EA Awards Three RNA-Seq Research Grants

The Associated Press

EA, a Quintiles company, awarded RNA-Seq grants to researchers at Brigham & Women's Hospital, Washington University in St. Louis, and Erasmus Medical College through the company's annual grant program, which supports genomic studies with high-potential to improve human health. An independent panel of judges selected the awardees, each of whom will receive EA next-generation sequencing and bioinformatic services, Illumina next-generation sequencing products and Golden Helix tertiary data analysis solutions.

"EA is dedicated to giving researchers access to the highest quality, most productive genomic approaches for more meaningful investigations of serious human disease. Grant awardees are conducting investigations that maximize the power of RNA-Seq data to provide an unbiased, global view of gene expression changes. We look forward to introducing these grant award winners to the many benefits of RNA-Seq and incorporating this method into their research so they can experience its biological advantages first hand," says EA President and CEO Steve McPhail.

EA, in conjunction with Golden Helix, will provide a host of analytic tools and services via their cloud-based RNA-Seq secondary analysis pipeline.

"We are excited to co-sponsor this year's RNA-Seq grant program with EA," says Christian Henry, Illumina's SVP and General Manager, Genomic Solutions. "The recent advances in transcriptome sequencing using our TruSeq RNA kits enable a deeper understanding of cancer biology by enabling access to low quality samples, such as FFPE samples. We congratulate the recipients and look forward to seeing the results of these exciting experiments."

EA's grant program includes three categories of RNA-Seq studies: RNA-Seq analysis of FFPE samples, biomarker discovery using whole transcriptome sequencing, and developmental coding and non-coding RNA expression. Awardees in each category are conducting studies that address pressing clinical and fundamental disease research issues. All projects will be completed this year and results presented in separate public forums.

The FFPE category awardee, Pim French, Ph.D., at Erasmus Medical Center in Rotterdam, aims to identify predictive markers for the subset of patients who responded positively to bevacizumab, an antibody therapeutic for glioblastomas, the most common and aggressive glial brain tumor subtype. French's project will involve sequencing the transcriptome of 80 low-quality, FFPE patient samples from the only randomized, controlled phase II trial for the therapeutic.

At Washington University School of Medicine in St. Louis, awardees Professor Samuel Klein, M.D., Latisha Love-Gregory, Ph.D., and Heather Lawson, Ph.D., focus on the mechanisms involved in adverse metabolic effects of excess body fat, which could impact therapeutic strategies for obesity.

"About 30% of obese individuals do not have obvious metabolic abnormalities, such as increased blood sugar or abnormal blood lipids. The reason why some obese people are protected from the adverse effects of excess body fat is not known, but likely involves differences in gene isoform expression and structure. This grant provides us the opportunity to identify genetic factors that predispose some people but not others to the harmful effects of obesity," explains Klein.

Klein, Love-Gregory, and Lawson will work with EA to profile the biomarkers in the transcriptomes of insulin responsive tissues from four categories of non-diabetic participants: lean; metabolically normal (insulin sensitive) obese; metabolically abnormal (insulin resistant) obese; and obese people before and after marked (20%) weight loss.

Unanswered questions about the neurological changes that cause schizophrenia are the target of research conducted by Assistant Professor Tracy Young-Pearse, Ph.D., at Brigham & Women's Hospital in Boston. "Many agree that disruptions in the development of the brain increase the underlying risk for schizophrenia. However, the molecular underpinning of schizophrenia remains an open question," she says.

Young-Pearse's recent studies operated on a low-throughput gene-by-gene basis by immunostaining and quantitative RT-PCR. Her collaboration with EA allows a genome-wide, unbiased expansion of those studies.

Using isogenic human stem cell lines modified with transcription activator-like effector nucleases (TALENs) to disrupt the schizophrenia-associated gene DISC1, Young-Pearse will collaborate with EA to profile changes in coding and noncoding RNA expression at several stages in differentiation. The data is expected to reveal the mechanisms altered by DISC1 disruption during neuronal development.

More details on the awardees' projects and the grant program, which will open for applications again early next year, are online at www.expressionanalysis.com.

About EA EA, a Quintiles Company provides cutting-edge genomic sequencing, gene expression, genotyping, and bioinformatics services to the world's largest pharmaceutical companies, diagnostic test developers, government agencies, and academic labs. All projects are conducted under clinical-grade quality control, ensured through CLIA certification, GLP compliance, and adherence to CLSI guidelines. EA's bioinformatics staff are key contributors to the Food and Drug Administration's MicroArray Quality Control (MAQC) and Sequencing Quality Control (SEQC) studies, which aim to improve standards and quality measures for reliable use of next-generation sequencing and gene expression technologies in clinical practice and regulatory decision-making. As part of its mission to improve human health, EA has donated more than $2.2 million towards academic genomic research grants and its "Leave Your Fingerprint on the Cure" Program for pediatric cancer

hosted at the American Society for Human Genetics annual meeting.

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