LC Sciences

Press Release – The Porcine microRNAome is Revealed

Results blaze a trail for advancement in pig biology as well the use of pigs as model organism for human biological and biomedical studies

Houston (August 19, 2010) Researchers from LC Sciences LLC and a collaboration of Universities[1] have established a porcine microRNAome, a complete catalog of all microRNAs expressed in the species *Sus scrofa*[2]. MicroRNAs (miRNAs) are small regulatory RNA molecules known to control a wide array of cellular functions such as growth and development and whose dysregulation has been associated with disease. The findings of this study lay the groundwork for a greater understanding of the species through further mapping of tissue- and stage-specific miRNAs.

The domestic pig is an important species from various standpoints. First, it is a major protein source in the human diet world-wide. Additionally, its anatomy, physiology, and genome size are very similar to the human species, and there has been increasing molecular genetic evidence showing the comparability of human and pig, making it a suitable model system for human biology. Pigs are now model animals for biomedical research of cardiovascular, immunological, cancer, diabetes, and a range of other diseases. Finally, the pig has become an important source of organs and tissue for transplantation into humans.

Prior to this study, miRbase[3], the primary public repository for miRNA sequence data, listed only 73 unique pig miRNAs, this out of a total of 10,883 database entries encompassing over 100 species. The number of miRNAs for pig was significantly lower than for other species with similar size genomes (such as Human with 894 miRNAs) suggesting the existence of far more pig miRNAs.

The researchers used advanced deep sequencing and developed bioinformatics technologies to analyze all the small RNA molecules that are transcribed from all the genes in the pig genome. After filtering, mapping, alignment and classification of all the reads, they had shown that the pig miRNAome has 777 unique miRNA sequences. The sequencing results will not only greatly enhance the utility of the pig microRNAome as the blueprint of advanced pathway network studies of miRNA and their target mRNAs, but also provide information on time-dependent variations of the microRNAome as to sequence lengths, counts, composition, genomic location, and the relative expression of conserved versus pig-specific miRNAs.

This first pig miRNAome report has opened a path for exploration and better understanding of pig molecular biology in cell growth and development, and for advanced pathway and function modeling in pig relevant to complex human diseases.

About microRNA – microRNAs are small non-protein-coding RNA molecules that function as regulators of gene expression by mature miRNAs targeting specific mRNAs. These interactions may result in variations in mRNA and/or protein expression.

About LC Sciences - LC Sciences is a leader in miRNA discovery and profiling offering flexible services and delivering high quality results based on our innovative µParaflo® custom microarray platform and the latest deep sequencing technologies. We have developed complementary bioinformatics tools necessary for extracting biological and functional information from large microRNA and miRNAome data sets. LC Sciences provides microfluidic made-to-order microarrays and delivers the most up-to-date genomics application tools for advancement in basic science and applied biomedical fields.

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