TWINCORE

TWINCORE – Seminar

Thursday October 19th, 2017, 5 p.m.
TWINCORE Lecture Hall

Exploration of RSV polymerase activities using mutagenesis and small molecule inhibitors

Rachel Fearns, Ph.D.

Respiratory syncytial virus (RSV) is the major cause of hospitalization significant cause of disease in the elderly and immunocompromised. As yet, there is no vaccine or effective antiviral treatment to control the virus. RSV has an RNA genome, which is transcribed to produce capped and polyadenylated mRNAs, and replicated to generate progeny genomes. RSV transcription and genome replication are both performed by a multi-functional viral RNA dependent RNA polymerase. In this presentation, I will provide an overview of the mechanisms underlying RSV transcription and genome replication, and then describe work performed with small molecule polymerase inhibitors, coupled with amino acid substitution analysis of the large polymerase subunit (L). This work sheds some light on the structure-function relationships of the polymerase as it performs its various activities.

Who is Rachel Fearns?

- Associate Professor, Dept. of Microbiology, Boston University School of Medicine.
- Faculty member, National Emerging Infectious Disease Laboratories, Boston University.

Rachel Fearns has spent the last twenty-one years researching the transcription/ replication mechanisms of a non-segmented negative strand RNA virus, respiratory syncytial virus (RSV). Her group has developed cell-based assays that allow different events in RSV transcription and RNA replication to be dissected, and they have expertise in generating and analyzing mutant recombinant versions of infectious RSV. They showed for the first time that it was possible to purify active RSV polymerase complexes, a breakthrough that allowed development of an assay in which RSV RNA synthesis is reconstituted in vitro using purified protein and RNA oligonucleotide templates. In more recent work, her group has begun to extend the techniques they have developed to other related viruses and to identify similarities and differences in transcription and replication mechanisms within the non-segmented negative strand RNA viruses.

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