Exiqon non-coding RNA Seminar

When?
Tuesday, 10 May 2016
09:00-14:00

Where?
Starling Hotel Lausanne (at EPFL)
Route Cantonale 31
CH-1025 Saint-Sulpice

Join us for this free non-coding RNA seminar

09.00 Welcome coffee
09:30 Welcome to seminar
09:35 **Role of non-coding RNAs in the control of β-Cell functions**
Prof. Romano Regazzi, PhD
Department of Fundamental Neurosciences,
University of Lausanne
10:10 **The long noncoding RNA WISPER controls cardiac fibrosis and remodeling**
Samir Ounzain, PhD
Department of Medicine,
University of Lausanne Medical School
10.45 Coffee break
11:05 **Exosomal microRNAs in urine – promising biomarkers for prostate cancer**
Peter Mouritzen, PhD
VP, Research & Development, Exiqon
11:40 General discussion
12:00 Lunch buffet

Prof. Romano Regazzi, PhD
University of Lausanne

Samir Ounzain, PhD
University of Lausanne

Peter Mouritzen, PhD
Exiqon

Please register at www.exiqon.com/seminars

For more information, please contact
Roman Kurek, PhD (rok@exiqon.com)

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Role of non-coding RNAs in the control of β-Cell functions

Prof. Romano Regazzi, PhD

Insulin secretion from pancreatic β-cells plays a central role in the control of body metabolism. Dysfunction and/or loss of β-cells can result in the release of insufficient insulin to cover the organism needs and in the development of diabetes mellitus. β-cell dysfunction is linked to major changes in gene expression.

We performed global profiling of pancreatic islets isolated from different animal models and found that diabetes manifestation is associated with changes in the expression of different classes of non-coding RNAs, including microRNAs, long non-coding RNAs and circular RNAs.

Detailed analysis of the role of the differentially expressed non-coding RNA molecules revealed that some of them promote glucose-induced insulin secretion, enhance β-cell proliferation and/or improve β-cell survival, suggesting that they contribute to adaptive changes in the functional β-cell mass in response to diminished insulin sensitivity of target tissues. In contrast, the alterations in the level of other non-coding RNAs result in β-cell dysfunction and death, probably contributing to the development of diabetes.

The balance between the changes in these groups of non-coding RNAs with opposing functional effects is likely to determine whether individuals can maintain blood glucose homeostasis or if they progress toward glucose intolerance and diabetes.

The long noncoding RNA WISPER controls cardiac fibrosis and remodelling

Samir Ounzain, PhD

Long noncoding RNAs are emerging as powerful regulators of cardiac development and disease. However, our understanding of the roles of these molecules in cardiac fibrosis and remodelling is limited. Using an integrated transcriptomic and epigenomic screen, we identified WISPER (WIsp2 SuPer-Enhancer associated RNA) as a cardiac fibroblast enriched lncRNA that potentially regulates cardiac fibrosis.

WISPER expression is significantly correlated with cardiac fibrosis both in a murine myocardial infarction (MI) model and in human patients suffering with aortic stenosis. In vitro loss-of-function approaches using modified antisense oligonucleotides (GapmeRs) demonstrated that WISPER is a tissue type specific regulator of cardiac fibroblast survival, proliferation and migration. Accordingly, GapmeR-mediated silencing of WISPER in vivo prevented and attenuated MI-induced fibrosis and remodelling in both preventative (GapmeR injection pre-injury) and therapeutic (GapmeR injection post-injury) experimental scenarios. Functionally, WISPER globally regulates cardiac fibroblast gene expression programs critical for cell identity, survival and proliferation.

Together, our findings identify WISPER as a novel cardiac fibroblast enriched super-enhancer associated lncRNA that represents an attractive therapeutic target to prevent cardiac fibrosis and pathological remodelling.

Exosomal microRNAs in urine - promising biomarkers for prostate cancer

Peter Mouritzen, PhD, VP R&D, Exiqon

MicroRNAs constitute a class of short RNAs which function as post-transcriptional regulators of gene expression. The expression patterns of microRNAs can accurately classify discrete tissue types and specific disease states which have positioned microRNAs as promising new biomarkers for diagnostic application in cancer.

We have developed a highly sensitive LNA™-based qPCR platform for microRNA detection, which enables profiling in biofluids where microRNA levels are extremely low. Thousands of biofluid samples including serum/plasma and urine have been profiled to determine normal reference ranges for circulating microRNAs as well as to identify biomarkers of disease.

To develop a non-invasive diagnostic test for prostate cancer, we have combined our LNA™-based qPCR with a recently developed exosome enrichment method, to identify several diagnostic microRNAs in cell free urine from non-prostate-massaged men with early stages of prostate cancer. The strongest signature consists of three microRNA which were identified in a cohort of 220 patients and validated in an independent cohort of similar size. The signature allows construction of receiver operating characteristic curves with areas under the curve from 0.95 - 0.90. We will discuss the importance of sample and data qualification which together with analysis method is crucial in securing high quality data from biofluids.