PLANT AND ANIMAL BIOLOGY
Accurate and actionable data for conservation, biodiversity, and biodiscovery

Sequencing to understand and protect species, populations, and ecosystems

As climate patterns change and ecosystems shift, scientists are turning to modern genomics technology to better understand and protect the species and populations with whom we share our world. PacBio® provides cutting-edge sequencing solutions that enable plant and animal biologists to discover and harness biological information for all organisms — big or small. From sea to sky, and everything in between, researchers are using genomic data that more accurately represents the complex biology of plants and animals to drive conservation efforts, capture biodiversity, and dive deeper into the unique biology of all organisms.
HiFi sequencing for the best of long and short reads

With PacBio HiFi sequencing, you no longer have to compromise between long read lengths and high accuracy.

HiFi reads

- Long read lengths up to 25 kb
- High read accuracy (99.9%)
- Easy library preparation
- Low coverage requirements
- Small file sizes to minimize compute time
- A single technology solution for a range of applications

A typical 20,000 bp HiFi read has ~8 incorrect bases
Insect biology

Marine biology

Plant and animal research

Applications to fuel plant and animal biology

Whole genome sequencing
Produce reference-quality genomes with phased haplotypes from even small-bodied organisms

Structural variant calling
Use high-sensitivity variant calls with low false discovery rate to gain actionable insights across populations

Targeted sequencing
Choose from flexible options to target regions to access to all variants — even in the most complex regions

RNA sequencing
Access full-length transcript sequences to identify novel genes and transcripts and improve genome annotation

Complex populations
Comprehensively characterize metagenomes with long, highly accurate, single-molecule reads — no assembly required

Plant and animal biology in action
Insect biology

Develop disease prevention methods, understand basic biology, and improve pest control using a population or a single individual.

Genomes to capture the vast diversity of insects

Over two decades ago, the first insect genome assembly was published in Science for Drosophila melanogaster, and since then, the insect biology scientific community has sequenced hundreds of genomes for insects, arthropods, and pests all over the world. Even though these genomes only represent 0.06% of the million different insect species on earth, scientists are quickly sequencing more insect genomes than ever before, because long-read sequencing allows scientists to efficiently assemble, phase, and capture genomic diversity from single-nucleotide polymorphisms to complex structural variants.

Sequence even the smallest organisms

Overcome DNA input barriers to sequencing small-bodied organisms

- **Standard HiFi workflow** — A HiFi sequencing approach requiring >300 ng input DNA
- **Ultra-low DNA input workflow** — A HiFi sequencing approach, with the addition of an amplification step, requiring 5 ng of input DNA

Overview of insect biology applications

Image adapted from Long Reads Are Revolutionizing 20 Years of Insect Genome Sequencing
Dive into the depths of marine ecosystems to study evolution, reveal insights into developmental biology, and address the challenges of climate change.

Genomes to protect marine biodiversity

Science may, at times, seem like a fishing expedition. But for those who are charting the depths of the 321 trillion gallons of water that make up Earth’s seas and oceans, the endeavor to collect genetic information is particularly difficult. The magnitude of global marine species diversity is immense, with thousands of species yet to be discovered and described. Luckily, the process of comprehensively characterizing the genetics of marine species is well underway. Many scientists are using HiFi sequencing to explore the genomes and transcriptomes of a wide variety of marine species and ecosystems. These studies are already adding to our understanding of how marine species adapt and evolve, shedding light on efforts to protect life in our lakes, rivers, oceans, and seas.

Environmental stressors

- PH
- Temperature

Detect effects with SMRT® sequencing
- DNA sequencing
  - Population variation
- RNA sequencing
  - Transcriptional compensation mechanisms
- Metagenomic sequencing
  - Shifting microbial communities

Sequencing applications for marine ecosystems

- Whole genome sequencing
  - Assemble high-quality genomes to better understand complex genotypes such as bioluminescence
- RNA sequencing
  - Understand how fish adapt to harsh environments with full-length transcriptome sequencing
- Complex populations
  - Dive into aquatic ecosystems by deconvoluting microbial life and understanding symbiosis
- Targeted sequencing
  - Identify, sequence, and multiplex genomic regions of interest without compromising amplicon size

Overview of Circulomics Nanobind technology

Minced tissue → Homogenize tissue → Lyse + pellet debris → Bind → Wash 3x → Elute with HMW DNA

- Step 1: Homogenize tissue
- Step 2: Lyse + pellet debris
- Step 3: Bind
- Step 4: Wash
- Step 5: Elute

Obtaining high-molecular weight DNA from the “hardest” organisms

It is no deep secret that isolating DNA from mollusks, corals, and other marine species is difficult. However, solutions from Circulomics’ Nanobind technology make it easier than ever to obtain high-quality DNA from marine specimens.
A genome fit for a giant: the California redwood

*Sequoia sempervirens* is one of the world’s fastest-growing conifers that live for hundreds of years. Once ubiquitous throughout the Northern Hemisphere, now only 5% of the original old-growth coastal redwood forest remains.

Changes in land plant genome assembly quality and availability over time

Image adapted from *Representation and participation across 20 years of plant genome sequencing*

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Workflow

With easy-to-use, high throughput sequencing, you can get the accuracy you need at an affordable cost.

Sample prep
- Flexible DNA input requirements down to 5 ng

Library prep
- Adjustable multiplexing options to maximize throughput

SMRT® sequencing
- Run a single SMRT® Cell 8M at a time or several consecutively for set it and forget it sequencing

Data analysis
- Use SMRT® Link, or open-source tools to analyze your HiFi data

This scalable workflow allows for sequencing 100s to 1000s of genomes per year.
REFERENCES
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4. Hotaling, S. et al. (2021) Long Reads Are Revolutionizing 20 Years of Insect Genome Sequencing Genome Biology and Evolution 13, 8, evab138
5. PacBio (2020) Application note - considerations for using the low and ultra-low DNA input workflows for whole genome sequencing
10. Circulomics: Nanobind Technology, Website