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SOLEXA COMPLETES FIRST FULL GENOME SEQUENCE WITH CLUSTER-SBS TECHNOLOGY

RESULTS PROVIDE END-TO-END EXPERIMENTAL DEMONSTRATION OF FUTURE DNA SEQUENCING TECHNOLOGY, LAY GROUNDWORK FOR HUMAN RE-SEQUENCING

HAYWARD, Calif. and CAMBRIDGE, U.K. (March 10, 2005) – Solexa, Inc. (Nasdaq: SLXA) today announced the completion of its first genome sequence, that of the virus Phi-X 174. The company announced genome coverage of 100%, accuracy of at least 99.93% and the detection of at least three mutations subsequently confirmed by conventional DNA sequencing techniques. This accuracy was achieved despite a number of sub-sequences, which are particularly difficult to sequence with certain other chemistries.

The work reported by Solexa today was completed using its breakthrough/completely novel sequencing biochemistry. This work provides end-to-end demonstration of a technology expected to sequence the DNA of individual humans for the detection of key disease-predisposing mutations. The genome sequence has already been repeated a number of times.

Over 1,000-times improvement in data generated per sample preparation

While the Phi-X 174 genome sequenced was small at just over 5,000 bases, the amount of sequence data generated was considerably larger. Whereas conventional DNA sequencing equipment typically delivers no more than approximately 1,200 bases per sample preparation, this Solexa experiment delivered more than three million bases from a single sample preparation. Thus sample preparation, which can be a major effort in large-scale DNA sequencing projects, can potentially be reduced by over 1,000-fold.

While impressive, these results significantly underestimate the amount of data available. In these experiments, because of the prototype nature of the hardware used, the instrument system was directed to image only 3% of the available area in its flow-cell. Thus the company estimates that more than 100 million bases of data were represented in a single flow cell, all from a single sample preparation. Solexa expects future experiments to substantially increase the fraction of data to be recovered. Ultimately later this year fully automated instrumentation is expected to allow hands-off capture of almost all available data.

Cluster technology, acquired in 2004, achieves record small feature sizes

The experiments being reported today all were conducted using DNA cluster technology, which was acquired by the company in early 2004 and has been significantly refined and developed since that time. Notably, the results were implemented with proprietary surface chemistry developed by the company. This approach has successfully achieved clusters so small that they are beyond the resolving power of the research microscope used to observe them. This achievement confirms Solexa's decision to move from earlier bead based work to clusters. The new approach provides high fluorescence signals while achieving submicron feature sizes, thereby enabling rapid and inexpensive detection of large numbers of DNA sequencing data points. Since instrument depreciation is a major contributor to the cost per data point, this is an important advancement. By lowering instrument costs per data point while simultaneously achieving extremely low reagent usage, the company anticipates that cluster technology may result in substantially lower sequencing costs.

While companies with competing technologies have developed novel DNA sequencing technologies based on beads spaced by as much as 50 microns apart, Solexa is now working with clusters as small as one-half a micron in radius. This density of sequence reads is up to 500 times higher than the bead-based approach. Thus reagent costs can be expected to scale in parallel, likely giving Solexa a substantial long-term cost advantage.

Sequencing By Synthesis (SBS) provides read lengths needed for future human re-sequencing

Since Solexa was founded, it has labored to increase the read length of the sequences it is able to determine. Bioinformatics analysis of the human genome reference sequence has shown that read lengths of 25 base pairs are the point of diminishing returns for increasing read-lengths in genome-scale re-sequencing work. At this level, up to 82% of the human genome can be uniquely associated with specific reads, even when those reads record mutations. Above this level, the percentage of the genome covered increases very slowly with increasing read length, due to the content of highly repetitive sequences (i.e., those of least importance to most researchers). Solexa has now achieved this read length in the Phi-X experiment and has obtained greater than a hundred thousand reads of this length on a wide range of sequence contexts. The sequencing technology is not fundamentally limited to this read length.

The sequence covered by Solexa in this demonstration of the "Cluster-SBS" technology includes a numbers of cases in which the same nucleotide occurs for many consecutive positions, a type of subsequence that can be problematic for other sequencing chemistries. The Solexa SBS chemistry reads through these by analysis of each incremental base in a stepwise fashion. This focus on accuracy is expected to be a key competitive advantage for the company. Re-sequencing is often used to look for very rare mutations, particularly in cancer samples. In these and other cases, even a modest error rate can create more false positives than real detected mutations.

The Pioneering Role of Phi-X 174

In making this announcement, the company noted that the Phi-X 174 virus was again playing a pioneering role. The first complete sequence of a genome was Φ X174 in 1978 by Fred Sanger and co-workers (J. Mol. Biol., 125, 225-246, 1978). He shared the Nobel Prize for Chemistry in 1980 for "...contributions concerning the determination of base sequences in nucleic acids". More recently, the first complete synthesis of a genome was described with Φ X174 by Craig Venter et al in 2003 (Proc. Natl. Acad. Sci. USA., 100, 15440-15445, 2003).

About Solexa

Solexa is developing DNA sequencing systems for the comprehensive and economical analysis of whole genomes. These systems are intended for use by customers in a wide range of applications from basic research through to the development and implementation of personalized medicine. The amount of information required about individual genomes depends upon the scientific application. Present methods generally provide insufficient information and are costly, which has inhibited progress, for instance in understanding the genetic components of common human diseases and the variable

response of individuals to drugs. The systems Solexa is developing are designed to provide very large amounts of information about individual genomes including the entire individual human genomic sequence, and to do so economically.

Solexa was formed by the recent combination of Solexa Limited with Lynx Therapeutics, Inc. Solexa will continue to provide high volume, short read DNA sequencing services from its Hayward production facility via the Lynx bead-based technology platform until the new fully automated Cluster-SBS instruments begin replacing the older systems later this year and into early 2006. The bead-based systems are mainly used for genome-wide, comprehensive gene expression and small RNA analysis, and the Cluster-SBS technology will enable sequencing services for the broad genome analysis community. Solexa expects to begin placing Cluster-SBS instruments in its production facility and development partner laboratories by the end of this year and to begin broad commercial sale of instruments in early 2006.

Conference Call Information

An investor conference call has been scheduled for Thursday, March 10, 2:00 p.m. Pacific Standard Time (5:00 p.m. Eastern Standard Time) to discuss the subject of this press release. To participate in the live call via telephone, please call (877) 815-7177 for domestic callers or (1) (706) 679-0753 for international callers. A telephone replay will be available for 48 hours following the conclusion of the call by dialing (800) 642-1687 (domestic) or (1) (706) 645-9291 (international), and entering reservation code 4620803.

The live conference call will be available via the Internet by visiting www.solexa.com, or on the investor resources section of the company's Web site at www.lynxgen.com. A recording of the call will be available for 14 days following the completion of the call.

This press release contains "forward-looking" statements, including statements related to the current views of Solexa management as to future products, product development, the expansion and success of Solexa's commercial application of its genomics technologies, and the future financial performance of Solexa. Any statements contained in this press release that are not statements of historical fact may be deemed to be forward-looking statements. Words such as "believes," "anticipates," "plans," "predicts," "expects," "envisions," "hopes," "estimates," "intends," "will," "continue," "may," "potential," "should," "confident," "could" and similar expressions are intended to identify forward-looking statements. There are a number of important factors that could cause the results of Solexa to differ materially from those indicated by these forward-looking statements including, among others, risks detailed from time to time in the Company's SEC reports, including its Annual Report on Form 10-K for the year ended December 31, 2003, as amended, its Quarterly Report on Form 10-Q for the period ended September 30, 2004 and its Proxy Statement/Prospectus filed pursuant to Rule 424(b)(3) on January 24, 2005. Solexa does not undertake any obligation to update forward-looking statements.

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