CBC SEMINAR ANNOUNCEMENT

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Influenza virus – Importance of RNA secondary structure

Influenza A virus is a real threat to human due to seasonal epidemics and occasional pandemics. Worldwide, there are about up to 0.5 million deaths each year caused by severe complications of influenza. Knowledge about the secondary structure of influenza RNA is still fragmentary. Recently, several studies showed the importance of influenza RNA folding as one of the factors guiding proper and efficient virus propagation. These findings indicate that both genomic and antigenomic influenza RNA secondary structures may be keys to understanding RNA functions and facilitating drug development. Results and perspectives of the studies of several influenza RNAs will be presented.

The collaborative research by the D.H. Turner and E. Kierzek groups revealed the conservation of the type A secondary structure motif in segment 7 (+)RNA containing 3′ splice site (1). The results suggest that segment 7 mRNA splicing can be controlled by a conformational switch between a pseudoknot and a hairpin structure, which exposes and hides the splice site, respectively. A combination of in vitro chemical and isoenergetic microarray mapping validated another two stable structures in segment 7 mRNA and segment 8 mRNA, which could have regulatory functions in viral gene expression (2,3).

Recently, intensive studies have been undertaken to determine the conserved secondary structure of segment 8 vRNA. The structure of the entire segment 8 vRNA (875 nt), containing universal, evolutionarily maintained structural motifs, is modeled on the basis of chemical and isoenergetic microarray mapping, and sequence/structure comparison (4).

References

Date: 24th November 2014 (Monday)
Time: 11:00am–12:30pm
Venue: NTU SPMS CBC Building Level 2, Conference Room
Host: Asst Professor Chen Gang