Novel Insights into Microbial and Viral Complexity

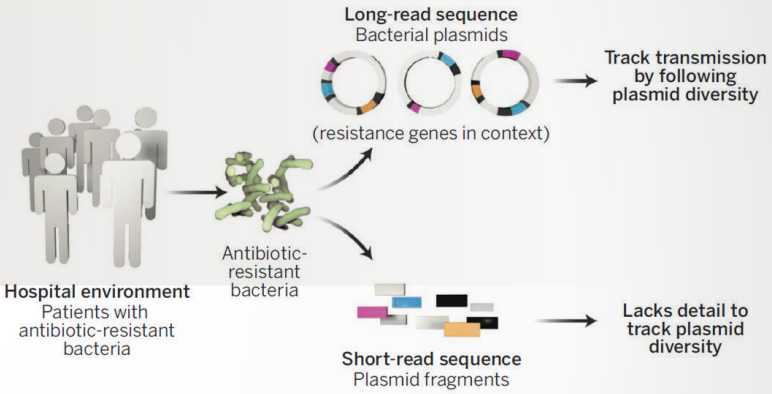
Fully characterize complete microbial genomes and populations affordably with SMRT® Sequencing, simultaneously detailing base modifications and mobile elements, quantifying low-level variants and achieving strain-level resolution within communities.

Complete Microbial Characterization in a Single Experiment

"We can now do it [investigate plasmid transfer] in the context of fully sequenced genomes because we now know every plasmid and what it carries. We're now doing a study that I think is fully informed."

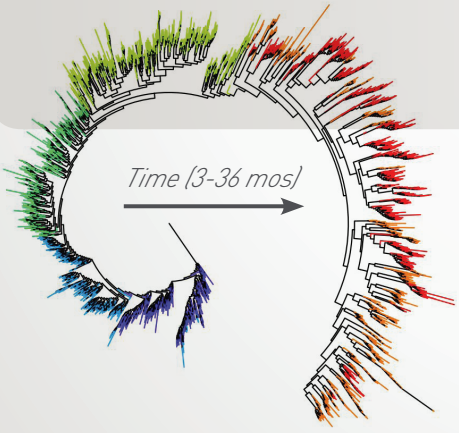
- Julie Segre, NHGRI[1]

- Generate gold-standard reference genomes
- Assess contribution of base modification on pathogenesis
- Understand the role of mobile elements in drug resistance and transmission



Long-read sequencing can resolve complete plasmids in order to track the dissemination of antimicrobial-resistance genes among pathogenic bacteria[2]

Investigate Viral Population Dynamics



- De-convolute complex mixtures of unique haplotypes
- Track evolution and phylogeny of viral populations
- Identify and quantify minor variants

"To understand within-host viral evolution, long high-quality sequences are absolutely necessary. PacBio is the only NGS technology that hits the sweet spot for length, accuracy and depth."

- Ben Murrell, UCSD CFAR[3]

HIV *env* sequences expand and diversify throughout infection[3]

PACIFIC BIOSCIENCES®

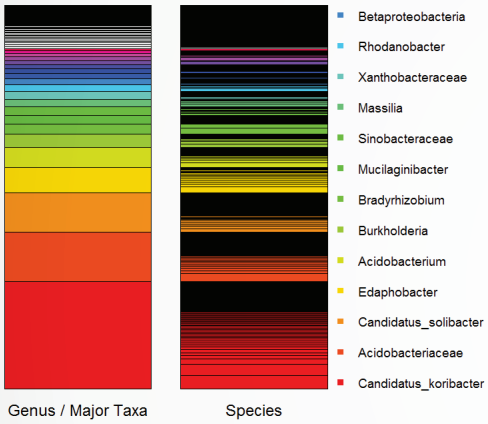
Detailed Examination of Microbial Communities

"SMRT Sequencing is a single molecule technique that can generate long reads (10-15 kb), is highly accurate and can distinguish methylated bases from the normal A,C,G,T. This latter property is unique as no other method can do that for N^6-methyladenine or N^4-methylcytosine without additional chemistry being involved."

- Rich Roberts, New England Biolabs[4]

- Discover novel genes with longer reads and contigs
- Identify and assign functions to community members with better genome assemblies
- Leverage epigenomic data to cluster contigs, including those from closely related strains

Full-length 16S



Species-level resolution of soil sample[5]

Whole-Genome Shotgun

De novo assembly string graph of Human Microbiome Mock Community B (HM-276D), from the Human Microbiome Project

Key References

1. GenomeWeb. (2014) PacBio Long Reads Assess Antibiotic Resistance Plasmids in Wake of Enterobacteriaceae Outbreak. Retrieved February 3, 2015 from https://www.genomeweb.com/sequencing/pacbio-long-reads-assess-antibiotic-resistance-plasmids-wake-enterobacteriaceae
2. Beatson and Walker. (2014) Tracking Antibiotic Resistance. *Science*. **345** (6203):1454-1455.
3. Murrell, et al. (2015) Full-length *env* Deep Sequencing in a Donor with Broadly Neutralizing V1/V2 Antibodies. Conference on Retroviruses and Opportunistic Infections (2015 CROI) Poster Presentation.
4. Naomi Attar. (2013) Rich Roberts discusses single-molecule sequencing technology. Retrieved February 3, 2015 from http://www.biomedcentral.com/biome/rich-roberts-discusses-single-molecule-sequencing-technology/
5. Bowman, et al. (2013) Analysis of Full-Length Metagenomic 16S Genes by SMRT® Sequencing. American Society for Microbiology (2013 ASM) Poster Presentation. Retrieved February 5, 2015 from http://files.pacb.com/pdf/Analysis_of_Full_Length_Metagenomic_16S_Genes_by_SMRT_Sequencing.pdf

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PN: VM102-020915