



Pacific Biosciences Selected for NSF Project to Rapidly Sequence Maize Pangenome

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SMRT Sequencing Chosen for Ambitious Effort to Generate Reference Genomes for 26 Maize Lines

MENLO PARK, Calif., July 10, 2018 (GLOBE NEWSWIRE) -- Pacific Biosciences of California, Inc. (Nasdaq:PACB), the leading provider of high-quality sequencing of genomes, transcriptomes and epigenomes, today announced that a multi-institutional consortium of maize researchers is using the Sequel[®] System to create a 26-line pangenome reference collection.

Led by faculty investigator R. Kelly Dawe, Distinguished Research Professor at the University of Georgia, the \$2.8 million National Science Foundation-funded [Plant Genome Research Project](#) will create comprehensive, high-quality assemblies of 25 inbreds known as the NAM founder lines, the most extensively researched maize lines that represent a broad cross section of modern maize diversity, as well as an additional line containing abnormal chromosome 10.

Leading maize researchers Matt Hufford, assistant professor at Iowa State University, and Doreen Ware, a computational biologist at USDA and Cold Spring Harbor Laboratory, will also participate in the project. Ware's lab was involved in creating the first reference genome for maize variety B73 in 2009, as well as an improved version in 2017.

PacBio[®] Single Molecule, Real-Time (SMRT[®]) Sequencing and BioNano Genomics optical mapping, which were essential in the creation of the groundbreaking 2017 B73 maize reference, will be used in the project.

Plant genomes are notoriously difficult to sequence, and maize is particularly challenging because the vast majority of its 2.3 Gb genome — a staggering 85 percent — is made up of highly repetitive transposable elements that other types of sequencing can't address. Understanding these regulatory and structural elements is crucial to modern breeding efforts that aim to improve productivity across marginal environments and under changing climate conditions.

Maize is also amazingly diverse. A study comparing genome segments associated with kernel color from two inbred lines revealed that 12 percent of the gene content was not shared — that's much more diversity within the species than between humans and chimpanzees, which exhibit more than 98 percent sequence similarity. The new project will create multiple reference genomes to reflect this diversity.

"By relying on a single type specimen as the sequence reference for most of the genetic information in maize, we may be missing much of the highly valuable natural variation in maize," Dr. Ware said.

"SMRT Sequencing will be essential as the team assesses the role of structural variation between the lines, such as presence-absence variation and copy number variation, in the determination of agronomic traits," she added.

"To go from a single reference to a broad perspective on the entire genetic repertoire of genes and gene expression patterns will be a major step forward in how we approach genome analysis in crops," said Dr. Dawe. "It's something that has not happened for any crop at this scale."

Kevin Corcoran, Senior Vice President for Market Development at Pacific Biosciences, commented: "Corn is one of the most important crops in the world, and a significant species of study for answering fundamental questions about how plants adapt to different environments. Other important crop species could also benefit from this approach, and commercial breeders are increasingly recognizing the value of creating multiple reference genomes. We are excited that our technology can contribute as scientists attempt to address the challenges of a changing world."

Industry leader Corteva Agriscience[™], Agriculture Division of DowDupont[™] (formerly DuPont Pioneer) has helped with the NSF pangenome project by carrying out the Bionano optical mapping phase of the project. Corteva is also using highly-accurate PacBio whole-genome sequencing to create its own extensive maize reference collection, and projects to create multiple high-quality reference genomes for other important crops have been announced by various research institutions. These include: the Arizona Genomics Institute, which is building reference genomes for 23 species of rice; the HudsonAlpha Institute for Biotechnology, which is creating several genomes for cotton, peanut and sorghum; the University of California at Davis, which is amassing a collection of genomes for wine grapes and other fruits; and Cornell University, which is using SMRT Sequencing to detail several varieties of coffee.

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[®]) 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[®] 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.

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 products or technologies for particular applications, studies or projects, the expected benefits of the Plant Genome Research Project, 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."

Pacific Biosciences undertakes no obligation to revise or update information in this press release to reflect events or circumstances in the future, even if new information becomes available.

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