SIMPLIFIED SOLUTIONS

Detect, track, and characterize pathogens to a new standard of completeness and precision. PacBio® solutions offer unmatched accuracy and long read lengths to support a wide range of pathogen surveillance applications.

“The tracking and reporting of PMQR [plasmid-mediated quinolone resistance] in these bacteria is essential for a one health strategy to identify emerging public health threats and is enhanced by long-read sequencing for de novo characterization of novel plasmids.”

— Patrick McDermott, Office of Research, Center for Veterinary Medicine, U.S. Food and Drug Administration

BACTERIAL WGS
Identify more outbreak clusters and resolve them faster with closed genomes and plasmids.

VIROLOGY
Fully phase complete viral genes or genomes to identify transmission routes and drug resistance.

HIFIVIRAL
Perform cost-effective COVID-19 surveillance at any scale with our simple-to-use, automatable kit.

16S/METAGENOMICS
Profile samples, without culturing, at strain-level resolution with highly accurate reads up to 10 kb in length.

LIBRARY PREP
SMRTbell® prep kit

SMRT® SEQUENCING
Sequel® Ile system

DATA ANALYSIS
SMRT® Link
Long-read sequencing reveals antimicrobial resistance and virulence genes in *salmonella enterica*\(^2\)

- 134 multidrug resistant isolates belonging to 33 serotypes were sequenced with PacBio, yielding 233 closed plasmids.
- The study found a correlation between heavy metal and multidrug resistance genes.
- "These details are important in assessing the nature of resistant microbial hazards in food and other sources."

Highly accurate long-read data improves the utility of microbiome data\(^3\)

"Both amplicon and metagenomic long-read approaches (LRA) yielded added microbiome data value in the form of higher confidence taxonomic and functional resolution and improved recovery of microbial genomes compared to traditional short-read methodologies (SRA)."

"Analysis with long-read sequencing platforms, such as PacBio, provides high-resolution chromosomal and plasmid maps to clearly define resistance gene-carrying vectors and events mediating spread."
— Lynn Bry, Department of Pathology, Brigham and Women’s Hospital\(^4\)

Rescue of a replication-deficient RSV attenuated vaccine candidate detected by long-read sequencing\(^5\)

- Serial passage of a vaccine candidate RSV strain under selective conditions led to the recovery of replication fitness.
- PacBio HiFi sequencing revealed minor variants with large internal deletions (LD) that were missed by short reads.
- The LD variants were the key to replication rescue.

The spread of carbapenem resistance in greater Boston area hospitals\(^4\)

- Clinically ordered testing identifies carbapenem-resistant Enterobacteriaceae at participating institutions, a subset of which undergo retrospective PacBio sequencing.
- Long-read sequencing revealed a shared 3 kb cassette driving the spread of the *blaNDM* gene, carried by diverse transposon and plasmid backbones.

Learn more about pathogen genomics:
pacb.com/microbial-genomics