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Single Molecule, Real-Time (SMRT) DNA Sequencing Technology From Pacific Biosciences to be Featured in 20 Presentations at the American Society for Microbiology 2014 Annual Meeting

Winner of Last Year's SMRT Grant Program Announced; "SMRTest Microbe" Grant Program Begins Worldwide

MENLO PARK, Calif., May 14, 2014 (GLOBE NEWSWIRE) -- Pacific Biosciences of California, Inc., (Nasdaq:PACB) provider of the PacBio® RS II system, announced today that its Single Molecule, Real-Time (SMRT®) DNA Sequencing technology will be featured in seven podium and 13 poster presentations at the 2014 American Society for Microbiology (ASM) annual meeting in Boston.

Of note, Nobel Laureate Sir Richard Roberts will host a session entitled "Bacterial Methylomes" (#227) on Tuesday, May 20 from 2-4:30 p.m. The session will include talks from scientists representing the Joint Genome Institute, Mount Sinai School of Medicine, the US Food and Drug Administration, Harvard School of Public Health and New England Biolabs. Also on May 20, at 4:00 p.m., Julie Segre of the National Institutes of Health will discuss her work using SMRT Sequencing in a talk entitled "Tracking Hospital Patients and Environment with Complete Genome Sequencing of Carbapenem-Resistant *Klebsiella pneumoniae* and other Enterobacteriaceae."

Jonas Korlach, Chief Scientific Officer for Pacific Biosciences commented: "SMRT Sequencing simplifies the genetic characterization of microbes by making high-accuracy finished *de novo* genome assembly rapid and affordable. Factors affecting virulence such as structural variation, horizontal gene transfer and methylation become readily apparent through comparison of these assemblies. These unique advantages have made SMRT Sequencing the gold standard for microbial sequencing, which is also evidenced by the rapidly increasing number of papers and genome announcements being published."

At last year's ASM annual meeting, Pacific Biosciences initiated a SMRT Grant Program to reward interesting proposals from attendees with free SMRT Cells and project support. The company announced today that the winner from last year was Michael Nelson of the University of Connecticut for his entry to sequence a putative novel Bacteroidete genus with importance to the digestive tract. Nelson experienced difficulty sequencing the genome of the type strain using short-read technologies, but using PacBio technology he was able to sequence the genome completely in one contig.

This year, Pacific Biosciences has opened up the SMRTest Microbe Grant Program to any eligible scientist. The scientist with the winning application will receive a free sequencing run on the PacBio RS II system using up to one SMRT Cell 8Pac and up to four library constructions for their project. More details, including the official rules of the Grant Program, are available at: www.pacb.com/smrtgrant.

A full listing of the podium and poster presentations featuring SMRT technology is listed [here](#), and more information about the ASM annual meeting is available at: <http://gm.asm.org/>. Pacific Biosciences will be exhibiting its technology at Booth #1034.

About the PacBio RS II and SMRT® Sequencing

Pacific Biosciences' Single Molecule, Real-Time (SMRT) Sequencing technology achieves the industry's longest read lengths, highest consensus accuracy^{i,ii} and the least degree of bias.ⁱⁱⁱ These characteristics, combined with the ability to detect many types of DNA base modifications (e.g., methylation) as part of the sequencing process, make the PacBio RS II an essential tool for many scientists studying genetic and genomic variation. The PacBio platform provides a sequencing solution that can address a growing number of complex medical, agricultural and industrial problems.

About Pacific Biosciences

Pacific Biosciences of California, Inc. (Nasdaq:PACB) offers the PacBio RS II DNA Sequencing System to help scientists solve genetically complex problems. Based on its novel Single Molecule, Real-Time (SMRT) technology, the company's products enable: targeted sequencing to more comprehensively characterize genetic variations; *de novo* genome assembly to more fully identify, annotate and decipher genomic structures; and DNA base modification identification to help characterize epigenetic regulation and DNA damage. By providing access to information that was previously inaccessible, Pacific Biosciences enables scientists to increase their understanding of biological systems.

ⁱ Koren et al., "Reducing assembly complexity of microbial genomes with single-molecule sequencing." *Genome Biology*, 14:R10.1 (2013).

ⁱⁱ Chin et al., "Nonhybrid, finished microbial genome assemblies from long-read SMRT sequencing data." *Nature Methods*, 10; 563-569 (2013).

ⁱⁱⁱ Ross et al. Characterizing and measuring bias in sequence data. *Genome Biol* 14: R51 (2013).

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