

Branford, USA, June 25, 2009

Roche Applied Science Announces Winners of the 454 Life Sciences' 10GB Grant Program

The two first-place winners will use the 10GB sequencing award to study African sleeping sickness drug resistance and ant fungal garden metagenomes.

Roche Applied Science announced today the winners of the 10 Gigabase Grant Program for DNA sequencing and transcriptome analysis studies. The program awards up to 10 gigabases of sequencing using the Genome Sequencer FLX System to individual researchers, institutions or corporations as selected by a team of external scientific reviewers representing the fields of plant and agriculture, human genetics and genomics, metagenomics and evolutionary biology. Due to the large number of strong applicants, two first place grants were awarded. One first-place winner, a team of researchers at the University of Bern, Switzerland, plan to use the technology of the 454 Sequencing System to uncover genetic mutations associated with drug resistance in a parasite species responsible for African trypanosomiasis (sleeping sickness). The other first-place winner is a team of researchers at the Emory University, Washington University, and the University of Wisconsin-Madison who plan to perform metagenomic analysis of the fungal gardens formed by leaf-cutting ants.

The 10 GB winning project in Europe, led by Pascal Mäser from the Institute of Cell Biology at the University of Bern, will use the award sequencing to uncover low-frequency genetic mutations in the parasite species *Trypanosoma brucei* subspecies which causes African sleeping sickness. The disease is most commonly found in Sub-Saharan Africa and is often fatal, a situation which is aggravated by the occurrence of drug-resistance strains. "We are excited about the opportunity to use the technology of 454 Sequencing System to identify the mutations underlying drug resistance in *T. brucei* subspecies," explained Mäser. "The data generated with the 10GB Grant Program will take us closer to developing DNA-based tests for the diagnostics of drug resistance in sleeping sickness."

The 10GB award in North America will support the sequencing efforts of the fungal garden ant project, led by Nicole Gerardo from Emory University, Cameron Currie from the University of Wisconsin, and George Weinstock from Washington University in St. Louis. For approximately 50

million years, leaf-cutting ants have been farming fungi for food. Like human agriculture, this ancient system is complex, involving symbiotic associations between farmers, crops, beneficial microbes and harmful pathogens.

“Building on previous ecological and evolutionary studies, we will utilize metagenomics, transcriptomics and genomics based on the 454 Sequencing System to explore the molecular processes underlying these intimate associations,” stated Nicole Gerardo. “While doing so, we will build an infrastructure to integrate community-based genome exploration with cross-disciplinary studies in genomics, molecular biology, developmental biology, ecology and evolution.”

Runner-up winners include projects to sequence the Arctic ice metagenome, examine the evolution of the drosophila genome, and perform genomic analysis of the silver fox.

Open to all researchers globally, this year’s grant program received a record number of registrants a testament to the increasing impact of sequencing as a tool in nearly all fields of biology. “We are pleased to see the adoption of the technology 454 Sequencing System across a wide range of scientific disciplines,” said Chris McLeod, President and CEO of 454 Life Sciences, a Roche company. “While one winning team will use the sequencing to deepen our understanding of one of the oldest and most complex symbiotic relationships described in nature, another will use the technology towards possible improvement of the treatment of a fatal human disease in the future. We are inspired by the scientific community and their ability to find new applications for the technology of the 454 Sequencing System.”

454 Life Sciences, a center of excellence of Roche Applied Science, develops and commercializes the innovative 454 Sequencing System for ultra-high-throughput DNA sequencing. Specific applications include de novo sequencing and re-sequencing of genomes, metagenomics, RNA analysis, and targeted sequencing of DNA regions of interest. The hallmarks of the 454 Sequencing System are its simple, unbiased sample preparation and long, highly accurate sequence reads, including paired-end reads. The technology of the 454 Sequencing System has enabled hundreds of peer-reviewed studies in diverse research fields, such as cancer and infectious disease research, drug discovery, marine biology, anthropology, paleontology, and many more.

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