*i*SEQ lunch seminar series

Wednesday 13 April 2016 at 12.00 – 13.00

Professor Harvey Lodish
Whitehead Institute for Biomedical Research,
Department of Biological Engineering and Biology, MIT.

Talk:
Lineage- specific long non-coding RNAs regulate development of erythrocytes, brown and white adipocytes, and probably every cell type.

Abstract:
To obtain a comprehensive view of how lncRNAs contribute to erythropoiesis, we performed and analyzed data from high depth RNA-sequencing on RNAs from erythroid progenitor cells and terminally differentiating erythroblasts. We focused on differentiation-induced lncRNAs, including novel erythroid-specific lncRNAs conserved in humans that are nuclear-localized and identified 13 erythroid-specific lncRNAs that are greatly induced during erythroid terminal differentiation. Importantly, shRNA-mediated loss-of-function assays reveal that all 13 are important for red cell formation. One intergenic lncRNA, LincRNA-EPS, prevents the apoptosis of progenitors that is normally induced by erythropoietin deprivation and represses expression of several proapoptotic genes including Pycard, a caspase activator. A second lncRNA is transcribed by the erythroid- specific enhancer of Band 3, encoding a major erythrocyte membrane protein.

To uncover brown adipose tissue (BAT)-specific long non-coding RNAs (lncRNAs), we used high depth RNA-sequencing on RNAs from mouse brown, inguinal white, and epididymal white fat. We identified ~1500 lncRNAs, including 127 BAT-restricted loci induced during differentiation and often targeted by key regulators PPARγ, C/EBPα and C/EBPβ. One of them, lnc-BATE1, is required for establishment and maintenance of BAT identity and thermogenic capacity. lnc-BATE1 inhibition impairs concurrent activation of brown fat and repression of white fat genes, and is partially rescued by exogenous lnc-BATE1 with mutated siRNA-targeting sites, demonstrating a *trans* function of lnc-BATE1
Thus diverse types of intergenic, enhancer, and antisense lncRNAs are expressed only in specific types of hematopoietic and adipose cells and are essential for their proper development; they participate in the regulatory circuitry underlying lineage-specific development.

Venue:
Merete Barker Auditory, The Lakeside Theatres, Aarhus University, Bartholins Allé 3, 8000 Aarhus C.

Refreshments:
Sandwiches will be provided. Therefore, please email Anne Hedemand (anne@biomed.au.dk) no later than 11 April 2016, if you would like to participate.

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