
Seminars 2015-16

Leveraging molecular biology and population genetics to reveal the natural history of clinically significant viral infections



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It is well accepted that RNA viruses exist as mixed populations of genomic sequences and these quasispecies populations are relevant to viral fitness and disease. It is unclear if the same is true for DNA viruses. A candidate quasispecies DNA virus is human cytomegalovirus (HCMV), where mixed genotype infections in patients have been repeatedly demonstrated. HCMV is a beta-herpesvirus and genetically, the most complex viral pathogen of humans with a ~235,000 bp dsDNA genome. To better understand this mixed genotype phenomenon, we adapted high throughput (deep) sequencing to generate genome-wide coverage of HCMV and analyze viral populations in clinical samples. We discovered that HCMV populations in the plasma.

See full abstract: laufercenter.stonybrook.edu/

Friday February 26, 2016

2:30 PM

Laufer Center Lecture Hall 101

Host: Tom MacCarthy

Refreshments following seminar