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PacBio Technology Resolves Complex Maize Genome, Driving Demand for Other Large-Scale AgBio Sequencing Projects

SMRT Sequencing Offers Significant Improvements for Reference Genomes at Much Lower Cost

MENLO PARK, Calif., June 22, 2017 (GLOBE NEWSWIRE) -- A [new publication in Nature](#) reveals the significant quality improvement afforded by Single Molecule, Real-Time (SMRT®) Sequencing for the maize genome, with implications for other complex crop and livestock genomes. This new PacBio® genome assembly, produced by scientists at Cold Spring Harbor Laboratory, the USDA's Agricultural Research Service, and other institutes, is an important resource for crop breeding and selection programs and serves as a model for how SMRT Sequencing can contribute to affordably improving other economically valuable crops.

Many plant genomes, including many of the major agricultural crops, are far more diverse within species than humans, increasing the importance of having multiple reference genomes for study. Maize is the most productive and widely grown crop in the world, and improvements in its fitness and yield will support farmers who earn significant income from this crop and contribute to efforts to meet the growing demand for affordable feedstocks. Previous genome assemblies for maize, generated with Sanger or short-read sequencing, were fragmented and missing complex repeat regions, limiting their utility to serve as the foundation for breeding and selection efforts. With its extremely long reads and very low bias, SMRT Sequencing can provide more complete information than short-read or Sanger sequencers and can support the generation of multiple, high-quality reference genomes.

The reported high-quality PacBio assembly significantly reduced gaps in the existing reference genome with a more than 50-fold increase in contiguity compared to the previous Sanger assembly. The scientists also corrected mistakes in previous assemblies, added data to difficult regions such as centromeres and regulatory sequences, and provided new gene annotations using PacBio's Iso-Seq® method. PacBio assemblies are also much higher quality than those produced with short-read sequence data because short-read assemblies are unable to represent the significant diversity and structural variation found in these plants.

This work can currently be completed at a cost of around \$20K per maize line using the company's newest sequencing platform, the Sequel® System, compared to the \$30M [cost](#) for the original maize genome reference. The cost and throughput improvements achieved with the Sequel System further enable the production of multiple high-quality reference genomes within species.

Doreen Ware of Cold Spring Harbor Laboratory and the USDA and senior author of the publication commented: "Implementing SMRT Sequencing allowed us to develop a higher-quality maize assembly than had been possible before. It is tremendously encouraging to realize we can now use this same approach for crops with even more complex genomes to generate agriculturally useful assemblies. We expect to use PacBio sequencing for additional assemblies of maize inbred lines, and to generate similar high-quality assemblies of other crop species."

"While this work was done on our older system, these impressive results are likely to drive demand for large-scale sequencing projects of crop genomes and we expect that much of this work will be done using our newer, lower-cost, high-throughput instrument, the Sequel System," said Kevin Corcoran, Senior Vice President of Market Development for Pacific Biosciences. "Various groups are already pursuing multiple-reference genome strategies for major crops including maize, sorghum, cotton, and soybean, as well as many specialty crops. This publication provides a roadmap for generating the high-quality assemblies that are needed in crop improvement programs, especially for very complex and repetitive plant genomes."

Publication details:

Yinping Jiao et al. [Improved maize reference genome with single-molecule technologies](#). *Nature* (2017) DOI: 10.1038/nature22971

For more information, please visit <http://www.pacb.com/research-focus/plant-animal-sciences/>.

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[®]) Sequencing 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, cost of using, quality or performance of, or benefits of using, products or technologies, 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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