CDB SEMINAR

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National Institutes of Health, Bethesda, Maryland, USA

Wednesday, July 20, 2011
16:00 - 17:00 A7F Seminar Room

Dissecting microRNA function using mouse genetics and genomics

Summary

In order to elucidate the impact of a microRNA on gene expression programs, we perform deep sequencing of RNA (RNA-seq), and compare the transcriptome of miRNA-deficient cells to wild type controls. Computational analyses allow us to detect specific gene expression signatures imposed by the miRNA.
I will illustrate using miR-155 as an example. This strategy uncovered a polycomb group protein as a direct miRNA target and its hitherto unsuspected role in regulating cytokine gene transcription.

In a second story, we consider Lin28 as a reprogramming factor. One well known function of Lin28 is to bind the let-7 family of miRNAs and inhibit their processing into mature miRNAs by targeting the precursors for uridylation and degradation. Interestingly, Lin28a is highly expressed in embryonic stem cells and not detectable in adult tissues. Conversely, let-7 is not detectable in embryonic stem cells and expressed upon differentiation. Furthermore, a paralog, Lin28b, is highly expressed during fetal hematopoiesis but not during adult hematopoiesis. I will discuss our latest understanding of Lin28 and let-7 function.

Host:
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