

SIMPLIFIED SOLUTIONS

Detect, track, and characterize pathogens to a new standard of completeness and precision. PacBio® solutions offer extraordinary 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, US Food and Drug Administration¹



BACTERIAL WGS

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



PATHOGEN SURVEILLANCE

Perform cost-effective pathogen surveillance at scale with targeted sequencing approaches.



VIROLOGY

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



16S/METAGENOMICS

Profile samples, without culturing, at strain-level resolution with highly accurate reads of ~10–15 kb.



LIBRARY PREP

SMRTbell® prep kit
HiFi plex prep kit 96



SMRT® SEQUENCING

Revio® system
Vega™ system

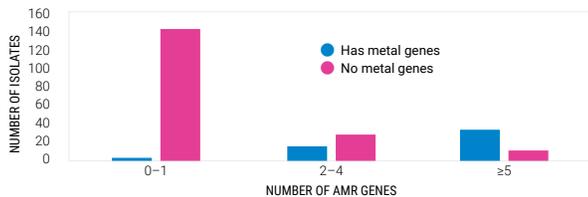


DATA ANALYSIS

SMRT® Link

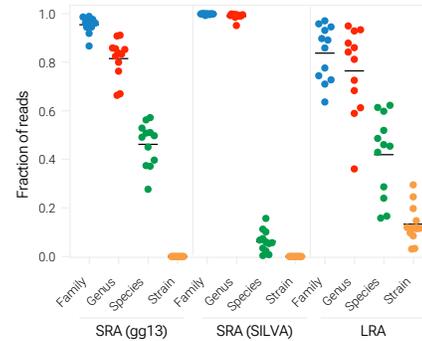
Long-read sequencing reveals antimicrobial resistance and virulence genes in *Salmonella enterica*²

- 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 data³

“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)”

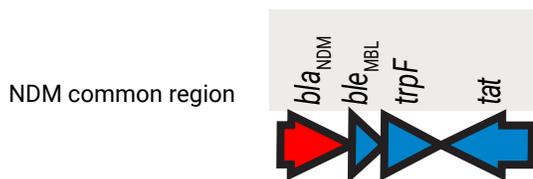


“Analysis with long-read sequencing platforms, such as PacBio, provides high-resolution chromosomal and plasmid maps to clearly define resistance gene-carrying vectors and events mediating spread.”

— Lynn Bry, Department of Pathology, Brigham and Women’s Hospital⁴

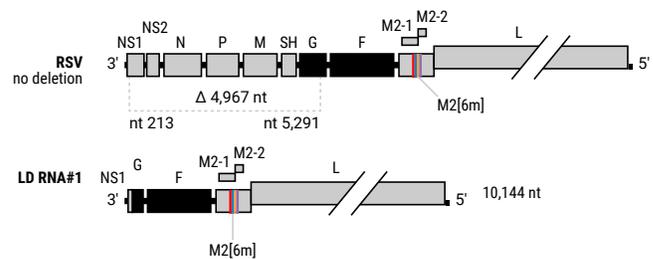
The spread of carbapenem resistance in greater Boston area hospitals⁴

- 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 bla_{NDM} gene, carried by diverse transposon and plasmid backbones.



Rescue of a replication-deficient RSV attenuated vaccine candidate detected by long-read sequencing⁵

- 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.



Learn more about our applications: pacb.com/microbial-genomics

1. Tyson, G. H. et al. (2019) Diverse fluoroquinolone resistance plasmids from retail meat *E. coli* in the United States. *Frontiers in Microbiology*.
2. Li, C. et al. (2021) Long-read sequencing reveals evolution and acquisition of antimicrobial resistance and virulence genes in *Salmonella enterica*. *Front Microbiol*.
3. Gehrig, J.L., et al. (2022) Finding the right fit: evaluation of short-read and long-read sequencing approaches to maximize the utility of clinical microbiome data. *Microb Genom*.
4. Pecora, N., et al. (2019) Diverse vectors and mechanisms spread New Delhi metallo-β-lactamases among carbapenem-resistant *Enterobacteriaceae* in the greater Boston Area. *Antimicrob Agents Chemother*.
5. Nouën C.L., et al. (2021) Rescue of codon-pair deoptimized respiratory syncytial virus by the emergence of genomes with very large internal deletions that complemented replication. *PNAS*.

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