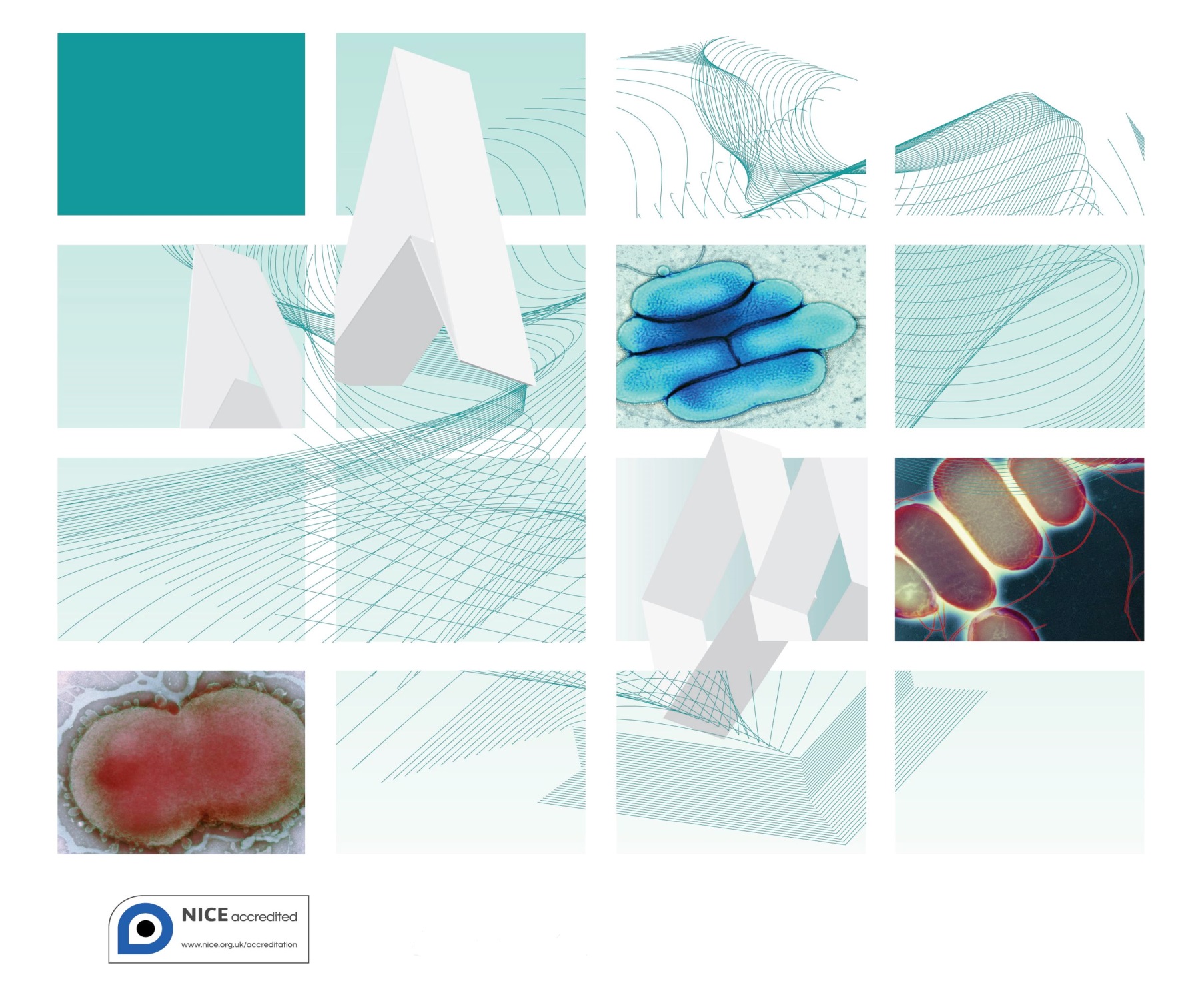
UK Standards for Microbiology Investigations

Identification of *Vibrio* species



Acknowledgments

UK Standards for Microbiology Investigations (SMIs) are developed under the auspices of Public Health England (PHE) working in partnership with the National Health Service (NHS), Public Health Wales and with the professional organisations whose logos are displayed below and listed on the website <http://www.hpa.org.uk/SMI/Partnerships>. SMIs are developed, reviewed and revised by various working groups which are overseen by a steering committee (see <http://www.hpa.org.uk/SMI/WorkingGroups>).

The contributions of many individuals in clinical, specialist and reference laboratories who have provided information and comments during the development of this document are acknowledged. We are grateful to the Medical Editors for editing the medical content.

For further information please contact us at:

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Microbiology Services

Public Health England

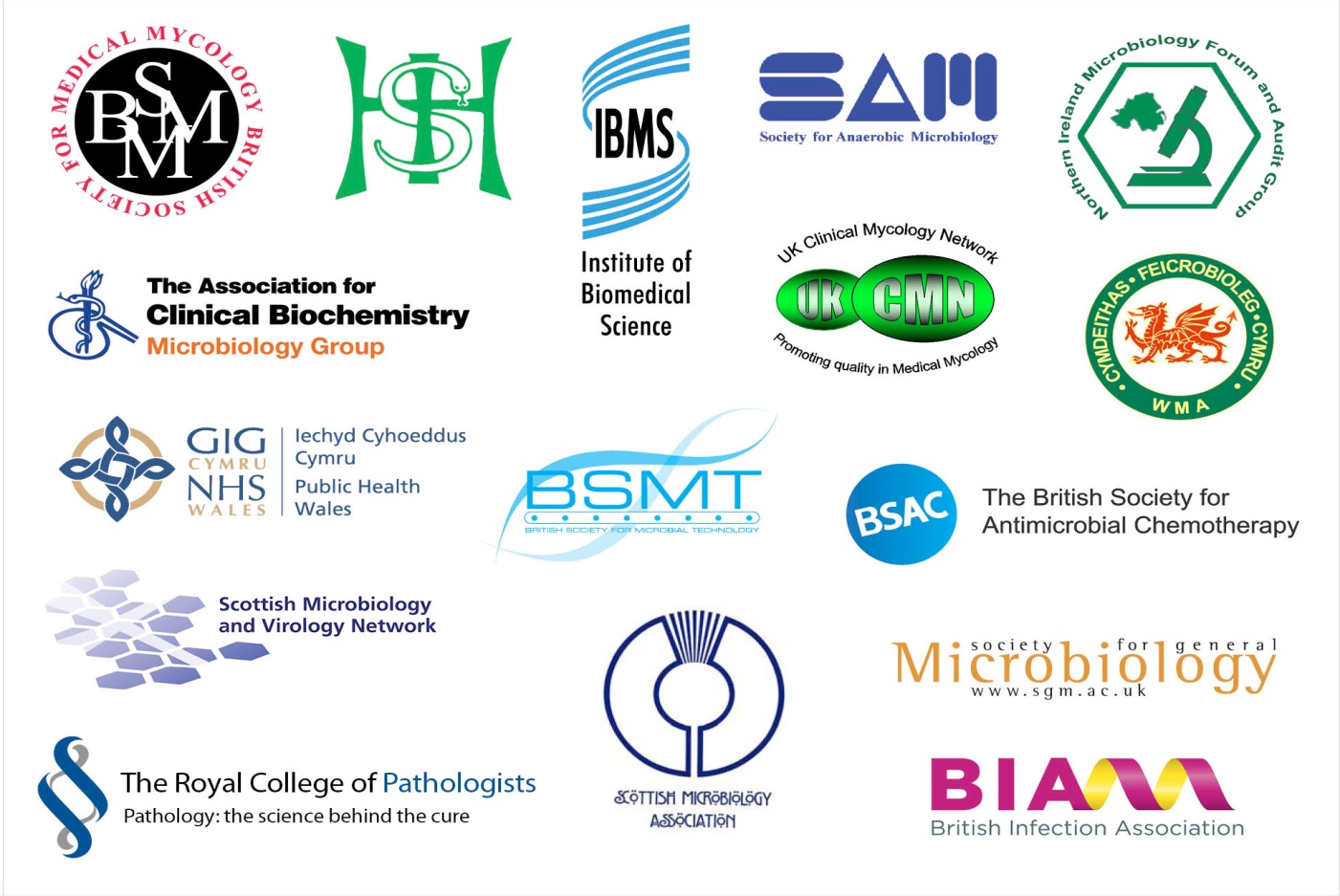
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UK Standards for Microbiology Investigations are produced in association with:



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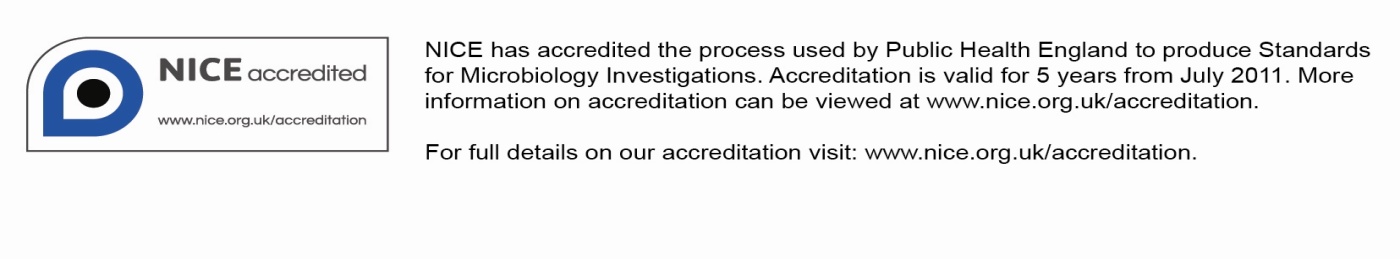
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Amendment Table

Each SMI method has an individual record of amendments. The current amendments are listed on this page. The amendment history is available from [standards@phe.gov.uk](mailto:standards@phe.gov.uk).

New or revised documents should be controlled within the laboratory in accordance with the local quality management system.

|  |  |
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| Amendment No/Date. | 4/ |
| Issue no. discarded. | 2.1 |
| Insert Issue no. |  |
| **Section(s) involved** | **Amendment** |
| Whole document. | Document has been transferred to a new template to reflect the Health Protection Agency’s transition to Public Health England.  Front page has been redesigned.  Status page has been renamed as Scope and Purpose and updated as appropriate.  Professional body logos have been reviewed and updated.  Standard safety and notification references have been reviewed and updated |

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| Issue no. discarded. | 2 |
| Insert Issue no. | 2.1 |
| **Section(s) involved** | **Amendment** |
| Whole document. | Document presented in a new format. |
| References. | Some references updated. |

UK Standards for Microbiology Investigations[[1]](#footnote-1)#: Scope and Purpose

Users of SMIs

* SMIs are primarily intended as a general resource for practising professionals operating in the field of laboratory medicine and infection specialties in the UK
* SMIs provide clinicians with information about the available test repertoire and the standard of laboratory services they should expect for the investigation of infection in their patients, as well as providing information that aids the electronic ordering of appropriate tests
* SMIs provide commissioners of healthcare services with the appropriateness and standard of microbiology investigations they should be seeking as part of the clinical and public health care package for their population

Background to SMIs

SMIs comprise a collection of recommended algorithms and procedures covering all stages of the investigative process in microbiology from the pre-analytical (clinical syndrome) stage to the analytical (laboratory testing) and post analytical (result interpretation and reporting) stages.

Syndromic algorithms are supported by more detailed documents containing advice on the investigation of specific diseases and infections. Guidance notes cover the clinical background, differential diagnosis, and appropriate investigation of particular clinical conditions. Quality guidance notes describe laboratory processes which underpin quality, for example assay validation.

Standardisation of the diagnostic process through the application of SMIs helps to assure the equivalence of investigation strategies in different laboratories across the UK and is essential for public health surveillance, research and development activities.

Equal Partnership Working

SMIs are developed in equal partnership with PHE, NHS, Royal College of Pathologists and professional societies.

The list of participating societies may be found at <http://www.hpa.org.uk/SMI/Partnerships>. Inclusion of a logo in an SMI indicates participation of the society in equal partnership and support for the objectives and process of preparing SMIs. Nominees of professional societies are members of the Steering Committee and Working Groups which develop SMIs. The views of nominees cannot be rigorously representative of the members of their nominating organisations nor the corporate views of their organisations. Nominees act as a conduit for two way reporting and dialogue. Representative views are sought through the consultation process.

SMIs are developed, reviewed and updated through a wide consultation process.

Quality Assurance

NICE has accredited the process used by the SMI Working Groups to produce SMIs. The accreditation is applicable to all guidance produced since October 2009. The process for the development of SMIs is certified to ISO 9001:2008.

SMIs represent a good standard of practice to which all clinical and public health microbiology laboratories in the UK are expected to work. SMIs are NICE accredited and represent neither minimum standards of practice nor the highest level of complex laboratory investigation possible. In using SMIs, laboratories should take account of local requirements and undertake additional investigations where appropriate. SMIs help laboratories to meet accreditation requirements by promoting high quality practices which are auditable. SMIs also provide a reference point for method development.

The performance of SMIs depends on competent staff and appropriate quality reagents and equipment. Laboratories should ensure that all commercial and in-house tests have been validated and shown to be fit for purpose. Laboratories should participate in external quality assessment schemes and undertake relevant internal quality control procedures.

Patient and Public Involvement

The SMI Working Groups are committed to patient and public involvement in the development of SMIs. By involving the public, health professionals, scientists and voluntary organisations the resulting SMI will be robust and meet the needs of the user. An opportunity is given to members of the public to contribute to consultations through our open access website.

Information Governance and Equality

PHE is a Caldicott compliant organisation. It seeks to take every possible precaution to prevent unauthorised disclosure of patient details and to ensure that patient-related records are kept under secure conditions.

The development of SMIs are subject to PHE Equality objectives <http://www.hpa.org.uk/webc/HPAwebFile/HPAweb_C/1317133470313>. The SMI Working Groups are committed to achieving the equality objectives by effective consultation with members of the public, partners, stakeholders and specialist interest groups.

Legal Statement

Whilst every care has been taken in the preparation of SMIs, PHE and any supporting organisation, shall, to the greatest extent possible under any applicable law, exclude liability for all losses, costs, claims, damages or expenses arising out of or connected with the use of an SMI or any information contained therein. If alterations are made to an SMI, it must be made clear where and by whom such changes have been made.

The evidence base and microbial taxonomy for the SMI is as complete as possible at the time of issue. Any omissions and new material will be considered at the next review. These standards can only be superseded by revisions of the standard, legislative action, or by NICE accredited guidance.

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Suggested Citation for this Document

Public Health England. (). Identification of *Vibrio* species. UK Standards for Microbiology Investigations. ID 19 Issue di+. <http://www.hpa.org.uk/SMI/pdf>.

Scope of Document

This SMI describes the identification of *Vibrio* species.

This SMI should be used in conjunction with other SMIs.

Introduction

Taxonomy

The genus *Vibrio* is a member of the family *Vibrionaceae* and consists of 103 recognised species. 12 species have been reclassified to other genera within the family1. Currently, only 10 species of the genus *Vibrio* have been incriminated in gastrointestinal and extra-intestinal diseases in man; the most important of these being *Vibrio cholerae*, the cause of cholera.

Characteristics

*Vibrio* species are straight or curved Gram negative non-spore forming rods, 0.5-0.8µm wide x 1.4-2.6µm long in size. They all grow at 20°C and most at 30°C. On blood agar, colonies are greyish, 2-3mm in diameter and colonies on thiosulphate citrate bile salt sucrose (TCBS) agar are either yellow or green. *Vibrio* species are facultative anaerobes and are motile by polar flagellum with sheaths. *V. cholerae* has a single polar flagellum with sheath. Some species, such as *V. parahaemolyticus* and *V. alginolyticus*, have both a single polar flagellum with sheath and thin flagella projecting in all directions, and the other species, such as *Aliivibrio fischeri* (formerly known as *V. fischeri*), have tufts of polar flagella with sheath. They are also mesophilic and chemoorganotrophic, and have a facultatively fermentative metabolism2.

All members of the genus *Vibrio*, with the exceptions of *V. metschnikovii* and *V. gazogenes* (non-human), are oxidase positive and reduce nitrates to nitrites3. They are usually sensitive to the vibriostatic agent O129 (2, 4-diamino-6, 7-diisopropylpteridine phosphate-150μg disc). Growth is stimulated by sodium ions (halophilic) - the concentration required is reflected in the salinity of their natural environment. *V. cholerae* (the causative agent of cholera) is not halophilic3.

*Vibrio* species are typically found in saltwater and in numerous sea-living animals, such as oysters, crabs or prawns, and has been known to cause fatal infections in humans during exposure. In humans, *Vibrio* species has been isolated from stool, vomitus, blood, or wound exudate cultures4,5.

The type species is *V. chloerae*.

The medically important *Vibrio* specie is;

V. *cholerae*

Cells are comma shaped gram negative, non-spore forming rods. The bacterium is   
1- 3 µm x 0.5-0.8 µm and is motile. It has a single polar flagellum. They grow at several temperatures - 4°C, 20°C, 30°C and 35 – 37 °C. On blood agar, colonies are strongly haemolytic except for strains of the classical biotype of *V. cholerae*, which are non-haemolytic. On TCBS agar, colonies are yellow and at least 2 mm in diameter after 18 – 24hrs incubation6.

*Vibrio cholerae* can be serogrouped into 155 groups on the basis of somatic O antigens. Serogroups O1 (classical and El Tor biotypes) and O139 are primarily responsible for cholera outbreaks. Epidemic strains of *V. cholerae* O1 can be differentiated into El Tor and classical biotypes, which is further subdivided into Inaba, Ogawa and Hikojima subtypes. Worldwide, *V. cholerae* El Tor is currently the predominant biotype and Ogawa the predominant subtype. Strains not belonging to serogroup O1 is generally referred to as *V. cholerae* non-O1 and can still cause illness in humans. In 1993 an outbreak of epidemic cholera began in Bengal caused by a new serogroup of non-O1 *V. cholerae*7. Although initial isolates of this serogroup (O139) were resistant to vibriostatic agent O129, recently isolated strains are sensitive7.

*V. cholerae* O1 depends on the detection of the O1 antigen on the surface of the bacterium, and therefore does not identify *V. cholerae* O139 strains.

*V. cholerae* O1 classical biotype is Voges-Proskauer (VP) negative and is sensitive to polymyxin (50 IU disc). *V. cholerae* O1 El Tor biotype is VP positive and is resistant to polymyxin8. They are oxidase positive, reduce nitrates, grow at 40°C, as well as utilize sucrose, α-ketoglutarate and also grow in the absence of Na+. These distinguish them from other species of *Vibrio*6.

Principles of Identification

Isolates from primary culture are identified by colonial appearance, Gram stain, serology (agglutination with specific antisera) and biochemical testing. If confirmation of identification is required, isolates should be sent to the Reference Laboratory. All identification tests should ideally be performed from non-selective agar.

Technical Information/Limitations

Oxidase Test

The oxidase test may give false negative results if performed from TCBS agar and so colonies should be sub-cultured to a non-selective medium such as blood agar before testing5.

Gram Stain

Gram stain is a relative rapid and easy procedure for diagnosis. The morphology of *Vibrio* species should be curved Gram negative rods on microscopic examination. Based on this characteristics, a Gram stain can promptly help differentiate *Vibrio* species from *Pseudomonas* species9.

Serology

Agglutination should be carried out with subcultures onto non-selective agar, because colonies can auto-agglutinate from TCBS agar, giving false-positive results7.

1 Safety Considerations10-26

*Vibrio cholerae* and *Vibrio parahaemolyticus* are Hazard Group 2 organisms, and in some cases the nature of the work may dictate full Containment Level 3 conditions. All laboratories should handle specimens as if potentially high risk.

*Vibrio cholerae* and *Vibrio parahaemolyticus* cause severe and sometimes fatal diseases. The infectious dose ranges between 106 and 1011 ingested *Vibrio* organisms. Laboratory-acquired infections have been reported27-29. Infection may be acquired either through ingestion, contact with non-intact skin or mucosa and accidental parenteral inoculation30. Vaccine is recommended for laboratory workers who may be regularly exposed to cholera in the course of their work. This would normally only include those working in reference laboratories or in laboratories attached to infectious disease units; guidance is given in the DH Green Book31. This vaccine confers protection specific to *V. cholerae* serogroup O1. Immunisation does not protect against *V. cholerae* serogroup O139 or other species of *Vibrio*31.

The most effective method for preventing laboratory-acquired infections is the adoption of safe working practices. Complying with these rules remains the top priority.

Refer to current guidance on the safe handling of all organisms documented in this SMI.

Laboratory procedures that give rise to infectious aerosols must be conducted in a microbiological safety cabinet.

The above guidance should be supplemented with local COSHH and risk assessments.

Compliance with postal and transport regulations is essential.

2 Target Organisms

*Vibrio species* commonly reported to cause human disease

*Vibrio cholerae* (serogroups 01 and 0139(Bengal)), *Vibrio parahaemolyticus, Vibrio vulnificus*

Other *Vibrio* species reported to have caused human disease

*Vibrio alginolyticus, Vibrio carchariae, Vibrio cholerae (*serogroups other than 01 and 0139*), Vibrio cincinnatiensis, Vibrio fluvialis, Vibrio furnissii, Vibrio metschnikovii, Vibrio mimicus,*

Any species of *Vibrio* may be found in faeces after the ingestion of seafood or water that contains them.

3 Identification

3.1 Microscopic Appearance

**Gram stain** (refer to [TP 39 - Staining Procedures](http://www.hpa.org.uk/SMI/pdf/Testprocedures))

Cells are Gram negative rods characteristically curved or comma-shaped but can also be straight. This characteristic appearance is not always observed when the organism is Gram stained from solid media.

3.2 Primary Isolation Media

Blood agar incubated in air at 35-37°C for 18-24hrs

TCBS agar incubated in air at 35-37°C for 18-24hrs

3.3 Colonial Appearance

On blood agar, colonies are 2-3mm in diameter. Some strains may be haemolytic.

On TCBS agar, colonies are at least 2 mm in diameter and yellow in the case of sucrose fermenters and green non-sucrose fermenters after 18-24hrs incubation. Cultures should be examined quickly after removal from the incubator as the yellow colouration of the colonies may revert to a green colour when left at room temperature. Organisms other than *Vibrio* species grow on TCBS. See table below.

|  |  |
| --- | --- |
| **Organism** | **Colour of colonies on TCBS** |
| *V. cholera* | yellow |
| *V. alginolyticus* | yellow |
| *V. cincinnatiensis* | yellow |
| *V. carchariae* | yellow/green |
| *V. fluvialis* | yellow |
| *V. furnissii* | yellow |
| *V. parahaemolyticus* | green |
| *V. metschnikovii* | yellow |
| *V. vulnificus* | green |
| *V. mimicus* | green |
| *Aeromonas* species | yellow |
| *Pseudomonas* species | blue/green\* |
| *Proteus* species | yellow/green\* |
| *Enterococcus* species | yellow |

\* The colonies are smaller than those produced by *Vibrio* species

3.4 Test Procedures

**Oxidase Test** ([TP 26 - Oxidase test](http://www.hpa.org.uk/SMI/pdf/Testprocedures))

*Vibrio* species are oxidase positive with the exceptions of *V. metschnikovii* and *V. gazogenes.*

**NOTE:** Oxidase test may give false negative results on media containing carbohydrates - subculture to nutrient or blood agar before testing.

Voges-Proskauer Test (optional)

The Voges-Proskauer test has been used to differentiate between the El Tor and classical biotype of *V. cholerae* O1. Classical biotypes usually give negative results; El Tor isolates are generally positive. A cherry red colour indicates a positive reaction.

Sensitivity to pteridine O129 (10 μg and 150 μg discs)

Pteridine 0129 is useful in the differentiation of *Vibrio* from other gram-negative bacteria especially *Aeromonas*, which are characteristically resistant to 0129.

Most *Vibrio* species are sensitive with 150μg but species differ with 10μg discs (some strains of *V. cholerae* O1 and O139 may be resistant to both disc contents).

Serology (agglutination with specific antisera)

Serotype identification is based on agglutination in antisera to type-specific O antigens. The use of specific antisera is one of the most rapid and specific methods of identifying *Vibrio* species.

**NOTE:** Agglutination should be carried out with subcultures onto non-selective agar, because colonies can auto-agglutinate from TCBS agar, giving false-positive results7.

Commercial Identification Systems

These tests may require supplementation with sodium chloride (NaCl). Laboratories must follow manufacturer’s instructions. Rapid tests and kits must be validated and be shown to be fit for purpose prior to use.

3.5 Further Identification

Rapid Molecular Methods

Molecular methods have had an enormous impact on the taxonomy of *Vibrio*. Analysis of gene sequences has increased understanding of the phylogenetic relationships of *Vibrio* and related organisms; and has resulted in the recognition of numerous new species. Molecular techniques have made identification of many species more rapid and precise than is possible with phenotypic techniques.

A variety of rapid identification and sensitivity methods have been developed for isolates from clinical samples; these include molecular techniques such as Real-time Polymerase Chain reaction (PCR), Pulsed Field Gel Electrophoresis (PFGE), Multilocus Sequence Typing (MLST), Multiple-Locus Variable-Number Tandem-Repeat Analysis (MVLA), Fluorescent Amplified Fragment Length Polymorphism (FAFLP), Whole Genome Sequencing (WGS) and Matrix Assisted Laser Desorption Ionisation Time-of-Flight (MALDI-TOF) Mass Spectrometry. All of these approaches enable subtyping of unrelated strains, but do so with different accuracy, discriminatory power, and reproducibility.

However, these methods remain accessible to reference laboratories only and are difficult to implement for routine bacterial identification in a clinical laboratory.

**Matrix-Assisted Laser Desorption/Ionisation - Time of Flight (MALDI-TOF) Mass Spectrometry**

Matrix-assisted laser desorption ionization–time-of-flight mass spectrometry (MALDI-TOF MS), which can be used to analyse the protein composition of a bacterial cell, has emerged as a new technology for species identification. This has been shown to be a rapid and powerful tool because of its reproducibility, speed and sensitivity of analysis. The advantage of MALDI-TOF as compared with other identification methods is that the results of the analysis are available within a few hours rather than several days. The speed and the simplicity of sample preparation and result acquisition associated with minimal consumable costs make this method well suited for routine and high-throughput use32.

This has been utilized to aid in both the detection and species-level identification of *Vibrio* species - Vibrio *parahaemolyticus*33. It has also been used to discriminate between closely related species, such as *Aeromonas* species, *Photobacterium damselae* (formerly *Vibrio damselae*) and *Grimontia hollisae* (formerly *Vibrio* *hollisae*)33*.*

Real-time Polymerase Chain reaction (RT-PCR)

PCR is usually considered to be a good method for bacterial detection as it is simple, rapid, sensitive and specific. The basis for PCR diagnostic applications in microbiology is the detection of infectious agents and the discrimination of non-pathogenic from pathogenic strains by virtue of specific genes. However, it does have limitations. Although the 16S rRNA gene is generally targeted for the design of species-specific PCR primers for identification, designing primers is difficult when the sequences of the homologous genes have high similarity.

PCR targeted to the *dnaJ* gene has been used successfully in the identification of *Vibrio* species - *Vibrio cholerae, Vibrio parahaemolyticus, Vibrio vulnificus, Vibrio mimicus*, and *Vibrio alginolyticus* 34. It has also been used to detect *V. vulnificus*- specific genes within 2hrs in the blood of patients with skin and soft tissue infections35.

Pulsed Field Gel Electrophoresis (PFGE)

PFGE detects genetic variation between strains using rare-cutting restriction endonucleases, followed by separation of the resulting large genomic fragments on an agarose gel. PFGE is known to be highly discriminatory and a frequently used technique for outbreak investigations and has gained broad application in characterizing epidemiologically related isolates. However, the stability of PFGE may be insufficient for reliable application in long-term epidemiological studies. However, due to its time-consuming nature (30hr or longer to perform) and its requirement for special equipment, PFGE is not used widely outside the reference laboratories36,37.

This has been used successfully to identify and discriminate between species of the genus *Vibrio*. It has also been used perform molecular subtyping of *Vibrio cholerae* 01 and 013938,39.

Multilocus Sequence Typing (MLST)

MLST measures the DNA sequence variations in a set of housekeeping genes directly and characterizes strains by their unique allelic profiles. The principle of MLST is simple: the technique involves PCR amplification followed by DNA sequencing. Nucleotide differences between strains can be checked at a variable number of genes depending on the degree of discrimination desired. The technique is highly discriminatory, as it detects all the nucleotide polymorphisms within a gene rather than just those non-synonymous changes that alter the electrophoretic mobility of the protein product. One of the advantages of MLST over other molecular typing methods is that sequence data are portable between laboratories and have led to the creation of global databases that allow for exchange of molecular typing data via the Internet40.

MLST has been extensively used as one of the main typing methods for analysing the genetic relationships within the genus *Vibrio*2. It has been very useful in the typing of *V. cholerae*. MLST has also been suggested to have better discriminatory ability than PFGE41.

This method has also been used for the detection of *V. parahaemolyticus* strains and in the recognition of evolutionary trends and emergence of *V. parahaemolyticus* clonal complexes, thus providing an early warning system42.

The drawbacks of MLST are the substantial cost and laboratory work required to amplify, determine, and proofread the nucleotide sequence of the target DNA fragments, making the method hardly suitable for routine laboratory testing.

Fluorescent Amplified Fragment Length Polymorphism (FAFLP)

Fluorescent Amplified Fragment Length Polymorphism is a high-resolution whole genome methodology used as a tool for rapid and cost-effective analysis of genetic diversity within bacterial genomes. It is useful for a broad range of applications such as identification and subtyping of microorganisms from clinical samples, for identification of outbreak genotypes, for studies of micro and macro-variation, and for population genetics.

FAFLP has numerous advantages over other DNA fingerprinting techniques because it assesses the whole genome for both conserved and rapidly evolving sequences in a relatively unbiased way. The number of fragments obtained for comparative purposes between isolates is significantly greater than pulsed-field gel electrophoresis (PFGE), therefore making it more discriminatory than PFGE and the FAFLP results are highly reproducible due to stringent PCR cycling parameters.

This robust and reproducible fingerprinting technique has been used to distinguish between *V. cholerae* O1 and non-O1 and non-O139 strains43. This has also shown that clinical isolates closely resemble environmental isolates in their genomic patterns44.

Multiple-Locus Variable-Number Tandem-Repeat Analysis (MVLA) also known as VNTR

Multiple-Locus Variable number tandem repeat Analysis (MLVA) is a method used to perform molecular typing of particular microorganisms. It utilizes the naturally occurring variation in the number of tandem repeated DNA sequences found in many different loci in the genome of a variety of organisms. The molecular typing profiles are used to study transmission routes, to assess sources of infection and also to assess the impact of human intervention such as vaccination and use of antibiotics on the composition of bacterial populations.

This has been used successfully in the subtyping of *Vibrio* species – *Vibrio cholerae* O1 and O139 serogroups45.

The method has proven very useful for detecting and investigating outbreaks, since it has the capacity to differentiate closely related strains. It also has comparable discriminatory power with PFGE. In addition, the combination of the two approaches (MVLA and PFGE) can further distinguish the strains from different sources and geographical regions of isolation45. The method is technically simple and inexpensive to perform.

Whole Genome Sequencing (WGS)

This is also known as “full genome sequencing, complete genome sequencing, or entire genome sequencing”. It is a laboratory process that determines the complete DNA sequence of an organism's genome at a single time. There are several high-throughput techniques that are available and used to sequence an entire genome such as pyrosequencing, nanopore technology, IIIumina sequencing, Ion Torrent sequencing, etc. This sequencing method holds great promise for rapid, accurate, and comprehensive identification of bacterial transmission pathways in hospital and community settings, with concomitant reductions in infections, morbidity, and costs.

This has been used successfully to explore the genome of *V. cholerae*. The *Vibrio cholerae* genome sequence provides a new starting point for the study of this organism's environmental and pathobiological characteristics. The genome sequence may also hopefully provide important clues to understanding the metabolic and regulatory networks that link genes on the two chromosomes46.

3.6 Storage and Referral

If required, save the pure isolate on a nutrient agar slope for referral to the Reference Laboratory.

4 Identification of *Vibrio* species Flowchart

The flowchart is for guidance only

5 Reporting

5.1 Presumptive Identification

If appropriate growth characteristics, colonial appearance, Gram stain of the culture and oxidase results are demonstrated.

5.2 Confirmation of Identification

Further biochemical tests and/or molecular methods and/or reference laboratory report.

5.3 Medical Microbiologist

Inform the medical microbiologist of all positive cultures from normally sterile sites, of all presumptive and confirmed *Vibrio* species that are known to be pathogenic or potentially pathogenic, and all isolates in outbreaks.

Inform the medical microbiologist if the request card bears information which suggests infection with *V. cholerae* or *V.* *parahaemolyticus*, according to local protocols eg

* Severe watery diarrhoea
* Suspected cholera
* History of foreign travel, or laboratory work
* Suspected food poisoning (especially cases involving consumption of seafood)

The medical microbiologist should also be informed of presumptive or confirmed *Vibrio* species in association with:

* Wound infection or (necrotising) myofasciitis
* Septicaemia
* History of foreign travel
* Contact with (brackish) water, fishing/eating fish or seafood (suggestive of infection with *V*. *vulnificus*, *Photobacterium damselae subsp. damselae* (formerly *V. damsela*)or *Aeromonas hydrophila sensu lato)*
* Medicinal use of leeches, as in plastic surgery (suggestive of infection with *Aeromonas hydrophila sensu lato*)
* Alcoholism, substance abuse, immunodeficiency
* Other serious medical condition such as cancer, or persons receiving treatment for cancer which induces neutropenia and/or mucositis

Follow local protocols for reporting to clinician.

5.4 CCDC

Refer to local Memorandum of Understanding.

5.5 Public Health England47-52

Refer to current guidelines on CDSC and COSURV reporting.

5.6 Infection Control Team

As cholera is a notifiable disease in the UK, for public health management of cases, contacts and outbreaks, all suspected cases should be notified to the local Public Health England Centre immediately. The infection control team should also be informed of presumptive and confirmed isolates of *Vibrio* species.

6 Referrals

6.1 Reference Laboratory

Contact appropriate devolved nation reference laboratory for information on the tests available, turn around times, transport procedure and any other requirements for sample submission: <http://www.hpa.org.uk/cfi/lep/default.htm>

Gastrointestinal Infections Reference Unit

Microbiology Services

Public Health England

61 Colindale Avenue

London

NW9 5EQ

Contact PHE’s main switchboard: Tel. +44 (0) 20 8200 4400

England and Wales <http://www.hpa.org.uk/webw/HPAweb&Page&HPAwebAutoListName/Page/1158313434370?p=1158313434370>

Scotland

<http://www.hps.scot.nhs.uk/reflab/index.aspx>

Northern Ireland

<http://www.belfasttrust.hscni.net/Laboratory-MortuaryServices.htm>

7 Notification to PHE47,48 or Equivalent in the Devolved Administrations49-52

The Health Protection (Notification) regulations 2010 require diagnostic laboratories to notify Public Health England (PHE) when they identify the causative agents that are listed in Schedule 2 of the Regulations. Notifications must be provided in writing, on paper or electronically, within seven days. Urgent cases should be notified orally and as soon as possible, recommended within 24 hours. These should be followed up by written notification within seven days.

For the purposes of the Notification Regulations, the recipient of laboratory notifications is the local PHE Health Protection Team. If a case has already been notified by a registered medical practitioner, the diagnostic laboratory is still required to notify the case if they identify any evidence of an infection caused by a notifiable causative agent.

Notification under the Health Protection (Notification) Regulations 2010 does not replace voluntary reporting to PHE. The vast majority of NHS laboratories voluntarily report a wide range of laboratory diagnoses of causative agents to PHE and many PHE Health protection Teams have agreements with local laboratories for urgent reporting of some infections. This should continue.

**Note:** The Health Protection Legislation Guidance (2010) includes reporting of HIV & STIs, HCAIs and CJD under ‘Notification Duties of Registered Medical Practitioners’: it is not noted under ‘Notification Duties of Diagnostic Laboratories’.

Other arrangements exist in Scotland49,50, Wales51 and Northern Ireland52.

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1. #Microbiology is used as a generic term to include the two GMC-recognised specialties of Medical Microbiology (which includes Bacteriology, Mycology and Parasitology) and Medical Virology. [↑](#footnote-ref-1)