“Epigenetics and Non-coding RNAs in Diabetic Complications & Metabolic Memory”

“Diabetes is associated with significantly accelerated rates of inflammation and multiple macro- and micro-vascular complications such as atherosclerosis and nephropathy. Abnormal activation of vascular cells, circulating monocytes and renal cells triggered by inflammatory genes has been implicated, but the underlying molecular mechanisms are not fully understood. We have examined the role of epigenetic mechanisms, including chromatin histone modifications, DNA methylation and non-coding RNAs in regulating the expression of genes associated with the pathology of diabetic vascular complications. We have also performed epigenome profiling and systems biology analyses to identify diabetes- and diabetes complication-specific epigenetic signatures genome-wide in mice, and in patients with type 1 diabetes, including patients experiencing metabolic memory. We also adopted translational approaches with small molecules and antisense oligonucleotide GapmeRs to interfere with diabetes induced changes in epigenetic marks and non-coding RNAs (microRNAs and lncRNAs). Together, our studies suggest that epigenetic factors play significant roles in the development of diabetic complications.”

Tuesday, December 4th, 2018
12:00p-1:00p
Rosenstiel Medical Science Building
4th Floor Auditorium