



Explore bacterial and fungal communities in detail across a range of niches with NCIMB's next-generation sequencing (NGS) metagenomics services.

Game-changing insight

Metagenomics is the study of genetic material recovered directly from environmental samples. It offers a game-changing insight into the microbial diversity within all kinds of environmental niches including water, soil, gut microbiomes, production facilities, fermenters and bioreactors.

Many microbes do not grow under laboratory conditions and consequently microbiology techniques that require growth only identify a fraction of the whole community within environmental samples. Metagenomics allows you to identify culturable and non-culturable taxa in one assay.

At NCIMB we offer a range of analyses for bacterial community analysis, including 16S or ITS based amplicon metagenomics and whole-genome shotgun approaches.

While amplicon approaches allow you to quickly understand taxonomic makeup and distribution, the whole-genome approach enables a full interrogation of the underlying genes and pathways within the ecosystem. Metagenomics paves the way to new insights into taxonomic identification, population stratification, differential abundance testing and understanding functional context.

Identifying microbiome dysbiosis

From the human gut to the oilfield reservoir, shifts in the microbiome can have a dramatic and sometimes devastating effect. For example, recent research has associated changes in human gut bacteria with a number of conditions including obesity and recurrent infection. Within the oil and gas sector, changes in the reservoir microbial community can result in costly souring. Metagenomics analysis guides understanding of these changes and can inform the next steps taken.

Metagenomics for food chain monitoring

16S metagenomics is a good option to consider when testing to identify food spoilage bacteria as it can capture sporulated bacteria which may not respond to being plated for identification. At NCIMB, we can also provide services for identifying animal species or contamination in food production chains by analysing the CO1 marker gene.

Defining terroir

Understanding the terroir of food and drink production can give important insights into what makes your product unique. From understanding the soil around vines and its impact on wine quality, to the makeup of the microbes in brewing processes, we can help you characterise your signature microbes and understand how production management might impact quality.



V3/V4 sequencing

We use the V3-V4 regions of the 16S gene in our standard 16S metagenomics service. If you have specific requirements for other variable regions, we can take care of the whole process from primer design to data analysis.

Whole-genome shotgun metagenomics

Whole-genome metagenomics sequences bulk DNA from an environmental niche. This allows not only taxonomic identification, but also a full interrogation of the underlying genes and pathways in the ecosystem.

Combine with qPCR

16S metagenomics is semi-quantitative and deals with the relative abundances of taxonomic groups. qPCR provides rapid quantitative information for an organism or group of organisms and is increasingly combined with NGS data for greater quantitative power.

Bioinformatics

Using the latest software and algorithms for metagenomic community analysis we can analyse microbiome data rapidly and accurately. Our bioinformatics capability scales to your project's requirements, with clearly summarised and visualised data.

16S/ITS metagenomics

Metagenomics based on PCR amplification of marker genes such as 16S and ITS offers a cost-effective way to understand the makeup of a bacterial or fungal community. If you are interested in exploring other marker genes, please talk to us about your requirements.

Amplicon sequence variant resolution

NCIMB focuses on ASVs or 'amplicon sequence variants' which provide greater resolution and consistent taxonomic labels and are replacing the previous focus on 'operational taxonomic units' (OTU's) for metagenomic taxonomic identification.

Fast turnaround

Our highly experienced and customer-focused staff offer a flexible and responsive service for next-generation sequencing metagenomics projects. We accept all kinds of sample types from extracted DNA through to unprocessed environmental samples.

For more information

For more information contact our Bioinformatics Delivery Manager, Dr Daniel Swan.

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