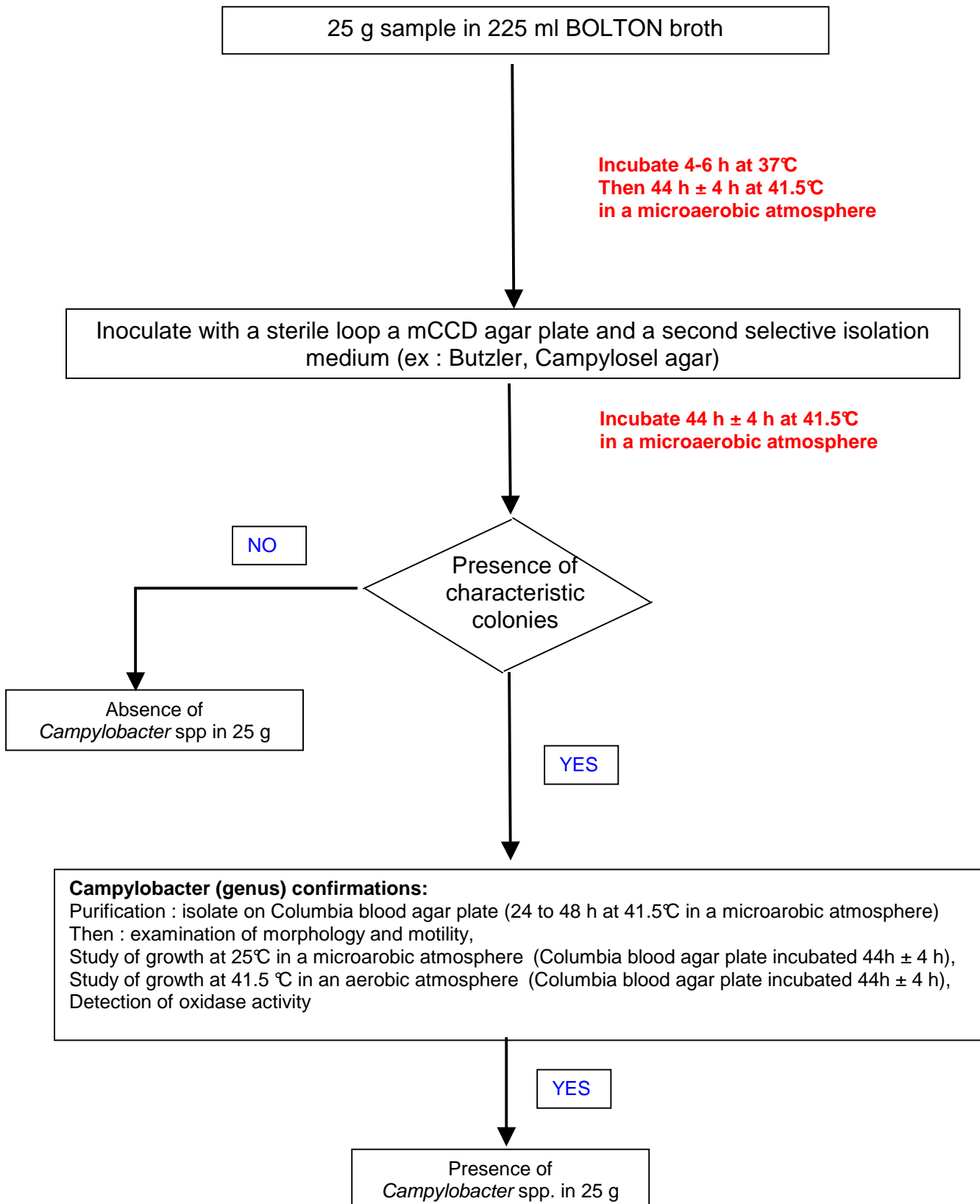
Virginie Ewe
Technical manager

APPENDICES

APPENDIX A

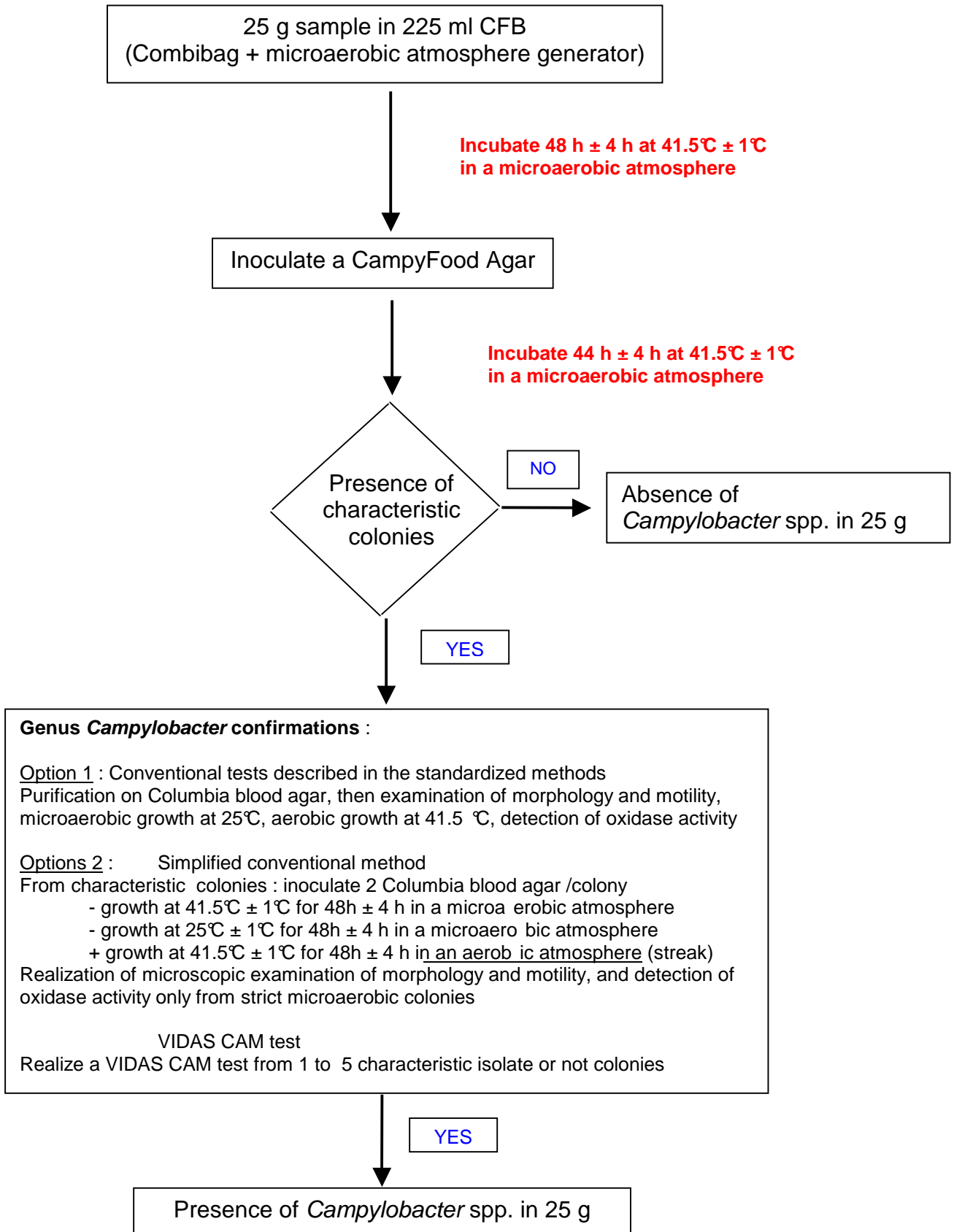
ANALYTICAL PROTOCOLS

EN ISO STANDARD 10272-1 : 2006 (#)



Alternative method

CampyFood Broth (CFB) –CampyFood Agar (CFA)



APPENDIX B

RELATIVE ACCURACY, RELATIVE SPECIFICITE,
RELATIVE SENSITIVITY

-

DETAILED RESULTS TABLES
FOR EACH SAMPLE CATEGORY

Total bacteria growth

∅ : no growth
 L = Low
 M = Medium
 H = High

Distribution of flora

presumptive colonies = *Campylobacter* spp colonies

A = pure culture of suspicious colonies
 B = mix with a majority of suspicious colonies
 C = mix with a minority of suspicious colonies
 D = mix with rare suspicious colonies
 E = absence of suspicious colonies
 (x) : x characteristic colonies of *Campylobacter* spp if x < 5

Conventional standardized methods tests

Reference method

Morphology	Oxidase	Motility	41,5°C microaerobic	41,5°C aerobic	25°C microaerobic	Conclusion	Result
BG-	+	+	+	-	-	corresponding tests	<i>Campylobacter</i> spp.

Simplified conventional tests

Alternative method

Morphology	Oxidase	Motility	41,5°C microaerobic	41,5°C aerobic	25°C microaerobic	Conclusion	Result
BG-	+	+	+	-	-	corresponding tests	<i>Campylobacter</i> spp.

Morphology, Oxidase detection and motility, realized only if negative growth culture in an aerobic atmosphere at 41,5°C, or in case of discordance

N.B. : during the validation study, all tests have been realized, including growth/ no growth test at 25°C in a microaerobic atmosphere

red FN (False Negative) result
 blue PS (Positive additional) result
 CA Artificial contamination of samples
 Cat. : category of products
 POUL : poultry products
 MP : other meat products
 EN : environment samples

Code	Sample	Cat.	CA	Reference method EN ISO 10272-1 (#)								Alternative method CampyFood Agar method										Comments		
				mCCDA	Butzler	Confirmation					Final result	Confirmations from CampyFood Agar (CFA)												
						Morphology	Oxidase	Motility	25°C microaerobic	41,5°C aerobic		Growth	GeneProbe	Final result (CFA Accuprobe)	Comparison	RFV	VT	Final result (CFA VIDAS CAM)	Comparison	Conventional tests	Final result (conventional CFA)		Comparison	
A2	Chicken with skin	POUL1	No	+HA	+HA	BG-	+	+	-	-	+	+HA	+	+	=	10227	2,14	+	+	=	corresponding	+	=	
A5	Chicken	POUL1	No	+HA	+HA	BG-	+	+	-	-	+	+MA	+	+	=	10958	2,29	+	+	=	corresponding	+	=	Molecular identification C.jejuni subsp. jejuni
B3	Chicken leg	POUL1	No	-HE	-ME	/	-	/	+	+	-	Ø	/	-	=	/	/	/	-	=	/	-	=	
B4	Chicken fillet	POUL1	No	+MB	+MB	BG-	+	+	-	-	+	+MB	+	+	=	11847	2,38	+	+	=	corresponding	+	=	
B5	Chicken breast	POUL1	No	+LB	+LB	BG-	+	+	-	-	+	+MB	+	+	=	10308	2,07	+	+	=	corresponding	+	=	
C2	Chicken with skin	POUL1	No	-HE	-HE	/	/	/	/	/	-	-LB	-	-	=	226	0,04	-	-	=	corresponding	-	=	
C3	Chicken wing	POUL1	No	+HB	+HB	BG-	+	+	-	-	+	+MC	+	+	=	10358	2,08	+	+	=	corresponding	+	=	
C4	Chicken leg	POUL1	No	-HE	-HE	/	/	/	/	/	-	-ME	/	-	=	/	/	/	-	=	/	-	=	
C6	Chicken with skin	POUL1	No	+HB	+HB	BG-	+	+	-	-	+	+LA	+	+	=	11197	2,25	+	+	=	corresponding	+	=	
D3	Sauté of duck	POUL1	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=	
E1	Chicken leg	POUL1	No	-HB	-HB	BG-	+	/	+	+	-	+MB	+	+	PS	617	0,12	+	+	PS	corresponding	+	PS	Ref. method : E. coli
E3	Chicken tenderloin	POUL1	No	-MB	-MB	BG-	+	+	+	+	-	-LA	-	-	=	386	0,08	-	-	=	no corresponding	-	=	
F1	Chicken tenderloin	POUL1	No	-ME	-ME	BG-	-	-	+	+	-	-ME	-	-	=	224	0,04	-	-	=	no corresponding	-	=	
F2	Chicken tenderloin	POUL1	No	+MB	+MB	BG-	+	+	-	-	+	+MB	+	+	=	9940	2,08	+	+	=	no corresponding	+	=	
F3	Chicken leg	POUL1	No	-ME	-ME	/	/	/	/	/	-	-Me(Ec)	/	-	=	/	/	/	-	=	/	-	=	
G2	Chicken leg	POUL1	No	+HB	+HB	BG-	+	+	-	-	+	+MB	+	+	=	229 9931	0,04 2,04	- +	+	=	corresponding	+	=	
G6	Chicken leg	POUL1	No	-LE	-LE	/	/	/	/	/	-	+MA	+	+	PS	10968	2,26	+	+	PS	corresponding	+	PS	
G9	Chicken leg	POUL1	No	-HE	-HE	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=	
H2	Chicken wing	POUL1	No	-ME	-ME	/	/	/	/	/	-	-LE	/	-	=	/	/	/	-	=	/	-	=	
H3	Chicken tenderloin	POUL1	No	+HB	+HB	BG-	+	+	-	-	+	+MB	+	+	=	9452	2,07	+	+	=	corresponding	+	=	
H4	Duck filets	POUL1	No	+MB	+MB	BG-	+	+	-	-	+	+MB	+	+	=	8678	1,90	+	+	=	corresponding	+	=	
H5	Chicken tenderloin	POUL1	No	+MC	-ME	BG-	+	+	-	-	+	+MB	+	+	=	9432	2,06	+	+	=	corresponding	+	=	
H6	Chicken wing with paprika	POUL1	No	-HE	-ME	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=	
H8	Chicken tenderloin	POUL1	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=	
I1	Sauté of turkey	POUL1	Yes	+HA	+HB	BG-	+	+	-	-	+	+HA	+	+	=	11629	2,54	+	+	=	corresponding	+	=	
I5	Turkey breast	POUL1	Yes	+HB	+HB	BG-	+	+	-	-	+	+MA	+	+	=	11279	2,47	+	+	=	corresponding	+	=	
I6	Sauté of turkey	POUL1	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=	
I9	Turkey breast	POUL1	No	-LE	-LE	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=	
L6	Giblets of poultry	POUL1	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=	
D6	Roasted chicken	POUL2	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=	
D7	Roasted chicken	POUL2	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=	
F5	Roasted chicken	POUL2	No	Ø	-HE	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=	
F6	Roasted, badly cooked chicken	POUL2	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=	
F13	Chicken in the juice	POUL2	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=	
H11	Roasted chicken	POUL2	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=	
I2	Roasted chicken	POUL2	Yes	+HA	+MB	BG-	+	+	-	-	+	+HA	+	+	=	11684	2,55	+	+	=	corresponding	+	=	
I3	Roasted chicken	POUL2	Yes	+HA	+HB	BG-	+	+	-	-	+	+HA	+	+	=	11312	2,47	+	+	=	corresponding	+	=	
I4	Roasted chicken	POUL2	Yes	+HA	+HA	BG-	+	+	-	-	+	+HA	+	+	=	11645	2,55	+	+	=	corresponding	+	=	
I7	Roasted chicken	POUL2	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=	
I8	Roasted chicken	POUL2	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=	
J6	Roasted chicken	POUL2	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=	
L4	Gizzards of poultry	POUL2	No	+HB	+HC	BG-	+	+	-	-	+	+MB	+	+	=	9647	1,91	+	+	=	corresponding	+	=	
L5	Chicken livers	POUL2	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=	
G4	Rinsing carcass	POUL3	No	-ME	-ME	/	/	/	/	/	-	+LB	+	+	PS	10102	2,08	+	+	PS	corresponding	+	PS	
G5	Rinsing carcass	POUL3	No	+MB	+MB	BG-	+	+	-	-	+	+LB	+	+	=	11422	2,35	+	+	=	corresponding	+	=	
G8	Rinsing carcass	POUL3	No	+MB	+MB	BG-	+	+	-	-	+	+MA	+	+	=	8978	1,85	+	+	=	corresponding	+	=	
H9	Rinsing carcass	POUL3	No	+MB	-ME	BG-	+	+	-	-	+	+MB	+	+	=	9330	2,04	+	+	=	corresponding	+	=	
H10	Rinsing carcass	POUL3	No	+MB	-ME	BG-	+	+	-	-	+	+MB	+	+	=	9678	2,12	+	+	=	corresponding	+	=	
L1	Rinsing carcass	POUL3	No	+MC	-LE	BG-	+	+	-	-	+	+HA	+	+	=	11253	2,23	+	+	=	corresponding	+	=	
L2	Rinsing carcass	POUL3	No	+LC	+LC	BG-	+	+	-	-	+	+MA	+	+	=	9400	1,86	+	+	=	corresponding	+	=	
L3	Rinsing carcass	POUL3	No	+MB	+MB	BG-	+	+	-	-	+	+MA	+	+	=	10414	2,06	+	+	=	corresponding	+	=	
A1	Skin of chicken neck	POUL4	No	+MB	+MA	BG-	+	+	-	-	+	+HA	+	+	=	10402	2,18	+	+	=	corresponding	+	=	
A3	Skin of chicken	POUL4	No	+HA	+HA	BG-	+	-	-	+	-	+MA	-	-	=	214	0,04	-	-	=	corresponding	-	=	
A4	Skin of chicken neck	POUL4	No	+HB	+HB	BG-	-	-	+	+	-	+HA	+	+	PS	11356	2,38	+	+	PS	corresponding	+	PS	Molecular identification C.jejuni subsp. jejuni
A6	Skin of chicken neck	POUL4	No	+MB	+MB	BG-	-	-	+	+	-	+MA	+	+	PS	9808	2,05	+	+	PS	corresponding	+	PS	Molecular identification C.jejuni subsp. jejuni
B1	Skin of chicken neck	POUL4	No	-HE	-LE	BG+	-	/	+	+	-	+LA (2)	-	-	=	223	0,04	-	-	=	no corresponding	-	=	Lactobacillus
B2	Skin of chicken neck	POUL4	No	+HB	+MB	BG-	+	+	-	-	+	+HA	+	+	=	11412	2,29	+	+	=	corresponding	+	=	
C1	Skin of chicken neck	POUL4	No	+HB	+HB	BG-	+	+	-	-	+	+MB	+	+	=	11477	2,31	+	+	=	corresponding	+	=	
C5	Skin of chicken neck	POUL4	No	+HB	+HB	BG-	+	+	-	-	+	+MA	+	+	=	11303	2,27	+	+	=	corresponding	+	=	
F4	Skin of chicken	POUL4	No	-HE	-HE	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=	
G1	Skin of chicken neck	POUL4	No	+HC	+HB	BG-	+	+	-	-	+	+MB	+	+	=	11585	2,38	+	+	=	corresponding	+	=	
G7	Skin of chicken neck	POUL4	No	+MB	-ME	BG-	+	+	-	-	+	+MA	+	+	=	11907	2,45	+	+	=	corresponding	+	=	
H1	Skin of chicken	POUL4	No	-HE	-HE	/	/	/	/	/	-	-LE	/	-	=	/	/	/	-	=	/	-	=	
H7	Skin of chicken neck	POUL4	No	+HB	+HC	BG-	+	+	-	-	+	+MB	+	+	=	9021	1,97	+	+	=	corresponding	+	=	

Code	Sample	Cat.	CA	Reference method EN ISO 10272-1 (#)							Alternative method CampyFood Agar method												
				mCCDA	Butzler	Confirmation					Final result	Confirmations from CampyFood Agar (CFA)											
						Morphology	Oxidase	Motility	25°C microaerobic	41,5°C aerobic		Growth	GeneProbe	Final result (CFA Accuprobe)	Comparison	RFV	VT	Final result (CFA VIDAS CAM)	Comparison	Conventional tests	Final result (conventional CFA)	Comparison	
B6	Pork chop	MP1	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
C7	Rib eye steak of ox	MP1	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
D1	Deep-frozen minced beef	MP1	No	Ø	Ø	/	/	/	/	/	-	-ME	/	-	=	/	/	/	-	=	/	-	=
D2	Deep-frozen minced beef	MP1	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
D5	Slice of bovine meat	MP1	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
D10	Sliced thinly by pork	MP1	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
E2	Pork chop	MP1	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
E4	Ground beef 5% fat	MP1	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
E5	Ground beef 20% fat	MP1	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
E6	Ground beef 5% fat	MP1	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
F8	Rib steak of ox	MP1	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
F9	Ground beef	MP1	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
F10	Ground beef	MP1	No	-LE	-ME	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
F11	Minced beef	MP1	No	-LE	-LE	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
F14	Fried beef	MP1	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
F15	Fried beef	MP1	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
G11	Floods pork chop	MP1	No	+HA	+HB	BG-	+	+	-	-	+	+HA	-	-	FN (FP)	10378	2,14	+	+	=	corresponding	+	=
G13	Beef tenderloin	MP1	Yes	+HA	+HB	BG-	+	+	-	-	+	+MA	+	+	=	10323	2,12	+	+	=	corresponding	+	=
J1	Ground beef	MP1	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
J3	Veal cutlet	MP1	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
J4	Beefsteak	MP1	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
L7	Calv kidney	MP1	No	Ø	Ø	/	/	/	/	/	-	-LB	-	-	=	270	0,05	-	-	=	/	-	=
L8	Pork kidney	MP1	No	-HE	-HE	/	/	/	/	/	-	-HE	/	-	=	/	/	/	-	=	/	-	=
M2	Slice of leg of lamb with bone	MP1	Yes	-LE	-LE	/	/	/	/	/	-	+HC	+	+	PS	9336	1,85	+	+	PS	corresponding	+	PS
M3	Leg of lamb without bone	MP1	Yes	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
M4	Pork tongue	MP1	No	-LE	-LE	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
N5	Calv kidney	MP1	No	+MA	+HA	BG-	+	+	-	-	+	+HA	+	+	=	10880	2,21	+	+	=	corresponding	+	=
N7	Lamb kidney	MP1	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
N9	Pork sirloin	MP1	Yes	-LB	+LB	BG-	+	+	-	-	+	+HA	+	+	=	10859	2,21	+	+	=	corresponding	+	=
N10	Pork filet mignon	MP1	Yes	+HB	+MA	BG-	+	+	-	-	+	+HC	+	+	=	11097	2,26	+	+	=	corresponding	+	=
N11	Veal chop	MP1	Yes	-HE	+HA	/	/	/	/	/	-	+HC	+	+	PS	10890	2,21	+	+	PS	corresponding	+	PS
O2	Heart of ox	MP1	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
O6	Slice of bovine meat	MP1	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
O8	Calv kidney	MP1	No	-HE	-HE	/	/	/	/	/	-	-ME	/	-	=	/	/	/	+	=	/	-	=
P14	Back of the knee of lamb	MP1	Yes	+HA	+HA	BG-	+	+	-	-	+	+HB	+	+	=	10192	1,98	+	+	=	corresponding	+	=
P15	Chopolatas	MP1	Yes	+HA	+HC	BG-	+	+	-	-	+	+HB	+	+	=	9931	1,93	+	+	=	corresponding	+	=
P16	Bib of ox	MP1	Yes	+HA	+HA	BG-	+	+	-	-	+	+HB	+	+	=	9911	1,92	+	+	=	corresponding	+	=
P17	Pork chop	MP1	Yes	+HA	+HB	BG-	+	+	-	-	+	+MB	+	+	=	9820	1,9	+	+	=	corresponding	+	=
P18	Sweetbread - Heart	MP1	Yes	+HA	+LB	BG-	+	+	-	-	+	-HE	/	-	FN	/	/	/	-	FN	/	-	FN
P19	Calv kidney	MP1	Yes	+HA	+HA	BG-	+	+	-	-	+	+MA	+	+	=	9892	1,92	+	+	=	corresponding	+	=
Q2	Calv liver	MP1	Yes	+HA	+HA	BG-	+	+	-	-	+	+HA	+	+	=	9748	1,89	+	+	=	corresponding	+	=
Q3	Beef tongue	MP1	Yes	+HA	+HA	BG-	+	+	-	-	+	+HA	+	+	=	9897	1,92	+	+	=	corresponding	+	=
Q6	Pork filet mignon	MP1	Yes	+HB	+HB	BG-	+	+	-	-	+	+HA	+	+	=	11465	2,22	+	+	=	corresponding	+	=
Q7	Pork filet mignon	MP1	Yes	+HA	+HA	BG-	+	+	-	-	+	+HA	+	+	=	10748	2,08	+	+	=	corresponding	+	=
Q8	Sirloin of ox	MP1	Yes	+HA	+HA	BG-	+	+	-	-	+	+HA	+	+	=	11125	2,16	+	+	=	corresponding	+	=
Q10	Pork filet mignon	MP1	Yes	Ø	Ø	/	/	/	/	/	-	+HA	+	+	PS	9651	1,87	+	+	PS	corresponding	+	PS
Q14	Rib nearby kills of pork	MP1	Yes	+HB	+HB	BG-	+	+	-	-	+	+HA	+	+	=	10661	2,07	+	+	=	corresponding	+	=

C8	Bib wipes shallot	MP2	No	Ø	Ø	/	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
C10	Ox balls	MP2	No	Ø	Ø	/	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
D9	Ox balls	MP2	No	Ø	Ø	/	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
E7	Chipolatas in herbs	MP2	No	Ø	Ø	/	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
E8	Sausage meat	MP2	No	Ø	Ø	/	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
E9	Chipolatas	MP2	No	Ø	Ø	/	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
F12	Rib nearly kills of pork	MP2	No	Ø	Ø	/	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
G12	Fried beef	MP2	Yes	+HB	+HB	BG-	+	+	-	-	-	+	+MB	-	-	FN (FP)	10297	2,12	+	+	=	corresponding	+	=
G14	Raw salsiccia Texas (porc)	MP2	Yes	+HA	+HA	BG-	+	+	-	-	-	+	+HA	+	+	=	10843	2,23	+	+	=	corresponding	+	=
J5	Deep-frozen minced beef with onions	MP2	No	Ø	Ø	/	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
L9	Leg of lamb slice	MP2	No	Ø	Ø	/	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
M1	Leg of lamb slice	MP2	Yes	-LB	-LB	/	/	/	/	/	/	-	-LE	-	-	=	280	0,05	-	-	=	/	-	=
O3	Porc belly	MP2	No	Ø	Ø	/	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
O4	Ox foot	MP2	No	Ø	-ME	/	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
P11	Chipolatas in herbs	MP2	Yes	+HC	+MB	BG-	+	+	-	-	-	+	+HB	+	+	=	11150	2,16	+	+	=	corresponding	+	=
P12	Strong merguez sausages	MP2	Yes	+HA	+HB	BG-	+	+	-	-	-	+	+HB	+	+	=	10180	1,97	+	+	=	corresponding	+	=
Q4	Mexican pork chop	MP2	Yes	+HA	+HA	BG-	+	+	-	-	-	+	+HA	+	+	=	10026	1,94	+	+	=	corresponding	+	=
Q11	Chopped pork	MP2	Yes	+HC	+HC	BG-	+	+	-	-	-	+	+HA	+	+	=	9856	1,91	+	+	=	corresponding	+	=
Q12	Calf kidney	MP2	Yes	+HA	+HA	BG-	+	+	-	-	-	+	+HA	+	+	=	9925	1,92	+	+	=	corresponding	+	=
C9	The moussaka	MP3	No	Ø	Ø	/	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
D4	The lasagnes of ox	MP3	No	Ø	Ø	/	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
D8	Rib steak cooks	MP3	No	Ø	Ø	/	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
E10	Pork cooked cheek	MP3	No	Ø	Ø	/	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
F7	Chicken sandwich	MP3	No	Ø	Ø	/	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
G10	Roasted chicken	MP3	No	Ø	Ø	/	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
J2	Sausages	MP3	No	Ø	Ø	/	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
J7	Chicken sandwich	MP3	No	Ø	Ø	/	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
J8	Chicken couscous	MP3	No	Ø	Ø	/	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
J9	Chicken sandwich	MP3	No	-MA	Ø	/	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
P13	Sliced thinly by pork wipes Tuscan	MP3	Yes	+HA	+HB	BG-	+	+	-	-	-	+	+HB	+	+	=	10477	2,03	+	+	=	corresponding	+	=
P20	Smoked palette without bone	MP3	Yes	+HA	+HA	BG-	+	+	-	-	-	+	+MB	+	+	=	9377	1,82	+	+	=	corresponding	+	=
Q1	Cutlet of pork's ham	MP3	Yes	+HA	+HA	BG-	+	+	-	-	-	+	+HA	+	+	=	9882	1,92	+	+	=	corresponding	+	=
Q5	Pork filet mignon	MP3	Yes	+HB	+HB	BG-	+	+	-	-	-	+	+HA	+	+	=	11029	2,14	+	+	=	corresponding	+	=
Q9	Pork filet mignon	MP3	Yes	Ø	Ø	/	/	/	/	/	/	-	+HA	+	+	PS	9531	1,85	+	+	PS	corresponding	+	PS
Q13	Bacon the old	MP3	Yes	+HA	+HA	BG-	+	+	-	-	-	+	+HA	+	+	=	10831	2,1	+	+	=	corresponding	+	=

Code	Sample	Cat.	CA	Reference method EN ISO 10272-1 (#)							Alternative method CampyFood Agar method												
				mCCDA	Butzler	Confirmation				Final result	Confirmations from CampyFood Agar (CFA)												
						Morphology	Oxidase	Motility	25°C microaerobic		41,5°C aerobic	Growth	GeneProbe	Final result (CFA Accuprobe)	Comparison	RFV	VT	Final result (CFA VIDAS CAM)	Comparison	Conventional tests	Final result (conventional CFA)	Comparison	
P1	Process water	ENV1	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
P2	Process water	ENV1	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
P3	Process water	ENV1	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
P4	Process water	ENV1	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
P5	Process water	ENV1	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
P6	Process water	ENV1	Yes	-HA	-HA	/	/	/	/	/	Yes	Ø	/	-	=	/	/	/	-	=	/	-	=
P7	Process water	ENV1	Yes	+HA	+HC	BG-	+	+	-	-	+	+HB	+	+	=	9950	1,93	+	+	=	corresponding	+	=
P8	Process water	ENV1	Yes	+HB	+HC	BG-	+	+	-	-	+	+HB	+	+	=	9733	1,89	+	+	=	corresponding	+	=
P9	Process water	ENV1	Yes	Ø	Ø	/	/	/	/	/	-	+HB	+	+	PS	11891	2,31	+	+	PS	corresponding	+	PS
P10	Process water	ENV1	Yes	Ø	Ø	/	/	/	/	/	-	-LE	/	-	=	/	/	/	-	=	/	-	=
Q20	Process water	ENV1	Yes	+HA	+HB	BG-	+	+	-	-	+	+HA	+	+	=	10869	2,11	+	+	=	corresponding	+	=
Q21	Process water	ENV1	Yes	-HE	-HE	/	/	/	/	/	-	-LE	/	-	=	/	/	/	-	=	/	-	=
Q22	Process water	ENV1	Yes	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
R3	Process water	ENV1	Yes	+HA	+HB	BG-	+	+	-	-	+	+HA	+	+	=	10770	2,24	+	+	=	corresponding	+	=
R4	Process water	ENV1	Yes	+HA	+HB	BG-	+	+	-	-	+	+HA	+	+	=	10880	2,26	+	+	=	corresponding	+	=
S5	Process water	ENV1	Yes	+HA	+HA	BG-	+	+	-	-	+	+HA	+	+	=	11639	2,47	+	+	=	corresponding	+	=
S6	Process water	ENV1	Yes	+HA	+HA	BG-	+	+	-	-	+	Ø	/	-	FN	/	/	/	-	FN	/	-	FN
S11	Process water	ENV1	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
S12	Process water	ENV1	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
K1	Whole raw hen surface	ENV2	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
K2	Whole raw chicken surface	ENV2	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
K3	Whole raw young cockerel surface	ENV2	No	+HA	+MB	BG-	+	+	-	-	+	+MA	+	+	=	9715	1,92	+	+	=	corresponding	+	=
K4	Whole raw chicken surface	ENV2	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
N13	Chicken taking	ENV2	No	-HE	-HE	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
N14	Chicken taking	ENV2	No	Ø	Ø	/	/	/	/	/	-	+HA	+	+	PS	9536	1,94	+	+	PS	corresponding	+	PS
N15	Hen taking	ENV2	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
O5	Pigeon taking	ENV2	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
Q15	Surface stainless table preparation	ENV2	Yes	+HA	+HA	BG-	+	+	-	-	+	+HA	+	+	=	11031	2,14	+	+	=	corresponding	+	=
Q16	Surface stainless table preparation	ENV2	Yes	+HA	+HA	BG-	+	+	-	-	+	+HA	+	+	=	11311	2,19	+	+	=	corresponding	+	=
Q17	Surface ground	ENV2	Yes	+HA	+HA	BG-	+	+	-	-	+	+HA	+	+	=	10710	2,08	+	+	=	corresponding	+	=
Q19	Surface ground	ENV2	Yes	+HA	+HA	BG-	+	+	-	-	+	+HA	+	+	=	10375	2,01	+	+	=	corresponding	+	=
R1	Surface stainless preparation	ENV2	Yes	+HA	+HB	BG-	+	+	-	-	+	+HA	+	+	=	10397	2,16	+	+	=	corresponding	+	=
R2	Surface stainless preparation	ENV2	Yes	+HA	+HB	BG-	+	+	-	-	+	+HA	+	+	=	10466	2,17	+	+	=	corresponding	+	=
R5	Surface tub of storage	ENV2	Yes	+HA	+HB	BG-	+	+	-	-	+	+HA	+	+	=	10765	2,24	+	+	=	corresponding	+	=
R7	Surface tub of storage	ENV2	Yes	+HA	+HB	BG-	+	+	-	-	+	+HA	+	+	=	10084	2,09	+	+	=	corresponding	+	=
S1	Surface ground	ENV2	Yes	+HA	+HA	BG-	+	+	-	-	+	+HA	+	+	=	100076	2,14	+	+	=	corresponding	+	=
S2	Surface ground	ENV2	Yes	+HA	+HA	BG-	+	+	-	-	+	+HA	+	+	=	11648	2,47	+	+	=	corresponding	+	=
S3	Surface tub of storage	ENV2	Yes	+HA	+HA	BG-	+	+	-	-	+	+HA	+	+	=	11428	2,43	+	+	=	corresponding	+	=
S8	Surface ground	ENV2	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
S9	Surface stainless preparation	ENV2	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
S10	Surface stainless preparation	ENV2	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
S13	Surface table	ENV2	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
S14	Surface flatware	ENV2	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
S15	Surface ground	ENV2	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
M5	Scraps from poultry gizzard	ENV3	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
N1	Scraps from tub with blood	ENV3	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
N2	Scraps from tub with dried blood	ENV3	No	-HE	-HE	/	/	/	/	/	-	+HA	+	+	PS	9512	1,93	+	+	PS	corresponding	+	PS
N3	Scraps from poultry liver	ENV3	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
N4	Scraps from hen workshop	ENV3	No	Ø	Ø	/	/	/	/	/	-	+HC	+	+	PS	11706	2,38	+	+	PS	corresponding	+	PS
N6	Scraps from chicken cut workshop	ENV3	No	+HB	+HB	BG-	+	+	-	-	+	+HB	+	+	=	10691	2,17	+	+	=	corresponding	+	=
N8	Scraps from cock cut	ENV3	No	+HB	+HA	BG-	+	+	-	-	+	+HA	+	+	=	9945	2,02	+	+	=	corresponding	+	=
N12	Scraps from chicken workshop	ENV3	No	+HB	+LC	BG-	+	+	-	-	+	+HB	+	+	=	9580	1,95	+	+	=	corresponding	+	=
O1	Scraps from chicken skin of leg	ENV3	No	-ME	-ME	/	/	/	/	/	-	+MC	+	+	PS	9506	1,93	+	+	PS	corresponding	+	PS
O7	Scraps from chicken skin of leg	ENV3	No	Ø	-ME	/	/	/	/	/	-	-LE(1)	/	-	=	/	/	/	-	=	/	-	=
O9	Scraps from chicken skin of leg	ENV3	No	-HE	-HE	/	/	/	/	/	-	-ME	/	-	=	/	/	/	-	=	/	-	=
O10	Scraps from chicken skin of leg	ENV3	No	-HE	-HE	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
O11	Scraps from chicken skin of leg	ENV3	No	-HE	-HE	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
O12	Scraps from pigeon leg	ENV3	No	-ME	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=
Q18	Scraps from turkey cut ground	ENV3	Yes	+HA	+HA	BG-	+	+	-	-	+	+HA	+	+	=	10352	2,01	+	+	=	corresponding	+	=
R6	Scraps from tub of storage	ENV3	Yes	+HA	+HB	BG-	+	+	-	-	+	+HA	+	+	=	10830	2,25	+	+	=	corresponding	+	=
S4	Scraps from tub of storage	ENV3	Yes	+HA	+HA	BG-	+	+	-	-	+	+HA	+	+	=	11514	2,44	+	+	=	corresponding	+	=
S7	Scraps from cut workshop ground	ENV3	No	Ø	Ø	/	/	/	/	/	-	Ø	/	-	=	/	/	/	-	=	/	-	=

APPENDIX C

INCLUSIVITY / EXCLUSIVITY

Inclusivity

Reference	Strain	Origin	Enumeration in 225 ml CFB before incubation	CFA
C4	<i>Campylobacter jejuni</i>	Evisceration turkey	60	+MA
C5	<i>Campylobacter coli</i>	Evisceration turkey	100	+MA
C6	<i>Campylobacter coli</i>	Evisceration turkey	120	+MA
C7	<i>Campylobacter jejuni</i>	Evisceration turkey	90	+MA
C8	<i>Campylobacter coli</i>	Evisceration turkey	130	+MA
C9	<i>Campylobacter jejuni</i>	Evisceration turkey	70	+MA
C10	<i>Campylobacter coli</i>	Evisceration turkey	110	+MA
C11	<i>Campylobacter jejuni</i>	Evisceration turkey	110	+MA
C12	<i>Campylobacter coli</i>	Evisceration turkey	120	+MA
C13	<i>Campylobacter coli</i>	Evisceration turkey	50	+MA
C14	<i>Campylobacter jejuni</i>	Evisceration turkey	100	+MA
C15	<i>Campylobacter jejuni</i>	Evisceration turkey	120	+MA
C16	<i>Campylobacter jejuni</i>	Evisceration turkey	130	+MA
C17	<i>Campylobacter jejuni</i>	Evisceration turkey	130	+MA
C18	<i>Campylobacter coli</i>	Evisceration turkey	5	+MA
C19	<i>Campylobacter coli</i>	Evisceration turkey	8	+MA
C20	<i>Campylobacter jejuni</i>	Evisceration turkey	30	+MA
C21	<i>Campylobacter coli</i>	Evisceration turkey	22	+MA
C22	<i>Campylobacter jejuni</i>	Poultry ressuage	4	+MA
C23	<i>Campylobacter coli</i>	Poultry ressuage	3	+MA
C24	<i>Campylobacter jejuni</i>	Poultry ressuage	18	+MA
C25	<i>Campylobacter jejuni</i>	Poultry ressuage	50	+MA
C26	<i>Campylobacter jejuni</i>	Poultry ressuage	45	+MA
C27	<i>Campylobacter jejuni</i>	Poultry ressuage	32	+MA
C28	<i>Campylobacter jejuni</i>	Poultry ressuage	32	+MA
C29	<i>Campylobacter jejuni</i>	Poultry ressuage	40	+MA
C30	<i>Campylobacter jejuni</i>	Poultry ressuage	21	+MA
C31	<i>Campylobacter jejuni</i>	Poultry ressuage	40	+MA
C32	<i>Campylobacter jejuni</i>	Poultry ressuage	42	+MA
C33	<i>Campylobacter jejuni</i>	Poultry ressuage	55	+MA
C34	<i>Campylobacter jejuni</i>	Poultry ressuage	60	+MA
C0	<i>Campylobacter jejuni s.jejuni</i>	Carcass of poultry	30	+MA
C1	<i>Campylobacter jejuni s.jejuni</i>	Chicken cutlet	32	+MA
C2	<i>Campylobacter jejuni s.jejuni</i>	Chicken skin of neck	40	+MA
C3	<i>Campylobacter jejuni s.jejuni</i>	Chicken cutlet	35	+MA
C35	<i>Campylobacter jejuni</i>	Evisceration turkey	40	+MA
C36	<i>Campylobacter jejuni</i>	Evisceration turkey	53	+MA
C37	<i>Campylobacter jejuni</i>	Evisceration turkey	55	+MA
C38	<i>Campylobacter jejuni</i>	Evisceration turkey	78	+MA
C39	<i>Campylobacter lari</i>	Collection	37,5	+HA
C42	<i>Campylobacter upsaliensis</i>	Collection	19	+MA
C43	<i>Campylobacter jejuni doylei</i>	Collection	25	+MA
C44	<i>Campylobacter lari</i>	Collection	125	+HA
C45	<i>Campylobacter lari</i>	Collection	50	+MA
C46	<i>Campylobacter lari subsp lari</i>	Collection	75	+HA
C47	<i>Campylobacter jejuni doylei</i>	Collection	43	+MA
C48	<i>Campylobacter lari</i>	Bordeaux hospital	40	+MA
C49	<i>Campylobacter upsaliensis</i>	Bordeaux hospital	32	+MA
C60	<i>Campylobacter coli</i>	Chicken ressuage	31	+MA
C61	<i>Campylobacter jejuni</i>	Chicken ressuage	33	+MA
C62	<i>Campylobacter coli</i>	Evisceration turkey	30	+MA
C63	<i>Campylobacter jejuni</i>	Evisceration chicken	16	+MA

Exclusivity

Reference	Strain	Origin	Enumeration in 225 ml nutritive broth before incubation	CFA	Comment
Ba 1	<i>Bacillus cereus</i>	Egg	7,00E+05	Ø	
Ba 6	<i>Bacillus mycoides</i>	Collection	4,00E+05	Ø	
Ba 17	<i>Bacillus pumilus</i>	Custard	3,20E+05	Ø	
EN 9	<i>Enterobacter agglomerans</i>	Pork belly	8,00E+05	Ø	
EN 16	<i>Enterobacter cloacae</i>	Environment surface	6,20E+05	-LE	Dark red colony with irregular board and darker center
EN 22	<i>Enterobacter amnigenus</i>	Jambon	5,70E+05	Ø	
KL 38	<i>Klebsiella oxytoca</i>	Collection	3,00E+05	Ø	
HA 31	<i>Hafnia alvei</i>	Minced meat	4,20E+05	Ø	
PS 30	<i>Pseudomonas aeruginosa</i>	Mullet fillet	5,00E+05	Ø	
PS 85	<i>Pseudomonas putida</i>	Collection	7,00E+05	Ø	
PS 86	<i>Pseudomonas putida</i>	Collection	6,80E+05	Ø	
PS 33	<i>Pseudomonas fluorescens</i>	Vegetables	5,20E+05	Ø	
EN 43	<i>Proteus mirabilis</i>	Meat product	7,50E+05	Ø	
ST 13	<i>Staphylococcus aureus</i>	CIP 7625	3,80E+05	Ø	
ST 20	<i>Staphylococcus epidermidis</i>	Smoked salmon	4,20E+05	Ø	
18	<i>Aeromonas hydrophila</i>	Collection	3,00E+05	Ø	
40	<i>Acinetobacter baumannii</i>	Minced pork	9,00E+04	-LE	Dark red colony with irregular board and darker center
Ec 13	<i>Escherichia coli</i>	Parsley	8,10E+05	Ø	
S 15	<i>Salmonella hadar</i>	Poultry	5,00E+05	Ø	
CIT 23	<i>Citrobacter freundii</i>	Vegetables	4,50E+05	Ø	
EN 72	<i>Shigella flexneri</i>	Collection	3,20E+05	Ø	
ESC 14	<i>Escherichia hermanii</i>	Food for animals	5,70E+05	Ø	
PS 12	<i>Pseudomonas fluorescens</i>	Mineral water	6,00E+05	Ø	
56	<i>Acinetobacter calcoaeticus</i>	Collection	1,90E+05	-HE	Opaque pinkish flat colony
58	<i>Arcobacter cryoaerophilus</i>	Collection	9,60E+04	-HE	Brilliant red colony without metallic reflection
59	<i>Arcobacter butzleri</i>	Collection	2,20E+05	-HE	Brilliant red colony without metallic reflection
57	<i>Proteus vulgaris</i>	Collection	1,40E+05	Ø	
43526	<i>Helicobacter pylori</i>	Clinical sample	9,00E+04	-HE	Brilliant pinkish red colony
43504	<i>Helicobacter pylori</i>	Clinical sample	9,00E+04	-HE	Brilliant pinkish red colony
62	<i>Vibrio parahaemolyticus</i>	Collection	9,60E+04	Ø	
C40	<i>Campylobacter fetus</i>	Collection	3,00E+01	+HA	Culture realized in CFB at 25°C, no growth at 41.5°C
C41	<i>Campylobacter fetus</i>	Collection	2,10E+01	+HA	Culture realized in CFB at 25°C, no growth at 41.5°C
E1	<i>Enterococcus faecalis</i>	Egg	3,60E+05	Ø	
E6	<i>Enterococcus faecalis</i>	ATCC 19433	1,70E+05	Ø	

Accuracy *Escherichia coli*
Aeromonas hydrophila

Growth Dark red colony with irregular board and darker center
Growth Red purple colony without metallic reflection

APPENDIX D

INTERLABORATORY STUDY - LIST AND DETAILED RESULTS OF PARTICIPANT LABORATORIES

Name of laboratory	Address	Country
ADRIA Développement	Département Recherche et Innovation ZI de Creac'h Gwen 29000 Quimper	France
AFSCA	Chaussée de Namur, 22 - BE 5030 GEMBLoux	Belgium
CONEGAN Labo conseil	5, Parc d'activités de la Trésorerie - 62126 WIMILLE	France
FOODMICRO Kft Laboratoire de microbiologie	H-1047 BUDAPEST, Fóti út 56 - Hongrie	Hungary
IDHESA (LDV 29)	22, Av. de la Plage des Gueux 29334 QUIMPER Cédex	France
Istituto Zooprofilattico Sperimentale del Lazio e Toscana di Roma - Sede Centrale Roma	Via Appia Nuova, 1411 - Roma - Italy	Italy
Istituto Zooprofilattico Sperimentale Umbria e Marche - Lab. Contaminanti Biologici	Via G. Salvemini, 1 06126 Perugia - Italy	Italy
LDA 01 Laboratoire Départemental d'Analyses de l'Ain	Plateforme ALIMENTEC - Rue Henri de Boissieu - 01060 Bourg-en-Bresse	France
LDA 35	24, rue Antoine Joly - 35031 RENNES	France
RIVM-LZO	Postbak 63 PO Box 1 - 3720 BA Bilthoven - The Netherlands	Netherlands
SILLIKER	P.O. Box 153 6710 BD EDE	Netherlands
SILLIKER - Cergy	10 Les Châteaux St Sylvère - 95011 Cergy Cédex	France
SVA	Travvågen, 20 - UPPSALA - Suède	Sweden
SVU Olomouc	Jakoubka ze Stribra 1 - 779 00 Olomouc	Czech Republic
Université de Gent	Dienst PROF. DR. IR. J. DEBEVERE Coupure Links 653 Blok B - 4de	Belgium
Veterinärmedizinische Universität	Institut für Feishtechnologie und lebensmittelwissenschaft veterinärplatz 1 -	Austria
VISAVET	Avda Puerta de Hierro, S/N Ciudad Universitaria - 28040 Madrid	Spain

= : corresponding result
 # : discrepant result
 / : not realized (no characteristic colony)

INDIVIDUAL RESULTS OF PARTICIPATING LABORATORIES

Laboratory A Analyses realized at Day 1

Code sample	Reference method EN ISO 10272-1 #				Comparison / Expected result	Code sample	Alternative method CFB - CFA			Comparison / Expected result
	Presence of characteristic CFU		Confirmation	Final result**			Presence of characteristic CFU on CFA	VIDAS CAM confirmation Test result	Final result	
	mCCDA	Campyloset								
27	-	-	-	-	=	5	+	-	-	=
28	-	-	-	-	=	6	-	/	-	=
35	-	-	-	-	=	9	-	/	-	=
36	-	-	-	-	=	10	+	+	+	#
41	-	-	-	-	=	13	-	/	-	=
42	-	-	-	-	=	14	-	/	-	=
43	-	-	-	-	=	19	-	/	-	=
44	-	-	-	-	=	20	+	+	+	#
29	-	-	-	-	#	3	+	+	+	=
30	-	-	-	-	#	4	+	+	+	=
31	-	-	-	-	#	11	+	+	+	=
32	-	-	-	-	#	12	+	+	+	=
39	-	-	-	-	#	17	+	+	+	=
40	-	-	-	-	#	18	+	+	+	=
45	-	-	-	-	#	23	+	+	+	=
46	-	-	-	-	#	24	+	+	+	=
25	-	-	-	-	#	1	+	+	+	=
26	-	-	-	-	#	2	+	+	+	=
33	-	-	-	-	#	7	+	+	+	=
34	-	-	-	-	#	8	+	+	+	=
37	-	-	-	-	#	15	+	+	+	=
38	-	-	-	-	#	16	+	+	+	=
47	-	-	-	-	#	21	+	+	+	=
48	-	-	-	-	#	22	+	+	+	=

Total flora 30°C of poultry meat (CFU/g) : 1,1.10⁹

**Important interfering flora

Laboratory B Analyses realized at Day 1

Code sample	Reference method EN ISO 10272-1 #				Comparison / Expected result	Code sample	Alternative method CFB - CFA			Comparison / Expected result
	Presence of characteristic CFU		Confirmation	Final result**			Presence of characteristic CFU on CFA	VIDAS CAM confirmation Test result	Final result	
	mCCDA	Campyloset								
27	-	-	-	-	=	5	-	/	-	=
28	-	-	-	-	=	6	-	/	-	=
35	-	-	-	-	=	9	-	/	-	=
36	-	-	-	-	=	10	-	/	-	=
41	-	-	-	-	=	13	-	/	-	=
42	-	-	-	-	=	14	-	/	-	=
43	-	-	-	-	=	19	-	/	-	=
44	-	-	-	-	=	20	-	/	-	=
29	-	-	-	-	#	3	+	+	+	=
30	-	+	+	+	=	4	+	+	+	=
31	-	+	+	+	=	11	+	+	+	=
32	-	+	+	+	=	12	+	+	+	=
39	-	+	+	+	=	17	+	+	+	=
40	-	+	+	+	=	18	+	+	+	=
45	-	+	+	+	=	23	+	+	+	=
46	-	-	/	-	#	24	+	+	+	=
25	-	+	+	+	=	1	+	+	+	=
26	-	+	+	+	=	2	+	+	+	=
33	+	-	+	+	=	7	+	+	+	=
34	-	+	+	+	=	8	+	+	+	=
37	-	+	+	+	=	15	+	+	+	=
38	-	+	+	+	=	16	+	+	+	=
47	-	+	+	+	=	21	+	+	+	=
48	-	+	+	+	=	22	+	+	+	=

Total flora 30°C of poultry meat (CFU/g) : 7,7.10⁹

**Important interfering flora

Laboratory C Analyses realized at Day 2

Code sample	Reference method EN ISO 10272-1 #				Comparison / Expected result	Code sample	Alternative method CFB - CFA			Comparison / Expected result
	Presence of characteristic CFU		Confirmation	Final result**			Presence of suspect CFU on CFA	VIDAS CAM confirmation Test result	Final result	
	mCCDA	Campyloset								
27	-	-	-	-	=	5	-	/	-	=
28	-	-	-	-	=	6	-	/	-	=
35	-	-	-	-	=	9	+	+	+	#
36	-	-	-	-	=	10	+	+	+	#
41	-	-	-	-	=	13	-	/	-	=
42	-	-	-	-	=	14	-	/	-	=
43	-	-	-	-	=	19	-	/	-	=
44	-	-	-	-	=	20	-	/	-	=
29	-	-	-	-	#	3	+	+	+	=
30	-	-	-	-	#	4	+	+	+	=
31	-	-	-	-	#	11	+	+	+	=
32	-	-	-	-	#	12	+	+	+	=
39	-	-	-	-	#	17	+	+	+	=
40	-	-	-	-	#	18	+	+	+	=
45	-	-	-	-	#	23	+	+	+	=
46	-	-	-	-	#	24	+	+	+	=
25	-	-	-	-	#	1	+	+	+	=
26	-	-	-	-	#	2	+	+	+	=
33	-	-	-	-	#	7	+	+	+	=
34	-	-	-	-	#	8	+	+	+	=
37	-	-	-	-	#	15	+	+	+	=
38	-	-	-	-	#	16	+	+	+	=
47	-	-	-	-	#	21	+	+	+	=
48	-	-	-	-	#	22	+	+	+	=

Total flora 30°C of poultry meat (CFU/g) : >3.10⁸

**Important interfering flora

= : corresponding result
 # : discrepant result
 / : not realized (no characteristic colony)

INDIVIDUAL RESULTS OF PARTICIPATING LABORATORIES

Laboratory D

Analyses realized at Day 1

Code sample	Reference method EN ISO 10272-1 #				Comparison / Expected result	Code sample	Alternative method CFB - CFA			Comparison / Expected result
	Presence of characteristic CFU		Confirmation	Final result**			Presence of characteristic CFU on CFA	VIDAS CAM confirmation Test result	Final result	
	mCCDA	Campyloset								
27	+	-	-	-	=	5	-	/	-	=
28	+	+	+	+	#	6	-	/	-	=
35	+	+	-	-	=	9	-	/	-	=
36	+	+	-	-	=	10	-	/	-	=
41	+	-	-	-	=	13	-	/	-	=
42	+	+	+	+	#	14	-	/	-	=
43	+	-	-	-	=	19	-	/	-	=
44	+	-	-	-	=	20	-	/	-	=
29	+	+	+	+	=	3	+	+	+	=
30	+	-	-	-	#	4	+	+	+	=
31	+	-	-	-	#	11	+	+	+	=
32	+	-	-	-	#	12	+	+	+	=
39	+	+	+	+	=	17	+	+	+	=
40	+	-	-	-	#	18	+	+	+	=
45	+	+	-	-	#	23	+	+	+	=
46	+	+	+	+	=	24	+	+	+	=
25	+	+	+	+	=	1	+	+	+	=
26	+	+	+	+	=	2	+	+	+	=
33	+	+	+	+	=	7	+	+	+	=
34	+	-	-	-	#	8	+	+	+	=
37	+	-	-	-	#	15	+	+	+	=
38	+	+	-	-	#	16	+	+	+	=
47	+	+	+	+	=	21	+	+	+	=
48	+	+	+	+	=	22	+	+	+	=

Total flora 30°C of poultry meat (CFU/g) : >3.10⁸

**Important interfering flora

Laboratory E

Analyses realized at Day 1

Code sample	Reference method EN ISO 10272-1 #				Comparison / Expected result	Code sample	Alternative method CFB - CFA			Comparison / Expected result
	Presence of characteristic CFU		Confirmation	Final result**			Presence of characteristic CFU on CFA	VIDAS CAM confirmation Test result	Final result	
	mCCDA	Campyloset								
27	+	+	+	+	#	5	-	/	-	=
28	+	+	+	+	#	6	-	/	-	=
35	+	+	+	+	#	9	-	/	-	=
36	+	+	+	+	#	10	-	/	-	=
41	+	+	+	+	#	13	-	/	-	=
42	+	+	+	+	#	14	-	/	-	=
43	-	-	-	-	=	19	-	/	-	=
44	-	-	-	-	=	20	-	/	-	=
29	+	+	-	-	#	3	+	+	+	=
30	+	+	-	-	#	4	+	+	+	=
31	+	+	+	+	=	11	+	+	+	=
32	+	+	+	+	=	12	+	+	+	=
39	+	+	+	+	=	17	+	+	+	=
40	+	+	+	+	=	18	+	+	+	=
45	+	+	+	+	=	23	+	+	+	=
46	+	+	+	+	=	24	+	+	+	=
25	+	+	+	+	=	1	+	+	+	=
26	+	+	+	+	=	2	+	+	+	=
33	+	+	-	-	#	7	+	+	+	=
34	+	+	-	-	#	8	+	+	+	=
37	+	+	-	-	#	15	+	+	+	=
38	+	+	-	-	#	16	+	+	+	=
47	+	+	+	+	=	21	+	+	+	=
48	+	+	+	+	=	22	+	+	+	=

Total flora 30°C of poultry meat (CFU/g) : 8,1.10⁷ UFC/g

Laboratory G

Analyses realized at Day 1

Code sample	Reference method EN ISO 10272-1 #				Comparison / Expected result	Code sample	Alternative method CFB - CFA			Comparison / Expected result
	Presence of characteristic CFU		Confirmation	Final result**			Presence of characteristic CFU on CFA	VIDAS CAM confirmation Test result	Final result	
	mCCDA	Campyloset								
27	-	+	+	+	#	5	-	/	-	=
28	-	+	+	+	#	6	-	/	-	=
35	-	+	+	+	#	9	+	+	+	#
36	+	+	+	+	#	10	-	+	+	#
41	-	-	-	-	=	13	-	/	-	=
42	-	-	-	-	=	14	+	-	-	=
43	-	-	-	-	=	19	+	-	-	=
44	+	-	-	-	=	20	+	-	-	=
29	-	-	-	-	#	3	+	+	+	=
30	-	-	-	-	#	4	+	+	+	=
31	-	-	-	-	#	11	+	+	+	=
32	+	-	-	-	#	12	+	+	+	=
39	+	-	-	-	#	17	+	+	+	=
40	-	-	-	-	#	18	+	+	+	=
45	-	-	-	-	#	23	+	+	+	=
46	+	+	+	+	=	24	+	+	+	=
25	+	+	+	+	=	1	+	+	+	=
26	+	-	-	-	#	2	+	+	+	=
33	+	-	-	-	#	7	+	+	+	=
34	-	+	+	+	=	8	+	+	+	=
37	+	+	+	+	=	15	+	+	+	=
47	-	-	-	-	#	16	+	+	+	=
48	+	+	+	+	=	21	+	+	+	=
48	-	+	+	+	=	22	+	+	+	=

Total flora 30°C of poultry meat (CFU/g) : >3.0.10⁸ UFC/g

**Important interfering flora

= : corresponding result
 # : discrepant result
 / : not realized (no characteristic colony)

INDIVIDUAL RESULTS OF PARTICIPATING LABORATORIES

Laboratory H

Analyses realized at Day 1

Code sample	Reference method EN ISO 10272-1 #				Comparison / Expected result	Code sample	Alternative method CFB - CFA			Comparison / Expected result
	Presence of characteristic CFU		Confirmation	Final result**			Presence of characteristic CFU on CFA	VIDAS CAM confirmation Test result	Final result	
	mCCDA	Campyloset								
27	-	-	/	-	=	5	-	/	-	=
28	-	-	/	-	=	6	-	/	-	=
35	-	-	/	-	=	9	-	/	-	=
36	-	-	/	-	=	10	-	/	-	=
41	-	-	/	-	=	13	-	/	-	=
42	-	-	/	-	=	14	-	/	-	=
43	-	-	/	-	=	19	-	/	-	=
44	-	-	/	-	=	20	-	/	-	=
29	-	-	/	-	#	3	+	+	+	=
30	-	-	/	-	#	4	+	+	+	=
31	-	-	/	-	#	11	+	+	+	=
32	-	-	/	-	#	12	+	+	+	=
39	-	-	/	-	#	17	+	+	+	=
40	+	+	+	+	=	18	+	+	+	=
45	-	-	/	-	#	23	+	+	+	=
46	-	-	/	-	#	24	+	+	+	=
25	-	+	+	+	=	1	+	+	+	=
26	+	+	+	+	=	2	+	+	+	=
33	+	+	+	+	=	7	+	+	+	=
34	+	+	+	+	=	8	+	+	+	=
37	+	+	+	+	=	15	+	+	+	=
38	-	-	/	-	#	16	+	+	+	=
47	+	+	+	+	=	21	+	+	+	=
48	+	+	+	+	=	22	+	+	+	=

Total flora 30°C of poultry meat (CFU/g) : >3,10⁸ UFC/g

**Important interfering flora

Laboratory J

Reception at D2 (13 °C)

Code sample	Reference method EN ISO 10272-1 #				Comparison / Expected result	Code sample	Alternative method CFB - CFA			Comparison / Expected result
	Presence of characteristic CFU		Confirmation	Final result**			Presence of suspect CFU on CFA	VIDAS CAM confirmation Test result	Final result	
	mCCDA	Campyloset								
27	-	-	-	-	=	5	+	-	-	=
28	-	-	-	-	=	6	+	-	-	=
35	-	-	-	-	=	9	-	/	-	=
36	-	-	-	-	=	10	+	-	-	=
41	-	-	-	-	=	13	-	/	-	=
42	-	-	-	-	=	14	+	-	-	=
43	-	-	-	-	=	19	-	-	-	=
44	-	-	-	-	=	20	-	-	-	=
29	-	-	-	-	#	3	+	+	+	=
30	-	-	-	-	#	4	+	+	+	=
31	-	-	-	-	#	11	+	+	+	=
32	-	-	-	-	#	12	+	+	+	=
39	-	-	-	-	#	17	+	+	+	=
40	-	-	-	-	#	18	+	+	+	=
45	-	-	-	-	#	23	+	+	+	=
46	-	-	-	-	#	24	+	+	+	=
25	-	-	-	-	#	1	+	+	+	=
26	-	-	-	-	#	2	+	+	+	=
33	-	-	-	-	#	7	+	+	+	=
34	-	-	-	-	#	8	+	+	+	=
37	-	-	-	-	#	15	+	+	+	=
38	-	-	-	-	#	16	+	+	+	=
47	-	-	-	-	#	21	+	+	+	=
48	-	-	-	-	#	22	+	+	+	=

Total flora 30°C of poultry meat (CFU/g) : 4,4.10⁹

**Important interfering flora

Laboratory K

Analyses realized at Day 1

Code sample	Reference method EN ISO 10272-1 #				Comparison / Expected result	Code sample	Alternative method CFB - CFA			Comparison / Expected result
	Presence of characteristic CFU		Confirmation	Final result**			Presence of characteristic CFU on CFA	VIDAS CAM confirmation Test result	Final result	
	mCCDA	Campyloset								
27	-	+	-	-	=	5	+	-	-	=
28	-	+	-	-	=	6	+	-	-	=
35	-	+	-	-	=	9	-	/	-	=
36	-	+	-	-	=	10	-	/	-	=
41	-	+	-	-	=	13	-	/	-	=
42	-	+	-	-	=	14	-	/	-	=
43	-	+	-	-	=	19	-	/	-	=
44	-	+	-	-	=	20	-	/	-	=
29	-	+	-	-	#	3	+	+	+	=
30	-	+	-	-	#	4	+	+	+	=
31	-	+	-	-	#	11	+	+	+	=
32	-	+	-	-	#	12	+	+	+	=
39	-	+	-	-	#	17	+	+	+	=
40	-	+	-	-	#	18	+	+	+	=
45	-	+	-	-	#	23	+	+	+	=
46	-	+	-	-	#	24	+	+	+	=
25	-	+	-	-	#	1	+	+	+	=
26	-	+	-	-	#	2	+	+	+	=
33	-	+	-	-	#	7	+	+	+	=
34	-	+	-	-	#	8	+	+	+	=
37	-	+	-	-	#	15	+	+	+	=
38	-	+	-	-	#	16	+	+	+	=
47	-	+	-	-	#	21	+	+	+	=
48	-	+	-	-	#	22	+	+	+	=

Total flora 30°C of poultry meat (CFU/g) : 9,4.10⁷

**Important interfering flora

= : corresponding result
 # : discrepant result
 / : not realized (no characteristic colony)

INDIVIDUAL RESULTS OF PARTICIPATING LABORATORIES

Laboratory L

Analyses realized at Day 1

Code sample	Reference method EN ISO 10272-1 #				Comparison / Expected result	Code sample	Alternative method CFB - CFA			Comparison / Expected result
	Presence of characteristic CFU		Confirmation	Final result**			Presence of characteristic CFU on CFA	VIDAS CAM confirmation	Final result	
	mCCDA	Campyloset						Test result		
27	+	+	+	+	#	5	-	/	-	=
28	-	-	-	-	=	6	-	/	-	=
35	+	+	+	+	#	9	+	-	-	=
36	-	-	-	-	=	10	+	-	-	=
41	-	-	-	-	=	13	-	/	-	=
42	+	+	+	+	#	14	-	/	-	=
43	+	+	+	+	#	19	-	/	-	=
44	+	+	+	+	#	20	-	/	-	=
29	+	+	+	+	=	3	-	/	-	#
30	+	+	+	+	=	4	-	/	-	#
31	+	+	+	+	=	11	+	/	-	#
32	-	-	-	-	#	12	+	+	+	=
39	-	-	-	-	#	17	+	+	+	=
40	-	-	-	-	#	18	+	+	+	=
45	+	+	+	+	=	23	+	+	+	=
46	+	+	+	+	=	24	+	+	+	=
25	+	+	+	+	=	1	-	/	-	#
26	-	-	-	-	#	2	-	/	-	#
33	+	+	+	+	=	7	+	+	+	=
34	+	+	+	+	=	8	+	+	+	=
37	+	+	+	+	=	15	+	+	+	=
38	-	-	-	-	#	16	+	+	+	=
47	+	+	+	+	=	21	+	+	+	=
48	+	+	+	+	=	22	+	+	+	=

Total flora 30°C of poultry meat (CFU/g) : 2,8.10⁹

Laboratory M

Analyses realized at Day 1

Code sample	Reference method EN ISO 10272-1 #				Comparison / Expected result	Code sample	Alternative method CFB - CFA			Comparison / Expected result
	Presence of characteristic CFU		Confirmation	Final result**			Presence of characteristic CFU on CFA	VIDAS CAM confirmation	Final result	
	mCCDA	Campyloset						Test result		
27	+	+	+	+	#	5	+	-	-	=
28	+	-	-	-	=	6	+	-	-	=
35	-	-	-	-	=	9	+	-	-	=
36	+	+	+	+	#	10	+	-	-	=
41	-	+	-	-	=	13	+	-	-	=
42	+	+	+	+	#	14	+	+	+	#
43	-	-	-	-	=	19	+	-	-	=
44	+	-	-	-	=	20	+	-	-	=
29	+	+	+	+	=	3	+	+	+	=
30	-	-	-	-	#	4	+	+	+	=
31	-	-	-	-	#	11	+	+	+	=
32	+	+	+	+	=	12	+	-	-	#
39	+	+	+	+	=	17	+	+	+	=
40	+	+	+	+	=	18	+	+	+	=
45	-	-	-	-	#	23	+	+	+	=
46	-	-	-	-	#	24	+	+	+	=
25	+	+	+	+	=	1	+	+	+	=
26	+	+	+	+	=	2	+	+	+	=
33	+	+	+	+	=	7	+	+	+	=
34	-	+	-	-	#	8	+	+	+	=
37	-	-	-	-	#	15	+	+	+	=
38	+	+	+	+	=	16	+	+	+	=
47	+	+	+	+	=	21	+	+	+	=
48	+	+	+	+	=	22	+	+	+	=

Total flora 30°C of poultry meat (CFU/g) : 3,6.10⁷

Laboratory N

Analyses realized at Day 1

Code sample	Reference method EN ISO 10272-1 #				Comparison / Expected result	Code sample	Alternative method CFB - CFA			Comparison / Expected result
	Presence of characteristic CFU		Confirmation	Final result**			Presence of characteristic CFU on CFA	VIDAS CAM confirmation	Final result	
	mCCDA	Campyloset						Test result		
27	-	-	-	-	=	5	-	/	-	=
28	-	-	-	-	=	6	+	+	+	#
35	-	-	-	-	=	9	-	/	-	=
36	-	-	-	-	=	10	-	/	-	=
41	-	-	-	-	=	13	-	/	-	=
42	-	-	-	-	=	14	-	/	-	=
43	-	-	-	-	=	19	-	/	-	=
44	-	-	-	-	=	20	-	/	-	=
29	-	-	-	-	#	3	+	+	+	=
30	-	-	-	-	#	4	+	+	+	=
31	-	-	-	-	#	11	+	+	+	=
32	-	-	-	-	#	12	+	+	+	=
39	-	-	-	-	#	17	+	+	+	=
40	-	-	-	-	#	18	+	+	+	=
45	-	-	-	-	#	23	+	+	+	=
46	-	-	-	-	#	24	+	+	+	=
25	-	-	-	-	#	1	+	+	+	=
26	-	-	-	-	#	2	+	+	+	=
33	-	-	-	-	#	7	+	+	+	=
34	-	-	-	-	#	8	+	+	+	=
37	-	-	-	-	#	15	+	+	+	=
38	-	-	-	-	#	16	+	+	+	=
47	-	-	-	-	#	21	+	+	+	=
48	-	-	-	-	#	22	+	+	+	=

Total flora 30°C of poultry meat (CFU/g) : 2,9.10⁷

**Important interfering flora

= : corresponding result
 # : discrepant result
 / : not realized (no characteristic colony)

INDIVIDUAL RESULTS OF PARTICIPATING LABORATORIES

Laboratory O Analyses realized at Day 1

Code sample	Reference method EN ISO 10272-1 #				Comparison / Expected result	Code sample	Alternative method CFB - CFA			Comparison / Expected result
	Presence of characteristic CFU		Confirmation	Final result**			Presence of characteristic CFU on CFA	VIDAS CAM confirmation Test result	Final result	
	mCCDA	Campyloset								
27	-	-	-	-	=	5	-	/	-	=
28	-	-	-	-	=	6	+	+	+	#
35	-	-	-	-	=	9	-	/	-	=
36	-	-	-	-	=	10	-	/	-	=
41	-	-	-	-	=	13	-	/	-	=
42	-	-	-	-	=	14	-	/	-	=
43	-	-	-	-	=	19	-	/	-	=
44	-	-	-	-	=	20	-	/	-	=
29	-	-	-	-	#	3	+	+	+	=
30	-	-	-	-	#	4	+	+	+	=
31	-	-	-	-	#	11	+	+	+	=
32	-	-	-	-	#	12	+	+	+	=
39	-	+	+	+	=	17	-	-	-	#
40	-	-	-	-	#	18	+	+	+	=
45	-	-	-	-	#	23	+	+	+	=
46	-	-	-	-	#	24	+	+	+	=
25	-	+	+	+	=	1	+	+	+	=
26	-	-	-	-	#	2	+	+	+	=
33	-	-	-	-	#	7	+	+	+	=
34	-	-	-	-	#	8	+	+	+	=
37	-	-	-	-	#	15	+	+	+	=
38	-	-	-	-	#	16	+	+	+	=
47	-	-	-	-	#	21	+	+	+	=
48	-	-	-	-	#	22	+	+	+	=

Total flora 30°C of poultry meat (CFU/g) : 2,9.10⁷

Laboratory P Analyses realized at Day 2

Code sample	Reference method EN ISO 10272-1 #				Comparison / Expected result	Code sample	Alternative method CFB - CFA			Comparison / Expected result
	Presence of characteristic CFU		Confirmation	Final result**			Presence of characteristic CFU on CFA	VIDAS CAM confirmation Test result	Final result	
	mCCDA	Campyloset								
27	-	-	-	-	=	5	-	/	-	=
28	-	-	-	-	=	6	-	/	-	=
35	-	-	-	-	=	9	+	+	+	#
36	-	-	-	-	=	10	-	/	-	=
41	-	-	-	-	=	13	-	/	-	=
42	-	-	-	-	=	14	-	/	-	=
43	-	-	-	-	=	19	-	/	-	=
44	-	-	-	-	=	20	-	/	-	=
29	-	-	-	-	#	3	+	+	+	=
30	-	-	-	-	#	4	+	+	+	=
31	-	-	-	-	#	11	+	+	+	=
32	-	-	-	-	#	12	+	+	+	=
39	-	-	-	-	#	17	+	+	+	=
40	-	-	-	-	#	18	+	+	+	=
45	-	-	-	-	#	23	+	+	+	=
46	-	-	-	-	#	24	+	+	+	=
25	-	-	-	-	#	1	+	+	+	=
26	-	-	-	-	#	2	+	+	+	=
33	-	-	-	-	#	7	+	+	+	=
34	-	-	-	-	#	8	+	+	+	=
37	-	-	-	-	#	15	+	+	+	=
38	-	-	-	-	#	16	+	+	+	=
47	-	-	-	-	#	21	+	+	+	=
48	-	-	-	-	#	22	+	+	+	=

Total flora 30°C of poultry meat (CFU/g) : 5,5.10⁷

**Important interfering flora which can mask *Campylobacter* spp

Laboratory Q Analyses realized at Day 1

Code sample	Reference method EN ISO 10272-1 #				Comparison / Expected result	Code sample	Alternative method CFB - CFA			Comparison / Expected result
	Presence of characteristic CFU		Confirmation	Final result**			Presence of characteristic CFU on CFA	VIDAS CAM confirmation Test result	Final result	
	mCCDA	Campyloset								
27	+	-	-	-	=	5	-	/	-	=
28	-	-	-	-	=	6	-	/	-	=
35	-	-	-	-	=	9	-	/	-	=
36	-	-	-	-	=	10	-	/	-	=
41	-	-	-	-	=	13	-	/	-	=
42	-	-	-	-	=	14	-	/	-	=
43	-	-	-	-	=	19	-	/	-	=
44	-	-	-	-	=	20	-	/	-	=
29	-	-	-	-	#	3	+	+	+	=
30	-	-	-	-	#	4	+	+	+	=
31	-	-	-	-	#	11	+	+	+	=
32	-	-	-	-	#	12	+	+	+	=
39	+	+	+	+	=	17	+	+	+	=
40	-	-	-	-	#	18	+	+	+	=
45	-	-	-	-	#	23	+	+	+	=
46	-	-	-	-	#	24	+	+	+	=
25	+	+	+	+	=	1	+	+	+	=
26	-	-	-	-	#	2	+	+	+	=
33	+	+	+	+	=	7	+	+	+	=
34	-	-	-	-	#	8	+	+	+	=
37	-	-	-	-	#	15	+	+	+	=
38	+	+	+	+	=	16	+	+	+	=
47	+	+	+	+	=	21	+	+	+	=
48	+	+	+	+	=	22	+	+	+	=

Total flora 30°C of poultry meat (CFU/g) : 8,7.10⁷

APPENDIX E

INTERLABORATORY STUDY - ACCORDANCE

ALTERNATIVE METHOD

Level L0

Laboratory	Nb of negatives expected	Nb of negatives obtained	Probability of negatives	Probability of negatives pairs	Probability of positives	Probability of positive pairs	Probability of identical result pairs
A	8	6	0,75	0,56	0,25	0,06	0,63
B	8	8	1,00	1,00	0,00	0,00	1,00
D	8	8	1,00	1,00	0,00	0,00	1,00
E	8	8	1,00	1,00	0,00	0,00	1,00
G	8	6	0,75	0,56	0,25	0,06	0,63
H	8	8	1,00	1,00	0,00	0,00	1,00
K	8	8	1,00	1,00	0,00	0,00	1,00
M	8	7	0,88	0,77	0,13	0,02	0,78
N	8	7	0,88	0,77	0,13	0,02	0,78
O	8	7	0,88	0,77	0,13	0,02	0,78
Q	8	8	1,00	1,00	0,00	0,00	1,00
Mean :							0,87
Accordance :							87%

Level L1

Laboratory	Nb of positives expected	Nb of positives obtained	Probability of positives	Probability of positives pairs	Probability of negatives	Probability of negative pairs	Probability of identical result pairs
A	8	8	1,00	1,00	0,00	0,00	1,00
B	8	8	1,00	1,00	0,00	0,00	1,00
D	8	8	1,00	1,00	0,00	0,00	1,00
E	8	8	1,00	1,00	0,00	0,00	1,00
G	8	8	1,00	1,00	0,00	0,00	1,00
H	8	8	1,00	1,00	0,00	0,00	1,00
K	8	8	1,00	1,00	0,00	0,00	1,00
M	8	7	0,88	0,77	0,13	0,02	0,78
N	8	8	1,00	1,00	0,00	0,00	1,00
O	8	7	0,88	0,77	0,13	0,02	0,78
Q	8	8	1,00	1,00	0,00	0,00	1,00
Mean :							0,96
Accordance :							96%

Level L2

Laboratory	Nb of positives expected	Nb of positives obtained	Probability of positives	Probability of positives pairs	Probability of negatives	Probability of negative pairs	Probability of identical result pairs
A	8	8	1,00	1,00	0,00	0,00	1,00
B	8	8	1,00	1,00	0,00	0,00	1,00
D	8	8	1,00	1,00	0,00	0,00	1,00
E	8	8	1,00	1,00	0,00	0,00	1,00
G	8	8	1,00	1,00	0,00	0,00	1,00
H	8	8	1,00	1,00	0,00	0,00	1,00
K	8	8	1,00	1,00	0,00	0,00	1,00
M	8	8	1,00	1,00	0,00	0,00	1,00
N	8	8	1,00	1,00	0,00	0,00	1,00
O	8	8	1,00	1,00	0,00	0,00	1,00
Q	8	8	1,00	1,00	0,00	0,00	1,00
Mean :							1,00
Accordance :							100%

REFERENCE METHOD

Level L0

Laboratory	Nb of negatives expected	Nb of negatives obtained	Probability of negatives	Probability of negatives pairs	Probability of positives	Probability of positive pairs	Probability of identical result pairs
A	8	8	1,00	1,00	0,00	0,00	1,00
B	8	8	1,00	1,00	0,00	0,00	1,00
D	8	6	0,75	0,56	0,25	0,06	0,63
E	8	2	0,25	0,06	0,75	0,56	0,63
G	8	4	0,50	0,25	0,50	0,25	0,50
H	8	8	1,00	1,00	0,00	0,00	1,00
K	8	8	1,00	1,00	0,00	0,00	1,00
M	8	5	0,63	0,39	0,38	0,14	0,53
N	8	8	1,00	1,00	0,00	0,00	1,00
O	8	8	1,00	1,00	0,00	0,00	1,00
Q	8	8	1,00	1,00	0,00	0,00	1,00
Mean :							0,84
Accordance :							84%

Level L1

Laboratory	Nb of positives expected	Nb of positives obtained	Probability of positives	Probability of positives pairs	Probability of negatives	Probability of negative pairs	Probability of identical result pairs
A	8	0	0,00	0,00	1,00	1,00	1,00
B	8	6	0,75	0,56	0,25	0,06	0,63
D	8	3	0,38	0,14	0,63	0,39	0,53
E	8	6	0,75	0,56	0,25	0,06	0,63
G	8	1	0,13	0,02	0,88	0,77	0,78
H	8	1	0,13	0,02	0,88	0,77	0,78
K	8	0	0,00	0,00	1,00	1,00	1,00
M	8	4	0,50	0,25	0,50	0,25	0,50
N	8	0	0,00	0,00	1,00	1,00	1,00
O	8	1	0,13	0,02	0,88	0,77	0,78
Q	8	1	0,13	0,02	0,88	0,77	0,78
Mean :							0,76
Accordance :							76%

Level L2

Laboratory	Nb of positives expected	Nb of positives obtained	Probability of positives	Probability of positives pairs	Probability of negatives	Probability of negative pairs	Probability of identical result pairs
A	8	0	0,00	0,00	1,00	1,00	1,00
B	8	8	1,00	1,00	0,00	0,00	1,00
D	8	5	0,63	0,39	0,38	0,14	0,53
E	8	4	0,50	0,25	0,50	0,25	0,50
G	8	5	0,63	0,39	0,38	0,14	0,53
H	8	7	0,88	0,77	0,13	0,02	0,78
K	8	0	0,00	0,00	1,00	1,00	1,00
M	8	6	0,75	0,56	0,25	0,06	0,63
N	8	0	0,00	0,00	1,00	1,00	1,00
O	8	1	0,13	0,02	0,88	0,77	0,78
Q	8	5	0,63	0,39	0,38	0,14	0,53
Mean :							0,75
Accordance :							75%

APPENDIX F

INTERLABORATORY STUDY - CONCORDANCE

ALTERNATIVE METHOD

Number of laboratories 11
 Number of negatives per laboratory 8

Level L0

Laboratory	Nb of negatives expected	Nb of negatives obtained	Inter-laboratory pairs with the same result	Total number of inter-laboratory pairs
A	8	6	460	640
B	8	8	584	640
D	8	8	584	640
E	8	8	584	640
G	8	6	460	640
H	8	8	584	640
K	8	8	584	640
M	8	7	524	640
N	8	7	524	640
O	8	7	524	640
Q	8	8	584	640
Total			5996	7040
Concordance	85,17%			

Number of laboratories 11
 Number of negatives per laboratory 8

Level L1

Laboratory	Nb of positives expected	Nb of positives obtained	Inter-laboratory pairs with the same result	Total number of inter-laboratory pairs
A	8	8	624	640
B	8	8	624	640
D	8	8	624	640
E	8	8	624	640
G	8	8	624	640
H	8	8	624	640
K	8	8	624	640
M	8	7	554	640
N	8	8	624	640
O	8	7	554	640
Q	8	8	624	640
Total			6724	7040
Concordance	95,51%			

Number of laboratories 11
 Number of negatives per laboratory 8

Level L2

Laboratory	Nb of positives expected	Nb of positives obtained	Inter-laboratory pairs with the same result	Total number of inter-laboratory pairs
A	8	8	640	640
B	8	8	640	640
D	8	8	640	640
E	8	8	640	640
G	8	8	640	640
H	8	8	640	640
K	8	8	640	640
M	8	8	640	640
N	8	8	640	640
O	8	8	640	640
Q	8	8	640	640
Total			7040	7040
Concordance	100,00%			

REFERENCE METHOD

Number of laboratories 11
 Number of negatives per laboratory 8

Level L0

Laboratory	Nb of negatives expected	Nb of negatives obtained	Inter-laboratory pairs with the same result	Total number of inter-laboratory pairs
A	8	8	520	640
B	8	8	520	640
D	8	6	428	640
E	8	2	196	640
G	8	4	320	640
H	8	8	520	640
K	8	8	520	640
M	8	5	376	640
N	8	8	520	640
O	8	8	520	640
Q	8	8	520	640
Total			4960	7040
Concordance	70,45%			

Number of laboratories 11
 Number of negatives per laboratory 8

Level L1

Laboratory	Nb of positives expected	Nb of positives obtained	Inter-laboratory pairs with the same result	Total number of inter-laboratory pairs
A	8	0	456	640
B	8	6	228	640
D	8	3	360	640
E	8	6	228	640
G	8	1	428	640
H	8	1	428	640
K	8	0	456	640
M	8	4	320	640
N	8	0	456	640
O	8	1	428	640
Q	8	1	428	640
Total			4216	7040
Concordance	59,89%			

Number of laboratories 11
 Number of negatives per laboratory 8

Level L2

Laboratory	Nb of positives expected	Nb of positives obtained	Inter-laboratory pairs with the same result	Total number of inter-laboratory pairs
A	8	0	312	640
B	8	8	264	640
D	8	5	312	640
E	8	4	320	640
G	8	5	312	640
H	8	7	284	640
K	8	0	312	640
M	8	6	300	640
N	8	0	312	640
O	8	1	320	640
Q	8	5	312	640
Total			3360	7040
Concordance	47,73%			