

Genomic analysis of the industrially relevant *Clostridium autoethanogenum* genome reveals potential role for CRISPR systems



Background

- *Clostridium autoethanogenum* is an acetogen capable of fermenting CO, CO₂ and H₂ into biofuels and chemicals and is currently used in an industrial setting.
- BESC worked in collaboration with LanzaTech, New Zealand, to produce an annotated genome sequence for *C. autoethanogenum*.

Approach

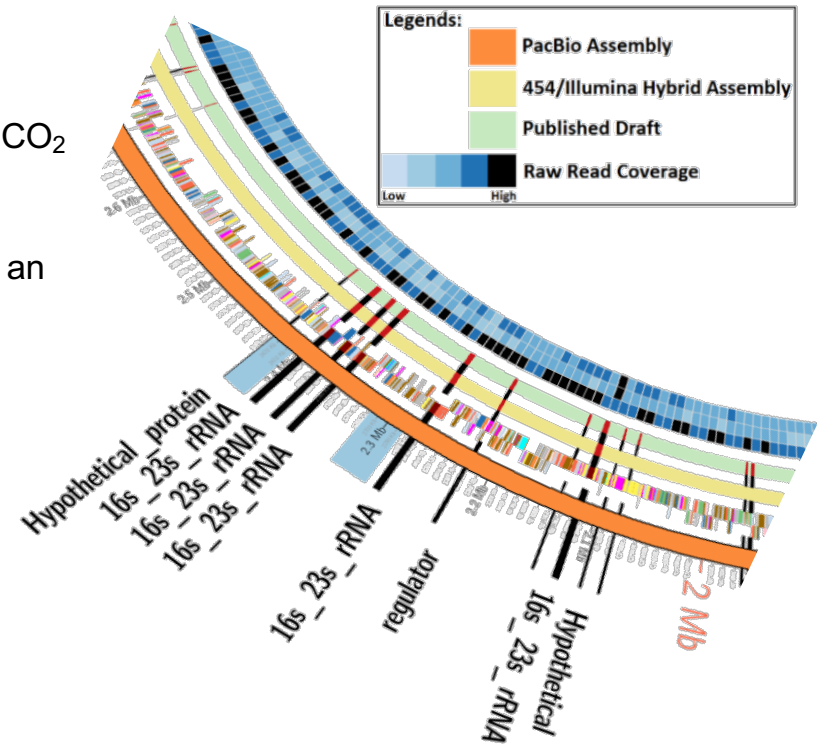
- PacBio sequencing generated long reads (~26 kb) and high coverage (~179x).
- Approach resulted in a closed, high-quality genome sequence for *C. autoethanogenum* without the need for further manual finishing.
- CRISPR (Clustered Regularly Interspaced Short Palindromic Repeats) systems among biotechnologically relevant Clostridia were classified and related to plasmid content and prophages.

Outcomes

- *C. autoethanogenum* genome only existed in draft form (100 contig) prior to this effort.
- Insights from genomes of related bacteria show key differences in presence of CRISPR bacterial defense systems.

Significance

- This study demonstrates value of PacBio single molecule sequencing in producing single contig finished genomes.
- Potential associations between plasmid content and CRISPR systems may have implications for historical industrial scale Acetone-Butanol-Ethanol (ABE) fermentation failures and future large scale bacterial fermentations.



Brown, S. D. *et al.*, "Comparison of single-molecule sequencing and hybrid approaches for finishing the genome of *Clostridium autoethanogenum* and analysis of CRISPR systems in industrial relevant Clostridia." *Biotechnology for Biofuels* 7:40, 2014.