

## Large-Scale Global Genome Projects Choose PacBio Sequencing to Help Decode Life

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### High-quality reference genomes for thousands of plant, animal and microbial species to be created using SMRT Sequencing

MENLO PARK, Calif., Sept. 13, 2018 (GLOBE NEWSWIRE) -- When creating a genomic ark of creatures great and small, scientists across the globe are turning to the comprehensive coverage and quality of long-read sequencing technology from Pacific Biosciences (Nasdaq:PACB), the leading provider of high-quality sequencing of genomes, transcriptomes and epigenomes.



Explore how high-quality genomes contribute to these critical scientific endeavors

Today, the [Vertebrate Genomes Project \(VGP\)](#), an international consortium of more than 150 scientists from 50 academic, industry and government institutions in 12 countries, released the first 15 of an anticipated 66,000 high-quality reference genomes that will eventually include all vertebrate species on Earth. These new genomes are the most complete genomes created to date for these species, and roughly double the number of high-quality animal reference genomes with comparable levels of combined contiguity, completeness and accuracy in the public domain.

The VGP is one of many large-scale international projects that have chosen PacBio® Single Molecule, Real-Time (SMRT®) Sequencing to generate some of the most complete genomes to date for thousands of plant, animal, fungal and bacterial species. These comprehensive catalogs of genetic code provide valuable resources to researchers in their quest to understand the biology, physiology, development and evolution of a multitude of living organisms, and will aid in their conservation.

“We are honored to work with world-class researchers to generate high-quality genome references and support large-scale efforts such as the VGP,” said Jonas Korfach, Chief Scientific Officer of Pacific Biosciences. “We are looking forward to continuing our involvement in projects like these to benefit science, society and the environment.”

Other major projects using or that recently used PacBio SMRT Sequencing include:

- The [Bird 10,000 Genomes \(B10K\) Project](#), which is aiming to generate representative draft genome sequences from all extant bird species; many of its members became founders of the The Genome 10,000 consortium ([G10K](#)), which evolved into the Vertebrate Genome Project;
- The [Bat1K initiative](#) to catalog the genetic diversity in 1,300 types of bats;
- Efforts to sequence nationally significant species, such as the [Sanger 25 Project](#) by the Wellcome Trust Sanger Institute and the Canada 150 Sequencing Initiative ([CanSeq150](#)) by Canada’s Genomics Enterprise.
- The [NCTC 3000 initiative](#) by the UK’s National Collection of Type Cultures to sequence the genomes of 3,000 strains of bacteria;
- [Whole Genome Assembly of the Maize NAM Founders](#), a multi-institutional effort to create a 26-line pangenome maize reference collection, one of many initiatives to sequence important agricultural crops to discover and utilize novel genes, traits and/or genomic regions for crop improvement and basic research;
- The [Functional Annotation of Animal Genomes Project \(FAANG\)](#), which is aiming to produce comprehensive maps of functional elements in the genomes of domesticated animal species;
- Marine and aquaculture efforts such as [The Aqua-Hundred Genome Project](#); and
- Insect initiatives, including the [i5k Project](#) to sequence 5,000 arthropod genomes and The Global Ant Genomics Alliance ([GAGA](#)) to sequence 200 ant species.

- The [Pan-Genome Analysis of Sorghum](#) project at the Donald Danforth Plant Science Center, which includes 15 sorghum lines covering the diversity of this important bioenergy, food, and feed crop. The project is supported through the Community Science Program (CSP) of the DOE Joint Genome Institute with PacBio sequencing at HudsonAlpha Institute for Biotechnology.
- The [Open Green Genomes Initiative](#), also supported by DOE Joint Genome Institute, which will generate high-quality genome assemblies and annotations for 35 species representing all major evolutionary lineages in the land plant tree of life.

Researchers are using PacBio's advanced technology to create high-quality reference genomes, which become highly curated representations of the species for the community to which all individuals of that species are compared. The information provided by these detailed DNA analyses can help in the conservation of animal species and their habitats; it may also have implications for the human species.

Bats, for instance, are reservoirs for some of the deadliest viral diseases, including Ebola and SARS (severe acute respiratory syndrome), but somehow they survive. Figuring out why could increase our understanding of immune function. Information gleaned from their genomes could also contribute to our understanding of human aging and boost agricultural productivity and ecosystem restoration, according to Sonja Vernes of the Max Planck Institute, a leader of the Bat1K initiative.

"The long-read sequencing technology from PacBio is allowing us to produce bat genomes of unprecedented quality and resolution as part of the Bat1K project," said Vernes. "This is going to be a big step forward for understanding how the genes and also the non-coding DNA in these genomes influence the weird and wonderful features of bats."

An infographic describing how high-quality genomes contribute to these critical scientific endeavors is available [here](#). More information about today's news from the VGP is available [here](#).

#### **About Pacific Biosciences**

Pacific Biosciences of California, Inc. (NASDAQ:PACB) offers sequencing systems to help scientists resolve genetically complex problems. Based on its novel Single Molecule, Real-Time (SMRT<sup>®</sup>) technology, Pacific Biosciences' products enable: *de novo* genome assembly to finish genomes in order to more fully identify, annotate and decipher genomic structures; full-length transcript analysis to improve annotations in reference genomes, characterize alternatively spliced isoforms in important gene families, and find novel genes; targeted sequencing to more comprehensively characterize genetic variations; and real-time kinetic information for epigenome characterization. Pacific Biosciences' technology provides high accuracy, ultra-long reads, uniform coverage, and the ability to simultaneously detect epigenetic changes. PacBio<sup>®</sup> sequencing systems, including consumables and software, provide a simple, fast, end-to-end workflow for SMRT Sequencing. More information is available at [www.pacb.com](http://www.pacb.com).

#### **Forward-Looking Statements**

All statements in this press release that are not historical are forward-looking statements, including, among other things, statements relating to future availability, uses, accuracy, quality or performance of, or benefits of using, products or technologies, the suitability or utility of methods, products or technologies for particular applications, studies or projects, the expected benefits of sequencing projects, and other future events. You should not place undue reliance on forward-looking statements because they involve known and unknown risks, uncertainties, changes in circumstances and other factors that are, in some cases, beyond Pacific Biosciences' control and could cause actual results to differ materially from the information expressed or implied by forward-looking statements made in this press release. Factors that could materially affect actual results can be found in Pacific Biosciences' most recent filings with the Securities and Exchange Commission, including Pacific Biosciences' most recent reports on Forms 8-K, 10-K and 10-Q, and include those listed under the caption "Risk Factors."

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