UC DAVIS PURCHASES IRYS SYSTEM FROM BIONANO GENOMICS TO ADVANCE GENOME MAPPING AND ASSEMBLY OF WHEAT RELATIVE

High Quality Draft of Ancestor Genome to Inform Understanding of Complex Wheat Genome

SAN DIEGO — Jan. 13, 2014—BioNano Genomics announced today the purchase of an Irys™ System by UC Davis to assist, among other projects, in completing the genome assembly of *Aegilops tauschii,* one of three progenitors of today's bread wheat. The team of researchers at UC Davis, led by Dr. Jan Dvorak, will use the Irys System in their workflow as they determine the sequence, location, and orientation of all genes and transposable elements of the *A. tauschii* genome. This information will be used to advance the assembly and analysis of the wheat genome sequence, which is known to be five times larger and significantly more complex than the human genome.

"Among the world's essential crops for human and animal food, the wheat genome has yet to be fully realized because of its complexity," said Erik Holmlin, president and CEO of BioNano Genomics. "The UC Davis team's research with *A. tauschii* will help determine how wheat genome is organized and contribute to the large international effort to decode the genome of one of the world's most important food crops."

"To date, very few high-quality assemblies are available for large and complex genomes, like wheat, because we have inaccurate, low-resolution physical maps on which to arrange DNA sequence information," stated Han Cao, Ph.D., founder and chief scientific officer of BioNano Genomics. "The Irys System provides a high-resolution genome map upon which DNA sequences can quickly and accurately be organized."

Ancestor Gives Clues to Today's Wheat

Bread wheat (*Triticum aestivum* L.) is a hexaploid species containing three different ancestral genomes (designated A, B, and D), each of which has seven pairs of chromosomes. In addition, approximately 90 percent of the wheat genome is made up of repetitive stretches of DNA, making the assembly of an accurate and complete genome map and genome sequence extremely difficult. As the progenitor to wheat's D genome, *A. tauschii* is a wild grass that spontaneously hybridized with cultivated tetraploid wheat 8,000 years ago, producing what we know today as bread wheat.

"In order to complete the sequence of a large genome, like that of wheat, we need to know how all the genes are organized within each chromosome and the length and location of the many long areas of repeats," said Ming-Cheng Luo, Ph.D., research geneticist in the Department of Plant Sciences at UC Davis and co-PI on the *A. tauschii* sequencing project. "Despite advances in high-throughput sequencing, accurate *de novo* assembly of a genome has previously been the weak link in genomics research."

To assemble a genome *de novo* (from scratch), scientists must determine how the small lengths of DNA sequences generated from short-read next generation sequencing (NGS) methods are organized in the whole genome. BioNano's Irys System is a genome mapping technology that fills a void in *de novo* assemblies by providing a high-resolution physical genome map to anchor and organize DNA sequence information to dramatically improve the fidelity of the final genome assembly.

"Last year, we worked with BioNano to generate Irys data that allowed us to quickly create and publish a high-resolution genome map of a particularly complex region of *Aegilops tauschii* genome," said Dr. Luo, "Based on the success of that collaboration, we have decided to acquire our own Irys system, and we will build upon that research to create an accurate draft of the entire D genome sequence. Once completed, the high-quality draft of *A. tauschii* D genome can be used by the global research community to predict gene locations and accelerate genome sequencing and assembly of wheat and its relatives."

New Technologies Are Reducing the Costs of Genome Research

Assembling a genome to completion has previously been an intractable problem because researchers have not been able to easily visualize repetitive elements and structural variations. All genomes contain structural variations, which include large sections of repeats, deletions, duplications, insertions, inversions, translocations, and copy-number variants.

BioNano's Irys System is an automated, long-read technology that allows for precise and accurate visualization of the underlying organization and structural variation of extended stretches of DNA.

"NGS methods, where the DNA is cut into smaller pieces to be sequenced, loses structural information making genome assembly an inaccurate, labor-intensive and costly task," said Dr. Luo. "With BioNano's Irys System, we can actually retain the long-range contiguity of the DNA, which allows us to accurately assemble and finish genomes as well as compare the structural variations that exist among different genomes to learn how an organism has genetically adapted to changing environments."

Dr. Cao added, "The hidden costs in sequencing are assembly, analysis, and annotation of the genome. Rapid and accurate *de novo* map assembly with BioNano's technology makes sequencing projects less expensive by streamlining the process and providing a genome map with unprecedented quality and accurate structural variation information. Our technology actually reduces backend analysis costs so that researchers can expand the number of genomes that can be studied, thus supporting more comprehensive surveys and comparisons among genomes."

Safeguarding Wheat's Future

The United Nations has said that harvest yield of wheat will need to increase by 60 percent by 2050 to meet the dietary needs for our expected population growth. However, wheat output has recently plateaued causing alarm in the wheat research and production community. A more complete genomic map of wheat and ultimately genome sequence could provide important information on how wheat adapts to drought, disease, and temperature changes.

Dr. Luo concluded, "With our recent grant from the National Science Foundation and the integration of the Irys System and the new high-throughput V2 chips into our workflow, we will be able to quickly complete a high-quality draft of the *A. tauschii* genome. By decoding the sequences of all genes and determining their locations and orientations relative to each other, wheat geneticists will be able to identify changes in the wheat genome that are responsible for the high productivity of modern cultivars. This knowledge and more efficient breeding techniques based on an accurate wheat genome sequence will accelerate breeding of new, more productive varieties."

To learn more: BioNano Genomics will be hosting a workshop at the upcoming International Plant and Animal Genomes Conference held in San Diego on Tuesday, January 14, at 1:30PM. Presentations will include results generated with the Irys System on wheat and other crop plants.

About Irys

Irys makes it possible to routinely and accurately detect genomic structural variation and to finish genome assemblies. The fully automated Irys benchtop instrument uses the IrysChip to uncoil and confine long DNA molecules in proprietary Nanochannel Arrays™ where they are uniformly linearized in a highly parallel display for high-resolution, single-molecule imaging. Irys does not employ DNA fragmentation or amplification, which are typical with next-generation sequencing. The result is sequence information over extremely long "reads" ranging from hundreds of kilobases to a megabase, where the sample's valuable structural information is preserved. Irys makes it possible for researchers to directly observe structural variants including replications, deletions, translocations and inversions.

About BioNano Genomics

Headquartered in San Diego, BioNano Genomics is delivering an altogether better way of gaining a fully informed understanding of genomes. The Company's platform provides researchers and clinicians the most comprehensive, organized and actionable picture of a genome with unprecedented insights into how the individual components of genomes are ordered, arranged, and interact with each other. BioNano Genomics works with institutions in life science, translational research, molecular diagnostics and personalized medicine. The Company is supported by private investors and grant funding from genomics programs at federal agencies, including the NIH and NIST-ATP.

www.BioNanoGenomics.com

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BioNano Media Contact
Jessica Yingling Ph.D.
Little Dog Communications
858.344.8091
jessica@litldog.com