



At NCIMB we have extensive experience of providing fast, confidential and accurate identification of bacterial and fungal isolates to Good Manufacturing Practice (GMP) standards.

Fast turnaround

Our experienced, customer-focused laboratory analysts offer a flexible and responsive service. We offer a range of turnaround times including same-day interim reporting of samples received before 10am. We also offer strain comparison and differentiation, qPCR and next generation sequencing. Pure cultures can be sent to us for identification as plates, slopes or broths.

We can also accept mixed cultures and other samples types such as water, slimes or contaminated products. Turnaround time for these sample types is slightly longer than for pure isolated cultures and results are usually available within three to ten days.

Validated genotypic bacterial and fungal identification

We use a variety of identification techniques and tailor our service to customer requirements. For identification of bacterial isolates, including mycoplasma, we undertake 16S ribosomal DNA gene sequencing, with 500 BP or full gene options available. For fungal identification, sequencing of the D2 region of the large subunit ribosomal DNA (D2 LSU), is usually the first technique we recommend. In both cases identification is obtained by examining sequences against validated MicroSEQ® databases.

If these approaches do not give a species level match, it can often be obtained by using additional data sources, or in the case of fungi, an alternative sequencing technique.

Strain to strain comparison and characterisation

Identification of bacteria to strain level can be valuable when tracing the source of objectionable organisms and with respect to the use of bacteria in manufacturing processes. 16S rDNA sequencing can be used for basic strain comparison when the full 16s gene (1500bp) is sequenced and we use multilocus sequence typing (MLST) or next generation sequencing (NGS) for comparison of closely related strains and strain characterisation.

Rapid quantitative information

For customers who require quantitative information, NCIMB offers a qPCR service. Quantitative polymerase chain reaction is a valuable method for establishing the presence or absence of an organism or group of organisms, whilst also providing very rapid quantitative information.



16S sequencing of bacterial isolates

We use 16S ribosomal DNA sequencing for primary identification of bacterial isolates, including mycoplasma. This technique rapidly identifies viable, non-viable and slow growing organisms, those with complex growth requirements, Gram variable isolates, and non-fermenters.

Next generation sequencing

We offer next generation sequencing for microbial community analysis and whole genome sequencing. This is a valuable technique for microbiome studies, the discovery of useful properties, searching for antibiotic resistance genes, identifying virulence factors and strain comparison.

Multilocus sequence typing (MLST)

MLST is a highly reproducible DNA sequencing-based technique used for strain to strain comparison and differentiation. Sequences of internal fragments of (typically) seven essential housekeeping genes, are used to characterise isolates.

D2 LSU and ITS fungal sequencing

Fungi can be identified by sequencing of the D2 region of the large subunit ribosomal DNA (D2 LSU) and sequencing of one or both of the internal transcribed spacer regions (ITS). We can combine these techniques, to obtain the most reliable species level identification.

qPCR

Quantitative polymerase chain reaction (qPCR) determines the presence or absence of an organism or group of organisms in a sample, whilst providing very rapid quantitative information. It is a useful method for monitoring populations.

Phenotypic testing

At NCIMB we are experienced in the use of morphological, physiological and biochemical tests and offer a variety of analyses. Please enquire for more information.

ACDP category

NCIMB does not accept active cultures of dangerous human pathogens or organisms isolated from clinical or diseased plant materials for identification. We cannot accept isolates known to be greater than ACDP category 2 and ACGM class 1.

For more information

For more information contact our identification services manager, Vikki Mitchell:

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