



CD Genomics

The Genomics Services Company



**How to
Accelerate Your
Infectious Pathogens Research
by Sequencing**

Why does infectious disease pathogen research matter?

Infectious diseases caused by various pathogens, such as viruses, bacteria, fungi, and parasites, remain a significant public health challenge worldwide. These diseases cause millions of deaths each year and have a severe impact on the global economy. Infectious diseases also have the potential to cause pandemics, as we have seen with the recent COVID-19 outbreak.

Sequencing infectious pathogens has revolutionized research in this field by providing a wealth of information about the pathogens' genetic makeup and how they spread. With the advancement of sequencing technology, researchers can now sequence the entire genome of an infectious pathogen and analyze its genetic diversity and evolution. Infectious disease pathogen research helps researchers better understand the pathogen's biology, including its transmission patterns and the mechanisms of resistance to drugs.

Pathogen Identification by High-throughput Technology: Revolutionizing the Fight Against Infectious Diseases

Sequencing technologies have been used in numerous infectious pathogen research applications.

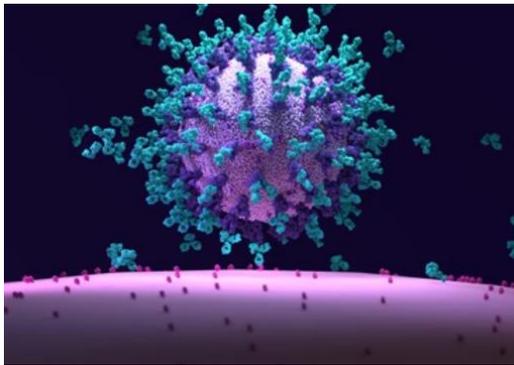
Identification of Pathogens

The characterization of viral genomic variation, intra-host variation, and viral quasispecies by high-throughput sequencing helps to identify and characterize pathogenic microorganisms, understand response mechanisms, and monitor the generation of new variants and strains. Metagenomics and metatranscriptomics allow us to determine which microorganisms are present and functionally associated with a specific disease in a healthy individual and how they relate to that disease.

Infectious Disease Surveillance

The COVID-19 pandemic showed that new tools are needed to find and track new pathogens like SARS-CoV-2. Extensive detection of pathogens, such as respiratory pathogens, and antibiotic resistance mutations through high-throughput technologies is important for pathogen discovery and traceability, infectious disease surveillance, prevention and control, treatment and prognosis.





Vaccine Development

Vaccines are biologically prepared using pathogenic microorganisms or their components or metabolites as starting materials for the prevention and treatment of corresponding human diseases. New safe and effective vaccines are further developed through research on pathogenic microorganisms and immune responses.

Drug Discovery and Development

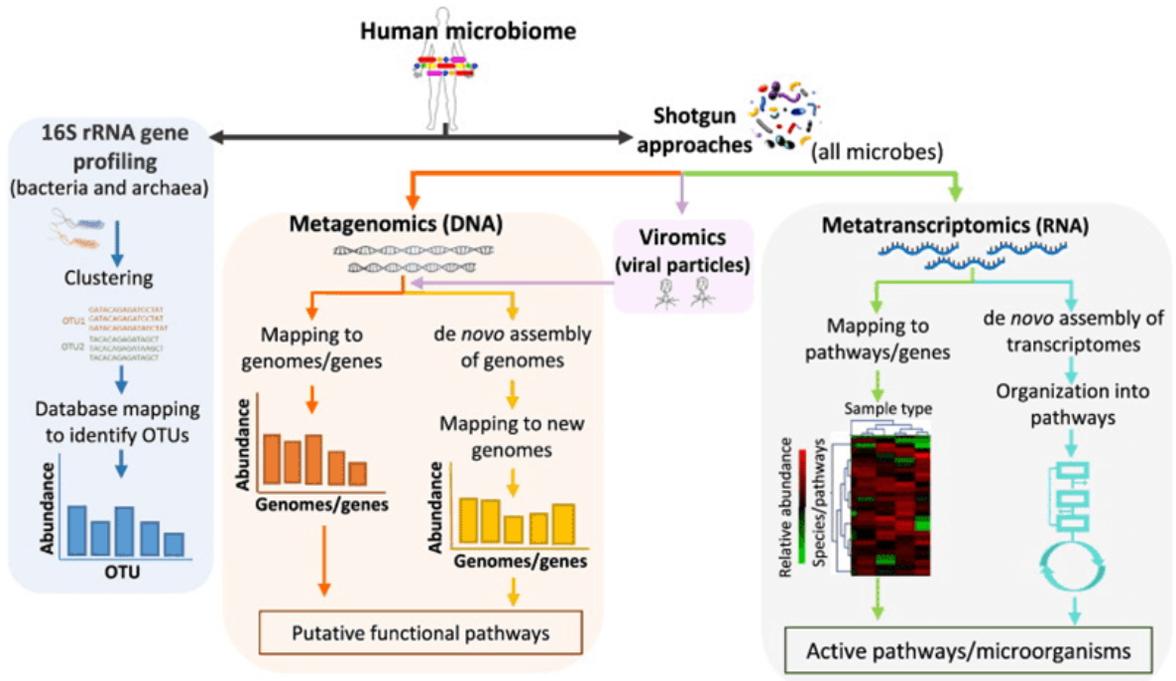
Currently, pathogen resistance is a challenging global health problem. Therefore, early and precise identification of pathogens, prediction of their susceptibility to drugs, and timely guidance of anti-infective therapy are essential to improve patient prognosis and control the emergence and spread of drug-resistant bacteria. By decrypting all nucleic acid information, we are able to provide researchers and important companies with data at the genetic level for further drug discovery and development.



Sequencing Approaches in Infectious Pathogens Research

Sequencing technologies can obtain partial or complete sequences of bacterial and viral genomes for infectious disease research, detection and surveillance. Targeted NGS (tNGS) can also detect genomic variants when relevant. Firstly, high-throughput sequencing technology dramatically increases the sensitivity of detection, allowing large-scale parallel detection of low-frequency mutations. Moreover, the target sequence regions can be optimally targeted by design to obtain higher sequencing depth and homogeneity.





A systems-level understanding of human microbiome. Bikel S., et al. Computational and Structural Biotechnology Journal. 2015, 13:390-401.

◆ 16S/18S/ITS Amplicon Sequencing

Based on the second-generation high-throughput technology to sequence 16S rRNA/18S rRNA/ITS and other genes, it can simultaneously detect dominant species, rare species and some unknown species in the samples, and obtain the composition of microbial communities in the samples as well as the relative abundance among them. It is of great theoretical and practical importance to reveal microbial diversity for studying the relationship between pathogens and hosts, pathogens and environment.

◆ Metagenome Sequencing

The total DNA/RNA of all pathogens/microorganisms and hosts in a sample can be sequenced and analyzed. The genomes of pathogens in a specific environment are used as the object of study to further explore the community functional activity, interactions of pathogens and their relationship with the environment and host, and to uncover potential biological significance based on the analysis of pathogen diversity, population structure and evolutionary relationships.



◆ Microbial Whole Genome Sequencing

Microbial whole genome sequencing is used to obtain the full-length genomes of pathogens, which, combined with downstream phenotyping techniques, can be used to explore the discovery of molecular mechanisms of pathogen-infected diseases, identify new mutants, study drug resistance, virulence or other functional gene analysis, etc.

◆ Virus Genome Sequencing

Virus sequencing has exploded during the COVID-19 pandemic, with a global effort to detect mutant strains such as Delta and Omicron and guide response strategies. This is because sequencing not only detects new variants, but also helps scientists track transmission pathways. When sequencing is combined with laboratory studies or epidemiological studies, it can answer questions about the basic biology of the virus, such as whether the virus is becoming more transmissible or whether the impact of infection is changing. It is also a tool that can help track the resistance of vaccines to evolving viruses.

◆ Targeted Capture Sequencing

PCR amplicon or hybrid capture sequencing technologies allow researchers and assay developers to focus on the specific pathogens being studied. Based on the sequence information, the species of pathogens in the sample can be determined. This allows for the quick and objective detection of a larger number of microorganisms, such as viruses, bacteria, fungi, parasites, etc., with the benefits of a clear pathogenic spectrum range and low sequencing costs, which can help with research on detecting infectious diseases and responding to large-scale outbreaks.

◆ Long-Read Sequencing

For complex structural variants (SVs), which are difficult to tackle due to read length limitation of NGS, Nanopore and PacBio SMRT sequencing can easily span large segments of SVs in the genome, which is highly targeted and requires less data, and can effectively identify structural variants and help to obtain more complete information.

◆ Metatranscriptomics

Metagenomics and metatranscriptomics allow us to find which microorganisms and functions are present in healthy individuals or are linked to a certain disease, as well as how they relate to that disease. Besides, those data can be correlated with disease onset or progression. Specifically, with transcriptomics, it is possible to assess whether gene expression is associated with a specific disease or state of deterioration.



Why Choose Our Infectious Pathogens Research Solution

At CD Genomics, we provide high-quality microbial sequencing services to support infectious pathogen research. Our team of experienced scientists uses state-of-the-art sequencing technologies and bioinformatics analysis to deliver accurate and reliable results.

Our sequencing services for microorganisms cover a wide range of uses, such as metagenomics, metatranscriptomics, whole-genome sequencing, and targeted sequencing.



With CD Genomics, you can expect:

Accurate and reliable results

Our microbial sequencing services are performed using high-quality equipment and rigorous quality control measures to ensure accurate and reliable results.

Experienced scientists

Our team of scientists has extensive experience in microbial sequencing and infectious disease research, providing you with expert guidance and support.

Comprehensive analysis

We use advanced bioinformatics tools to provide a comprehensive analysis of microbial sequencing data, including strain identification, gene annotation, and functional analysis.

Customized solutions

We work closely with our clients to develop customized sequencing solutions that meet their unique research needs, from sample preparation to data analysis.

Contact CD Genomics for more inspiration and service content.