第 550 回 難研セミナー
第 123 回 難治疾患共同研究拠点セミナー

下記により難研セミナーを開催しますので、多数御来聴下さい。
※このセミナーは Tokyo RNA Club の一部として学外にもご案内しています。
※発表言語は英語です。

記

日　時：２０１６年７月２５日（月）１７：１５～１８：１５
場　所：歯学部特別講堂（歯科棟南４階）
演　者：Takayuki Nojima
（*Sir William Dunn School of Pathology, University of Oxford, UK*）
演　題：Catch RNA polymerase II in act; Genome-wide analysis of nascent RNA in mammalian cells.

要　旨：In the past several years, many milestones of transcription study have been shown by high-throughput sequencing (seq) technology. Total RNA-seq method is frequently used to demonstrate a genome-wide transcription landscape, showing most of genome region generates transcripts including protein-coding and non-coding genes. However, extremely unstable RNA (such as pre-mRNA processing intermediate and antisense RNA) could not be detected due to limitation of total RNA-seq method mainly picking up steady state RNA.

RNA processing is tightly connected to RNA polymerase II (Pol II) transcription. The C-terminal domain (CTD) of Pol II largest subunit is dynamically phosphorylated during nascent transcription to allow efficient and regulated recruitment of RNA processing factors. Recently I have developed native elongating transcript-sequencing technique for mammalian cells (mNET-seq) using a selection of CTD phosphorylation specific Pol II antibodies[1,2]. Interestingly, mNET-seq revealed a splicing intermediate are specifically associated with serine 5-phosphorylated (S5P) CTD Pol II[1]. Combined with mNET-seq technology and mass spectrometry of human Pol II elongation complexes, I found distinctive patterns of transcription and RNA processing for protein-coding and long intergenic noncoding RNA.

Overall mNET-seq and mass spectrometry analysis will be powerful techniques to explore the complex life of nascent RNA in mammalian cells.

References

1. Nojima et al. ***Cell*** 161, 526-540, 2015
2. Nojima et al., ***Nature Protocols*** 11, 413-428, 2016

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