

# QMS

# **Quality in Microbiology Scheme**

# **Scheme Description**

# LGC Standards Proficiency Testing

1 Chamberhall Business Park Chamberhall Green Bury, BL9 0AP UK.

Telephone:	+44 (0) 161 762 2500
Fax:	+44 (0) 161 762 2501
Email:	qms@lgcgroup.com
Website:	www.lgcstandards.com



# Record of issue status and modifications

ISSUE	ISSUE DATE	DETAILS	AUTHORISED BY
2	15/08/08	General review and update of scheme description	M. Whetton
3	Aug 2009	Operational issues common to all schemes moved into General Protocol. List of abbreviations added. New analytes added: Shigella and combined yeast and mould. Changed name of E.sakazakii to Cronobacter sakazakii	T.Noblett
4	Aug 2010	Added trial for Bifidobacterium. Included samples for microbial analysis of tea/herbs/spices trialled in previous year.	T.Noblett
5	Jan 2011	Added qualitative test for Enterobacteriaceae and updated address	T.Noblett
6	Aug 2011	Sample 16 -removed qualitative test for Enterobacteriaceae and E.coli. Added Bifidobacterium sample trialled in 2011. Added Presence/absence sample for E.coli, Enterobacteriaceae and coliforms.	Karen Cliff
7	Sep 2012	Updated units and ranges. Added enumeration tests for sample 18F/D	T.Noblett
8	Mar 2013	Added trial for the enumeration of <i>Campylobacter</i> species (sample 32)	T.Noblett
9	Sept 2013	Included microbiological method codes	T.Noblett
10	Sept 2014	Added <i>Staphylococcus</i> species and <i>Bacillus</i> species enumeration to sample 17. Added CampyCount method to sample 32. Added <i>Lactobacillus</i> species to sample 27. Inclusion of traceability information in Appendix A. Inclusion of subcontracting information in 'Test Materials' section.	K.Cliff
11	Sept 2015	Included samples previously included in QMIS, i.e. identification test, Salmonella serology, paper exercise. Methods updated Removed Hard copy report information	K.Cliff A. McCarthy
12	Aug 2016	Updated details for Sample 35 regarding setting of assigned value by formulation	T.Noblett

# Notes:

Where this document has been translated, the English version shall remain the definitive version

# Scheme Aims and Organisation

The primary aim of the Quality In Microbiology (QMS) is to enable laboratories performing the microbiological analysis of food and dairy products to monitor their performance and compare it with that of their peers. QMS also aims to provide information to participants on technical issues and methodologies relating to testing of food and dairy products.

The QMS scheme year operates from January to December. Further information about QMS, including test material availability, round despatch dates and reporting deadlines, are available on the current QMS application form.

# **Test Materials**

Details of test materials available in QMS are given in Appendix A. The test parameters are continually reviewed to ensure they meet the needs of current laboratory testing and regulatory requirements.

Test material batches are tested for homogeneity for at least one test parameter where deemed appropriate. Details of homogeneity tests performed and results are given in the QMS Scheme Reports.

Some aspects of the scheme, such as test material production, homogeneity testing and stability assessment, can from time to time be subcontracted. When subcontracting occurs, it is placed with a competent subcontractor and LGC is responsible for this work. The planning of the scheme, the evaluation of performance and the authorisation of the final report will never be subcontracted.

#### Statistical Analysis

Information on the statistics used in QMS can be found in the General Protocol and in the Scheme Report. Methods for determining assigned values and the values for SDPA used for individual samples are given in Appendix A

#### Methods

Methods are listed in Appendix A and PORTAL. Please select the most appropriate method from the list. If none of the methods are appropriate, then please report your method as 'Other' and record a brief description in the Comments Section in PORTAL.

Abbreviations for microbiological method codes can be found in Appendix A. The time and temperature of incubation does not need to be reported.

#### **Results and Reports**

QMS results are returned through our electronic reporting software, PORTAL, full instructions for which are provided by email. However, participants may request result submission forms on which to report and return results if they are unable to report through electronic means. This will incur an additional charge.

QMS reports will be available on the website within 10 working days of round closure. Participants will be emailed a link to the report when it is available.

# **APPENDIX A - Description of abbreviations used**

#### Assigned Value (AV)

The assigned value may be derived in the following ways:

From the robust mean (RMean). This is the median of participant results after the removal of test results that are inappropriate for statistical evaluation, e.g. miscalculations, transpositions and other gross errors. Generally, the assigned value will be set using results from all methods, unless the measurement is considered method-dependant, in which case the assigned value will be set by method as illustrated in the report tables. For some analytes, where there is a recognised reference method for that type of measurement, this may be used as the assigned value for a particular analyte i.e. it would be applied to results obtained by any method.

Traceability: Assigned values which are derived from the participant results, or a sub-set of the results are not traceable to an international measurement standard. The uncertainty of assigned values derived in this way is estimated from the participant results, according to ISO 13528.

 From a formulation value (Formulation). This denotes the use of an assigned value derived from sample preparation details, where known and exact quantities of analyte have been used to prepare the sample.

Traceability: Assigned values calculated from the formulation of the test sample are traceable, via an unbroken metrological traceability chain, to an international measurement standard. The measurement uncertainty of the assigned value is calculated using the contributions from each calibration in the traceability chain.

 From a qualitative formulation (Qual Form). This applies to qualitative tests where the assigned value is simply based on the presence/absence of the analyte in the test material.

Traceability: Assigned values calculated from the qualitative formulation of the test sample are traceable to a certified reference standard or a microbiological reference strain.

 From expert labs (Expert). The assigned value for the analyte is provided by an 'expert' laboratory.

Traceability: Assigned values provided by an 'expert' laboratory may be traceable to an international measurement standard, according to the laboratory and the method used. The uncertainty of measurement for an assigned value produced in this way will be provided by the laboratory undertaking the analysis. Details of traceability and the associated uncertainty will be provided in the report for the scheme/round.

# Range

This indicates the concentration range at which the analyte may be present in the test material.

# SDPA

The SDPA represents the 'standard deviation for proficiency assessment' which is used to assess participant performance for the measurement of each analyte. This may be a fixed value (as stated), a percentage (%) of the assigned value or based on the robust standard deviation of the participant measurement results, either across all methods or by method depending on whether the measurement made is method dependent (see assigned value).

# Units

This indicates the units used for the assessment of data and in which participants should report their results. For some analytes in some schemes participants may have a choice of which units to report their results, however, the units stipulated in this scheme description are the default units to which any results reported using allowable alternative results will be converted to.

# DP

This indicates the number of decimal places to which participants should report their measurement results.

# **APPENDIX A**

Sample 03Salmonella enumerationSupplied as:1 x 10g skimmed milk powder

Analyte	Method	AV	Range	SDPA	Units	DP
Enumeration of Salmonella species	XLD agar BG agar Plate count agar MPN	RMean	0 to 100,000	log <sub>10</sub> 0.35	cfu g <sup>-1</sup>	0

# Sample 04Cronobacter speciesSupplied as:1 x 25g skimmed milk powder

Analyte	Method	AV	Range	SDPA	Units	DP
Detection of Cronobacter species	Enrichment/culture PCR	Qual Form	0 to 1000	NA	cfu 25g <sup>-1</sup>	NA

Sample 05	Osmophilic yeast and mould
Supplied as:	1 x 10g skimmed milk powder or oatmeal

Analyte	Method	AV	Range	SDPA	Units	DP
Enumeration of osmophilic yeast	Dichloran 18 agar	RMean	0 to 100,000	log <sub>10</sub> 0.35	cfu g⁻¹	0
Enumeration of osmophilic mould	Rose Bengal agar					

Sample 06 Supplied as: Salmonella species (detection)

Analyte	Method	AV	Range	SDPA	Units	DP
Detection of Salmonella species	Enrichment/culture	Qual Form	0 to 1000	NA	cfu 25g <sup>-1</sup>	NA
	PCR					
	VIDAS					
	ELISA					
	TECRA					

# QMS Scheme DescriptionSample 07Listeria species (detection)Supplied as:1 x 25g skimmed milk powder or oatmeal

Analyte	Method	AV	Range	SDPA	Units	DP
Detection of <i>Listeria</i> species Detection of <i>L.monocytogenes</i>	Enrichment/culture PCR RAPID L.MONO VIDAS ELISA	Qual Form	0 to 1000	NA	cfu 25g <sup>-1</sup>	NA

#### Sample 08 Supplied as:

# Listeria species (enumeration)

1 x 10g skimmed milk powder or oatmeal

Analyte	Method	AV	Range	SDPA	Units	DP
Enumeration of <i>Listeria</i> species Enumeration of <i>L.monocytogenes</i>	Aloa agar Palcam agar	RMean	0 to 100,000	log <sub>10</sub> 0.35	cfu g <sup>-1</sup>	0

# Sample 09 Supplied as:

# Enterococci

1 x 10g skimmed milk powder or oatmeal

Analyte	Method	AV	Range	SDPA	Units	DP
Enumeration of Enterococci	KF agar KAA agar	RMean	0 to 100,000	log <sub>10</sub> 0.35	cfu g⁻¹	0
	Slanetz & Bartley agar					

# Sample 10 Supplied as:

# **Clostridium species**

Analyte	Method	AV	Range	SDPA	Units	DP
Detection of <i>Clostridium</i> species	Enrichment/culture RC agar PCR	Qual Form	0 to 100,000	NA	cfu 10g⁻¹	NA
Enumeration of <i>C.perfringens</i>	TSC agar OPSP agar IS agar	RMean	0 to 100,000	log <sub>10</sub> 0.35	cfu g⁻¹	0

# QMS Scheme DescriptionSample 11Spore countsSupplied as:1 x 10g skimmed milk powder or oatmeal

Analyte	Method	AV	Range	SDPA	Units	DP
Enumeration of mesophilic aerobic spores	Plate count agar 30C	RMean	0 to 100,000	log <sub>10</sub> 0.50	cfu g⁻¹	0
Enumeration of thermophilic aerobic spores	Plate count agar 55C	RMean	0 to 100,000	log <sub>10</sub> 0.50	cfu g⁻¹	0

# Sample 12 Supplied as:

# **Shigella species** 1 x 25g oatmeal

AnalyteMethodAVRangeSDPAUnitsDPDetection of Shigella speciesEnrichment/culture<br/>RAPID TESTQual Form0 to 1000NAcfu 25g<sup>-1</sup>NA

#### Sample 13 Supplied as:

# Vibrio species

1 x 25g oatmeal

Analyte	Method	AV	Range	SDPA	Units	DP
Detection of Vibrio species	Enrichment/culture	Qual Form	0 to 1000	NA	cfu 25g⁻¹	NA
Detection of V. parahaemolyticus	RAPID TEST					

# Sample 14Yersinia speciesSupplied as:1 x 25g skimmed milk powder

Analyte	Method	AV	Range	SDPA	Units	DP
Detection of Y.enterocolitica	Enrichment/culture RAPID TEST	Qual Form	0 to 1000	NA	cfu 25g⁻¹	NA

# Sample 15 Supplied as:

# Anaerobes

Analyte	Method	AV	Range	SDPA	Units	DP
Total anaerobic mesophilic count	Plate count agar RC agar	RMean	0 to 100,000	log10 0.35	cfu g <sup>-1</sup>	0

QMS Scheme Description

Analyte	Method	AV	Range	SDPA	Units	DP
Enumeration of anaerobic sulphite-reducing bacteria	IS agar TSC agar	RMean	0 to 100,000	log10 0.35	cfu g⁻¹	0
Enumeration of mesophilic anaerobic spores	Plate count agar RC agar	RMean	0 to 100,000	log10 0.50	cfu g⁻¹	0

# Sample 16 Supplied as:

**TVC/indicator organisms** 1 x 10g skimmed milk powder or oatmeal

Analyte	Method	AV	Range	SDPA	Units	DP
Total aerobic mesophilic count	Plate count agar Milk plate count agar Petrifilm	RMean	0 to 100,000	log <sub>10</sub> 0.35	cfu g <sup>-1</sup>	0
Enumeration of coliforms	VRBA Petrifilm COLI ID MPN	RMean	0 to 100,000	log <sub>10</sub> 0.35	cfu g <sup>-1</sup>	0
Enumeration of Enterobacteriaceae	VRBGA Petrifilm MPN	RMean	0 to 100,000	log <sub>10</sub> 0.35	cfu g <sup>-1</sup>	0
Enumeration of <i>E. coli</i>	TBX agar VRBA Petrifilm COLI ID MPN	RMean	0 to 100,000	log <sub>10</sub> 0.35	cfu g <sup>-1</sup>	0

Sample 17 Supplied as:

# Staphylococcus/Bacillus species

Analyte	Method	AV	Range	SDPA	Units	DP
Enumeration of Staphylococcus species	Baird parker agar	RMean	0 to 100,000	log <sub>10</sub> 0.35	cfu g⁻¹	0
Enumeration of coagulase positive	Petrifilm					
staphylococci	Rapid Staph					
Enumeration of Bacillus species	MYP agar	RMean	0 to 100,000	log <sub>10</sub> 0.35	cfu g⁻¹	0
Enumeration of <i>B.cereus</i>	PEMBA agar			-	-	
	COMPASS BC agar					
	Bacillus cereus agar					

	QMS Scheme Description
Sample 18	Low-level indicator organisms
Supplied as:	1 x 10g skimmed milk powder or oatmeal

Analyte	Method	AV	Range	SDPA	Units	DP
Detection of <i>E.coli</i>	Enrichment/culture RAPID TEST MPN Petrifilm	Qual Form	0 to 1000	NA	cfu 10g <sup>-1</sup>	NA
Detection of Enterobacteriaceae	Enrichment/culture Petrifilm MPN	Qual Form	0 to 1000	NA	cfu 10g <sup>-1</sup>	NA
Detection of coliforms	Enrichment/culture COLI ID MPN Petrifilm	Qual Form	0 to 1000	NA	cfu 10g <sup>-1</sup>	NA
Enumeration of <i>E.coli</i>	TBX agar VRBA Petrifilm COLI ID MPN	RMean	0 to 1000	log <sub>10</sub> 0.35	cfu g <sup>-1</sup>	0
Enumeration of Enterobacteriaceae	VRBGA Petrifilm MPN	RMean	0 to 1000	log <sub>10</sub> 0.35	cfu g⁻¹	0
Enumeration of coliforms	VRBA Petrifilm COLI ID MPN	RMean	0 to 1000	log <sub>10</sub> 0.35	cfu g <sup>-1</sup>	0

# Sample 20 Supplied as:

# Thermotolerant coliforms

Analyte	Method	AV	Range	SDPA	Units	DP
Enumeration of <i>E. coli</i> Enumeration of thermotolerant coliforms	VRBA 44	RMean	0 to 100,000	log <sub>10</sub> 0.35	cfu g⁻¹	0

Analyte	Method	AV	Range	SDPA	Units	DP
Detection of Campylobacter species	Enrichment/culture	Qual Form	0 to 1000	NA	cfu 25g⁻¹	NA

# Sample 22E.coli O157Supplied as:1 x 25g skimmed milk powder or oatmeal

Analyte	Method	AV	Range	SDPA	Units	DP
Detection of <i>E.coli</i> O157	Enrichment/culture IMS REVEAL PCR ELISA VIDAS	Qual Form	0 to 1000	NA	cfu 25g <sup>-1</sup>	NA

#### Sample 23 Supplied as:

Sample 24

Supplied as:

# Yeast and Mould

1 x 10g skimmed milk powder or oatmeal

Analyte	Method	AV	Range	SDPA	Units	DP
Enumeration of yeast	OGYE agar	RMean	0 to 100,000	log <sub>10</sub> 0.35	cfu g⁻¹	0
Enumeration of mould	Dichloran 18 agar				_	
Enumeration of yeast and mould	Malt extract agar					
	Rose Bengal agar					
	DRBC agar					
	YGC agar					
	Petrifilm					

# Lactic acid bacteria

Analyte	Method	AV	Range	SDPA	Units	DP
Enumeration of lactic acid bacteria	MRS agar AM agar Rogosa agar Petrifilm	RMean	0 to 100,000	log <sub>10</sub> 0.35	cfu g <sup>-1</sup>	0

# Sample 25PsychrotrophsSupplied as:1 x 10g oatmeal

Analyte	Method	AV	Range	SDPA	Units	DP
Enumeration of aerobic psychrotrophs	Plate count agar 21 C Plate count agar 6.5 C	RMean	0 to 100,000	log <sub>10</sub> 0.35	cfu g⁻¹	0

# Sample 26Pseudomonas speciesSupplied as:1 x 10g skimmed milk powder or oatmeal

Analyte	Method	AV	Range	SDPA	Units	DP
Enumeration of <i>Pseudomonas</i> species	CF agar CN agar	RMean	0 to 100,000	log <sub>10</sub> 0.35	cfu g <sup>-1</sup>	0

# Sample 27Probiotic bacteriaSupplied as:1 x 10ml vial to represent 10g sample (once reconstituted in 10ml diluent)

Analyte	Method	AV	Range	SDPA	Units	DP
Enumeration of <i>Bifidobacterium</i> species	TOS-MUP agar	RMean	0 to 100,000	log <sub>10</sub> 0.35	cfu g⁻¹	0
Enumeration of <i>Lactobacillus</i> species	AM agar MRS agar MRS-OX agar Rogosa agar	RMean	0 to 100,000	log <sub>10</sub> 0.35	cfu g <sup>-1</sup>	0

# Sample 28Salmonella in teaSupplied as:1 x 10ml vial plus 25g tea matrix

Analyte	Method	AV	Range	SDPA	Units	DP
Detection of Salmonella species	Enrichment/culture	Qual Form	0 to 1000	NA	cfu 25g <sup>-1</sup>	NA
	PCR					
	VIDAS					
	ELISA					
	TECRA					

# Sample 29Indicator organisms in teaSupplied as:1 x 10ml vial plus 10g tea matrix

Analyte	Method	AV	Range	SDPA	Units	DP
Total aerobic mesophilic count	Plate count agar Milk plate count agar Petrifilm	RMean	0 to 100,000	log <sub>10</sub> 0.35	cfu g <sup>-1</sup>	0
Enumeration of coliforms	VRBA Petrifilm COLI ID MPN	RMean	0 to 100,000	log <sub>10</sub> 0.35	cfu g <sup>-1</sup>	0
Enumeration of coagulase positive staphylococci	Baird parker agar Petrifilm Rapid Staph	RMean	0 to 100,000	log <sub>10</sub> 0.35	cfu g⁻¹	0
Enumeration of yeast and mould	OGYE agar Dichloran 18 agar Malt extract agar Rose Bengal agar DRBC agar YGC agar Petrifilm	RMean	0 to 100,000	log <sub>10</sub> 0.35	cfu g <sup>-1</sup>	0

# Sample 30 Supplied as:

# Salmonella in herbs

1 x 10ml vial plus 25g herb matrix

Analyte	Method	AV	Range	SDPA	Units	DP
Detection of Salmonella species	Enrichment/culture PCR	Qual Form	0 to 1000	NA	cfu 25g <sup>-1</sup>	NA
	VIDAS					
	ELISA					
	TECRA					

Sample 31 Supplied as:

# Salmonella in spices

1 x 10ml vial plus 25g spice matrix

Analyte	Method	AV	Range	SDPA	Units	DP
Detection of Salmonella species	Enrichment/culture PCR VIDAS	Qual Form	0 to 1000	NA	cfu 25g <sup>-1</sup>	NA

#### QMS Scheme Description

Analyte	Method	AV	Range	SDPA	Units	DP
	ELISA					
	TECRA					

# Sample 32Campylobacter enumerationSupplied as:1 x 10ml vial to represent 10g sample (once reconstituted in 10ml diluent)

Analyte	Method	AV	Range	SDPA	Units	DP
Enumeration of Campylobacter species	Karmali agar CCDA agar Skirrow agar CampyCount agar	RMean	0 to 100,000	NA	cfu g <sup>-1</sup>	0

# Sample 33Identification Test (non-pathogen)Supplied as:Participants will be provided with a vial of freeze-dried material containing a single organism which will<br/>need to be cultured on non-selective agar before test. The sample may contain biosafety level 1 or 2<br/>organisms, including Staphylococcus, Bacillus and Clostridium, but will not contain the recognised food<br/>pathogens such as Salmonella, Listeria, Campylobacter or toxigenic *E.coli*. The organism may be<br/>identified to family, genus or species level.

Analyte	Method	AV	Range	SDPA	Units	DP
Identification of unknown organism	Morphological e.g Gram reaction, appearance Serological e.g. slide agglutination, ELISA Biochemical e.g. API, VITEK, Biolog Protein analysis e.g. electrophoresis Genotypic e.g. PCR, ribotyping, BAX Spectrometry e.g. MALDI-TOF	Formulation	NA	NA	NA	NA

	QMS Scheme Description
Sample 34	Salmonella identification
Supplied as:	Participants will be provided with a vial of freeze-dried material containing a strain of Salmonella which will need to be cultured on non-selective agar before test. The organisms should be identified to correct group or serovar

Analyte	Method	AV	Range	SDPA	Units	DP
Salmonella identification	Serological e.g. slide agglutination, ELISA Protein analysis e.g. electrophoresis Genotypic e.g. PCR, ribotyping, BAX Spectrometry e.g. MALDI-TOF	Formulation	NA	NA	NA	NA

# Sample 35 Supplied as:

# Paper exercise

Participants will be provided with a photograph and a scenario in order to count the number of colonies and calculate the number of microorganisms in the original sample.

Analyte	Method	AV	Range	SDPA	Units	DP
Counting of colonies and	Visual count only	Formulation	0 to 300	Greater of	cfu/ml or	NA
calculation of number of				robust SD or	cfu/g	
microorganisms				log 0.05	_	

# ABBREVIATIONS FOR MICROBIOLOGICAL METHOD CODES

AM = Acidified MRS	MRS-OX = MRS Oxgall
BG = brilliant green agar	OGYE = Oxytetracycline-Glucose Yeast Extract agar
CCDA = Charcoal-cefoperazone-deoxycholate agar	OPSP = Oleandomycin phosphate sulphadiazine polymyxin
CF = Cetrimide fucidin cephalosporin agar	PEMBA = Polymyxin-pyruvate-egg yolk-mannitol-bromthymol blue
CN = Cetrimide nalidixic acid agar	agar
DRBC = dichloran rose Bengal	PCR = Polymerase chain reaction
ELISA = Enzyme-linked immunosorbent assay	RC = Reinforced Clostridial agar
IMS = Immuno-magnetic separation	TBX = Tryptone Bile X-glucuronide agar
IS = Iron sulphite agar	TOS MUP = TOS proprionate agar + LiMUP
KAA = Kanamycin aesculin agar	TSC = Tryptone sulphite cycloserine agar
KF = KF Streptococcus agar	VRBA = Violet red bile agar
MPN = Most probable number	VRBGA = Violet red bile glucose agar
MYP = Mannitol Egg Yolk Polymyxin Agar	YGC = Yeast glucose chloramphenicol agar
MRS = de Mann, Rogosa & Sharpe	XLD = Xylose lysine deoxycholate agar

All analytes will also have 'OTHER' as a method choice in case your method is not listed