National Reference Laboratory for bacteriological contamination of bivalve molluscs

Generic protocol - Enumeration of *Escherichia coli* in bivalve molluscan shellfish by the colony-count technique (based on ISO 16649-2)

Note: For official control testing in the UK, either this document or the NRL generic protocol for enumeration of *Escherichia coli* in bivalve molluscan shellfish by the most probable number (MPN) technique (based on ISO 16649-3) must be used

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History of Procedure

Issue	Date	Section	Changes
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1. Introduction

The risks of infectious human diseases acquired from the consumption of bivalve molluscan shellfish (BMS) are internationally recognised. These health hazards are largely due to the phenomenon of filter-feeding whereby BMS concentrate and retain various bacterial and viral pathogens, often derived from sewage contamination of their growing waters. The risks of exposure to infectious agents are compounded by the traditional consumption of raw, or only lightly cooked, BMS. Historically, enteric bacteria, such as faecal coliforms, have been adopted as surrogate indicator organisms to assess the quality of bivalve shellfish flesh, and, consequently, to predict the risk of exposure to enteric pathogenic viruses.

In the UK, the criteria for laying down the microbiological standards for BMS are set out in Retained Regulation (EC) 2017/625 (Anon, 2017a) and Retained Regulation (EC) 2073/2005 (Anon, 2005a) for classification and end product testing respectively. In these regulations *Escherichia coli* is used as an indicator of faecal contamination of shellfish and the reference method for enumeration of *E. coli* is stated as the most probable number (MPN) technique based on ISO 16649-3 (Anon, 2015). These regulations further stipulate that alternative methods may be used if they are validated according to the criteria in ISO 16140.

In 2010, the RIKILT Institute of Food Safety, Wageningen University, the Netherlands undertook a validation study (Jacobs-Reitsma and Pol-Hofstad, 2010) to demonstrate the suitability of a colonycount (pour plate) protocol for enumeration of *E. coli* that it had developed based upon ISO 16649-2 (Anon, 2001) as an alternative method to the MPN. This validation was carried out according to ISO 16140:2003 (Anon, 2003). The validation was certified at the time by MicroVal as an independent certification body and further approved by Cefas as the EURL. A further validation study on the colony-count method using the original study data was carried out by the National Institute for Public Health and the Environment, the Netherlands, in 2021 (Pol-Hofstad and Jacobs-Reitsma, 2021) to reflect updated validation criteria in ISO 16140-2:2016 (Anon, 2016).

The colony-count method is currently listed as one of two accepted alternative methods in the EU Community Guide to the Principles of Good Practice for the Microbiological Classification and Monitoring of Bivalve Mollusc Production and Relaying Areas with regard to Implementing Regulation 2019/627 (Anon, 2021).

2. Scope

This protocol has been produced with reference to ISO 16649-2 (Anon, 2001), relevant parts of other ISO standards referenced in Section 11, and the two validation studies carried out in the Netherlands (Jacobs-Reitsma and Pol-Hofstad, 2010; Pol-Hofstad and Jacobs-Reitsma, 2021). In the context of this test detectable *E. coli* expresses β -glucuronidase activity at 44±1°C.

Note: This method has only been validated for BMS and is not recommended for analysis of other marine shellfish species e.g. gastropods and echinoderms.

3. Principle

The method used to enumerate *E. coli* in BMS is a pour plate, colony-count technique. Diluted bivalve shellfish homogenate is mixed with TBGA/TBX medium in sterile Petri dishes and incubated at $37\pm1^{\circ}$ C for 4 ± 0.5 hours (resuscitation step). The inoculated TGBA/TBX plates are then transferred to $44\pm1^{\circ}$ C for a further 18-24 hours. *E. coli* is confirmed by the presence of blue/green colonies within the medium indicative of β -glucuronidase activity.

Note: Strains of *E. coli* that do not grow at $44\pm1^{\circ}$ C and those that are β -glucuronidase negative, such as *E. coli* O157 and some other strains of pathogenic *E. coli*, will not be detected by this method.

4. Safety precautions

Standard microbiology safety precautions should be applied throughout. Laboratories should perform a full risk assessment before performing this procedure. Homogenisation of bivalve shellfish should be performed in a Class II safety cabinet to reduce the risk of infection from aerosol inhalation. *E. coli* should be handled in accordance with ACDP category 2 guidelines.

5. Equipment

- Waring blender and jars or Stomacher and stomacher bags
- Class II safety cabinet
- Refrigerator at 3±2°C
- Sterile glassware
- Protective gloves single use
- Safety gloves for example a chain mail glove
- Incubator at 37±1°C and 44±1°C
- Electric top pan balance
- Pipette filler and graduated pipettes or automatic pipettor and pipette tips of a range of sizes e.g. 1ml and 10ml. For handling shellfish homogenates (1 in 2 and 1 in 20 dilutions) open-ended pipettes may be necessary due to high concentrations of particulate matter
- Shucking knife, oyster cracker or other suitable equipment for opening and dissecting shellfish
- Food grade plastic bags
- Steamer, microwave or equivalent apparatus for melting prepared media
- Waterbath at 44-47°C
- Sterile 90mm Petri dishes

6. Media

- Peptone salt solution (PSS) (referred to as Maximum Recovery Diluent (MRD) in the UK)
- Tryptone bile glucuronide agar (TBGA/TBX)

7. Microbiological reference cultures for performance testing and controls

The NRL recommends the use of the positive and negative controls throughout the procedure. The strains and criteria included in Table 1 are recommended for use as a minimum.

Table 1: Microbiological reference strains used for control purposes

Media type	Control strain	WDCM ^a	Criteria	Characteristic reaction	Strain choice ^c
	Escherichia coli	00202	Blue to blue- green colonies	β-glucuronidase positive (weak)	2
Tryptone bile	Escherichia coli	00012 or 00013	Blue to blue- green colonies	β -glucuronidase positive	1
glucuronide agar (TBGA/TBX)	Enterococcus faecalis	00009 or 00087	Total inhibition	no growth	1
	Pseudomonas aeruginosa		White to beige colonies	β-glucuronidase	1
	Citrobacter freundii b	00006	colornes	negative	

^a Follow the link (<u>http://www.phe-culturecollections.org.uk/products/bacteria/WDCMStrains.aspx</u>) to obtain NCTC number for WDCM reference strains.

^b Following the sub-culturing of *C. freundii* onto TBGA/TBX plates, growth is not always present. We therefore recommend the use of *P. aeruginosa* over *C. freundii*.

^c Reference strains given in ISO 16649-3 for use in performance testing. Strain selection: 1 - Laboratory must select 1 strain from the list provided; 2 - Strain to be used as a minimum.

8. Procedures

8.1. Sample transport and receipt

Samples must be placed in an intact food grade plastic bag and properly packed in a cool box with ice packs – packed in this manner they should reach a temperature between 0°C and 10°C within 4 hours and then maintain this for at least 24 hours¹. For samples where less than 4 hours have elapsed between collection from the production area and receipt at the laboratory, the internal cool box air temperature (or between-bivalve shellfish sample temperature) should be less than the temperature recorded at the time of sampling. Samples from harvesting areas should have been rinsed (but not immersed) and drained at time of sampling. A sample should be regarded as unsatisfactory if on receipt at the laboratory the sample is frozen, the container is leaking, the shellfish are covered in mud or immersed in water or mud/sand.

The sample transport criteria given here are extracted from ISO 6887-3 (Anon, 2020). The use of alternate sample transport criteria may be acceptable, where verification studies have been undertaken and the results of those studies demonstrate that there is no significant effect on the quality of the test results. For Official Controls, it is recommended that verification studies

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¹ A temperature data logger may be used to monitor the sample temperature during transit. The data logger must be held in a central position within the cool box and not allowed to come into contact with the ice packs. If the logger has not been activated or is found to be in contact with the ice packs on arrival at the laboratory, then the temperature of the shellfish sample itself should be measured using an appropriately calibrated temperature probe.

supporting the use of sample transport criteria outside of the ranges given in ISO 6887-3 are approved by the relevant Competent Authority (CA).

Note: The UK NRL has carried out studies on the effect of extended storage time and elevated temperatures on certain species of BMS. The report of this work can be accessed using the following web link <u>https://www.cefas.co.uk/nrl/information-centre/nrl-reports/</u>

8.2. Sample storage

Upon receipt in the laboratory the temperature of the samples should be recorded. Samples should be examined immediately - if storage in the laboratory is necessary then samples should be stored at 3±2°C and should be processed within 24 hours of collection. If microbiological analysis cannot be initiated within 24 hours of sample collection, an upper limit of 48 hours should be used.

8.3. Sample selection

Choose shellfish that are alive according to the following criteria:

- Reaction or movement of exposed flesh after touching using a sterile shucking knife.
- Shellfish open and close of their own accord.
- A tap on the shell causes closing or movement.
- Tightly closed shellfish.

Discard all dead shellfish and those with obvious signs of damage. Select the appropriate number depending on the species (Appendix 1). More shellfish can be used, if necessary, to produce the required volumes for each analysis.

8.4. Sample preparation

Any mud and sediment adhering to the shellfish should be removed prior to opening the shellfish by rinsing/scrubbing under cold, running tap water of potable quality. Shellfish should not be reimmersed in water as this may cause them to open. Open all selected shellfish as described below ².

8.4.1. Preparation of BMS using the oyster cracker

Sterilise the blade of the oyster cracker before use (see Figure 1 and Figure 2). Place a single animal in a weighing dish on the platform underneath the blade. Lower the lever so that the blade engages the hinge of the shellfish, then fully pull the lever down so that the blade separates the shells. Using a sterilised shucking knife cut the muscle and scrape the meat of both shells into the sterilised container. Transfer any liquor collected in the weighing boat into the sterilised container.

² Alternative suitable equipment can be used to open bivalve shellfish.

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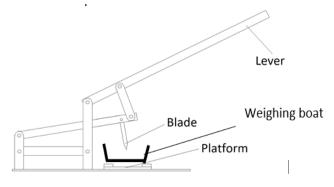


Figure 1: Oyster cracker apparatus



Figure 2: Opening an oyster using an oyster cracker

8.4.2. Preparation of BMS using a shucking knife

Open all selected shellfish as described below using a sterilised shucking knife or equivalent and empty meat and liquor into a sterile container. If sterilised by heating allow the knife to cool before using. When opening shellfish, ensure that the hand holding the shellfish is protected with a heavy-duty safety glove to prevent cuts.

8.4.2.1. Oysters and clams

Insert the knife between the two shells towards the hinge end of the animal. Push the knife further into the animal and prise open the upper shell, allowing any liquor to drain into the sterilised container. Push the blade through the animal and sever the muscle attachments by sliding across the animal. Remove the upper shell and scrape the contents of the lower shell into the sterilised container.

8.4.2.2. Mussels and cockles

Insert the knife in between the shells of the animal and separate the shells with a twisting motion of the knife. Collect the liquor from the animal in the sterilised container then cut the muscle between the shells and scrape the contents into the sterilised container.

8.5. Dilution and homogenisation

Weigh the sterilised container and calculate the weight of the contents by subtracting the weight of the pre-weighed container to the nearest gram.

Note: Complete either sections 8.5.1 or 8.5.2.

8.5.1. Homogenisation in a blender

Measure 1ml of sterile PSS per 1g of shellfish (\pm 2ml) using a measuring cylinder. Place contents of sterilised container into a 1 litre blender jar³ with the PSS from the measuring cylinder and homogenise at high speed for approximately 1 minute (4 bursts of 15 seconds with at least 5

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³ If shellfish are particularly small, it may be necessary to use a smaller blender to achieve a consistent homogenate.

seconds between bursts) in a class two microbiological laminar flow cabinet. Decant the contents (1 in 2 dilution) back into the sterilised container.

8.5.2. Homogenisation using a stomacher

Place the contents of the sterilised container into at least three stomacher bags (e.g. place three stomacher bags inside each other to avoid small pieces of shell from puncturing the bags). Remove excess air from the bags and operate the stomacher for 2-3 minutes. Transfer 50g of homogenised shellfish into another set of 3 stomacher bags, add 50ml of PSS and homogenise for a further 2-3 minutes. After homogenisation decant the contents (1 in 2 dilution) into a new sterilised container.

Note: Results from proficiency testing distributions of cockles have tended to give lower *E. coli* concentrations following stomaching than following blending. NRL advice is therefore to use blending for samples of cockles and other small species such as clams.

8.5.3. Preparation of 1 in 20 dilution

Make a further decimal dilution (1 in 20) using the 1 in 2 dilution as prepared in 8.5.1 or 8.5.2 by adding 1ml of the 1 in 2 dilution to 9ml of PSS.

Note: it may be necessary to use an open-ended pipette to transfer shellfish homogenate due to high concentrations of particulate matter.

8.6. Inoculation and incubation

Melt TBGA/TBX medium using a steamer, microwave or equivalent, then leave to cool in a waterbath at 44-47°C.

Inoculate 5 sterile Petri dishes (90mm diameter) with 2ml of the 1 in 2 dilution. Inoculate 2 sterile Petri dishes (90mm diameter) with 2ml of the 1 in 20 dilution. Use a new sterile pipette for each dilution.

Pour approximately 15-18ml melted and cooled TBGA/TBX medium into each Petri dish. Carefully mix the inoculum with the medium by gentle swirling and allow the mixture to solidify, with the Petri dishes standing on a cool horizontal surface.

Incubate the TGBA/TBX plates inverted for 4 hours at 37±1 °C, followed by 18–24 hours at 44±1 °C.

Note: it may be necessary to use an open-ended pipette to transfer shellfish homogenate due to high concentrations of particulate matter.

Note: The time which elapses between the distribution of the inoculum in a dish and pouring of the medium shall not exceed 15 min.

8.7. Counting the colony forming units

After incubation examine all inoculated TBGA/TBX plates for the presence of typical i.e. blue to blue-green colonies. Record the number of typical colonies on each of the five plates inoculated with the 1 in 2 dilution and each of the two plates inoculated with the 1 in 20 dilution. Atypical colonies should not be included in the count.

Note: in this protocol the maximum countable number of typical colonies for a set of plates at a single dilution is set at a level that corresponds to an average of 150 typical colonies per plate i.e. 750 colonies in total for a set of 5 plates or 300 colonies in total for a set of 2 plates (8.8.1). It is not possible for a set of plates to average \leq 150 typical colonies and to meet the requirements on the reliability of colony counts of parallel plates (8.8.2) where a single plate within the set contains \geq 192 typical colonies.

Therefore, where a count of \geq 192 typical colonies is reached for any single plate, the entire set at the affected dilution can be considered to be above the maximum countable number, and the remaining plates in the set do not need to be counted.

8.8. Test results

Test results are generated from the colony counts for all plates (8.7). The counts may be checked against the maximum countable number and for acceptable reliability, and results calculated and reported as described in sections 8.8.1 to 8.8.4. Alternatively, the Shellfish colony-count calculator can be used (8.8.5). This calculator simultaneously takes into account the maximum countable number, carries out checks for acceptable reliability, calculates the result and shows how the result should be expressed when reporting.

8.8.1. Maximum countable number of colonies

In this protocol the maximum countable number of typical colonies for a set of plates at a single dilution is set at a level that corresponds to an average of 150 typical colonies per plate i.e. 750 colonies in total for a set of 5 plates or 300 colonies in total for a set of 2 plates.

Where the maximum countable number of colonies is exceeded for the set of plates using the 1 in 2 dilution, calculation of results should be carried out using the colony count at the 1 in 20 dilution. However, if the results at the 1 in 20 dilution are rejected due to unacceptable variation between the counts on the two plates (8.8.2), then results should be reported as >15000 E. coli per 100g.

Where the maximum countable number of colonies is exceeded for the set of plates using the 1 in 20 dilution, then results should be reported as >150000 E. coli per 100g.

8.8.2. Determination of the reliability of colony counts on parallel plates

To ensure reliable results, the pattern of individual colony counts for all parallel plates within a set at a single dilution should be assessed for acceptable levels of variability using a *G*-test approach (e.g. Sokal and Rohlf, 2012) as recommended in ISO 7218 (Anon, 2013) and detailed (for 2 parallel plates) in ISO 14461-2 (Anon, 2005b).

For 5 parallel plates (1 in 2 dilution), determine the χ^2 statistic for the set using the following equation:-

$$\chi^{2} = \left\{ 2 \left[C_{a} \cdot \ln\left(\frac{C_{a}}{(\sum C)/5}\right) + C_{b} \cdot \ln\left(\frac{C_{b}}{(\sum C)/5}\right) + C_{c} \cdot \ln\left(\frac{C_{c}}{(\sum C)/5}\right) + C_{d} \cdot \ln\left(\frac{C_{d}}{(\sum C)/5}\right) + C_{e} \cdot \ln\left(\frac{C_{e}}{(\sum C)/5}\right) \right] \right\}$$

where

 C_a is the count on the first plate, C_b is the count on the second plate,..., C_e is the count on the fifth plate

 $\sum C$ is the sum of the counts on all five plates

The variability between the parallel counts is considered acceptable where χ^2 is less than or equal to 13.277 (the critical value of χ^2 for p=0.01 and 4 degrees of freedom).

For 2 parallel plates (1 in 20 dilution), determine the χ^2 statistic for the set using the following equation:-

$$\chi^{2} = \left\{ 2 \left[C_{\mathrm{a}} \cdot \ln \left(\frac{C_{\mathrm{a}}}{(\sum C)/2} \right) + C_{\mathrm{b}} \cdot \ln \left(\frac{C_{\mathrm{b}}}{(\sum C)/2} \right) \right] \right\}$$

where

 C_a is the count on the first plate and C_b is the count on the second plate

 $\sum C$ is the sum of the counts on both plates

The variability between the parallel counts is considered acceptable where χ^2 is less than or equal to 6.635 (the critical value of χ^2 for p=0.01 and 1 degree of freedom).

Alternatively, for 2 parallel plates the acceptability of the counts can be determined using the table in Appendix 2.

Where colony counts on a set of parallel plates at one dilution are not acceptable according to the above criteria, then calculation of results should be carried out using the colony counts at the other dilution. Where parallel plate counts at both dilutions are not acceptable then the test result should be considered as **Void**. This should occur in <1% of cases.

Note: if using the colony-count calculator (8.8.5), all steps described in this section are carried out automatically.

8.8.3. Determination of the reliability of colony counts at successive dilutions

To ensure reliable results, the ratio between the total counts (the sum of all plates) at the 1 in 2 and 1 in 20 dilutions should be assessed for acceptability using a *G*-test approach (e.g. Sokal and Rohlf, 2012) as recommended in ISO 7218 (Anon, 2013) and detailed (for successive dilutions where the same numbers of plates are used) in ISO 14461-2 (Anon, 2005b).

Determine the χ^2 statistic for the ratio of the total counts at the two dilutions using the following equation:-

$$\chi^{2} = \left\{ 2 \left[\sum upper \cdot \ln \left(\frac{\sum upper}{10.0 \cdot (\sum upper + \sum lower)/10.4} \right) + \sum lower \cdot \ln \left(\frac{\sum lower}{0.4 \cdot (\sum upper + \sum lower)/10.4} \right) \right] \right\}$$

where

 $\sum upper$ is the total count of the 5 plates at the 1 in 2 dilution

 \sum lower is the total count of the 2 plates at the 1 in 20 dilution

The ratio between the total counts at the two dilutions is considered acceptable where χ^2 is less than or equal to 6.635 (the critical value of χ^2 for p=0.01 and 1 degree of freedom).

Alternatively, the acceptability of the ratio of the total counts at the two dilutions can be determined using the table in Appendix 3.

Where the ratio between the total colony counts at the two dilutions is not acceptable according to the above criteria, then the test result should be considered as **Void**. This should occur in 1% of cases.

Note: if using the colony-count calculator (8.8.5), all steps described in this section are carried out automatically.

8.8.4. Calculation and reporting of results

Results are calculated using colony counts for all plates retained after the checks described in 8.8.1, 8.8.2 and 8.8.3. Where there are no issues with exceedance of the maximum countable number (8.8.1) or reliability of the counts at either dilution according to 8.8.2 and 8.8.3, then counts from all plates must be used in the calculation even if e.g. no colonies are present at the 1 in 20 dilution.

Where the sum of colony counts, $\sum C$, of all retained plates is ≥ 10 , calculate the result *N* (in *E. coli* per 100g) as a weighted mean using the following equations depending on which dilutions are retained:-

If plates at 1 in 2 and 1 in 20 dilutions are retained:

$$N = 100 \cdot \left(\frac{\sum C}{5.2}\right)$$

If plates at 1 in 2 dilution only are retained:

$$N = 100 \cdot \left(\frac{\Sigma C}{5}\right)$$

If plates at 1 in 20 dilution only are retained:

$$N = 100 \cdot \left(\frac{\sum C}{0.2}\right)$$

Round off the results to two significant figures and report as *N E. coli* per 100g.

Example:

Where individual plate counts at the 1 in 2 and 1 in 20 dilutions are (10,15,8,11,14) and (0,1) respectively:-

$$N = 100 \cdot \left(\frac{(10 + 15 + 8 + 11 + 14 + 0 + 1)}{5.2}\right)$$
$$N = 100 \cdot \left(\frac{59}{5.2}\right) = 1134.62$$

Results are rounded off to two significant figures and reported as 1100 E. coli per 100g.

Where the sum of colony counts, $\sum C$, of all retained plates is between 4 and 9, calculate the result *N* (in *E. coli* per 100g) as a weighted mean using the above equations.

Round off the results to two significant figures and report as *N E. coli* per 100g estimated.

Example:

Where individual plate counts at the 1 in 2 and 1 in 20 dilutions are (2,1,2,2,1) and (0,0) respectively:-

$$N = 100 \cdot \left(\frac{(2+1+2+2+1+0+0)}{5.2}\right)$$
$$N = 100 \cdot \left(\frac{8}{5.2}\right) = 153.85$$

Results are rounded off to two significant figures and reported as **150** *E. coli* per **100g** estimated.

Where the sum of colony counts of all retained plates is between 1 and 3, the result should be reported as present, *<N E. coli* per 100g, where N is calculated using the above equations, substituting 4 for $\sum C$ as follows:-

If plates at both dilutions are retained report the results as present, <77 E. coli per 100g

If plates at 1 in 20 dilution only are retained report the results as **present**, **<2000** *E. coli* **per 100g**

Where no colonies are present on the retained plates, the result should be reported as *N E. coli* per 100g, where N is calculated using the above equations, substituting 1 for $\sum C$ as follows:-

If plates at both dilutions are retained report the results as <19 E. coli per 100g

If plates at 1 in 20 dilution only are retained report the results as <500 E. coli per 100g

Note: if using the colony-count calculator (8.8.5), all steps described in this section are carried out automatically.

8.8.5. Use of the Shellfish colony-count calculator

The shellfish colony-count calculator is available from the NRL website (<u>NRL Laboratory</u> <u>Protocols - Cefas</u>).

• Download and open a copy of the colony-count calculator from the website.

Note: only cream-coloured cells can be overwritten, all other cells are locked.

- Each row of the calculator will generate results for a single sample (there are enough rows for 100 samples example details have been added to row 5 but can be overwritten).
- Add the sample name or unique identifier to column B.
- Add the colony counts for the 5 plates at the 1 in 2 dilution to columns D to H.
- Add the colony counts for the 2 plates at the 1 in 20 dilution to columns J and K.

Note: where the maximum countable number for either set was exceeded and the full count not completed (8.7), the set can be "blocked out" on the calculator by adding any number \geq 151 to all relevant columns.

- Where the variability between counts on parallel plates within a set is unacceptable, "!!!!!" will appear in column Y (1 in 2 dilution) and/or column AG (1 in 20 dilution).
- Where the ratio between total counts at the two dilutions is unacceptable, "!!!!!" will appear in column AP.
- Raw and rounded results calculated using the 1 in 2 dilution only, the 1 in 20 dilution only and both dilutions are shown in columns AW to BJ.
- Results (to be reported in *E. coli* per 100g), taking into account exceedance of maximum countable numbers at one or both dilutions, all checks for acceptability, expression of results at low colony counts (<10) and rounding of results to two significant figures, are shown in column CD. These result cells are conditionally colour-coded according to the classification bracket in which the results sit:-
 - ≤230 shaded green
 - o 240 700 shaded yellow
 - o 710 4600 shaded peach
 - o 4700 46000 shaded pink
 - \circ >46000 shaded red

Results that are ambiguous in terms of classification brackets (>15000, <2000, <500) are shaded grey and void results are shaded black with yellow text.

Note: where final results are shown in the form "*N* estimated", these should be reported as "*N E. coli* per 100g estimated".

• Lower and upper 95% confidence limits (section 9) are provided in columns CF and CG for information.

9. Uncertainty of test results

Uncertainty inherent in any test method, i.e. instruments, media, analyst performance etc can be assessed by the repeatability and reproducibility of test results. These should be monitored through control tests analysed alongside sample tests, through in-house comparability testing between analysts and through external inter-comparability exercises, which would highlight any uncertainties within the test methods.

The inclusion of the measurement of uncertainty (MU) or confidence limits for the result is not required when reporting but it is recommended that laboratories determine, as part of their quality procedure, the MU for the reported results and provide this information on request.

ISO 7218 (Anon, 2013) includes a formula for determination of theoretical confidence intervals for colony-count methods; the confidence interval becomes narrower in relative terms as the colony count increases. According to this formula, the confidence interval for a result of 230 *E. coli* per 100g obtained using results at both 1 in 2 and 1 in 20 dilutions and derived from a colony count of 12 is 100 - 360. The confidence interval for a result of 4600 *E. coli* per 100g derived from a colony count of 239 is 4000 - 5200. These intervals are included as an output on the calculation spreadsheet (8.8.5).

ISO 19036 (Anon, 2006) gives guidance on the estimation of MU for quantitative determinations in food microbiology.

10. Quality control

Quality control systems offer a laboratory a mechanism to control preventable inaccuracies within a procedure.

10.1. Proficiency testing

In order to comply with the requirements of Retained Regulation (EC) No. 2017/625 (Anon, 2017a), laboratories undertaking microbiological examination of official control samples of shellfish for *E. coli* and/or *Salmonella* spp. are expected to take part in the UKHSA/Cefas Shellfish EQA scheme (for further information contact <u>foodeqa@ukhsa.gov.uk</u>) and NRL proficiency test distributions⁴. These schemes provide an independent assessment of a laboratory's performance against other

⁴ It was agreed at the Laboratory network meeting in 2018 that laboratories analysing OC samples should take part in at least 2 EQA (UKHSA/Cefas) schemes and 1 whole animal distribution per year.

participants and can help improve the performance of the laboratory.

10.2. Trend monitoring

To ensure continuing intra-comparison of test results, trend analysis should be undertaken by regularly reviewing laboratory performance in the Shellfish EQA scheme. Results should be assessed against the participants' median and plotted graphically showing performance over time. This enables recognition of unusual trends in performance compared to other laboratories and allows for appropriate follow-up action. An Excel spreadsheet for this purpose is given at the Shellfish EQA Scheme web page (<u>https://www.gov.uk/government/publications/shellfish-schemetrend-analysis</u>).

In addition, laboratories should keep a check on the number of results which fail acceptability checks for variability of parallel counts at the 1 in 2 and 1 in 20 dilutions or for the ratio of total counts at successive dilutions. For each of these checks, it is expected that 1% of samples will provide unacceptable results. If a higher proportion is observed, this should be investigated.

10.3. Internal Quality Assurance (IQA)

It is recommended that regular (e.g. monthly) monitoring using known levels of target organism are examined to ensure routine *E. coli* procedures continue to be efficient and effective. An example for assessing quantitative methods is the use of LenticuleTM discs.

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12. Appendices

12.1. Appendix 1: Sample sizes of shellfish required for *E. coli* analysis

The following sample sizes are recommended for inclusion in the homogenisation step (the recommended number for sampling is 10 % greater to allow for morbidity in a proportion of animals on receipt at the laboratory).

Туре	Common name ⁵	Scientific name ⁶	Sample size ⁷
Scallops	Mediterranean scallop	Pecten jacobaeus	10 - 12
	King (Great Atlantic) scallop	Pecten maximus	10 - 12
	Queen scallop	Aequipecten (Chlamys) opercularis	15 - 30
	Variegated scallop	Mimachlamys (Chlamys) varia	10 - 18
Oysters	Pacific oyster	Magallana (Crassostrea) gigas	10 - 18
	Portuguese oyster	Magallana (Crassostrea) angulata	10 - 18
	European flat oyster	Ostrea edulis	10 - 18
Mussels	Blue or common mussel	Mytilus edulis	15 - 30
	Mediterranean mussel	Mytilus galloprovincialis	10 - 30
	Northern horse mussel	Modiolus modiolus	10 - 12
	Bearded horse mussel	Modiolus barbatus	15 - 30
Ark Clams	Ark clam	Barbatia barbata	15 - 25
	Noah's ark shell	Arca noae	15 - 30
Clams	Smooth clam	Callista chione	10 - 30
	Striped venus clam	Chamelea gallina	40 - 80
	Rayed artemis	Dosinia exoleta	18 - 35
	Hard clam	Mercenaria mercenaria	12 - 18
	Palourde (Grooved carpet shell)	Ruditapes (Tapes/Venerupis) decussatus	18 - 35
	Manila clam	Ruditapes (Tapes) philippinarum	18 - 35
	Banded carpet shell	Polititapes (Venerupis) rhomboides	20 - 25
	Pullet carpet shell	Venerupis corrugata (senegalensis)	20 - 25
	Warty venus clam	Venus verrucosa	15 - 30
	Atlantic surf clam (Thick trough shell)	Spisula solida	30 - 50
	Cut trough shell	Spisula subtruncata	70 - 90
	Bean clam	Donax spp.	30 - 50
	Wedge shell clam	Donax trunculus	40 - 80
	Common cockle	Cerastoderma edule	30 - 50
	Soft shell clam (Sand gaper)	Mya arenaria	10 - 12

⁵ Species of relevance provided by European NRLs.

NRL generic protocol - Enumeration of E. coli in bivalve molluscan shellfish by the colony-count technique

⁶ Scientific names are those used by the World Register of Marine Species at the time of writing, however commonly used alternatives for genus or species names are shown in brackets.

⁷ Number of shellfish to be tested for *E. coli*. Retained Regulation (EC) No. 2073/2005 specifies a minimum of 10 animals of any species should be examined. Sample sizes given in this table have been provided by European NRLs. The weight of shellfish flesh and liquor should be at least 50g for the *E. coli* method (for very small species such as *Donax* spp. a minimum amount of 25g is permitted). For species not given in the table, sufficient shellfish should be opened to achieve this minimum weight of flesh and liquor, with the provision that a minimum of ten animals should be used for very large species. In general, the more shellfish that are included in the initial homogenate, the less the final result will be influenced by the inherent animal-to-animal variation in *E. coli* concentration.

Razor Clams	Pacific geoduck	Panopea generosa	10 - 12
and	Sword razor	Ensis ensis	10 - 12
Geoducks	Razor shell	Ensis magnus (arcuatus)	10 - 12
	Atlantic razor clam (Jacknife		
	clam)	Ensis leei	10 - 12
	Pod razor	Ensis siliqua	10 - 12
	Grooved razor shell	Solen marginatus	10 - 12

12.2. Appendix 2: Limits of acceptable variability for colony counts of two parallel Petri dishes

For a set of two parallel Petri dishes at a single dilution, variability between the plates is acceptable provided that for a given upper plate count as shown in the "Upper colony count" column in the table below, the lower plate count in the set of two plates is no lower than the number shown in the "Lower colony count" column e.g. where the upper count in the set of two plates is 100, the other plate must contain at least 67 colonies for variability to be acceptable.

Colon	y count	Colon	y count		Colon	count	1	Colony	/ count
Upper	Lower	Upper	Lower		Upper	Lower		Upper	Lower
1	0	44	24		87	57	1	130	92
2	0	45	24		88	58	1	131	93
3	0	46	25		89	58	1	132	94
4	0	47	26		90	59	1	133	95
5	1	48	27		91	60	1	134	96
6	1	49	27		92	61	1	135	96
7	1	50	28		93	62	1	136	97
8	1	51	29		94	62	1	137	98
9	2	52	29		95	63	1	138	99
10	2	53	30		96	64	1	139	100
1	3	54	31		97	65		140	101
12	3	55	32		98	66		141	102
13	4	56	32		99	67		142	102
14	4	57	33		100	67		143	103
15	5	58	34		101	68		144	104
16	5	59	35		102	69		145	105
17	6	60	36		103	70		146	106
8	6	61	36		104	71		147	107
9	7	62	37		105	71]	148	107
)	7	63	38		106	72	1	149	108
	8	64	39		107	73	1	150	109
2	9	65	39		108	74]	151	110
	9	66	40		109	75		152	111
	10	67	41		110	76		153	112
5	11	68	42		111	76		154	113
6	11	69	42		112	77		155	113
7	12	70	43		113	78		156	114
8	12	71	44		114	79		157	115
9	13	72	45		115	80		158	116
30	14	73	46		116	81		159	117
1	14	74	46		117	81		160	118
32	15	75	47		118	82		161	119
33	16	76	48		119	83		162	120
34	16	77	49		120	84		163	120
35	17	78	50		121	85		164	121
86	18	79	50		122	86		165	122
7	19	80	51		123	86		166	123
38	19	81	52		124	87		167	124
39	20	82	53		125	88		168	125
40	21	83	54		126	89		169	125
41	21	84	54		127	90		170	126
42	22	85	55		128	91		171	127
43	23	86	56		129	91		172	128

12.3. Appendix 3: Limits of acceptable ratios for colony counts at successive dilutions

For a set of five parallel Petri dishes at the 1 in 2 dilution and two parallel dishes at the 1 in 20 dilution, the ratio between the total counts at the two dilutions is acceptable provided that for a given total count at the 1 in 2 dilution as shown in the below table, the total count at the 1 in 20 dilution falls within the lower and upper limits in the table e.g. where the total count at the 1 in 2 dilution is 100, the total count at the 1 in 20 dilution must be at least 1 and no more than 10 for the ratio to be acceptable.

1 in 2	1 in 20		
Total	Lower	Upper	
count	limit	limit	
0	0	1	
1	0	1	
2	0	1	
3	0	2	
4	0	2	
5	0	2	
6	0	2	
7	0	2	
8	0	2	
9	0	2	
10	0	3	
11	0	3	
12	0	3	
13	0	3	
14	0	3	
15	0	3	
16	0	3	
17	0	3	
18	0	4	
19	0	4	
20	0	4	
21	0	4	
22	0	4	
23	0	4	
24	0	4	
25	0	4	
26	0	4	
27	0	4	
28	0	4	
29	0	5	
30	0	5	
31	0	5	
32	0	5	
33	0	5	
34	0	5	
35	0	5	
36	0	5	
37	0	5	
38	0	5	
39	0	5	
40	0	6	
41	0	6	
42	0	6	
43	0	6	
44	0	6	

1 in 2	1 in 2 1 in 20				
Total	Lower	Upper			
count	limit	limit			
45	0	6			
45	0	6			
40	0	6			
47	0	6			
49	0	6			
50	0	6			
51	0	6			
52	0	6			
53	0	7			
54	0	7			
55	0	7			
56	0	7			
57	0	7			
58	0	7			
59	0	7			
60	0	7			
61	0	7			
62	0	7			
63	0	7			
64	0	7			
65	0	7			
66	0	8			
67	0	8			
68	0	8			
69	0	8			
70	0	8			
71	0	8			
72	0	8			
73	0	8			
74	0	8			
75	0	8			
76	0	8			
77	0	8			
78	0	8			
79	0	8			
80	0	9			
81	0	9			
82	0	9			
83	0	9			
84	0	9			
85	1	9			
86	1	9			
87	1	9			
88	1	9			
89	1	9			

1 in 2	1 in 20			
Total	Lower	Upper		
count	limit	limit		
90	1	9		
91	1	9		
92	1	9		
93	1	9		
94	1	9		
95	1	10		
96	1	10		
97	1	10		
98	1	10		
99	1	10		
100	1	10		
101	1	10		
102	1	10		
103	1	10		
104	1	10		
105	1	10		
106	1	10		
107	1	10		
108	1	10		
109	1	10		
110	1	11		
111	1	11		
112	1	11		
113	1	11		
114	1	11		
115	1	11		
116	1	11		
117	1	11		
118	1	11		
119	1	11		
120	1	11		
121	1	11		
122	1	11		
123	1	11		
124	1	11		
125	1	11		
126	1	12		
127	1	12		
128	1	12		
129	1	12		
130	1	12		
131	1	12		
132	1	12		
133	1	12		
134	1	12		

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173 2 14	
174 2 15	
175 2 15	
176 2 15	
177 2 15	
177 2 15 178 2 15 179 2 15	

1 in 2	1 in 2 1 in 20				
Total	Lower	Upper			
count	limit	limit			
180	2	15			
181	2	15			
182	2	15			
183	2	15			
184	2	15			
185	2	15			
186	2	15			
187	2	15			
188	2	15			
189	2	15			
190	2	15			
191	2	16			
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202	2	16			
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205	2	16			
206	2	16			
207	3	16			
208	3	17			
209	3	17			
210	3	17			
211	3	17			
212	3	17			
213	3	17			
214	3	17			
215	3	17			
216	3	17			
217	3	17			
218	3	17			
219	3	17			
220	3	17			
221	3	17			
222	3	17			
223	3	17			
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Total	Lower	Upper
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Total	Lower	Upper
count	limit	limit
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Total	Lower	Upper
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494	10	32

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Total count	Lower limit	Upper limit
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Total	Lower	Upper
count	limit	limit
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583	12	37
584	12	37

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Total	Lower	Upper
count	limit	limit
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629	14	39

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Total	Lower	Upper
count	limit	limit
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674	15	41

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Total	Lower	Upper
count	limit	limit
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717	16	43
718	16	43
719	16	44

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