



June 9, 2011 - Enabling microRNA Discoveries - 250th peer-reviewed publication made possible by μ Paraflo[®] custom microarray technology

Houston, TX – LC Sciences, a life sciences company leading the development of innovative microRNA (miRNA) analysis and discovery technologies, announced today the publication of over 250 peer-reviewed studies using the company's microarray service for analyzing miRNA expression profiles. These studies, by leading researchers in the field, represent significant steps toward realizing these small regulatory RNA's potential as biomarkers and therapeutic targets.

MiRNAs have proven to be an extremely important part of the gene expression regulation mechanism of a wide variety of cellular processes. This is evident in the amount of relevant findings by LC Sciences' customers being translated into published reports and the diverse range of study areas that these publications encompass: cancer research, neuroscience, cardiovascular research, reproductive biology, plant science, microbiology, immunology and stem cell research. LC Sciences' miRNA profiling service, powered by its μ Paraflo[®] custom microarray technology, provides quick, reliable, fully analyzed datasets enabling researchers to immediately move forward with groundbreaking research.

The miRNA field is still nascent, and it is advancing rapidly. The race to discovery has produced a continuous stream of new miRNA sequences as well as routine revisions of inaccurate or incomplete sequences. This fluidity has caused many microarrays with static content to fall away and has fueled reports of the wholesale replacement of microarrays by new methods such as RNA-Seq. But the nimble, customizable format of the μ Paraflo[®] array has given it staying power, not only by enabling it to keep current with all known miRNAs, but also by making use of data generated by RNA-Seq. These custom arrays have benefited from RNA-sequencing generating novel content that other arrays are unable to capture and take advantage of.

The 250th study, entitled "Wolbachia uses host microRNAs to manipulate host gene expression and facilitate colonization of the dengue vector *Aedes aegypti*." appeared in the May 31st issue of *PNAS* and was one of a group of articles published recently by LC Sciences' customers describing microarray expression analysis of miRNAs recently discovered through RNA Sequencing.

Researchers at the University of Queensland, Australia studied the underlying mechanisms of host manipulation by a widespread endosymbiont. Using microarrays, they show that the miRNA profile of the mosquito, *Aedes aegypti*, is significantly altered by a life-shortening strain of *W. pipientis* bacteria. This is extremely important work as introduction of Wolbachia into mosquitoes has been proposed as a method for malaria control. They found that a host miRNA (aae-miR-2940) is induced after *W. pipientis* infection in both mosquitoes and cell lines.

This study illustrates the versatility of μ Paraflo[®] from a couple of perspectives. First, mosquito, an important though non-model species was the target of interest here and mosquito arrays, as well as arrays from any of the 153 species listed in the miRBase public sequence database, are readily available from LC Sciences. Second, custom content (novel miRNA sequences from an earlier sequencing study on the same species) was quickly integrated into the content of the insect array providing an even richer expression dataset. Though all the previously described, known insect miRNAs were also present on the arrays, several custom sequences were

significantly differentially expressed in infected mosquitoes and a custom sequence turned out to be one that became a focus of the investigation. Dr. Sassan Asgari, lead researcher for the study, commented that microarrays "...provided an affordable approach to the study of differential expression of small RNAs and miRNAs in particular."

"We are very excited about the announcement of the 250th peer-viewed publication by one of our microarray customers," says Chris Hebel, VP of Business Development at LC Sciences. "We were the first to provide a microarray expression profiling service for miRNA back in 2005 and proud to be still going strong in the face of rapidly advancing technologies, while many other less adaptable arrays, have fallen away. Despite the apparent advantages of new technologies such as RNA-Seq, microarrays have been the gene expression workhorse for many years and continue to be a robust, affordable solution. High-throughput RNA sequencing is still significantly more expensive and it won't be until there is sufficient multiplexing of samples when we finally do reach a cost approaching that of microarrays. Of course more samples means less coverage per sample, and I think we're still trying to figure out just how much coverage is required for robust expression data from deep sequencing and therefore what level of multiplexing can ultimately be reached. Meanwhile, RNA-Seq has become an amazing tool for discovery of novel miRNAs and continues to provide new content for our custom microarrays."

About μ Paraflo[®] Technology - The μ Paraflo[®] technology is a microfluidic platform for *in situ* parallel synthesis of biomolecular chips and miniaturization of bioassays including hybridization, binding and enzymatic reactions. This unique platform technology is based on pico-liter microfluidic reaction devices and a digital light controlled synthesis method that employs conventional oligonucleotide or peptide synthesis chemistry; a completely programmable process. The seamless integration of these multidisciplinary technologies enables a significant advance in parallelization, miniaturization, customization, and automation.

About LC Sciences - LC Sciences offers discovery, profiling and validation services for microRNA and other small RNAs. Services include deep sequencing for discovery applications, microarrays for differential expression profiling and validation/confirmation of newly discovered microRNAs, and qRT-PCR for quantitation of microRNA expression levels. These comprehensive services are designed to be one-stop and produce the results needed to quickly advance your biological and biomedical research. Combining the latest deep sequencing technology with our μ Paraflo[®] on chip synthesis technology offers unprecedented flexibility and customization capability.

More information about LC Sciences is available at www.lcsciences.com.

Hussain M, Frentiu FD, Moreira LA, O'Neill SL, Asgari S. (2011) **Wolbachia uses host microRNAs to manipulate host gene expression and facilitate colonization of the dengue vector *Aedes aegypti***. *Proc Natl Acad Sci USA* 108(22), 9250-55. [[abstract](#)]

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