Functional Genomics & Metabolism

Distinguished Seminar

Friday, February 6, 14:00-15:00 PM

BMB Seminar room (V18-501-1)

"Transcriptional termination and links to RNA processing/decay pathways"

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Host: Asst. Prof. Kedar Natarajan

Abstract

Transcription termination is critical for partitioning of the genome into transcription units (TUs). In metazoans, the Cleavage and Polyadenylation (CPA) and Integrator (INT) complexes constitute the two main activities dictating RNA polymerase II (RNAPII) termination at the ends of mRNA and snRNA TUs, respectively. Moreover, both CPA and INT have been implicated in the termination of transcription of lncRNA genes. Hence, an RNA biotype-centric view of transcription termination is insufficient. Here, we take an unbiased approach to monitor CPA and INT activities genome-wide. We find that INT is specifically required for termination of transcription on relatively short and intron-less TUs. In fact, our data are consistent with a model where INT is generally responsible for promoter proximal transcription termination of RNAPII that fails to enter elongation mode, and it appears that most, if not all, protein coding genes, are subjected to some degree of premature INT-controlled promoter proximal termination. In a parallel study, we investigate nuclear RNA decay by the RNA exosome and its co-factors. We demonstrate that substrates of the Nuclear EXosome Targeting (NEXT) complex arise from transcripts terminated at heterogenous and predominantly non-polyadenylated 3'ends often covering kb-wide genomic regions. These 3'ends coincide with INT terminated transcripts, establishing a link between the two processes.