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EXPLORE PLANT + ANIMAL MICROBIOLOGY IN HIGH RESOLUTION

IMPROVE CROP YIELDS, ADVANCE LIVESTOCK HEALTH, AND PRESERVE BIODIVERSITY WITH A MORE COMPLETE VIEW OF PLANT AND ANIMAL MICROBIOLOGY

Bacteria, viruses, and fungi have critical influences on the health of plants, animals, and ecosystems. Study microbes, microbiomes, and phytobiomes in high resolution with HiFi sequencing.
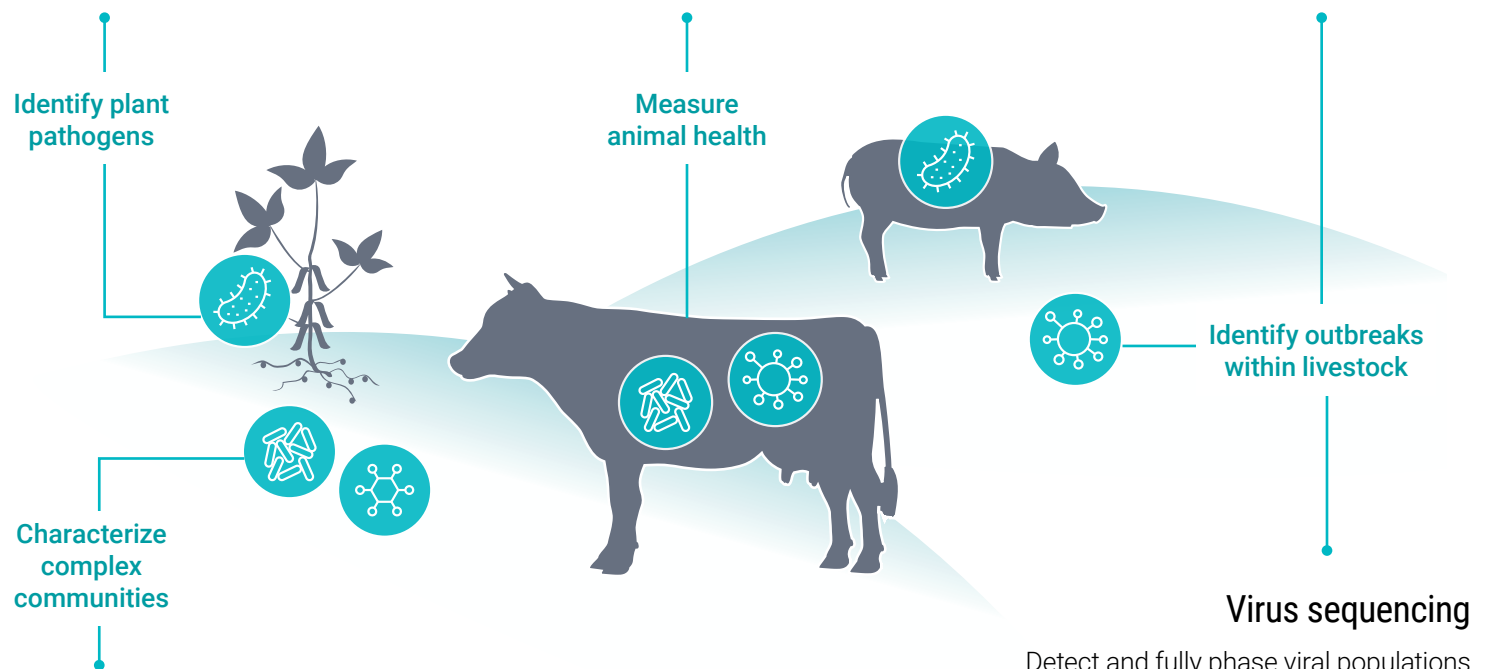
Microbial WGS

Sequence entire microbial genomes and plasmids to understand host-microbe dynamics.

Metagenome sequencing

Characterize soil, water, plant, and animal microbial communities to understand how microbiota influence ecosystem health and productivity.

Targeted sequencing

Capture and quantify pathogens or genes of interest to understand the drivers of disease.

Identify plant pathogens

Measure animal health

Identify outbreaks within livestock

Characterize complex communities

Full-length 16S sequencing

Profile bacteria in soil, water, and complex ecosystems with species-level resolution.

Virus sequencing

Detect and fully phase viral populations to understand global threats to plant and animal health.

"Repeats render TAL effector genes nearly impossible to assemble using next-generation short reads... long-read, single molecule real-time (SMRT) sequencing solves this problem"

— Adam J Bogdanove, Cornell University[1]

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Decrypting the bacterial drivers of virulence[2]

- *Xanthomonas* TAL effectors bind plant host DNA to upregulate specific genes, causing disease

- Highly repetitive TALE genes can't be assembled with short reads, limiting mechanistic studies

- 11 new closed PacBio® *Xanthomonas translucens* genomes will help identify critical genes involved in pathogen virulence and adaptation in cereals and forage grasses
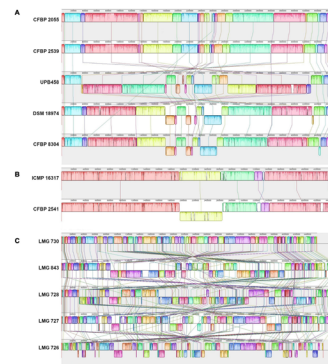
A species level view of the rhizosphere with full-length 16S[3]

- Waterlogging is an increasing contributor to low crop yields

- The rhizosphere can promote adaptation, but the key species and functions involved remain unclear

- In a recent soybean study, PacBio full-length 16S yielded a higher-resolution view of the rhizosphere than short or synthetic long reads

- Better 16S data ruled out soil type as a driver of rhizosphere restructuring while identifying clades linked to flooding tolerance
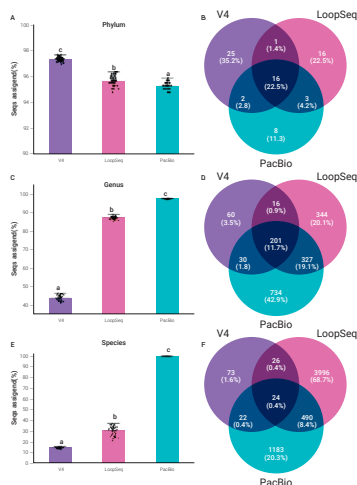
Better metagenome assemblies drive deeper insights[4]

- HiFi and Hi-C data yielded 428 HQ MAGs from a sheep fecal sample, of which 220 are lineage resolved

- The authors cite high accuracy as the key to getting closed MAGs from samples with closely related strains

- Better assemblies enable better functional characterization, as seen by the higher recovery of biosynthetic gene clusters with HiFi versus noisy long reads

Learn more about plant and animal microbes:
pacb.com/plant-animal-micro

KEY REFERENCES

1. Booher, N.J., et al. (2015) Single molecule sequencing of *Xanthomonas oryzae* genomes reveals a dynamic structure and complex TAL effector gene relationships. *Microb Genom*, 1(4). Doi: 10.1099/mgen.0.000032.
2. Goettelmann, F., et al. (2022). Complete genome assemblies of All Xanthomonas translucens pathotype strains reveal three genetically distinct clades. *Front Microbiol*, 12. doi: 10.3389/fmicb.2021.817815
3. Yu, T., et al. (2022) Effects of Waterlogging on Soybean Rhizosphere Bacterial Community Using V4, LoopSeq, and PacBio 16S rRNA Sequence. *Microbiology* spectrum, 10(1), e0201121.
4. Bickhart, et al. (2022) Generating lineage-resolved, complete metagenome-assembled genomes from complex microbial communities. *Nature Biotechnology*, 40. 711-719.

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