The Genome Sequencer FLX System

Metagenomics and Microbial Diversity

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454 SEQUENCING

Metagenomics and Microbial Diversity

Get the complete picture with long sequence reads

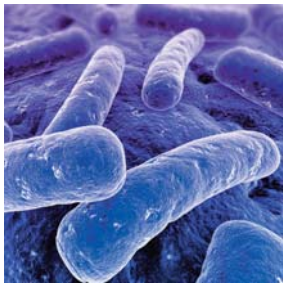
Obtaining an unbiased view of the phylogenetic composition and functional diversity within a microbial community is a central objective of metagenomic analysis. Until now, technical and economic constraints limited the depth of analysis necessary for obtaining a representative picture of microbial and viral communities, their metabolic profiles, and their adaptation dynamics.

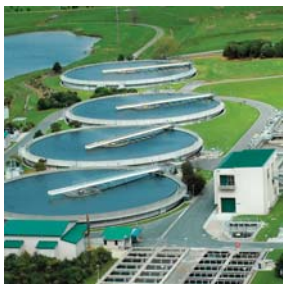
The Genome Sequencer FLX System, with its long, highly accurate reads, enables a comprehensive view into the diversity and metabolic profile of your metagenome of interest. Learn how 454 Sequencing systems can help you answer your research questions.

Microbial and metabolic diversity

Gene content

Viral pathogens





Metatranscriptomics – Environmental expression profiles

Microbial abundance

Signature profile of a specific environment

Microbial and metabolic diversity — Obtain an unprecedented picture of diversity with long specific reads

- Gain an in-depth perspective into the diversity and metabolic profile of an environmental habitat with rapid shotgun or bacterial 16S sequencing.
- Use long 400 bp sequence reads to achieve the specificity needed for comparison with nucleotide and protein databases.
- Survey an environment in a single GS FLX Titanium run or less, without traditional cloning steps.
- Assemble long reads into contigs to gain whole or partial genome information.

Microbial abundance — Gain unbiased insights into the relative representation of species within a habitat

- Count environmental gene tags (sequence reads specific for a species or a gene) to analyze the relative abundance of microbial species under varying environmental conditions.

Gene content — Discover new genes in unculturable species

- Discover genes quickly and make proper functional predictions within gene-rich microbiomes through the GS FLX System's sequencing depth and long, accurate reads.
- Screen microbiomes for enzymes of interest such as proteases or polymerases, and rapidly amplify them from the sample.

Metatranscriptomics — Analyze gene expression within microbial communities

- Analyze microbial diversity and gene regulation simultaneously within diverse environments through rapid gene expression profiling.
- Perform functional annotation with long sequence reads that unambiguously distinguish similar transcripts in a complex sample.
- Survey an environmental transcriptome in a single GS FLX Titanium run or less.

Viral pathogen detection — Only long reads can find "the needle in the haystack"

- Analyze viral outbreaks quickly and accurately by sequencing fragments of amplified RNA preparations from infected individuals.
- Identify the viral pathogen by matching the long reads to nucleotide or protein databases.

Signature profiling — Identify the molecular footprint of specific environments

- Take advantage of the GS FLX Titanium's long shotgun reads for straight forward analysis of a wide range of parameters unique to a specific environment.
- In a single instrument run, establish the signature profile of a microbial community by determining its members, predicting their function, and detecting their relative abundance.

Publicly available bioinformatic tools for 454 metagenomic analysis:

1. The SEED database/metagenomics RAST server: **http://metagenomics.nmpdr.org/**
2. NCBI non-redundant Clusters of Orthologs, COG: **http://www.ncbi.nlm.nih.gov/COG/**
3. Kyoto Encyclopedia of Genes and Genomes, KEGG: **http://www.genome.jp/kegg/**
4. MEGAN: **http://www-ab.informatik.uni-tuebingen.de/software/megan/welcome.html**
5. CARMA: **http://www.cebitec.uni-bielefeld.de/brf/carma/carma.html**
6. Integrated Microbial Genomes with Microbiome samples, IMG/M: **http://img.jgi.doe.gov/m**
7. CAMERA: **http://camera.calit2.net**
8. Publicly available 16S databases: *e.g.,* **http://rdp.cme.msu.edu/**

Selected References

Microbial and metabolic diversity
Dinsdale EA *et al.* (2008) Functional metagenomic profiling of nine biomes. *Nature*. **452**(7187):629-32.

Microbial abundance
McKenna P *et al.* (2008) The macaque gut microbiome in health, lentiviral infection, and chronic enterocolitis. *PLoS Pathog.* **4**(2):e20.

Gene content
Turnbaugh PJ *et al.* (2006) An obesity-associated gut microbiome with increased capacity for energy harvest. *Nature*. **444**:1027-1031.

Metatranscriptomics
Frias-Lopez J *et al.* (2008) Microbial community gene expression in ocean surface waters. *PNAS*. **105**(10):3805-10.

Viral pathogen detection
Cox-Foster DL *et al.* (2007) A metagenomic survey of microbes in honey bee colony collapse disorder. *Science*. **318** (5848):283-7.
Palacios G *et al.* (2008) A new arenavirus in a cluster of fatal transplant-associated diseases. *N Engl J Med.* **358**(10):991-8.

Signature profiling
Dinsdale EA *et al.* (2008) Functional metagenomic profiling of nine biomes. *Nature*. **452**(7187):629-32.

More references can be found at ***www.454.com***

"The 454 Sequencing platform is rapidly democratizing high-throughput sequencing by allowing individual investigators to produce datasets on the level of a genomic center. My lab can now go into a new ecosystem and determine what the microbes and viruses are doing in a matter of weeks, instead of years. Not only can we figure out the functions of the microbes at a much faster rate, we can do a much better job because of the more detailed information provided by the long, accurate reads."

— Forest Rohwer,
Associate Professor,
San Diego State University

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