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

**COMPLETE MICROBIAL CHARACTERIZATION IN A SINGLE EXPERIMENT**
- Generate gold-standard reference genomes
- Assess contribution of epigenetics to pathogenesis
- Understand the role of mobile elements in drug resistance and transmission

**INVESTIGATION OF VIRAL POPULATION DYNAMICS**
- Deconvolute complex mixtures of unique haplotypes
- Track evolution and phylogeny of viral populations
- Identify and quantify minor variants

"WE CAN NOW [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

"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

pacb.com/microbe
DETAILED EXAMINATION OF MICROBIAL COMMUNITIES

- 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

Whole-Genome Shotgun
De novo assembly string graph of Human Microbiome Mock Community B [HM-276D], from the Human Microbiome Project

“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 N6-METHYLANADENINE OR N4-METHYLCYTOSINE WITHOUT ADDITIONAL CHEMISTRY BEING INVOLVED.”

—RICH ROBERTS, NEW ENGLAND BIOLABS

KEY REFERENCES